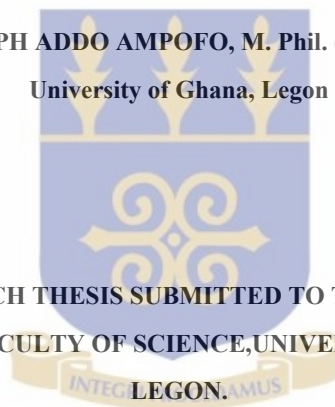


**STUDIES ON THE OCCURRENCE AND DIVERSITY OF
BACTERIA IN FISH CULTURE SYSTEMS IN GHANA WITH
SPECIAL REFERENCE TO SPECIES PATHOGENIC TO
FISH AND HUMANS**

BY

JOSEPH ADDO AMPOFO, M. Phil. (Botany)
University of Ghana, Legon

**A PH.D. RESEARCH THESIS SUBMITTED TO THE DEPARTMENT
OF BOTANY, FACULTY OF SCIENCE, UNIVERSITY OF GHANA,**



SEPTEMBER, 2000

£+117?



DECLARATION

I certify that this work presented in this thesis, 'Studies on the occurrence and diversity of bacteria in fish culture systems in Ghana with special reference to species pathogenic to fish and humans' was done entirely by me in the Department of Botany, University of Ghana, Legon, from September 1996 to July 1999.

This thesis does not contain any material previously published or written by another person except where due reference is made in the text, and to the best of my knowledge the work does not contain any material previously submitted for a degree in any University.



Joseph Addo Ampofo
University of Ghana,
Legon.

Date&

Prof. (Emeritus) G. C. Clerk

Supervisor

• 5, 2002.

TO GOD BE THE GLORY

DEDICATED

TO

THE FAMILY

And

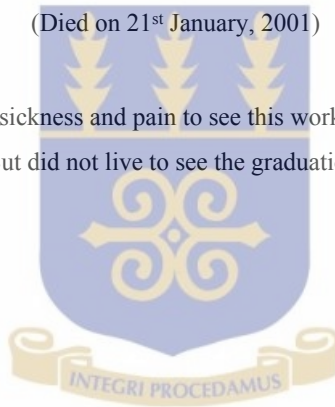
MY LATE FATHER

MR. SAMUEL ADDO AMPOFO

(Died on 21st January, 2001)

Who lived through sickness and pain to see this work done and presented;

But did not live to see the graduation.



ABSTRACT

The occurrence and diversity of bacteria in selected fish culture ponds from three regions in Ghana, Aduabenba Farms, Agyeman Farms, Aheto Farms, Akuse Kpong Farms, ARDEC Station, Asare Farms, Boadi Farm, Boahen Farms, Boateng Farms, Frimpong Farms, K.K. Farms, Pacific Farms and Sagoe Farms and three open systems, Kpong Head Pond, Volta River and Weija Dam were studied over a period of three years, 1996 - 1999.

Bacterial populations from the different fish culture systems studied consisted essentially of about the same bacterial species, but the predominating species varied with each culture system. Subtyping of the bacterial strains recovered from the different environments, and comparing the species present was a valuable tool to determine the correlations between the flora of the different environments. Since the studies involved large numbers of isolates, simple laboratory methods combined with automated data evaluation and presentation were used.

The Phene-Plate (PhP) system for biochemical finger printing of bacteria, which is based on measurements of the kinetics of biochemical tests, performed in microplates, was employed. The system included mathematical models to calculate the diversity (D_i) of the bacterial flora within each of the different environments, as well as the similarities between bacterial populations in the different environments as the population similarity coefficient (S_p).

The PhP system was used to type 80 colonies at a time from each of the cultured systems, open systems and the sewage fed ponds. The PhP system had the advantage of calculating the diversity index of the bacterial population present in each of the farm, as well as calculating the similarity coefficient between the population of bacteria in the different environments. From each one of the six different cultured ponds receiving different types of fertilizers, three rivers representing three open systems and the four serial sewage-fed ponds, a total of 7990 isolates were typed.

The results indicated that the diversity among the bacterial populations from the fish culture systems were generally high with mean diversity above 0.95 in all cases. Mean D_i

for the cow manure-fertilized ponds was 0.977, the mean for poultry manure-fertilized ponds was 0.981, and that for pig manure-fertilized ponds was 0.952. The rest were, blood waste-fertilized ponds, 0.989; chemically fertilized ponds, 0.972; ponds with no fertilization, 0.989; the open systems, 0.950; and the sewage-fed ponds, 0.971. These results indicated that the bacterial populations were very high in each community and consisted of many different bacterial types or strains.

Comparison of results obtained for the populations of bacteria present in the different fertilization type ponds to that of the open systems showed mean population similarity (Sp) coefficient values below 0.50. This was an indication of different populations with high diversities that were similar in their pattern of distribution. Similarly, comparison of the results of all the serial ponds of the sewage-fed ponds showed mean population similarity (Sp) coefficient with values below 0.50. Comparison of the results of ponds I and III, however, gave Sp value above 0.50, indicating that there were certain periods of sampling when the populations were not related. Biochemical and morphological tests, as well as the API 20NE and 2IE, were used to identify some selected bacteria picked randomly from the plates and used as the reference data for the PhP procedure.

Twenty-five species of bacteria were identified as associated with the fish culture systems in this study. The identified bacteria included one genus of spiral and curved bacteria, *Campylobacter* sp.; one genus of Gram-negative aerobic rod, *Pseudomonas* sp.; sixteen genera of Gram-negative facultative anaerobic rods, *Actinobacillus* sp., *Aeromonas* sp., *Citrobacter* sp., *Edwardsiella* sp., *Enterobacter* sp., *Escherichia* sp., *Flavobacterium* sp., *Hafnia* sp., *Klebsiella* sp., *Pasteurella* sp., *Proteus* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Vibrio* sp. and *Yersinia* sp.; one Gram-negative anaerobic bacterium, *Bacteroides* sp.; three Gram-positive cocci, *Micrococcus* sp., *Staphylococcus* sp. and *Streptococcus* sp.; two endospore-forming rods, *Bacillus* sp. and *Clostridium* sp.; and one Actinomycete, *Corynebacterium* sp.

Pseudomonas sp. was the most dominant species of most ponds; cow manure-fertilized ponds, blood waste-fertilized ponds, chemically fertilized ponds, sewage-fed ponds, ponds with no fertilization and in the open systems. Poultry manure-fertilized ponds and pig manure-fertilized ponds had *Salmonella* sp. and *Streptococcus* sp., respectively, as the most dominant species.

Physico-chemical parameters found to have positive correlation with the bacterial populations in the fish culture systems were acidity, air temperature, alkalinity, ammonium, biochemical oxygen demand, calcium ion, chloride, conductivity, magnesium ion, pH, phosphate ion, silicon dioxide, sulphate ion, suspended solids, total dissolved solids, total hardness, turbidity and water temperature.

Fish from the various culture systems harboured, bacteria belonging to the 25 genera isolated from the different culture systems in the blood, gut and muscles and on the gills and skin. Generally, higher bacterial populations were associated with the gills, gut and skin than the blood and muscle. Although *Pseudomonas* sp. was most abundant species in the sewage-fed ponds and was present in considerable quantities in the five fish tissues, *Salmonella* sp. was the most important isolate of the gills, muscle and skin. Pathogenic bacteria were isolated from inhabitants of communities associated with ponds that received all sorts of fertilizers and even with ponds that were not fertilized.

All the organic manures mostly used to fertilize fish ponds, cow manure, poultry manure, pig manure, blood waste and sewage water, supported growth to varying degrees of eight experimentally introduced pathogenic bacteria, *Pseudomonas* sp. KI-MTC-001K, *Shigella* sp. KI-MTC-002K, *Enterobacter* sp. KI-MTC-003K, *Klebsiella* sp. KI-MTC-004K, *Citrobacter* sp. KI-MTC-005K, *Proteus* sp. KI-MTC-006K, *Salmonella* sp. KI-MTC-007K, and *Vibrio parahaemolyticus* KI-MTC-008K. The best growth was recorded in the *Pseudomonas* sp. KI-MTC-001K tests and the poorest in the *Vibrio parahaemolyticus* KI-MTC-008K tests.

Resident bacteria were detected in all eleven feed types commonly used in feeding the fish. Highest count of 4.28 log₁₀ CFU g⁻¹ heterotrophic bacteria count of feed was recorded for fufu waste while banana waste recorded the least count of 2.85 log₁₀ CFU g⁻¹. Enormous quantities of heterotrophic bacteria, from 6.17 to 6.86 log₁₀ CFU g⁻¹, occurred in blood waste, cow manure and poultry manure, used as organic manure.

The bacterial population of the water, and, level of bacterial contamination of the fish of sewage-fed ponds was not remarkably different from those of ponds fertilized with blood waste, cow manure, chemical fertilizer, pig manure and poultry manure, and, ponds and open systems which were not fertilized. It was concluded that sewage fertilization could

serve two purposes. First, it could be a means of sewage disposal for small rural communities, and secondly, increasing the potential yields of fish ponds.

If four or more linearly arranged and inter-connected ponds were prepared with slow-flowing water moving through the system, sufficient solanization would purify the water to render the last pond bacteriologically safe for fish culture.

TABLE OF CONTENTS

	Page
DECLARATION	i
DEDICATION	ii
ABSTRACT	iii
LIST OF TABLES	xiv
LIST OF FIGURES	xix
LIST OF PLATES	xxvi
CHAPTER ONE. INTRODUCTION AND LITERATURE REVIEW	
Diversity of bacteria in nature	1
Quality of water of fish culture	2
Water as a bacteriological medium	6
Waterborne bacteria and their significance	6
Bacterial diseases of farmed fishes	7
Faecal coliform in fish culture system	8
Fish as potential vectors of human bacterial pathogens	10
Culture of fish in treated wastewater	11
Culture of fish in untreated wastewater	13
Role of bacteria in self-purification of water bodies	14
Marine farming	14
Freshwater farming	16
Objective of the research programme	18
CHAPTER TWO. MATERIALS AND GENERAL METHODS	
I. MATERIALS	19
A. Sampling Sites	19
i. Aduabenba farms.....	19
ii. Agyeman farms	19
iii. Aheto farms	19
ix. Akuse Kpong farms	20

v.	ARDEC station	21
vi.	As are farms	21
vii.	Boadi farms	22
viii.	Boahen farms	22
ix.	Boateng farms	22
x.	Frimpong farms	22
xi.	KK farms	23
xii.	Kpong Headpond	23
xiii.	Pacific farms	23
xiv.	Sagoe farms	23
xv.	Volta River	23
xvi.	Weija dam	23
B.	Reference Bacterial Strains	24
II.	GENERAL METHODS	25
A.	Sampling for bacteriological study	25
1.	Sampling of water and sediment	25
2.	Sampling of the fish	25
B.	Methods of sterilization	26
C.	Media for culturing the bacteria	27
1.	Preparations with dehydrated media	27
	Bismuth sulphite agar	27
	Blood agar base	27
	Brain heart infusion broth	28
	Brilliant green agar	28
	Brilliant green bile broth	28
	Cereus selective agar	28
	Desoxycholate citrate agar	28
	EC medium	28
	Eosin methylene blue agar	29
	KF streptococcus agar	29
	Lactose broth	29
	Lauryl tryptose broth	29
	Litmus milk	29
	MacConkey agar	29

MacConkey broth	30
Mannitol selenite broth base	30
M.R.V.P. medium	30
Nutrient agar	30
Nutrient broth	30
SS agar	30
Standard plate count agar	31
Staphylococcusmediumno.IIO	31
Thiosulphate citrate bile salt agar	31
Triple sugar iron	31
Trypticase soy agar	31
Tryptone water	31
2. Preparation of blood agar	32
3. Preparation of neomycin blood agar	32
4. Preparation of sodium azide broth	33
D. Quantitative estimation of bacterial flora	33
1. Heterotrophic bacterial density determination	33
2. Total coliform counts	34
3. Faecal coliform counts	34
4. Faecal streptococci counts	34
E. Isolation and identification of bacteria	35
1. Isolation	35
2. Determination of characteristics of isolates	35
Colony characteristics	35
Morphology of isolates	35
Gram stain reaction	35
Endospore staining	36
Indole test	36
Methyl red and Voges-Proskauer tests	36
Citrate utilization test	37
Oxidase test	37
Cell motility	37
Nitrate reduction	37
Catalase test	38

Production of hydrogen sulphide	38
Gelatin hydrolysis	38
Starch hydrolysis	38
Urease test	38
Sugar utilization	38
3. Selective culture of bacteria isolated	39
F. The Phene Plate (PhP) system.....	40
1. PhP suspending substrate	40
Bromothymol blue stock solution	40
Preparation of the suspending substrate	40
2. Pre-cultivation of bacteria	41
3. Preparation of bacterial suspension and inoculation	
of rapid screening PhP plates	41
4. Incubation of PhP plates	41
5. Reading of test results	42
G. Physico-chemical parameters of the pond water	42
1. Temperature	42
2. Hydrogen-ion concentration	42
3. Acidity	42
4. Alkalinity	43
5. Calcium and magnesium ions	43
6. Total hardness	44
7. Chloride ion	44
8. Phosphate ion	45
9. Ammonium nitrate	45
10. Nitrate and nitrite ion	46
11. Sulphate ion	46
12. Silica	47
13. Dissolved oxygen	47
14. Biochemical oxygen demand	47
15. Total Dissolved solids and suspended solids	48
16. Turbidity	49
17. Conductivity	49
H. Statistical Analysis	50

I. Experimental Precautions	50
-----------------------------	----

CHAPTER THREE. EXPERIMENTAL DETAILS

A. Physico-chemical parameters of water of the cultured ponds and open system	51
B. Quantitative estimation of the bacterial flora of water of the cultured ponds and open system	52
C. Isolation of pure cultures and identification of bacterial flora of water of the cultured ponds and open system	52
D. Bacterial flora of fish from cultured ponds and open system	54
E. Bacterial populations of fish feed types and organic fertilizers ...	54
F. Survival of selected bacterial pathogens introduced into organic manures used in fertilizing fish ponds	55
G. Case study of Akuse fish ponds: Bacteria-fish relationship in sewage treatment plant wastewater	56
H. Health status of the fish farmers and some consumers of fish	56

CHAPTER FOUR. RESULTS

A. Physico-chemical parameters of water of the cultured ponds and open systems	58
1. Cow manure-fertilized ponds	58
2. Poultry manure-fertilized ponds	60
3. Pig manure-fertilized ponds	68
4. Blood waste-fertilized ponds	73
5. Chemically-fertilized ponds	75
6. Pond without any form of fertilizer	78
7. Open systems	80
B. Isolation of pure cultures and identification of bacterial flora of water of the cultured ponds and open system	85
1. Cow manure-fertilized ponds	85
2. Poultry manure-fertilized ponds	99
3. Pig manure-fertilized ponds	103
4. Blood waste-fertilized ponds	107
5. Chemically-fertilized ponds	107

6. Pond without any form of fertilizer	112
7. Open systems	112
C. Analysis of the diversities of the bacterial flora from the cultured ponds and the open systems	118
1. Cow manure-fertilized ponds	118
2. Poultry manure-fertilized ponds	118
3. Pig manure-fertilized ponds	124
4. Blood waste-fertilized ponds	135
5. Chemically fertilized ponds.....	143
6. Non fertilized ponds	152
7. Open systems	155
D. Similarities between bacterial populations from the different sampling sites	164
E. Bacterial flora of fish from cultured ponds and open systems	166
1. Fish cultured in cow manure-fertilized ponds	166
2. Fish cultured in poultry manure-fertilized ponds	168
3. Fish cultured in pig manure-fertilized ponds	172
4. Fish cultured in blood waste-fertilized ponds	172
5. Fish cultured in chemically fertilized ponds	175
6. Fish cultured in ponds with no fertilization	180
7. Fish cultured in the open systems	180
F. Bacterial populations of fish feed types and organic fertilizers.....	186
G. Survival of selected pathogenic bacteria introduced into organic manures used in fertilizing fish ponds	188
1. Survival of <i>Pseudomonas</i> sp. KI-MTC-001K	188
2. Survival of <i>Shigella</i> sp. KI-MTC-002K	188
3. Survival of <i>Enterobacter</i> sp. KI-MTC-003K	192
4. Survival of <i>Klebsiella</i> sp. KI-MTC-004K	192
5. Survival of <i>Citrobacter</i> sp. KI-MTC-005K	192
6. Survival of <i>Proteus</i> sp. KI-MTC-006K	192
7. Survival of <i>Salmonella</i> sp. KI-MTC-007K	192
8. Survival of <i>Vibrio parahaemolyticus</i> KI-MTC-008K	193
H. Case study of Akuse fish ponds: Bacteria-fish relationship in sewage treatment plant wastewater	194

1. Physico-chemical parameters	194
2. Bacterial flora of the four Akuse ponds	199
3. Analysis of the diversities of the bacterial flora	205
4. Similarities between the bacterial populations for the different ponds	216
5. Bacterial flora of fish cultured in sewage water	216
I. Health status of the fish farmers and some consumers of fish.....	220
CHAPTER FIVE. GENERAL DISCUSSION	224
SUMMARY	243
APPENDICES	249
ACKNOWLEDGEMENT	300
REFERENCES	302

LIST OF TABLES

Taxonomy of bacterial pathogens of fishes.....	9
Physico-chemical parameters and bacterial population level of Aduabenba Farm cultured pond.....	59
Physico-chemical parameters and bacterial population level of Boateng Farm cultured pond.....	61
Physico-chemical parameters and bacterial population level of Agyeman Farm cultured pond.....	62
Physico-chemical parameters and bacterial population level of ARDEC 20 cultured pond.....	64
Physico-chemical parameters and bacterial population level of Asare Farm cultured pond.....	66
Physico-chemical parameters and bacterial population level of Frimpong Farm cultured pond.....	67
Physico-chemical parameters and bacterial population level of Boadi Farm cultured pond.....	69
Physico-chemical parameters and bacterial population level of KK Farm cultured pond.....	71
Physico-chemical parameters and bacterial population level of Pacific Farm cultured pond.....	72
Physico-chemical parameters and bacterial population level of Boahen Farm cultured pond.....	74
Physico-chemical parameters and bacterial population level of Aheto Farm cultured pond.....	76
Physico-chemical parameters and bacterial population level of Sagoe Farm cultured pond.....	77
Physico-chemical parameters and bacterial population level of ARDEC 3 cultured pond.....	79
Physico-chemical parameters and bacterial population level of Kpong Headpond open system.....	81
Physico-chemical parameters and bacterial population level of Volta River open system.....	82

Table 2p	Physico-chemical parameters and bacterial population level of Weija dam open system.....	84
Table 3	Characteristics of the bacterial isolates from the cultured ponds and open systems.....	86 - 94
Table 4a	Bacterial species isolated from Aduabenba Farm cultured pond in 1996 - 1999.....	97
Table 4b	Bacterial species isolated from Boateng Farm cultured pond in 1996 - 1999.....	98
Table 4c	Bacterial species isolated from Agyeman Farm cultured pond in 1996 - 1999.....	100
Table 4d	Bacterial species isolated from ARDEC 20 pond in 1996 - 1999.....	101
Table 4e	Bacterial species isolated from Asare Farm cultured pond in 1996 - 1999.....	102
Table 4f	Bacterial species isolated from Frimpong Farm cultured pond in 1996 - 1999.....	104
Table 4g	Bacterial species isolated from Boadi Farm cultured pond in 1996 - 1999.....	105
Table 4h	Bacterial species isolated from KK Farm cultured pond in 1996 - 1999.....	106
Table 4i	Bacterial species isolated from Pacific Farm cultured pond in 1996 - 1999.....	108
Table 4j	Bacterial species isolated from Boahen Farm cultured pond in 1996 - 1999.....	109
Table 4k	Bacterial species isolated from Aheto Farm cultured pond in 1996 - 1999.....	110
Table 4l	Bacterial species isolated from Sagoe Farm cultured pond in 1996 - 1999.....	III
Table 4m	Bacterial species isolated from AREDC 3 pond in 1996 - 1999.....	113
Table 4n	Bacterial species isolated from Kpong Headpond open system in 1996 - 1999.....	114
Table 4o	Bacterial species isolated from Volta River open system in 1996 - 1999.....	115

Table 4p	Bacterial species isolated from Weija dam open system in 1996 - 1999.....	117
Table 5a	Diversities among bacterial flora in cow manure-fertilized ponds ...	118
Table 5b	Diversities among bacterial flora in poultry manure-fertilized ponds	124
Table 5c	Diversities among bacterial flora in pig manure-fertilized ponds....	135
Table 5d	Diversities among bacterial flora in blood waste-fertilized ponds....	143
Table 5e	Diversities among bacterial flora in chemically fertilized ponds	152
Table 5f	Diversities among bacterial flora in non-fertilized ponds.....	152
Table 5g	Diversities among bacterial flora in the open systems	155
Table 6	Population similarities between the various study areas.....	164-165
Table 7a	Mean total number of bacterial isolates occurring in tissues of fish from cow manure-fertilized ponds.....	167
Table 7b	Mean total number of bacterial isolates occurring in tissues of fish from poultry manure-fertilized ponds.....	170
Table 7c	Mean total number of bacterial isolates occurring in tissues of fish from pig manure-fertilized ponds.....	173
Table 7d	Mean total number of bacterial isolates occurring in tissues of fish from blood waste-fertilized ponds.....	176
Table 7e	Mean total number of bacterial isolates occurring in tissues of fish from chemically fertilized ponds.....	178
Table 7f	Mean total number of bacterial isolates occurring in tissues of fish from ARDEC 3 pond with no fertilization.....	181
Table 7g	Mean total number of bacterial isolates occurring in tissues of fish from the open system.....	183
Table 8	The bacterial load present in feed types and organic manures used in the fish ponds.....	187
Table 9a	Growth of <i>Pseudomonas</i> sp. KI-MTC-001K in UV-sterilized pond water containing different types of organic matter.....	189
Table 9b	Growth of <i>Shigella</i> sp. KI-MTC-002K in UV-sterilized pond water containing different types of organic matter.....	189
Table 9c	Growth of <i>Enterobacter</i> sp. KI-MTC-003K in UV-sterilized pond water containing different types of organic matter.....	189
Table 9d	Growth of <i>Klebsiella</i> sp. KI-MTC-004K in UV-sterilized pond water containing different types of organic matter.....	190

Table 9e	Growth of <i>Citrobacter</i> sp. KI-MTC-005K in UV-sterilized pond water containing different types of organic matter.....	190
Table 9f	Growth of <i>Proteus</i> sp. KI-MTC-006K in UV-sterilized pond water containing different types of organic matter.....	190
Table 9g	Growth of <i>Salmonella</i> sp. KI-MTC-007K in UV-sterilized pond water containing different types of organic matter.....	191
Table 9h	Growth of <i>Vibrio parahaemolyticus</i> KI-MTC-008K in UV-sterilized pond water containing different types of organic matter.....	191
Table 10a	Physico-chemical parameters and bacterial population of Akuse pond I for 1996 -1999.....	195
Table 10b	Physico-chemical parameters and bacterial population of Akuse pond II for 1996 -1999.....	196
Table 10c	Physico-chemical parameters and bacterial population of Akuse pond III for 1996 -1999.....	197
Table 10d	Physico-chemical parameters and bacterial population of Akuse pond IV for 1996 -1999.....	198
Table 11a	Bacterial species isolated from Akuse pond I in 1996 - 1999.....	200
Table 11b	Bacterial species isolated from Akuse pond II in 1996 - 1999.....	201
Table 11c	Bacterial species isolated from Akuse pond III in 1996 - 1999....	202
Table 11d	Bacterial species isolated from Akuse pond IV in 1996 - 1999.....	203
Table 12	Diversities among the bacterial flora of sewage-fertilized ponds....	205
Table 13	Population similarities between the Akuse ponds.....	216
Table 14	Mean total number of bacterial isolates occurring in tissues of fish from sewage-fertilized ponds.....	217
Table 15	Bacterial species isolated from stool of fishermen associated with different fish culture sites.....	221



LIST OF FIGURES

Fig. 1	Sequence of experiments carried out on the bacterial isolates	53
Fig. 2a	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Aduabenba Farm (Aduabenba 1).....	119
Fig. 2b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Aduabenba Farm (Aduabenba 2).....	119
Fig. 2c	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Aduabenba Farm (Aduabenba 3).....	120
Fig. 2d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Aduabenba Farm (Aduabenba 4).....	120
Fig. 2e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Aduabenba Farm (Aduabenba 5).....	121
Fig. 2f	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Boateng Farm (Boateng 1).....	121
Fig. 2g	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Boateng Farm (Boateng 2).....	122
Fig. 2h	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Boateng Farm (Boateng 3).....	122
Fig. 2i	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Boateng Farm (Boateng 4).....	123
Fig. 3a	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Agyemang Farm (Agyeman 1).....	125
Fig. 3b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Agyemang Farm (Agyeman 2).....	125
Fig. 3c	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Agyemang Farm (Agyeman 3).....	126
Fig. 3d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Agyemang Farm (Agyeman 4).....	126
Fig. 3e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Agyemang Farm (Agyeman 5).....	127
Fig. 3f	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from ARDEC 20 pond (Ardec20 1).....	127
Fig. 3g	Dendrogram showing UPGMA clustering of the bacterial isolates	

	for August 1997 from ARDEC 20 pond (Ardec20 2).....	128
Fig. 3h	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1998 from ARDEC 20 pond (Ardec20 3).....	128
Fig. 3i	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1998 from ARDEC 20 pond (Ardec20 4).....	129
Fig. 3j	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1999 from ARDEC 20 pond (Ardec20 5).....	129
Fig. 3k	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1997 from Asare Farm (Asare 1).....	130
Fig. 3l	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1997 from Asare Farm (Asare 2).....	130
Fig. 3m	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1998 from Asare Farm (Asare 3).....	131
Fig. 3n	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1998 from Asare Farm (Asare 4).....	131
Fig. 3o	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1999 from Asare Farm (Asare 5).....	132
Fig. 3p	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1997 from Frimpong Farm (Frimpon 1).....	132
Fig. 3q	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1997 from Frimpong Farm (Frimpon 2).....	133
Fig. 3r	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1998 from Frimpong Farm (Frimpon 3).....	133
Fig. 3 s	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1998 from Frimpong Farm (Frimpon 4).....	134
Fig. 3t	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1999 from Frimpong Farm (Frimpon 5).....	134
Fig. 4a	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1997 from Boadi Farm (Boadi 1).....	136
Fig. 4b	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for August 1997 from Boadi Farm (Boadi 2).....	136
Fig. 4c	Dendrogram showing UPGMA clustering of the bacterial isolates	
	for February 1998 from Boadi Farm (Boadi 3).....	137
Fig. 4d	Dendrogram showing UPGMA clustering of the bacterial isolates	

	for August 1998 from Boadi Farm (Boadi 4).....	137
Fig. 4e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Boadi Farm (Boadi 5).....	138
Fig. 4f	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from KK Farm (KK 1).....	138
Fig. 4g	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from KK Farm (KK 2).....	139
Fig. 4h	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from KK Farm (KK 3).....	139
Fig. 4i	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from KK Farm (KK 4).....	140
Fig. 4j	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from KK Farm (KK 5).....	140
Fig. 4k	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Pacific Farm (Paci 1).....	141
Fig. 4l	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Pacific Farm (Paci 2).....	141
Fig. 4m	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Pacific Farm (Paci 3).....	142
Fig. 4n	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Pacific Farm (Paci 4).....	142
Fig. 4o	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Pacific Farm (Paci 5).....	144
Fig. 5a	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Boahen Farm (Boahen 1).....	144
Fig. 5b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Boahen Farm (Boahen 2).....	145
Fig. 5c	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Boahen Farm (Boahen 3).....	145
Fig. 5d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Boahen Farm (Boahen 4).....	146
Fig. 5e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Boahen Farm (Boahen 5).....	146
Fig. 6a	Dendrogram showing UPGMA clustering of the bacterial isolates	

	for February 1997 from Aheto Farm (Aheto 1).....	147
Fig. 6b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Aheto Farm (Aheto 2).....	147
Fig. 6c	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Aheto Farm (Aheto 3).....	148
Fig. 6d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Aheto Farm (Aheto 4).....	148
Fig. 6e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Aheto Farm (Aheto 5).....	149
Fig. 6f	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Sagoe Farm (Sagoe 1).....	149
Fig. 6g	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Sagoe Farm (Sagoe 2).....	150
Fig. 6h	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Sagoe Farm (Sagoe 3).....	150
Fig. 6i	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Sagoe Farm (Sagoe 4).....	151
Fig. 6j	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Sagoe Farm (Sagoe 5).....	151
Fig. 7a	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from ARDEC 3 pond (Ardec3 1).....	153
Fig. 7b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from ARDEC 3 pond (Ardec3 2).....	153
Fig. 7c	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from ARDEC 3 pond (Ardec3 3).....	154
Fig. 7d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from ARDEC 3 pond (Ardec3 4).....	154
Fig. 7e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from ARDEC 3 pond (Ardec3 5).....	156
Fig. 8a	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Kpong headpond (Kpong 1).....	156
Fig. 8b	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Kpong headpond (Kpong 2).....	157
Fig. 8c	Dendrogram showing UPGMA clustering of the bacterial isolates	

	for February 1998 from Kpong headpond (Kpong 3).....	157
Fig. 8d	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Kpong headpond (Kpong 4).....	158
Fig. 8e	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Kpong headpond (Kpong 5).....	158
Fig. 8f	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Volta river (Volta 1).....	159
Fig. 8g	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Volta river (Volta 2).....	159
Fig. 8h	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Volta river (Volta 3).....	160
Fig. 8i	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Volta river (Volta 4).....	160
Fig. 8j	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Volta river (Volta 5).....	161
Fig. 8k	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Weija dam (Weija 1).....	161
Fig. 8l	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Weija dam (Weija 2).....	162
Fig. 8m	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Weija dam (Weija 3).....	162
Fig. 8n	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Weija dam (Weija 4).....	163
Fig. 8o	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Weija dam (Weija 5).....	163
Fig. 9a	Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from cow manure-fertilized ponds.....	169
Fig. 9b	Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from poultry manure-fertilized ponds.....	171
Fig. 9c	Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from pig manure-fertilized ponds.....	174
Fig. 9d	Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from blood waste-fertilized ponds.....	177

Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from chemically fertilized ponds	179
Mean values and L.S.D (95%) intervals between the bacterial flora offish tissues from non fertilized ponds.....	.182
Mean values and L.S.D (95%) intervals between the bacterial flora offish tissues from the open systems.....	185
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Akuse pond I (Akusel 1).....	206
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Akuse pond I (Akusel 2).....	206
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Akuse pond I (Akusel 3).....	207
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Akuse pond I (Akusel 4).....	207
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Akuse pond I (Akusel 5).....	208
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Akuse pond II (Akusell 1).....	208
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Akuse pond II (Akusell 2).....	209
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Akuse pond II (Akusell 3).....	209
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Akuse pond II (Akusell 4).....	210
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Akuse pond II (Akusell 5).....	210
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Akuse pond III (Akuselll 1).....	211
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Akuse pond III (Akuselll 2).....	211
Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Akuse pond III (Akuselll 3).....	212
Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Akuse pond III (Akuselll 4).....	212

Fig. IOo	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Akuse pond III (AkuseIII 5).....	213
Fig. IOp	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1997 from Akuse pond IV (AkuseIV 1).....	213
Fig. IOq	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from Akuse pond IV (AkuseIV 2).....	214
Fig. IOr	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1998 from Akuse pond IV (AkuseIV 3).....	214
Fig. 10s	Dendrogram showing UPGMA clustering of the bacterial isolates for August 1998 from Akuse pond IV (AkuseIV 4).....	215
Fig. IOt	Dendrogram showing UPGMA clustering of the bacterial isolates for February 1999 from Akuse pond IV (AkuseIV 5).....	215
Fig. 11	Mean values and L.S.D (95%) intervals between the bacterial flora of fish tissues from sewage-fertilized ponds.....	219
Fig. 12	Number of individuals of fishing communities associated with ponds treated with cow manure (1), pig manure (2), poultry manure (3), blood waste (4), chemical (5), sewage (6), and no manure (7), and open system (8), harbouring the indicated pathogenic bacteria.....	222 -223

LIST OF PLATES

Plate 1a	Point of discharge of sewage into the Akuse I — IV ponds	20
Plate 1b	Fishermen fishing in the Akuse II pond	20
Plate 2	ARDEC 20 pond showing hen coop from which droppings of poultry fall directly into pond	21
Plate 3	Piggery house standing close to Boadi Farms pond. Droppings of pigs are washed daily into pond	22
Plate 4	Landing site at New Galilea of the Weija Dam	24
Plate 5a	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Aeromonas</i> species cultured on TCBS agar.....	95
Plate 5b	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Bacillus</i> species showing endospores.....	95
Plate 5c	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Clostridium</i> species showing endospores.....	95
Plate 5d	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Corynebacterium</i> species cultured on blood agar	95
Plate 5e	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Escherichia</i> species cultured on Eosin Methylene Blue agar	95
Plate 5f	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Flavobacterium</i> species cultured on blood agar.....	95
Plate 5g	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Klebsiella</i> sp. KI-MTC-004K cultured on MacConkey agar...	96
Plate 5h	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Staphylococcus</i> species cultured on blood agar.....	96
Plate 5i	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Salmonella</i> sp. KI-MTC-007K cultured on Brilliant Green agar	96
Plate 5j	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Serratia</i> species cultured on blood agar.....	96
Plate 5k	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Micrococcus</i> species cultured on blood agar.....	96
Plate 5l	Photomicrograph [Nikon, 100x, oil immersion objective] of one of the <i>Vibrio parahaemolyticus</i> KI-MTC-008K cultured on TCBS agar...	96

CHAPTER ONE

INTRODUCTION AND LITERATURE REVIEW

Diversity of Bacteria in Nature

Bacteria form a large group of chemoheterotrophic (saprophytic and parasitic) and autotrophic (photoautotrophic and chemoautotrophic) microorganisms widely distributed in the environment. Each of the major ecosystems in the world is populated with bacteria that may be unique to the particular ecosystem. The bacteria exist in populations, which can greatly affect the chemical and physical properties of their habitats. The bacteria in a particular ecosystem are represented by different morphological forms and many different species. Adaptation is a complex long-term adjustment in biochemistry or genetics that enables an organism to grow in its environment. Environmental factors fundamentally affect the function of metabolic enzymes, and that survival in changing environment is largely a matter of enzymatic flexibility. Most populations' existence also depends on the presence of other populations. For example, anaerobic species may exist in association with facultative anaerobes, which remove traces of oxygen, thus creating anaerobic conditions. Their interactions, on the other hand, may include competition, generally for limiting sources of food, and production of toxic metabolites, which tend to inhibit the growth of other species.

Bacteria in an ecosystem can be identified to the level of genus and species based on microscopic morphology (the shape and size of cells, Gram stain reaction, details shown by other differential stains, and special structures, including flagella, granules, capsules and endospores); macroscopic morphology (appearance of colonies, including texture, size, shape, pigment, speed of growth and reactions with special media); physiological characteristics (response to numerous diagnostic tests for determining the presence of specific enzymes **and** nutritional **and** oxygen requirements); serological analysis (response of bacterial cultures to antibodies that are known to be specific for a given species or genus of bacterium); chemical analysis (for the types of specific chemical substances that the bacterium has, such as proteins and fatty acids); and genetical analysis (analysing the DNA for its total percentage of guanine and cytosine - the G/C content - which may be indicative of its

relationship to other bacteria, and determination of degree of similarity of DNA molecules in cultures that would indicate genetic relationships - using DNA probes) (Cowan and Liston, 1994).

Surface water ecosystems such as ponds, lakes, rivers and oceans differ to a considerable extent in size, physical make-up and chemical content. An aquatic ecosystem is structured and it contains significant gradients or local differences in composition. Factors that contribute to the development of zones in aquatic systems are sunlight, temperature, aeration and dissolved nutrient content. These variations create numerous macro- and micro-environments for communities of organisms. Large bodies of standing water, for example, develop gradients in temperature or thermal stratification. Oxygen also forms a gradient that varies with depth. Of all the characteristics of water, the greatest range occurs in nutrient levels. Bacterial populations of many of these ecosystems have been studied to varying degrees (Cowan and Liston, *op. cit.*) The water ecosystems contain both native species of bacteria that grow in nature only in such an environment and terrestrial species that are passively carried to them.

Fish culture systems constitute a unique type of aquatic ecosystem. They are overpopulated with fish, oyster or other organisms under culture, and they receive, at intervals, fish feed that maintains a high level of nutrients in the water, while the water is frequently disturbed. Their bacterial flora may, therefore, vary in many aspects from those of other standing freshwater bodies.

Quality of Water of Fish Cultures

Tolerance limits of water quality of fish cultures depend very much on the species cultivated. It is, therefore, important to consider only the water quality parameters that have significance in assessing environmental impact. These are mainly dissolved oxygen, pH, carbon dioxide, ammonia, nitrites, nitrates, hydrogen sulphide, pesticides and turbidity. The optimum levels of many of these are not accurately known for many species, but based on long-term sub-lethal toxicity tests with chemicals and experience in experimental and production farms, "safety levels" have been proposed (Tiews, 1981).

In salmonid and warm water crustacean culture, dissolved oxygen levels are not allowed to go below 5 mg/l for more than a few hours. Eel (*Anguilla japonius*), carp (*Cyprinus carpio*) and tilapia (*Oreochromis niloticus*) can tolerate lower levels of 3 - 4 mg/l. According to Swingle (1969) and Boyd (1981), warm water fish survive at dissolved oxygen levels as low as 1 mg/l, but the growth is slowed down with prolonged exposure. The desirable level is above 5 mg/l.

In water used for intensive fish culture, free carbon dioxide levels fluctuate typically from 0 mg/l in the afternoon to 5 - 10 mg/l at daybreak with no obvious ill-effects on fish (Parks *et al.*, 1975). Higher concentrations of free carbon dioxide, even up to 60 mg/l may be tolerated provided that dissolved oxygen concentrations are high.

Un-ionized ammonia (NH₃) is toxic to fish, but the ammonium ion (NH₄⁺) is not toxic (Downing and Merckens, 1955; Boyd, 1981). According to EIFAC (1973), levels of ammonia for short-term exposure with no undue ill-effect lie between 0.6 and 2.0 mg/l, but, normally, the maximum tolerable concentration is considered to be 0.1 mg/l (Tiews, *op cit*). Un-ionized ammonia becomes more toxic when the level of dissolved oxygen is low, but this is of little importance in pond farms as the toxicity decreases with increasing carbon dioxide concentration, which is usually the case when the dissolved oxygen is high.

Available information on safety limits of nitrites (NO₂) is very limited, although studies indicate that nitrite may be a significant factor in channel catfish (*Heterobranchus bidorsalis*) ponds. The suggested maximum level for prolonged exposure in hard freshwater is 0.1 mg/l. The suggested maximum nitrate (NO₃) levels are below 100 mg/l.

Un-ionized hydrogen sulphide (H₂S) is extremely toxic to fish at concentrations that may occur in natural waters as well as in aquaculture farms. It has been demonstrated that high concentrations of hydrogen sulphide could result in poor growth of channel catfish (Bonn and Follis, 1967). Bioassays of several species of fish suggest that any detectable concentration of hydrogen sulphide should be considered detrimental to fish production (Boyd, 1981).

Many pesticides, particularly insecticides, are extremely toxic to fish. Acute toxicity values for several commonly used insecticides range from 5 to 100 mg/l¹ (Cope, 1964), and on longer exposure even lower concentrations may be toxic. Even when they do not cause mortality of the species under culture, they may affect the growth of food organisms and this reduces their growth and productivity.

Turbidity is also an important water quality, which a fish farmer has to control. Turbidity caused by suspended soil particles has usually no direct effect on fish and shellfish, but it restricts light penetration and limits photosynthesis. Besides, sedimentation of soil particles can destroy benthic communities and smother fish eggs. Turbidity caused by plankton is not harmful to fish, but clay turbidity exceeding 20,000 mg/l¹ (of particulate matter) causes behavioural reactions in many species of fish and appreciable mortality occurs at turbidities above 175,000 mg/l¹ (of particulate matter).

There is much concern about possible contamination of fish and its products by trace metals and organo-chlorines because of reported poisoning cases in many parts of the world. Several trace metals; dioxins, dibenzofurans and coplanar polychlorinated biphenols (PCBs) have been identified as the causative contaminants in the aquatic environments. The trace elements that are of greatest concern are mercury and cadmium. The Minimata disease caused by contamination of fish by mercury in discharges of a chemical factory, in Minimata Bay in Japan in the 1950's is a well-known tragedy (Mason, 1991). Since then, a number of other mercury poisoning cases due to eating contaminated fish have been reported (Mason, *op. cit.*). As a result, internationally accepted standards for trace elements in marine fish and shellfish have been set out (Nauen, 1983). The median standard for mercury in fish and shellfish is 0.5 µg/g¹ wet weight, with a range of 0.1-1.0 µg/g¹ wet weight. Such accumulations do not appear to have been reported from aquaculture products so far. Though mercury is usually accumulated in lethal concentrations by only long-lived predatory species such as tuna (*Thunnus thunus*) and swordfish (*Xiphias gladius*), the possibility of smaller farmed fish accumulating it in significant quantities in areas of excessive local contamination cannot be ruled out (Pillay, 1992).

Cadmium is another trace metal that is highly toxic to mammals, but is not known to have caused any public health problems in humans. However, there is much concern about possible cadmium contamination in Japan, resulting in the "itai-itai" syndrome (an unusual disease of a rheumatic nature), believed to be caused by the discharge of cadmium-rich effluent from a zinc mining company into the River Jintsu. The waters of the river were used for irrigation of rice fields, and consumption of rice from the affected area, containing high levels of cadmium, is thought to be the principal cause of the disease (Pillay, *op. cit.*). The median standards laid down for cadmium in fish and shellfish are 0.3 and 1.0 ngg⁻¹ wet weight, respectively (Pillay, *op. cit.*).

Another trace metal of concern as an environmental contaminant is lead, especially because of its possible impact on children. Concentrations of lead in seafood, however, are quite low and are unlikely to be a public health threat. Copper and arsenic are also important contaminants of food products, but there appears to be no reports of any significant bioaccumulation of these in cultured fish products. Copper is of low toxicity to mammals and the arsenic found in most aquatic organisms is principally organic in nature. Concentrations of inorganic arsenic in aquatic species is very low (generally below 0.5 ngg⁻¹ wet weight) and are thus of little toxicological effect (Pillay, *op. cit.*).

Organochlorines are known to be toxic to aquatic organisms and terrestrial animals, but their direct toxicity to humans is low and there are few known instances of their public health impacts. The few groups of organochlorines that are potential hazard to humans include dioxins, especially 2,3,7,8-tetrachlorodibenzo-p-dioxins (TCDD), dibenzofurans and certain polychlorinated biphenols (PCBs) (Chen and Hsu, 1986).

Residues of organochlorine pesticides and PCBs have been detected in aquatic species, but have been of importance only on a local scale (Pillay, 1992), insufficient to cause any public concern. Shellfish such as mussels have been found to accumulate DDT and coplanar PCBs in significant quantities in highly polluted areas and can thus pose public health problems if such areas are used for their culture. The effects of chronic-low-level exposure to such contaminants in humans are not sufficiently known.

Water as a Bacteriological Medium

Because water is such an excellent solvent, natural water supplies are actually dilute solutions of many substances. There is probably no truly pure water, even in laboratories where multiple distillations yield highly purified samples, because minute amounts of the components of glass or other containers dissolve in the distillates. Because of these dissolved substances pure water is far from free of viable bacteria.

Many bacteria reproduce in water; among the genera that will grow in water of unquestionable potable quality are *Achromobacter*, *Citrobacter*, *Crenothrix*, *Desulfovibrio*, *Escherichia*, *Pseudomonas*, *Streptococcus* and *Xanthomonas*. Pseudomonads are frequently found in surprisingly large numbers in potable waters, and they have been repeatedly and consistently found in every conceivable water source. This apparently results from the innate ability of many species of *Pseudomonas* to produce enzymes that enable them to utilize traces of a wide variety of compounds including thymol, cresol, chlorophenols, and nitrophenols as their sole source of carbon (Tabak *et al.*, 1964). These and many other more readily assimilable source of carbon, when present in water, yield surprisingly high populations when inoculated with Pseudomonads. In addition to being adaptable to diverse sources of carbon, these and some other species grow very well at temperatures slightly above freezing and proliferate to a remarkable degree at 0°C. The ability to grow well at 0°C is restricted mostly to strains of *Pseudomonas* and others, such as, *Achromobacter*, *Flavobacterium*, and *Micrococcus*.

Water-borne Bacteria and Their Significance

The health of fish is very dependent on water quality, that is, the chemical, physical and microbial content of the water. While the presence of some obligate pathogens such as *Aeromonas salmonicida* or *Renibacterium salmonarum* in water is taken to indicate the presence of fish disease on a farm, the presence of many other genera, such as Vibrios or motile aeromonads is the norm rather than the exception. Thus the bacterial load in water *per se* does not relate to possible health hazard. Indeed, the majority are beneficial saprobes involved in the numerous re-cycling processes.

Spoilage of fish could be distinguished from disease caused by obligate parasites. Bacterial spoilage of fish food is caused by psychrophilic strains of *Achromobacter*, *Flavobacterium* and *Pseudomonas*. Spoilage of stored fish and fish products is caused by some of the bacteria resident on the live fish, as well as other species contaminating the organism after death. Frazier (1958) stated that species of *Clostridium*, *Micrococcus* and *Proteus* are the major spoilage bacteria with species of *Flavobacterium* and *Pseudomonas* being the main spoilage bacteria at near freezing temperatures. *Bacillus*, *Clostridium*, *Escherichia*, *Proteus*, *Pseudomonas* and *Serratia* species have also been identified as spoilage organisms.

Environmental factors such as eutrophication, create conditions favourable for disease outbreaks. Bacterial populations in natural waters are related to the trophic state. Grimaldi *et al*, (1973), for example, found pathogenic fungal infections to be common in alpine lakes, and Korzeniewski and Korzeniewska (1982) found higher bacterial counts in the vicinity of rainbow trout (*Salmo gairdnesi*) cages in Lake Letowo in Poland, evidently as a result of environmental changes brought about by waste discharges from the cages.

Bacterial Diseases of Farmed Fishes

Many studies have shown that bacteria belonging mostly to the genera *Aeromonas*, *Corynebacterium*, *Myxobacterium*, *Pseudomonas*, and *Vibrio* cause infectious diseases in fish (Roberts, 1978). Diseases in marine fishes caused by bacteria belonging to the genus *Vibrio* and, *Aeromonas* and *Pseudomonas* in fresh water fishes have been reported in many culture systems (Kabata, 1985).

Some species of bacteria only cause disease if the animal host is in a physiologically weakened state. Disease also occurs if the bacteria are present in such large numbers that they overwhelm the host defenses or cause deterioration of the environment. These are opportunistic pathogens. In contrast, obligate pathogens live only within their respective hosts.

Most bacterial infections begin on mucus membranes. In order to initiate infection, the bacterium must reach the susceptible organ and adhere to the epithelial cells. In certain diseases, the bacteria may remain localized at the mucosal surface and cause

damage by liberating toxins. In most cases, however, infection is caused by the pathogen penetrating the epithelium and then growing in the sub-mucosa or spreading even further. Successful invasion depends on the ability of the pathogen to out-compete the normal microflora for nutrients. Small breaks or lesions in the mucosal membrane also facilitate spread of pathogens. Some examples of fish diseases cited by Munro (1982) are shown in Table 1.

Faecal Coliform in Fish Culture System.

Of much concern in fisheries also is the contamination of fishes by faecal coliforms in polluted waters (Caldreich and Clarke, 1966). In every country where a fish inspection programme exists, the load of faecal coliforms in farmed, feral or processed fish is evaluated to verify whether the harvest or product presents a health hazard or not (Blackwood, 1978; Fapohunda *et al.*, 1994). Their presence in fish intended for human consumption may constitute a potential danger not only in causing disease, but also because of the possible transfer of antibiotic resistance from aquatic bacteria to human infecting bacteria from non-aquatic sources (Olayemi *et al.*, 1991).

Table 1

Taxonomy of bacterial pathogens of fishes (after Roberts, 1978)

Family	Genus	Species	Main pathological features of infected fish
Cytophagaceae (gliding bacteria)	<i>Flexibacter</i>	<i>F. columnaris</i> ^b <i>F. psychrophila</i> ^{a,b} <i>F. marinus</i> ^{a,b}	Gill and skin lesions
Pseudomonadaceae	<i>Pseudomonas</i>	<i>Ps. fluorescens</i> <i>Ps. anguilliseptica</i> ^a	Septicaemias and haemorrhage
Enterobacteriaceae	<i>Edwardsiella</i> <i>Yersinia</i>	<i>E. tarda</i> <i>Y. ruckerif</i>	Septicaemias, haemorrhage and skin lesions
Vibrionaceae	<i>Vibrio</i> <i>Aeromonas</i>	<i>V. anguillarum</i> <i>V. species</i> <i>A. hydrophilla</i> <i>A. salmonicida</i>	Septicaemias, haemorrhage and skin lesions
Uncertain but Gram-negative	<i>Flavobacterium</i> <i>Pasteur el la</i> <i>Haemophilus</i>	<i>Flavobacterium species</i> <i>Past. piscicida</i> ^{a,h} <i>H. piscium</i>	Skin lesions, haemorrhage and septicaemias Granulomas Skin lesions, septicaemias and Haemorrhages
Streptococcaceae	<i>Streptococcus</i>	<i>Str. faecalis</i> <i>Streptococcus species</i>	Granulomas, haemorrhage
Norcardiaceae	<i>Nocardia</i>	<i>N. asteroides</i> <i>N. kampfch</i> ^b	Granulomas especially tubercles !
Uncertain but Gram-positive	Uncertain	<i>Renib acterium salmoninarum</i> ^{a,b}	Bacterial kidney disease granulomas in salmonids, haemorrhage
Bacillaceae	<i>Clostridium</i>	<i>Cl. botulinum</i>	Intoxication, granulomas especially tubercles
Mycobacterium	<i>Mycobacterium</i>	<i>M. fortuitum</i> <i>M. marinum</i>	Intoxication, granulomas especially tubercles

^a Not listed in Bergey's; 8^l Edition

^b Not listed in 'Approved lists of bacterial names'.

The coliform group of bacteria comprises mainly of species of the genera *Citrobacter*, *Enterobacter*, *Escherichia* and *Klebsiella*. *E. coli*, the predominant species of the faecal coliforms, has been found in the intestinal tract of fish (Newman *et al*, 1972), and on the gills, in the muscles and on the skin (Ogbondeminu, 1993), when sewage water has been used to rear the fish. Salle (1964) reported that the most heavily contaminated parts are the intestines and the skin. Presence of *E. coli* in water or food invariably indicates the possible presence also of the causative organisms of many gastro-intestinal diseases (DHSS, 1991). Thus, fish caught in polluted water have been found to cause infection in human (Caldreich and Clarke, 1966; van Duijn, 1973). According to Allen and Hopher (1969), most of the epidemics attributed to wastewater sources are from raw sewage gaining access to food eaten directly by man, or from contamination of water supply systems by untreated sewage. *E. coli* is reported to be one of the commonest causes of food poisoning in many areas throughout the world, including Europe (Pennings *et al*, 1994), United States of America (Beuchart, 1996), South America (Utsunomiya *et al*, 1995) and the Far East (Haque *et al*, 1994).

The indicator bacteria of faecal contamination are aerobic (facultatively anaerobic), oxidase negative, weakly motile, gram-negative and non-spore-forming rods. They do not liquefy gelatin but do form indole, coagulate milk, and ferment arabinose, fructose, glucose, lactose, maltose, and mannitol but do not ferment saccharose. On Endo agar these bacteria form characteristic red colonies with a golden metallic sheen, dark red colonies, and rose colonies with a dark center. Also on Eosin-Methylene Blue (EMB) agar, *E. coli* colonies produce a characteristic green metallic sheen.

Fish as Potential Vectors of Human Bacterial Pathogens

Fishes may be vectors of other bacterial pathogens of humans besides the water-borne species. Fish and crustaceans caught from marine waters are generally expected to be free of potentially pathogenic bacteria normally associated with warm-blooded land animals and humans (Thatcher and Clark, 1968; Shewan, 1970). However, when caught from estuarine waters, and from lakes, rivers and ponds, their microflora may reflect the degree of contamination of the environment. Levels of

pollution, especially from domestic sources, of freshwater bodies have increased within the last ten years (Biney, 1982).

Wild fish in endemic areas have been known to harbour Enterobacteriaceae that cause disease in humans or other warm-blooded animals. Vibrios causing epidemics such as cholera have been isolated after varying intervals following experimental inoculation of the fish. Eventually, the residual bacterial cells lost their virulence (Pillay *et al*, 1954), but there is no evidence that any of the pathogens have become systemic under fish culture conditions.

Some human pathogens survive and multiply in the gut, mucus, and tissues of fish and thus render the fish a potential vector of human disease for long periods. *Vibrio parahaemolyticus* is a typical example. This organism is indigenous to certain areas of the sea, and can maintain itself in and on fish usually without causing overt symptoms of disease. Severe gastrointestinal infection is caused by consuming uncooked fish containing this bacterium. Because of its importance in human medicine, *V. parahaemolyticus* is one of the few fish-borne pathogens that has been extensively studied (Twedt *et al*, 1969). Allen *et al*, (1979), in relevant studies, found faecal streptococci and other organisms associated with human diseases (species of *Aeromonas*, *Escherichia*, *Klebsiella*, *Pseudomonas*, and *Salmonella*) only in gut contents of small Pacific salmon and rainbow trout grown in domestic wastewater-fertilized ponds, and none in other visceral organs or musculature. A fish pathogen *Pseudomonas flourescens* is so similar to the human pathogen *Pseudomonas aeruginosa* that separation of the two taxonomically is very difficult (Bullock, 1964).

Culture of Fish in Treated Wastewater

Aquaculture is becoming an important source of proteins in both developed and developing countries, and today provides about one-fifth of fish consumed world-wide. A growing trend in fish farming is to feed the fish with waste products from human activities, such as urban or agricultural waste, or aquatic plants that have been used for purification of sewage water. In this way, waste products are transformed into high quality proteins.

Properly planned use of municipal wastewater alleviates surface water pollution problems and not only conserves valuable water resources but also takes advantage of the nutrients contained in sewage to culture the fish. The nitrogen and phosphorous content of sewage might reduce or eliminate the requirements for commercial fertilizers.

Municipal wastewater is mainly comprised of water together with relatively small concentrations of suspended and dissolved organic and inorganic solids. Among the organic substances present are carbohydrates, fats, proteins and their decomposition products. The inorganic substances may include a number of potentially toxic elements such as arsenic, cadmium, chromium, copper, lead, mercury and zinc. Even if toxic materials are not present in concentrations likely to affect humans, they might be at phytotoxic levels and the wastewater will be unsuitable for agricultural purposes. Furthermore, the possible presence of human pathogenic organisms should be borne in mind when wastewater is used for aquaculture. Advisedly, wastewater for aquaculture should be treated before use.

Primary and secondary treated waste effluents have successfully been used to grow the Nile tilapia *Oreochromis niloticus* (L.) (Khalil and Hussein, 1997). The growth rate of fish reared in treated wastewater was significantly higher than that of fish reared in the natural habitat. The results showed that the growth rate of the Nile tilapia in secondary and primary effluents was higher than that reared in underground water. Ishak (1986) found that the growth rate of *O. niloticus* in the Nile water and cage culture showed an average daily gain of 1.02g fish⁻¹. Bayoumi and Khalil (1988) recorded an average daily gain of 0.82 - 1.08g fish⁻¹ for *O. niloticus* in fisheries at Lake Manzaka in Egypt. It has also been shown that fish reared in treated effluents matured much earlier (7 months) than those reared in underground water (8.5 months) and that fry grown in treated water ponds were found to be healthy (Bardach *et al*, 1972; Balarin, 1979; Bayoumi and Khalil, *op. cit.*) The better performance had been attributed mainly to high levels of nutritive salts; particularly, phosphate and nitrate, in the sewage.

Culture of Fish in Untreated Wastewater

Application of fertilizers to ponds has been found to substantially increase yield. However, the continued increase in cost of commercial fertilizers is making the practice unprofitable. This has, accordingly, diverted interest to other sources of enrichment of the water, such as animal manure. Heavy introduction of organic wastes causes algal blooms, providing feed for the fish, and also serves as a source of nutrients for microorganisms present in the water. Animal wastes are used to fertilize pond farms in many countries and are considered superior to inorganic fertilizers in producing and maintaining desirable species of planktonic and benthic organisms in fresh and brackish water ponds (Pillay, 1992).

In integrated livestock-cum-fish farming, the animals are raised near or above fishponds so that the faecal matter and other waste materials can be discharged directly into the ponds. Total solid contents of animal waste are high. For example, for pigs and poultry, it is reported to be 268 - 509 g dry weight day⁻¹ animal⁻¹ (Whetstone *et al*, 1974) while the solid content of duck waste was estimated to be 50.5 g wet weight day⁻¹ duck⁻¹ (Woynarovich, 1980).

Use of pig and poultry manure to fertilize fish ponds has been reported in many parts of Asia (Bardach *et al*, 1972; Buck *et al*, 1979; de Guzman and Chia, 1978; Hopkins *et al*, 1980; Woynarovich, 1979). In Ghana poultry waste, and, cow and pig dung are mostly used to fertilize fish ponds. Some farmers make regular application at three or four months intervals. Others depend on visual observation and add the waste according to the colour of the pond water. Others do it once in the life time of the pond.

As manuring causes organic enrichment it may also hasten the deterioration of the water quality making the aquatic environment favourable for the growth, sustenance and multiplication of pathogenic bacteria that are hazardous to man through fish handling and consumption. Pathogenic bacteria such as *Citrobacter*, *Edwardsiella*, *Enterobacter*, *Escherichia coli*, *Klebsiella* and *Serratia* are easily introduced into the aquatic environment (Cohen and Shuval, 1973; Cuelin, 1962; Evison and James, 1973; Rao *et al*, 1968; Rudolfs *et al*, 1950).

Use of human sewage is not basically different from the application of animal wastes, but there are serious constraints to its use, due largely to aesthetic reasons and the possibility of spreading human diseases. On the contrary, recent studies in which sewage was used to grow fish biomass for predatory fish (Edwards *et al.*, 1987) showed that both the predatory fish and the forage fish were safe for human consumption.

The Role of Bacteria in Self-purification of Water bodies.

The advantages in the use of animal and domestic waste in fish culture are generally determined by rate of decomposition and mineralization of solid matter and the rate at which nutrients are released to support plankton or benthic production. The solids, which settle at the bottom of the pond, are decomposed anaerobically yielding carbon dioxide, ammonia and hydrogen sulphide. Aerobic decomposition takes place at the upper levels or zones of the water body producing carbon dioxide, nitrite, nitrogen and sulphur. These are utilized by algae which in turn produce oxygen by photosynthesis. This oxygen, along with dissolved atmospheric oxygen is utilized in aerobic decomposition processes (Pillay, 1992).

Marine Farming

There are two major farming systems which are differently managed, namely, Marine farming and Freshwater farming. Marine farming has a long history. The earliest type of farming was the raising of oysters. Aristotle discussed the cultivation of oysters in Greece and Pliny gave details of Roman oyster-farming in the early decades of the Christian Era. Records concerning the regulation of salt or brackish ponds for raising milkfish (*Chanos chanos*) in Java date back to the 15th Century (Pinchot, 1973).

Oysters are particularly appropriate for marine farming because their spawn can be collected and used for 'seeding' new areas of cultivation. An oyster produces more than 100 million eggs at a single spawning. The egg soon develops into a free-swimming larval form, known as a veliger, which settles to the bottom after two or three weeks. Veligers attach themselves to any clean surface and develop into miniature adult oysters, called 'spat'. At this point the oyster farmer distributes a supply of 'cultch' clean material with a smooth hard surface, such as old oyster shell

or ceramic tile. A set of spat settles on the cultch which is then used to seed new oyster beds.

The bottom of the new oyster bed is prepared by removing as many natural enemies of the oyster as possible. The oyster bed is then fenced to prevent the return of the natural enemies. The oysters are moved after a few years to **claires**, special fattening areas where the water is rich in diatoms. This produces oysters of improved taste and colour. When the oysters have reached marketable size, they are moved again to shallow water, where they must stay closed for longer periods at low tide (Holt, 1969; Pinchot, 1973; Ryther and Matthiessen, 1969).

There is also the comparatively recently developed method of suspension culture. This method, pioneered in Japan, is now spreading to the rest of the world. The spat are collected on shells that are strung in long bundles and immersed in tidal water. The strings, which do not touch the bottom, are sometimes attached to stakes but more generally are attached to rafts (Pinchot, 1973). This method has a number of advantages over growth at the sea bottom. The oysters are protected from predators and from silting, and they feed on the suspended food in the entire column of water. The result is faster growth, rounder shape and superior flavour. The suspension culture technique has long been used in Europe to raise mussels.

The farming of fish in the sea is more difficult than the farming of bivalves. First, the fish, being motile, must be held in ponds. Secondly, the salt water species breed only at sea. This means that the fry have to be caught where and when they occur naturally. Often the supply is not adequate (Holt, 1969; Pinchot, 1973). In spite of such handicaps pond farming is remarkably productive.

Lagoons of atolls are also used for marine fish farming. The fish are protected from predators and harvesting is easier. There are hundreds of coral atolls in the Pacific and Indian Oceans rich in nutrients that support fish life. The simple procedure used is to leave the passage between the lagoon and ocean open so that new species drift into the lagoon on their own. The practice follows the principle of ecology by working with nature to establish balanced, stable communities rather than by supporting large single crops artificially (Holt, 1969; Pinchot, 1973).

Freshwater Farming

Husbandry of aquatic organisms, though a novelty to Africa, has been practiced through the ages. Oyster culture, for instance, thrived in ancient Rome and Gaul. There are earlier, less certain reports of artificial propagation of fish; the legendary Chinese croesus, Fan-Li, of the fifth century B.C., is said to have reared carps in ponds. Although the description of their arrangement is reminiscent of the legendary well-filled system of ancient Chinese social organization, its authenticity is not established. It has been speculated that aquaculture may have even more remote roots in the highly organized ancient water-oriented civilizations of the Near East, in which fish were an important dietary component (Bardach *et al*, 1972).

Aquaculture is by no means restricted to food production. Sport fishermen have for centuries relied on hatcheries to supplement wild stocks and will increasingly do so in the future as recreational needs among developed nations grow in the face of increasing environmental degradation. Bait organisms are cultured for both sport and commercial purposes. Propagation of ornamental fish and plants constitutes an important industry in some areas. Goldfish (*Carassius auratus*) and other species are commercially reared for use as laboratory animals (Bardach *et al* {*op. cit.*}) Aquaculture also contributes to human nutrition through the production of unicellular algae for use in animal feeds. Human and other animal waste is sometimes used in this process in a manner that is ecologically sound and, under certain conditions, perhaps less costly than traditional sewage disposal methods.

Freshwater aquaculture involves a complete control of stocking which is achieved through the use of artificial enclosures so constructed as to preclude the entry of wild fish. Earthen ponds are the oldest and most common of such enclosures. Less common are enclosures constructed of either cement or wood. Floating net cages are becoming increasingly popular in recent years. Another method that merits special mention is raft culture of sessile invertebrates and macroscopic algae. High productivity is achieved by feeding the stock directly.

Bardach, *et al.* {*op. cit.*}) reported that only few species of African food fish have been cultured, even experimentally. There is, infact, no record of native tradition of aquaculture in Alrica south of the Sahara, even though the African freshwater fish

fauna is very large and diverse, reaching an apex of complexity in the Stanley Pool of the Congo River, which reportedly contains more species of fish than any other body of freshwater in the world. Fish culture in Africa as currently practiced was largely initiated by Europeans who, probably, for reasons of familiarity, have concentrated on exotic species, plus the easy-to-breed members of the genus *Tilapia* (Family: Cichlidae). A few of the native fishes other than *Tilapia* sp. have been cultured, in some cases with good results.

Fish Farming in Ghana

Fish constitutes about 55% of human animal protein intake in Ghana (Nyanteng, 1981). According to FAO's estimate (FAO, 1990) the sources of fish supply in Ghana are marine (85.4%), inland fishery (14.5%), and aquaculture (0.01%). There is extensive exploitation of the marine fishes, and some such as *Sardinella* species are already over-exploited. The Volta lake which contributes 74.6% of inland fish harvest is approaching its maximum yield level at the current rate of 35000 to 45000 tons year⁻¹ (FAO, *op. cit.*)

The need to supplement fish production through fish culture was recognized about four decades ago. In 1953, the Fisheries Department (Ministry of Agriculture) started building earth ponds in the northern part of the country in order to raise fish seed for the stocking of dams in an experimental but extensive fish culture programme (Balarin, 1988).

There are at present over 120ha of government and private fish ponds in the country with an estimated production level of about 325 tonnes year⁻¹ (Denyoh, 1985). Owusu-Frimpong (1989) recorded a total of 136 earth ponds with total surface area of 46.43ha in 24 fish farms in southern Ghana. The sizes of the ponds in the individual farms ranged from 0.03ha to 0.84ha. Tilapias and catfishes were the most commonly cultured fish species. These were cultured in both monoculture and polyculture systems in 87.5% of the fish farms. Pond fertilization and supplementary feeding, respectively, were carried out by 83.3% and 79.2% of the farmers. Fertilizer application which is necessary to enhance the natural productivity of ponds was done on one or more occasions in the life of the fish pond. Most (about 80%) of the farmers used organic fertilizers including poultry manure, cattle manure, sheep

manure and pig manure, with the poultry manure being the most popular. Owusu-Frimpong (1989) estimated the rate of application of the fertilizers as 0.07 - 1.46 tonnes hectare⁻¹ year⁻¹ with an average of 0.63 tonnes hectare⁻¹ year⁻¹ compared to the recommended rate in the tropics of 10 - 30 tonnes hectare⁻¹ year⁻¹ (Smith, 1985). The average fish yield was estimated at 1.07 tonnes hectare⁻¹ year⁻¹ by Owusu-Frimpong (*op. cit.*) He stated that field yield was influenced by several constraints including the management of the ponds, high cost of capital, improper pond construction, unavailability of water at critical times, inadequate fish seed, lack of stock improvement, inadequate feeding, escape of fish, predators, excessive aquatic vegetation, inadequate extension services, and, poor fish yield and marketing arrangements.

Objectives of the Research Programme

Knowledge of the population diversity of microbial organisms and their relation to organisms in the fish pond ecosystem is very important. This knowledge makes possible the prediction of the rate of decomposition and the types of nutrient cycling possible in the pond. It also offers the chance to predict the possible fish and human diseases that could break out.

This work was carried out to investigate:

- (a) the bacterial flora of selected fish farms in different regions in the country
- (b) the bacterial flora of fertilizers and feed introduced into the fish ponds
- (c) the comparative bacterial populations of the different fish ponds
- (d) the effect of fertilizer on bacterial populations of the fish ponds
- (e) the bacterial populations at different levels of sewage treatment plant being used for commercial fish farming
- (f) the bacterial flora of bodies of fish of the fish ponds, and
- (g) the health status of humans working on fish farms which use sewage water.

CHAPTER TWO

MATERIALS AND GENERAL METHODS

I. MATERIALS

A. Sampling Sites

Fish farms used in this study were ponds being used for commercial purposes, and which retained water throughout the year. They were drainable and had well conditioned dykes and were fertilized with only one type of fertilizer. Sixteen fish farms in all were selected: nine in the Ashanti Region, four in the Eastern Region and three in the Greater Accra Region. Except where otherwise indicated, the ponds were stocked with both catfish and tilapia together.

i. Aduabenba Farms

The farm is located at New Dedeesua in the Bosomtwi Kwanwoma District of the Ashanti Region. There were four ponds of an average size of 100 x 70m. The ponds were fertilized with cow manure, and the fish were fed on groundnut bran and wheat bran.

ii. Agyeman Farms

The farm is located at Asotwe-Ejisu in the Ejisu-Juaben District in the Ashanti region. There were three ponds each measuring 60 x 60m. The ponds were fertilized with poultry manure, and the fish were fed on corn chaff, groundnut bran and rice bran.

iii. Aheto Farms

Aheto farm is located at Ashaiman in the Tema District of the Greater Accra Region. There were five ponds each measuring 80 x 60m. The ponds were fertilized with inorganic fertilizer and the fish were given rice bran.

iv. Akuse Kpong Farms

The Kpong farm is located at Akuse in the Manya Krobo District of the Eastern Region. The ponds served as sewage treatment ponds for the township as well as a commercial fish farm (Plate 1a and 1b). There were seven ponds - three pairs of ponds namely, Akuse I, Akuse II and Akuse III, and a single isolated pond Akuse IV. Each pond measured 100 x 100m. All ponds were stocked with tilapia only. Corn chaff was occasionally given as supplementary feed.



Plate 1a



Plate 1b

Plate 1a Point of discharge of sewage into the Akuse I - IV ponds.

Plate 1b Fishermen fishing in the Akuse II pond.

v. ARDEC Station

The Aquaculture Research Development Centre (ARDEC) located at Akosombo in the Asuogyaman District of the Eastern Region belongs to the Water Research Institute of the Council for Scientific and Industrial Research. Two ponds were selected and were labelled as ARDEC 3 and ARDEC 20. They were all stocked with tilapia only. Each pond measured 0.5 hectare. Hen coop was constructed directly above ARDEC 20 so that the droppings of the poultry fell into the ponds (Plate 2). This served as the source of food for the fish stocked in the pond. Fish in ARDEC 3 were fed with wheat bran.



Plate 2 ARDEC 20 pond showing hen coop from which droppings of poultry fall directly into pond.

vi. Asare Farms

The farm is located at Patasi, a suburb of Kumasi in the Ashanti Region. There were 11 ponds each measuring 50 x 20m. The ponds were fertilized with poultry manure and the fish given groundnut bran and kitchen waste.

vis. Boadi Farms

The farm is located at Ahensan-Asokore in the Sekyere-East District of the Ashanti region. There were five ponds each measuring 120 x 100m. The ponds were fertilized with pig manure (Plate 3), and the fish given groundnut bran and rice bran.



Plate 3 Piggery house standing close to Boadi Farms pond. Droppings of pigs are washed daily into pond.

viii. Boafaem Farms

The farm is located at Ahodwo a suburb of Kumasi in the Ashanti Region. There were eight ponds each measuring 40 x 30m. Blood meal was used to fertilize the ponds and the fish given groundnut bran.

ix. Boateng Farms

The farm is located at Ofoase-kokoben in the Amansie East District of the Ashanti Region. There were three ponds, each measuring 60 x 60m. The fish were given kitchen waste and groundnut bran and the ponds were fertilized with cow manure.

x. Frimpomg Farms

The farm is located at Kunsun in the Ahafo Ano South District of the Ashanti Region. There were six ponds each measuring 100 x 80m. The ponds were fertilized

with poultry manure, and the fish fed on groundnut bran, rice bran and brewery spent grain.

xi. K K Farms

The farm is located at Nkawie Panyin in the Nkawie District of the Ashanti Region. There were five, 40 x 30m, ponds. Pig manure was used as manure and the fish fed on groundnut bran.

xii. Kpong Head Pond.

This is a dam constructed on the lower Volta river at Kpong, a town in the Manya Krobo District of the Eastern Region. The dam was constructed to supply water to the eastern part of Accra and the Eastern Region. This served as an open system of fish culture.

xiii. Pacific Farms

This is located at Lashibi in the Tema District of the Greater Accra Region. There were nine ponds each measuring 90 x 60m. The ponds were fertilized with pig manure and the fish given wheat bran.

xiv. Sagoe Farms

This farm is located at Brofoyeduru in the Kumasi District of the Ashanti Region. There were four ponds each measuring 100 x 80m. The ponds received inorganic fertilizer. The fish were fed on groundnut bran and rice bran.

xv. Volta River

The Volta River extends from the northern part of the country to the southern part covering an area of about 8482km² or 36% of the surface area of Ghana. For this study a sampling site was selected at Akosombo, a landing site for fishermen and close to the ARDEC station. This served as an open system of fish culture.

xvi. Weija Dam

The Weija dam was constructed at Weija a town in the Ga District of the Greater Accra Region. It was constructed to provide water for the western parts of Accra. It also served as an open system of fish culture (Plate 4).



Plate 4 Landing site at New Galilea of the Weija Dam.

B. Reference Bacterial Strains:

Eight pathogenic bacterial strains, viz. *Pseudomonas* sp. KI-MTC-001K, *Shigella* sp. KI-MTC-002K, *Enterobacter* sp. KI-MTC-003K, *Klebsiella* sp. KI-MTC-004K, *Citrobacter* sp. KI-MTC-005K, *Proteus* sp. KI-MTC-006K, *Salmonella* sp. KI-MTC-007K, and *Vibrio parahaemolyticus* KI-MTC-008K were supplied by the Microbiology and Tumourbiology Centre of the Karolinska Institute, Stockholm, Sweden to be used for this study.

The Public Health and Reference Laboratory, Korle Bu Teaching Hospital, Accra, also supplied the following bacterial strains which were used as reference strains in the PhP Method of bacterial typing; *Bacteriodes* sp. JA001, *Corynebacterium* sp. JA002, *Flavobacterium* sp. JA003, *Proteus* sp. JA004, *Pseudomonas* sp. JA005, *Salmonella* sp. JA006, *Staphylococcus* sp. JA007, *Streptococcus* sp. JA008, *Enterobacter* sp. JA009, *E. coli* JA010, *Aeromonas* sp. JA011, *Campylobacter* sp. JA012, *Citrobacter* sp. JA013, *Serratia* sp. JA014, *Klebsiella* sp. JA015, *Micrococcus* sp. JA016, *Bacillus* sp. JA017 and *Edwardsiella* sp. JA018.

II. GENERAL METHODS

A. Sampling for Bacteriological Study

Samples of water and sediment of the ponds and samples of the fishes were taken once every month from September 1996 to May 1999. The water and sediment samples were taken on the same day.

1. Sampling of Water and Sediment

Three locations were selected for collection of water and sediment samples for each pond: (a) area close to the point where water entered the pond, (b) the centre of the pond, and (c) the area close to the point where water drained off from the pond. Samples of the sediment were taken at the site where the water samples were collected. The sample containers were labelled appropriately indicating the type of sample, sampling station, and, date and time of sampling.

Sampling of Water

Water samples were taken at a depth of about 25cm with wide-mouthed 300ml borosilicate glass sample bottles. The stopper of the bottle was removed at the collection site and the bottle plunged quickly after that into the water. It was allowed to fill up to the neck and then brought out of the water and stoppered. The filled bottles were taken to the laboratory in a thermo-insulated container set at 4°C.

Sampling of Sediment

A 'bottom-grab' was used to collect the sediment samples. The contraption has jaws at the bottom that were manipulated to open after it had been lowered into the pond to scoop the sediment without disturbing the layers, thus, it lifted up the deposit with the top layer uppermost. After the 'bottom-grab' had been pulled up, the seal of the opening at the top was pulled out and the topmost layer of deposit was carefully taken with a sterile spatula and put in a sterile specimen tube.

2. Sampling of the Fish

Cast net was used with the assistance of the fish farmers and in some cases personnel from the Fisheries Department of the Ministry of Agriculture to collect fish samples from the various ponds. For each pond five live tilapias only were randomly selected

from the catch at each sampling time. The fish were placed in labelled sterile polypropylene bags and their condition at the time of collection noted.

Sterile cotton bud was used to take a swab from the surface of the fish immediately upon collection from the pond. The cotton bud was placed immediately in 5ml sterile peptone water in screw-capped test tube, labelled and kept at 4°C and transported to the laboratory. The fish were kept at 4°C in labelled polypropylene bags and transported to the laboratory within three hours. In cases where the distance was too far to cover in three hours, the fish was transported live to the laboratory in labelled polypropylene bags containing water from the pond.

In the laboratory each fish was rinsed with de-ionized water for about two minutes and the surface of the fish decontaminated by dipping it in ethyl alcohol and flamed. The fish was aseptically dissected and parts of the gills, gut and muscle were taken for analysis. Blood sample was also collected using a sterile syringe. Each tissue was homogenized separately in a blender in sterile phosphate buffered saline PBS of pH 7.2 to achieve a 10% w/v suspension of fish.

B. Methods of Sterilization

All media and plastic bottles and containers were sterilized by autoclaving at 1.1 kg cm⁻² steam pressure at 121°C for 15 minutes, using the model Wolf Sterilmatic, except otherwise stated.

Glassware were washed with detergent and rinsed in several changes of tapwater and finally with distilled water. The glassware were dried in Gallenkamp Drying Cabinet set at 60°C.

Dried Petri dishes were fitted with lids and packed into metal cannisters. Pipettes were grouped according to capacities and put into separate metal cannisters. Other glassware were wrapped in aluminium foil. All the glassware were sterilized in hot air oven, Charles Hearson & Co Ltd. model, at 160°C for 3 hours holding time. They were allowed to completely cool before removal.

The walls and benches of the inner chamber of the inoculating room were wiped with methylated spirit and the room was then sprayed with a solution of 5% phenol in 70% alcohol before the inoculating chamber was used. Incubating chambers were similarly sterilized.

The inoculating room was sterilized by cleaning the floor with antiseptic (dettol) solution and the room sprayed with 1% antiseptic (dettol) solution, after which the ultra-violet light was turned on for at least one hour just before the room was used. Inoculating loops were dipped into 95% ethanol and flamed until red hot.

C. Media for Culturing the Bacteria

1. Preparations with Dehydrated Media

Commercially available media, prepared according to the manufacturer's recommendations were used wherever possible. Media not commercially available were prepared according to directions found in the pertinent literature (Speck, 1976; Todd-Sanford, 1969).

Bismuth Sulphite Agar [Difco]

An amount of 52g of the powder was suspended in one litre of distilled water or deionized water and boiled for 1 - 2 minutes to dissolve. The precipitate was evenly dispersed by gentle agitation and the medium dispensed in aliquots of 15ml into Petri dishes.

Blood Agar Base [Oxoid]

An amount of 40g of the dehydrated Blood Agar Base [Oxoid] was dissolved in one litre of distilled water and heated to mix completely. The medium was autoclaved and allowed to cool to 40 - 50°C. Sterile defibrinated rabbit blood (7%) was aseptically added to the sterile Blood agar base and the mixture stirred gently to mix avoiding formation of air bubbles. The blood agar was dispensed aseptically in aliquots of 15ml into sterile Petri dishes.

Brain-Heart Infusion (BHI) Broth [bioMerieux]

An amount of 37g of the powder was dissolved in one litre of distilled water and aliquots of 50ml were dispensed into 250ml Erlenmeyer flasks and autoclaved. For the cultivation of anaerobes, the medium was used on the same day of preparation.

Brilliant Green Agar [Oxoid]

An amount of 50g of the powder was suspended in one litre of distilled water. The medium was heated while stirring until it boiled, and was then autoclaved.

Brilliant Green Bile (2%) Broth [Oxoid]

An amount of 40g of the powder was added to one litre of distilled water. The medium was mixed well by stirring and dispensed into test tubes containing inverted Durham's tubes. The test tubes were fitted with screw caps and autoclaved.

Cereus Selective Agar [Merck]

An amount of 43g of dehydrated Cereus selective agar base was suspended in 900 ml of demineralized water and heated in a boiling water bath to mix thoroughly. The medium was autoclaved, allowed to cool to about 50°C and mixed with 100 ml of sterile egg-yolk emulsion [Merck, cat. no. 1.03784] and 0.1 0.001g/l of polymyxin B sulphate. The medium was then poured into Petri dishes and allowed to harden.

Desoxycholate Citrate Agar (DCA) [Bacto]

An amount of 45g of the dehydrated medium was dissolved in one litre of distilled water and boiled for 20 minutes to dissolve completely. Aliquots of 20 ml were poured into sterile Petri dishes.

EC Medium [Difco]

An amount of 37g of the dehydrated medium was suspended in one litre of distilled or deionized water and warmed to dissolve completely. The medium was dispensed in aliquots of 5 ml into screw capped test tubes containing inverted Durham's tubes and autoclaved.

Eosin Methylene Blue Agar [Oxoid]

One tablet of the Eosin Methylene Blue agar was dissolved in 5 ml of distilled and autoclaved. The medium was cooled to 60°C and agitated in order to oxidize the methylene blue.

KF Streptococcus Agar [Oxoid]

An amount of 76.4g of the dehydrated medium was suspended in one litre of distilled water and heated while agitating and allowed to boil for 15 minutes. The medium was allowed to cool to 50°C and 1 ml of sterile aqueous 1% solution of 2,3,5-Triphenyl-tetrazolium chloride added aseptically. The medium was sterilized by autoclaving and aliquots of 15 ml poured into Petri dishes.

Lactose Broth [bioMerieux]

An amount of 13g of the powder was dissolved in one litre of distilled water. For double strength solution, 26g of the powder was dissolved in one litre of distilled water. The solutions were dispensed in aliquots of 10 ml into screw capped test tubes containing inverted Durham's test tubes and autoclaved.

Lauryl Tryptose Broth [Oxoid]

An amount of 35.6g of the powder was added to one litre of distilled water and dispensed in aliquots of 10ml into screw capped test tubes containing inverted Durham's tubes and autoclaved.

Litmus Milk [Oxoid]

One litre of distilled water was gradually added to 100g of the powder while stirring the mixture. The suspension was strained through a muslin and aliquots of 10ml of the filtrate were put in screw capped test tubes and autoclaved.

MacConkey Agar (MAC) [bioMerieux]

An amount of 50g of the dehydrated medium was dissolved in one litre of distilled water. This was autoclaved and aliquots of 20ml were dispensed into sterile Petri dishes.

MacConkey Broth [bioMerieux]

An amount of 35g of the powder was dissolved in one litre of distilled water to prepare a standard concentration of the medium while double strength medium was prepared by dissolving 70g of the powder in one litre of distilled water. The solutions prepared were dispensed in 10ml quantities into screw capped test tubes. An inverted Durham's tube was placed in each test tube and the tubes partially closed and autoclaved.

Mannitol Selenite Broth Base [Oxoid]

An amount of 19g of the powder was added to one litre of distilled water to which 4g of sodium biselenite [Oxoid L121] had been added. The medium was warmed while stirring to dissolve the powder. The medium was then poured into screw capped test tubes to a depth of five centimetres. The medium was then sterilized by boiling in a water bath for 15 minutes.

M.R.V.P. Medium [Oxoid]

An amount of 15g of the powder was added to one litre of distilled water and mixed well by stirring. The medium was dispensed in aliquots of 5 ml into screw capped test tubes and autoclaved.

Nutrient Agar (NA) [Sigma]

An amount of 31 g of the dehydrated medium was dissolved in one litre of distilled water. This was sterilized by autoclaving and aliquots of 20ml were then dispensed into sterile Petri dishes, while the medium was still molten.

Nutrient Broth [Oxoid]

An amount of 13g of the powder was dissolved in one litre of distilled water. The suspension was mixed well and distributed into aliquots of 50ml into 250ml Erlenmeyer flasks and autoclaved.

SS Agar [Difco]

An amount of 60g of the powder was suspended in one litre of distilled water and heated to boil to dissolve the powder completely. Aliquots of 20ml of the medium

were poured into Petri dishes which were then partially opened for about two hours to allow the medium to dry.

Standard Plate Count Agar (SPCA) [Oxoid]

An amount of 23.5g of the powder was suspended in one litre of distilled water. The suspension was mixed thoroughly by stirring and heated while agitating and allowed to boil for one minute. The medium was autoclaved, cooled to 45 - 50°C and dispensed in aliquots of 20ml into Petri dishes. The sterilized medium was used within 3 hours.

Staphylococcus Medium No. 110 [Oxoid]

An amount of 150g of the powder was suspended in one litre of distilled water. The mixture was boiled to dissolve the powder and autoclaved.

Thiosulphate Citrate Bile Salt (TCBS) Agar [Oxoid]

An amount of 88g of the dehydrated medium was dissolved in one litre of distilled water and boiled to dissolve completely. Aliquots of 20 ml were poured into sterile Petri dishes

Triple Sugar Iron (TSI) [bioMerieux]

An amount of 59.4g of the powder was suspended in one litre of distilled water and mixed thoroughly by stirring. It was then heated to boil for 1 - 2 minutes and dispensed into tubes. The medium was autoclaved at 118°C for 15 minutes. The tubes with medium were inclined while cooling to obtain slants with butts, with the butt length at least twice the diameter of the tube.

Trypticase Soy Agar [Oxoid]

An amount of 30g of the powder was dissolved in one litre of distilled water. This was autoclaved and aliquots of 20ml were dispensed into sterile Petri dishes.

Tryptone Water [Oxoid]

An amount of 15g of the powder was added to one litre of distilled water. The medium was mixed well by stirring and dispensed in aliquots of 5 ml into screw capped test tubes and autoclaved.

2. Preparation of Blood Agar

Blood agar was prepared by mixing sterile blood from rabbit obtained as described below and sterile blood agar base (Oxoid). The blood agar base was previously sterilized at 121°C for 15 minutes and kept liquefied at a temperature between 47°C and 50°C in a water bath. Half a millilitre of the oxalated blood was placed in the centre of a sterile Petri dish using sterile pipette. Sterile blood agar base liquefied and kept at between 47°C and 50°C was added to fill the Petri dish. They were mixed thoroughly by rotating the plate and the mixture then allowed to solidify.

To prepare the media in test tubes, aliquots of 5.0c.c of blood agar base were poured into test tubes and kept at 47°C to 50°C in a water bath. The oxalated blood (0.25cc.) was aseptically added to each tube and rotated vigorously to mix. The test tubes were then placed in an inclined position to obtain slants as the medium solidified.

The rabbit was placed on a board and lightly anesthetized with chloroform. The skin over its heart was shaven and the exposed skin painted with iodine to sterilize the area.

A 5.0c.c Luer syringe with needle previously sterilized in the dry heat oven at 170°C for 2 hours was used to withdraw 5.0c.c of blood from the heart. The blood was put in a 100c.c wide mouth bottle and 10 drops of 20% solution of sodium oxalate were added and then sterilized at 170°C for two hours. The bottle was shaken vigorously to oxalate the blood.

3. Preparation of Neomycin Blood Agar

A stock solution of 70,000 [j.g/ml neomycin was prepared from 0.5g neomycin sulphate (containing 0.35g neomycin base) in 5 ml of sterile distilled water. A working solution of 17,500 [j.g/ml was prepared from a mixture of 2 ml of the stock solution and 6 ml of sterile distilled water.

One millilitre of the working neomycin sulphate solution was added to 250 ml blood agar base to give a concentration of 70 [j.g/ml. The medium was thoroughly mixed and poured into sterile Petri dishes.

4. Preparation of Sodium Azide Broth (Hannay and Norton, 1947)

Sodium azide broth was prepared with the following ingredients

Peptone	10.0g
Sodium chloride	5.0g
Dipotassium hydrogen phosphate (K_2HPO_4)	5.0g
Potassium dihydrogen phosphate (KH_2PO_4)	2.0g
Glucose	5.0g
Yeast extract	3.0g
Sodium azide	0.25g
Bromocresol purple (1.6% ethanolic solution)	2ml
Distilled water	1L

The pH was adjusted to 7.3 by adding dilute sodium hydroxide solution. It was sterilized by autoclaving.

D. Quantitative Estimation of Bacterial Flora

1. Heterotrophic Bacterial Density Determination

Viable heterotrophic bacterial populations were determined for all the water and sediment samples from each sampling area using the heterotrophic plate count procedure (APHA, 1995) at $30 \pm 0.5^\circ C$ and $37 \pm 0.5^\circ C$. The Standard Plate Count Agar (Oxoid) (SPCA) was used. Serial dilutions of the water and sediment samples were separately made using sterile Phosphate buffer solution. Plate counts were made using appropriate dilutions of each sample. Standard volume of the sample was mixed with liquefied ($45^\circ C$) SPCA, in a sterile Petri dish and the mixture allowed to solidify. One set of Petri dishes was incubated at $30^\circ C$ and another set at $37^\circ C$ for 48 hours. Bacterial colonies which developed were counted using the Karl Kolb Colony Counter (Model D-6072), and the value obtained was converted to number of Colony Forming Units per millilitre of pond water.

2. Total Coliform Counts

The standard Most Probable Number (MPN) method was employed (APHA, *op. cit.*) to determine the number of total coliform present. The presumptive test involved a series of five subsets of fermentation tubes each containing aliquots of 10ml of sterile MacConkey broth. Each subset contained three tubes, and each tube had an inverted Durham tube to collect any gas produced by fermentation. The five subsets were inoculated with water inocula sizes of 10, 1.0, 0.1, 0.01 and 0.001ml, respectively. After 48 hours of incubation at $37 \pm 0.5^{\circ}\text{C}$, the tubes were evaluated for gas production. Gas production and/or acid formation was presumptive evidence of coliforms. The number of positive and negative tubes in each subset was tallied and the set of numbers was applied to a statistical table. From that standard, the most probable concentration of coliform was estimated as MPN ml⁻¹.

3. Faecal Coliform Counts

The Most Probable Number (MPN) method was used. Aliquots of 5ml of sterile EC medium (Difco) in boiling tubes containing Durham's tubes were separately inoculated with contents of all positive reaction tubes of the total coliform MPN test. Each tube was inoculated with three drops of the cultures carried by a 3mm-diameter loop. The tubes were placed upright in a water bath set at $44 \pm 0.5^{\circ}\text{C}$ for 24 hours. All tubes which showed production of gas and growth within 24 hours were considered positive for faecal coliform, and the MPN value calculated.

4. Faecal streptococci Counts

The Most Probable Number (MPN) method was employed using sterile Sodium Azide broth. Aliquots of 10ml of double and single strengths of the medium in boiling tubes were inoculated with different volumes of the water sample as described in 2 above. The tubes were incubated at $37 \pm 0.5^{\circ}\text{C}$ for 48 hours. Tubes in which acid was formed after the 48 hours were confirmed by inoculating fresh sterile Sodium Azide broth in tubes with their contents. Tubes showing acid formation after 48 hours were regarded as positive and the MPN value was calculated.

E. Isolation and Identification of Bacteria

1. Isolation

A total of 40 colonies were selected at random from the culture plates of each sample and sub-cultured. Twenty colonies were picked from the Blood Agar plates. The other twenty were picked from the SS Agar, TCBS Agar and Neomycin Blood Agar plates.

2. Determination of Characteristics of Isolates

The tests outlined below were carried out on each isolate following the procedures described by Bailey and Scott (Finegold and Baron, 1986) and Cheesbrough (1994) to enable an identification to the generic and species levels with the aid of the Bergey's Manual of Determinative Bacteriology (Holt *et al*, 1994).

Colony Characteristics

The colony size, margin pattern, profile and pigmentation were recorded for each isolate.

Morphology of Isolates

The morphological characteristics considered were shape, size and arrangement of cells, presence or absence of endospores, the position of endospores, if present, and presence or absence of capsules.

Gram Stain Reaction

An air dried smear of a pure colony of the isolate on a clean slide was fixed by gently passing it over the flame of a spirit lamp and stained as follows: the slide was flooded with crystal violet solution for 10 - 30 seconds. The slide was then rinsed with tapwater, shaking off all excess fluid. The slide was again flooded with Lugol's iodine solution and kept on the surface without drying for twice the time allowed for the crystal violet stain. The slide was again rinsed with tapwater, shaking off all excess fluid.

The smear was then decolorized with absolute ethanol for 10 seconds and rinsed under running tap until no more blue dye came off the smear. Carbon fuschin was

used to counterstain the smear for 30 seconds. The slide was rinsed with tapwater and the slide allowed to dry. The stained smear was then examined microscopically under oil immersion.

Gram positive cells stained blue/violet, while Gram negative cells stained red/pink.

Endospore Staining

Malachite green staining procedure was used. A thin air-dried smear on a clean slide, was fixed and flooded with hot 5% Malachite green solution and left for five minutes. It was then washed with distilled water and counter-stained with 0.5% aqueous Safranin solution for 30 seconds, rinsed with distilled water and allowed to dry in air before examining microscopically under oil immersion.

The endospore stained green and the vegetative part of the cell stained red.

Indole Test (Kovae's Method)

Half a milliliter of Kovae's reagent was added to a 2-day old tryptone broth culture and gently shaken. A pink colour in a ring was developed around the interface between the broth and the alcoholic reagent in the case of a positive reaction.

Methyl red (MR) and Voges-Proskauer (VP) Tests

The same substrate broth, MR/VP broth, was used for both tests. The bacterium was inoculated below the surface of the medium in a tube (5 ml per tube) and incubated at 35 - 37°C for 5 days. The contents of the tube was divided into 2.5 ml each for the methyl red and Voges-Proskauer tests.

To 2.5 ml of suspension, 0.6 ml (6 drops) of VP reagent A (alpha-naphtol) was added, followed by addition of 0.2 ml of VP reagent B (40% potassium hydroxide). The tube was shaken gently and allowed to stand for 15 minutes. The presence of pink colour in the medium was indicative of positive test. Negative test appeared colourless or yellow.

The remaining 2.5 ml of substrate was simultaneously tested for acidity by adding 0.5 ml Methyl red reagent. A red colour was indicative of positive test. For a negative test the indicator changed to yellow.

Citrate Utilization Test

The surface of an agar slant of Simmons' Citrate agar was inoculated with the bacterium. The tube was fitted with a loose cap and incubated up to 4 days at 35 - 37°C. Growth of the organism on the slant, with reversion of the colour indicator from green to blue or turquoise blue was evidence of a positive test. Luxuriant growth on the slant without the blue colour was also taken as positive test.

Oxidase Test

A disc of filter paper was placed into a sterile plastic disposable Petri dish and moistened with several drops of freshly prepared 1% aqueous solution of tetramethyl-p-phenylene diamine dihydrochloride. A small portion of the colony to be tested (not more than 24 hours old) was removed with a wooden stick and smeared on the moistened filter paper. Positive test showed a change to blue or purple colour within 10 minutes.

Cell Motility

This was done by growing the bacterium in a semisolid medium (SIM). The medium was prepared as butt 5 cm deep and was inoculated by stabbing vertically in the centre with a straight wire carrying the inoculum to a depth of approximately 2 cm.

After overnight incubation, motility was evident as a hazy growth extending into the agar from the stab line. With non-motile bacteria, growth was limited to the line of inoculation.

Nitrate Reduction

Inoculated nitrate broth in tubes was incubated at 37°C overnight. To the contents of each tube were added a few drops of 1% hydrochloric acid, 0.5 ml each of 0.2% solution of sulphonilamide and 0.1% N-naphthol ethylene diamine hydrochloride. Nitrate reduction was indicated by a pink colour development.

To detect further reduction of nitrite to nitrogen or hydroxylamine, a small amount of zinc dust was then added. There was no colour change when nitrite reduction occurred, while a pink colour developed following inability to reduce nitrite.

Catalase Test

A bit of the colony of each isolate was put in a drop of distilled water on a clean slide. A drop of hydrogen peroxide was then added to the suspension. A positive reaction was shown by the formation of bubbles.

Production of Hydrogen sulphide

Triple Sugar Iron (TSI) agar slants in screw capped test tubes were inoculated with each of the isolates and incubated at 37°C for 24 - 48 hours. There was blackening of the medium in the case of isolates which produced sulphide.

Gelatin Hydrolysis

Tubes of nutrient gelatin were inoculated by stabbing with a straight platinum wire carrying the bacterium. The tubes were incubated at 37°C for seven days, after which they were transferred to the refrigerator overnight. Gelatin hydrolysis had taken place in tubes in which the medium remained watery after the overnight refrigeration.

Starch Hydrolysis

Starch agar plates were inoculated and incubated for two days at 37°C. The plates were then flooded with iodine solution. There was a white hallow around cultures which had digested the starch.

Urease Test

Urea broth in tubes were inoculated with the different isolates and incubated at 37°C for two days. A change of colour from yellow to red indicated a positive reaction.

Sugar Utilization

Tubes of peptone water containing a sugar component and Andrade's indicator and inverted Durham's tubes were inoculated and incubated at 37°C for three days. The medium changed to red when acid was formed while gas produced by the bacterium was trapped in the Durham's tube. The sugars tested were fructose, glucose and mannitol.

3. Selective Culture of Bacterial isolated

The fish samples collected from each pond and water samples from the respective ponds were separately used to inoculate different bacteriological media which were selected to ensure the recovery of a wide variety of bacteria present. Selective media were used to increase the chance of isolating specific bacterial species which might be present in small numbers were:

BISMUTH SULPHIDE AGAR (BiS) - specifically to detect *Salmonella typhi*.

BLOOD AGAR (BA) general medium to detect more fastidious organisms as well as many common organisms.

BRILLIANT GREEN AGAR - for isolating *Salmonella*, other than *S. typhosa*.

CENTRIMIDE AGAR (PA) selective medium for members of the genus *Pseudomonas*.

EC MEDIUM for differentiating and enumerating coliforms.

EOSIN METHYLENE BLUE AGAR for differentiating *Escherichia coli* and *Enterobacter aerogenes*.

KF STREPTOCOCCUS AGAR - for isolating and enumerating *Streptococci* (*Enterococci*).

LACTOSE BROTH - for isolating coliform organisms.

LITMUS MILK MEDIUM for diagnostic tests involving lactose fermentation, and digestion and coagulation of casein, including the typical stormy clots produced by *Clostridium perfringes*.

MacCONKEY AGAR (MAC) - for detecting Gram negative bacteria.

MacCONKEY BROTH - for isolating and enumerating coliforms.

MANNITOL SELENITE BROTH - for the enrichment of Salmonellae.

SS AGAR - for detecting *Salmonella* and *Shigella* groups.

THIOSULPHATE-CITRATE-BILE SALTS SUCROSE AGAR (TCBS) - selective medium for *Vibrio cholerae* and *Vibrio parahaemolyticus*.

TRIPLE SUGAR IRON (TSI) - for identifying Gram negative enteric bacilli based on the fermentation of dextrose, lactose and sucrose, and, hydrogen sulphide production.

TRYPTICASE SOY AGAR (TSA) - general growth medium.

Forty isolates were randomly selected from plates of each test for the study. Each colony was identified to the generic level and the frequency of occurrence of each

genus in the selected 40 colonies determined. In cases where tissue parts could not produce a total of 40 colonies, all isolates were identified and the frequency based on the total number of colonies.

The selected 40 colonies consisted of (a) 20 colonies selected from all growths appearing on the Blood agar plates, (b) the other 20 from cultured plates of SS agar, TCBS agar, and Neomycin Blood agar.

F. The Phene Plate (PhP) System - Finger Printing of Bacteria in Microplates

1. PhP Suspending Substrate

This consisted of a solution of 0.1% Proteose peptone and 0.011% bromothymol blue in distilled water.

Bromothymol blue stock solution (0.11%)

An amount of 1.1 g of bromothymol blue was dissolved in 90ml of distilled water. Ten milliliters of 1M NaOH were added and stirred until the indicator was completely dissolved and then made up to one litre with distilled water. The solution was autoclaved and stored.

Preparation of the Suspending Substrate

An amount of 100ml of the indicator stock solution was mixed with 900ml of distilled water, and amended as follows for various purposes.

- 1g of Proteose peptone was added to it for general bacterial culture
- 0.5g of Proteose peptone was added to the 1L for *Klebsiella* and *Vibrio* sp. For *Vibrio*, 2% NaCl was also added.
- 2g of Proteose peptone, 0.5g Yeast extract and 5g of NaCl were added for assaying *Staphylococcus* and *Enterococcus*.

The pH of the substrate was adjusted to pH 7.8 - 8.5 and the solution divided into 100 - 200ml portions in capped flasks, autoclaved and stored in the refrigerator until needed.

2. Pre-cultivation of Bacteria

The bacteria to be tested were first pre-cultivated on appropriate agar media such as Blood agar, Brain Heart Infusion agar, Brilliant Green agar, Cereus selective agar, Deoxycholate Citrate agar, Eosin Methylene Blue agar, KF Streptococcus agar, MacConkey agar, Nutrient agar, Standard Plate Count agar, SS agar, Staphylococcus Medium, Triple Sugar Iron. The same pre-cultivation conditions were used for all strains in the test series.

3. Preparation of Bacterial Suspension and Inoculation of Rapid

Screening PhP plates

A multichannel pipette with sterile tips was used to fill all wells in the PhP plate with suspending substrate. Then, 0.320 - 0.375ml of the substrate was dispensed into all eight wells of 'Column 1' in the plate, and 0.150ml into all the other wells. A sterile toothpick was used to remove a single bacterial colony from the agar plate and suspend it in 'Column 1' of row A. With another toothpick another bacterial colony was removed and suspended in 'Column 1' of row B. This was repeated until all the 'Column 1' of all eight rows have been inoculated with different bacterial colonies. The plates were left for at least one hour, after which the bacterial suspensions in the first column were homogenized by gently sucking up and blowing down a couple of times with the aid of the multichannel pipette.

Quantities of 25µl of the bacterial suspensions in the first column were then transferred to all the other wells in each row with the multichannel pipette. Colonies suspected to be anaerobic were covered with sterile paraffin oil.

Each plate was covered by a sterile lid and put in a wet chamber to avoid drying.

4. Incubation of PhP plates

The plates were incubated at 37°C. In order to avoid drying of the plates they were incubated in the wet chambers. The colour of each well was assessed after 16, 40 and 64 hours of incubation.

5. Reading of Test Results

An optical microplate reader connected to a computer with the PhP software was used. Three readings were made, after 16, 40 and 64 hours, respectively. The absorbance was measured at 620nm.

G. Physico-Chemical Parameters of the Pond Water

Physico-chemical parameters of the water from the sampling sites were determined. Water samples for such determination were taken routinely on bi-monthly basis and at the same time that samples were taken for bacteriological studies. Methods employed were as described in the APHA (1995).

1. Temperature

A mercury-in-glass thermometer with calibrations of -10°C to 100°C was used to take the water temperature at each sampling site.

2. Hydrogen-ion concentration (pH)

This was determined with an electrode pH meter, model Piccolo by Hanna HI 1280.

3. Acidity

Samples were collected in borosilicate glass bottles and transported to the laboratory at below 10°C. The titration method was used. Before use, the electrodes and titration vessel were rinsed with distilled water and drained.

An amount of 20 ml of the sample was pipetted into titration flasks and 0.02N sulphuric acid (H₂SO₄) gradually added, 5 ml at a time, until the pH was reduced to pH 4 or less. The electrodes were removed and five drops of 30% H₂O₂ added to the solution and boiled for 2-5 minutes. The temperature of the sample was allowed to drop to room temperature and standard alkali added, 0.05 ml at a time. After each addition, the sample was mixed thoroughly but gently with a magnetic stirrer. This was continued until a constant pH 9 was achieved. Acidity was calculated from the volume of the alkali titrant used, its normality, the normality of the H₂SO₄ and the volume of H₂SO₄ applied. Acidity was calculated from:

$$\text{Acidity, as mg CaCO}_3/\text{L} = \frac{\text{ITA} \times \text{B}}{\text{ml sample}} - (\text{C} \times \text{D} \times 50,000)$$

where,

A = ml NaOH titrant used

B = normality of NaOH

C = ml H₂SO₄ used, and

D = normality of H₂SO₄

4. Alkalinity

The procedure for the determination of acidity as described above was followed substituting standard acid for standard sodium hydroxide (NaOH), and titration done to pH 4.5 or lower.

The alkalinity was calculated from the volume of the standard acid used and its normality, i.e.

$$\text{Alkalinity, mg CaCO}_3/\text{L} = \frac{A \times N \times 50.000}{\text{ml sample}}$$

where,

A = ml standard acid used, and

N = normality of standard acid.

5. Calcium and Magnesium ions

Determinations were made using the flame Atomic Absorption Spectrometric method. Samples were filtered immediately after collection with vacuum filter containing a filter support of plastic, through a pre-washed ungridded 0.45µm-pore-diameter membrane filter. Filtration was done at a pressure of 70 to 130 kPa. After the filtration the sample was acidified to pH 2 with concentrated nitric acid (HNO₃) and analyzed.

Atomic Absorption Spectrometer model Varian AA-1275 was used. The installation of the hollow-cathode lamp, setting of the wavelength dial and slit width, amount of current applied, optimization of wavelength to get the desired energy, installation of suitable burner head, adjustment of flow rate and adjustment of acetylene to value specified were all done according to the manufacturer's operating manual.

Aspiration of a blank consisting of deionized water containing the same concentration of acid in standard and sample, the aspiration of the nebulizer to obtain

maximum response, standardization of the instrument were done according to the procedure as laid out in the APHA (1995),

For the determination of calcium and magnesium ions, 100 ml of the sample was diluted with 10 ml lanthanum solution before being aspirated. The nebulizer was rinsed with aspirating water containing 1.5 ml concentrated HNO₃ l^l. The blank sample was aspirated and the instrument zeroed. The sample was aspirated and the absorbance value recorded.

6. Total Hardness

The Ethylenediaminetetraacetic acid and its sodium salts (EDTA) Titrimetric method was used. An amount of 25 ml of sample was diluted with an equal volume of distilled water in a porcelain casserole. One milliliter of buffer (ammonium chloride, ammonium hydroxide, and magnesium salt of EDTA in distilled water) was added. One drop of Eriochrome Black T indicator was added and standard EDTA titrant slowly added with continuous stirring until the last reddish tinge disappeared. Few drops of the titrant were added at 3 5 seconds interval until the end point of blue solution was obtained. The hardness was calculated as follows (APHA, 1995)

$$\text{Hardness} = \frac{A \times B \times 1000}{\text{ml sample}}$$

where:

A = ml titration for sample

B = mg CaCO₃ equivalent to 1.00 ml EDTA titrant.

7. Chloride Ion

The Argentometric Method was used. One milliliter potassium chromate (K₂Cro₄) indicator solution was added to 100 ml of the water sample and directly titrated with standard silver nitrate (AgNO_a) titrant to a pinkish yellow end point.

A reagent blank value was established by titrating standardized AgNO₃ titrant with a blank of 0.2 to 0.3 ml.

The amount of chloride ion in the sample was calculated based on values for the sample and the blank and the normality of the AgNO₃ used, i.e.

$$\text{mg Cl}^-/\text{L} = \frac{(A - B) \times N \times 35.450}{\text{ml sample}}$$

where,

A = ml titration for sample

B = ml titration for blank, and

N = normality of AgNO_3

8. Phosphate Ion

The Ascorbic Acid Method was employed. Fifty milliliters of the sample to be tested were pipetted into 125-ml Erlenmeyer flask, 0.05 ml (1 drop) of phenolphthalein indicator added and 5N H_2SO_4 was added drop by drop to the red colour solution formed to discharge the colour. Eight milliliters combined reagent were added and mixed thoroughly. After 10 30 minutes the absorbance of each sample was measured at 880nm, using reagent blank as the reference solution.

9. Ammonium Nitrate

The Titrimetric Method was used. To 50 ml of the sample diluted to 500 ml, was added 25 ml of borate buffer solution and the mixture adjusted to pH 9.5 with 6N NaOH.

The distillation apparatus was steamed out with a 500 ml water and 20 ml borate buffer adjusted to pH 9.5. The sample mixture was distilled at a rate of 6 to 10 ml min^{-1} with the tip of the delivery tube dipping into the acid receiving solution. The distillate was collected in a 500 ml Erlenmeyer flask containing 50 ml indicator, boric acid solution.

The ammonia in the distillate was titrated with standard 0.02N H_2SO_4 titrant until a pale lavender colour was obtained. A blank was used in place of the sample.

The ammonium nitrate was calculated using the formula (APHA, *op. cit.*)

$$\text{mg NH}_3\text{-N/L} = \frac{(A - B) \times 280}{\text{ml sample}}$$

where;

A = volume of H_2SO_4 titrated for sample (ml)

B = volume of H_2SO_4 titrated for blank.

10. Nitrate and Nitrite Ions

The Cadmium Reduction Method was employed using the Reduction Column TP-1730 Tudor Scientific Glass Co. and Spectrophotometer. The Column consists of two pieces of tubing joined end to end and packed with Cadmium granules treated with copper sulphate ($CuSO_4$). This method is based on the principle that nitrate (NO_3^-) is reduced almost quantitatively to nitrite (NO_2^-) in the presence of Cadmium.

An amount of 25 ml of sample was added to 75 ml ammonium chloride-EDTA solution and mixed thoroughly. The mixed sample was poured into the column and collected at a rate of 7 to 10 ml min^{-1} . The first 25 ml was discarded and the rest collected in a flask to which 2.0 ml of the colour reagent was immediately added to 50 ml of the collected sample and mixed. The absorbance was measured against a distilled water reagent blank at 543 nm.

Standard solutions of NO_3^- -N and NO_2^- -N solutions were prepared separately in volumes of 0.5, 1.0, 2.0, 5.0 and 10.0 ml and reductions carried out for NO_3^- and NO_2^- . Standard curves were obtained by plotting the absorbance of standards against NO_3^- -N and NO_2^- -N concentrations. Nitrate and nitrite ion concentrations were computed from the standard curves.

11. Sulphate Ion

The Turbidimetric Method was employed. An amount of 100 ml of water sample was measured into a 250-ml Erlenmeyer flask and 20 ml buffer solution added and mixed in a stirring apparatus. The buffer consisted of magnesium chloride, sodium acetate, potassium nitrate and acetic acid in distilled water. A spoonful of barium chloride ($BaCl_2$) was added and stirred at constant speed for 60 seconds. The solution was poured into the absorption cell of a photometer and the Turbidity measured at 5 minutes.

Sulphate concentration in sample was estimated by comparing Turbidity reading with a calibration curve prepared by carrying SO_4 standards through the entire procedure

directly from the calibration curve after subtracting sample absorbance before adding the BaCl₂.

12. Silica

One milliliter of 1 + 1 hydrochloric acid and 2.0 ml ammonium molybdate reagent were added in rapid succession to 50 ml of the water sample. The solution was mixed by inverting the cocked flask six times and letting it stand for 10 minutes, then 2.0 ml oxalic acid solution was added and mixed thoroughly. The presence of yellow colour was read after within two to 15 minutes, counting from the time when the oxalic acid was added. A permanent colour standard for visual determination of silica was prepared using potassium chromate and borax solutions.

13. Dissolved Oxygen

The water sample was collected in a 300-ml bottle and one milliliter manganese sulphate solution added immediately, followed by addition of one milliliter alkali-iodide-azide reagent. The bottle was stoppered carefully to exclude air bubbles and mixed by inverting the bottle a few times. When precipitate formed had settled sufficiently (to approximately half the bottle volume) leaving a clear supernatant above the manganese hydroxide floe, 1.0 ml concentrated H₂SO₄ was added. The bottle was restoppered and the content mixed by inverting several times until dissolution was completed.

Exactly 201 ml of the prepared solution in the bottle was pipetted into an Erlenmeyer flask. While constantly swirling the flask, the sample was titrated with 0.025M Na₂S₂O₃ solution to a pale straw colour. A few drops of starch solution were added and titration continued to first disappearance of the blue colour. The number of drops of the titrant added was used to calculate the amount of dissolved oxygen present in the water exposed to water-saturated air at atmospheric pressure (101.3 kPa).

14. Biochemical Oxygen Demand (BOD)

An amount of 250 ml special BOD bottles were over-filled with the sample at collection point and 1 ml each of phosphate buffer, magnesium sulphate, calcium chloride, and ferric chloride solutions per litre of water added.

Samples of caustic alkalinity or acidity were neutralized to pH 6.5 - 7.5 with a solution of H₂SO₄ or NaOH.

The initial DO value was immediately determined using the method described for dissolved oxygen. The BOD bottles containing the desired dilutions, dilution water blanks and glucose-glutamic acid checks were incubated at 20 ± 1°C. After 5 days incubation the DO in sample dilutions, blanks, and checks were again determined.

The BOD of sample was calculated using the formula (APHA, 1995).

$$\text{BOD}_5, \text{ mg/L} = \frac{P_i - D_2}{P}$$

where:

D₁ = DO of diluted sample immediately after preparation (mg l⁻¹)

D₂ = DO of diluted sample after 5 days incubation at 20°C (mg l⁻¹)

p = decimal volumetric fraction of sample used.

15. Total Dissolved Solids and Suspended Solids

An amount of 25 ml of sample was pipetted onto a cleaned glass-fibre and filtered with applied vacuum. Three successive washings with 10-ml volumes of reagent grade water were made, allowing complete drainage between washings, by continuing suction for about 3 minutes after filtration was completed.

The total filtrate (with washings) was transferred to pre-weighed evaporating dish and the filtrate evaporated to dryness in a drying oven set at 180 ± 2°C for 1 hour. It was cooled in a desiccator. The process was repeated until a constant weight was obtained. At the same time the filter was carefully removed from the filtration apparatus and transferred to an aluminium weighing dish as a support. This was dried in the oven set at 105 ± 2°C for 1 hour and cooled in the desiccator. The process was repeated until a constant weight was obtained.

The total dissolved solids was calculated as follows (APHA, *op. cit.*)

$$\text{Total dissolved solids/L} = \frac{(A - B) \times 1000}{\text{sample volume}}$$

where

A = weight of dried residue and dish (mg)

B = weight of dish (mg)

The total suspended solids was calculated using the formula

$$\text{Total suspended solids/L} = \frac{(C - D) \times 1000}{\text{sample volume}}$$

where

C = weight of filter and dried residue (mg)

D = weight of filter (mg).

16. Turbidity

Turbidity was measured immediately without altering the original sample conditions such as temperature and pH by the Nephelometric Method. Air and other gases trapped in the sample were removed by addition of a non-foaming type surfactant before the measurement. The sample was then agitated gently and time allowed for air bubbles to disappear. Sample was then poured into a cell and Turbidity read from the instrument display. Turbidity was corrected to the nearest NTU.

17. Conductivity

Conductivity meter model Wagtech 8733 was used. The temperature probe was rinsed three times with 0.01M KCl. With the probe in standard KCl solution, the meter was adjusted to read 1412 $\mu\text{mho/cm}$ automatically adjusting the cell constant. The sample resistance was then measured in the cell.

Conductivity was calculated by the formula (APHA, 1995)

$$\text{Conductivity,} = \frac{(1000000) (c)}{R_m[1 + 0.019 (t - 25)]}$$

where

c = cell constant (cm^{-1})

R_m = measured resistance of sample (ohms)

t = temperature of measurement

H. Statistical Analyses

The Multiple-Sample Comparison Analysis (Statgraphics Plus, 1995) software was used to compare significant differences, correlations and homogeneity between the physico-chemical and bacteriological parameters, as well as the means of bacterial flora in the blood, gill, gut, muscle and skin of fish from the various sampling sites.

Clustering of correlations and Sp coefficient were performed according to the unweighted-pair group method using average linkages (UPGMA) method. The phenotypic diversity (Di) of the bacterial population in each water sample was calculated as Simpson's index of diversity. All data handling, including optical readings, calculations of correlation coefficients, diversity indices, and Sp values, as well as clustering and printing of dendograms were performed using the software (BioSys inova, Stockholm) (Kuhn and Mollby, 1993).

I. Experimental Precautions

The following safety measures were strictly adhered to in carrying out this work;

- (i) Laboratory coat was worn whenever working, and the coat was decontaminated by washing with dettol™ disinfectant after use.
- (ii) Working tables was always decontaminated by wiping with 70% alcohol before and after completion of work.
- (iii) Protective gloves were worn for all procedures that involved direct contact with infectious materials.
- (iv) The laboratory was always kept clean, neat and free of materials not pertinent to the laboratory work.
- (v) Hands were disinfected with alcohol before and after handling infectious materials.
- (vi) Suitable labels were placed on vessels and reagent bottles.
- (vii) Inoculating pins, wire loops, metal forceps and pipette tips were flame sterilised with hooded Bunsen burner.
- (viii) The necks of specimen bottles, Erlenmeyer flasks, culture bottles and tubes were flamed after removing and placing caps and rubber bungs.
- (ix) Media and glassware were autoclaved before being used.

CHAPTER THREE

EXPERIMENTAL DETAILS

The investigation consisted of numerous studies which were carried out simultaneously over three years and the order of presentation of the Experimental Details does not, therefore, signify a sequence of the various experiments.

A. Physico-Chemical Parameters of Water of the Cultured Ponds and Open System

The physico-chemical characteristics of the ponds which naturally affect the fishes and bacterial flora in diverse ways were monitored throughout the course of study.

For each pond or open system the following parameters were studied using water samples from one particular site:

- (a) acidity, alkalinity, conductivity and pH.
- (b) Concentrations of ammonium nitrate, calcium ions, chloride ions, magnesium ions, phosphate ions, nitrate ions, nitrite ions, sulphate ions and silica.
- (c) Amount of dissolved oxygen.
- (d) Amount of total dissolved solids.
- (e) Biochemical oxygen demand.
- (f) Level of turbidity of the water; the features listed from (a) to (f) were likely to be affected by water periodically brought by rain. Records of rainfall for the different localities for the entire period of study were considered necessary for meaningful discussion of the experimental data obtained. These were provided by the Ghana Meteorological Services and the Surface Water Division of Water Research Institute and are presented in Appendix 9.
- (g) Temperature of the water measured at three places at the study area at approximately 11.00am. Because the water temperature would be affected by the atmospheric temperature, both temperatures were measured simultaneously.

B. Quantitative Estimation of the Bacterial Flora of Water of the Cultured Ponds and Open System

The population of heterotrophic and coliform bacteria of the water of the various ponds and the two open systems were studied. The bacterial population of the top layer of the sediment of the ponds was also determined. The standard plate count with Standard Plate Count Agar (SPCA) as growth medium was used. Pond water and sediment suspension dilutions of 1:10⁶ were used in all the tests. Duplicate plates were prepared for each sample serial dilutions and the mean number of colony forming units (CFU) determined after incubation at 37°C for 48 hours.

Densities of coliforms were determined for all the samples by the Most Probable Number (MPN) technique as stated in the Materials and Methods. The MPN technique was found to be more suitable for this work than the Membrane Filtration (MF) technique, due to the turbid nature of the water samples. The three-tube method was used. MacConkey broth and Brilliant Green Bile broth were used for the presumptive and confirmatory tests, respectively. Total coliform plates were incubated at 37 ± 0.5°C for 48 hours. Faecal coliforms were identified with the EC medium incubated at 44°C for 24 hours and faecal streptococci with Sodium azide broth incubated at 37°C for 48 hours.

C. Isolation of Pure Cultures and Identification of Bacterial Flora of Water of the Cultured Ponds and Open System

The flow chart shown on the next page describes the sequence of experiments carried out. Forty colonies were selected and identified to the generic level in each test.

Efforts were made to identify, where possible, some isolates to the species level. These were used as reference strains in subsequent studies. Confirmation of bacteria to the species level was made with the API bioMerieux (API 20 E and API 21 NE).

The Phene-Plate (PhP) system has been described in 'Materials and General Methods'. The inoculated plates were incubated at 37°C and the absorbance value (A₆₂₀) of each well measured after 16, 40 and 64 hours with a microplate reader. The biochemical fingerprint of each isolate was calculated as a mean absorbance value

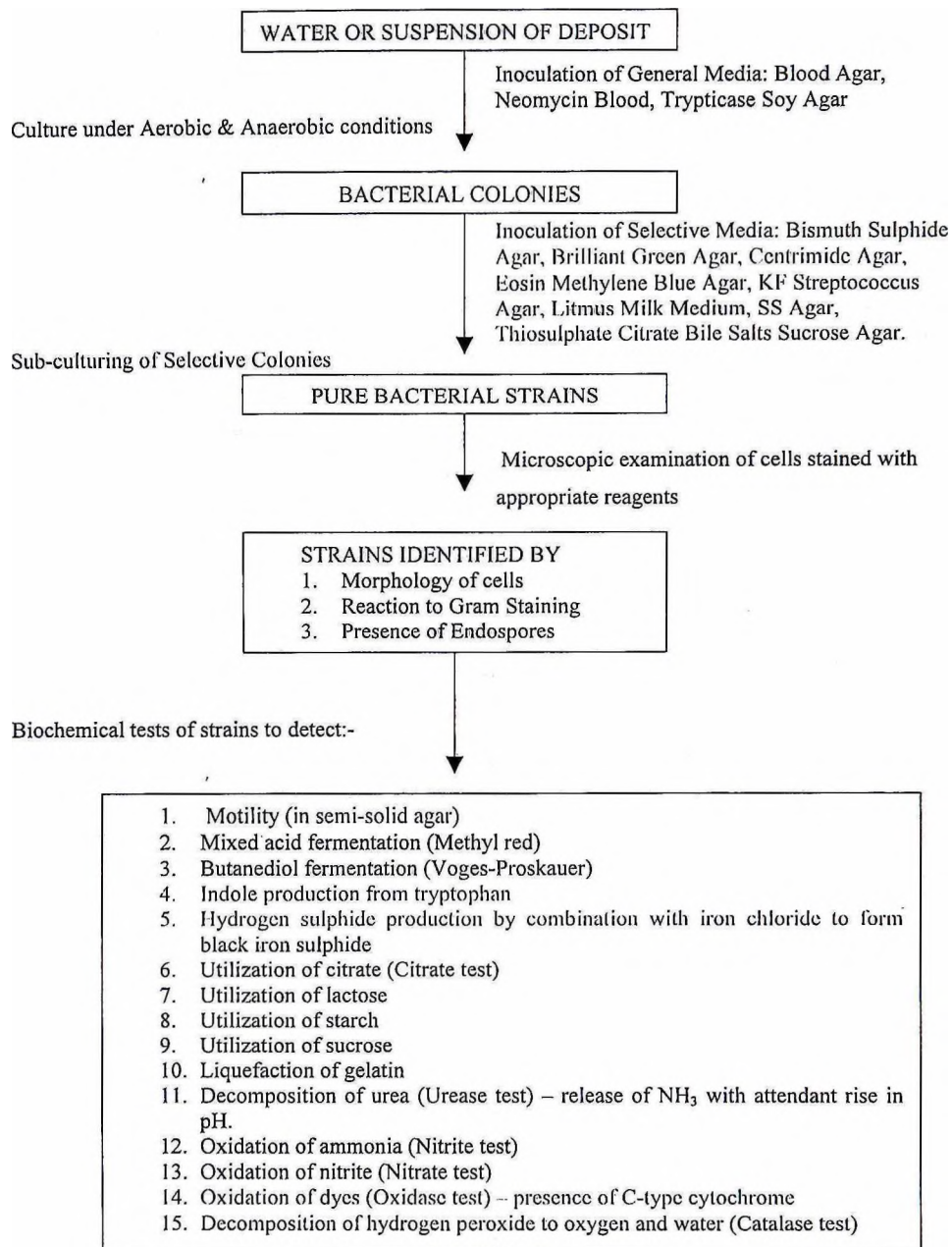


Fig . 1 Sequence of experiments carried out on the bacterial isolates.

for each well over all the three readings, viz. at 16, 40 and 64 hours. The similarities between isolates were expressed as correlation coefficients, and isolates showing correlation coefficients to each other higher than 0.975 (the identity level) were assigned the same PhP type. The similarities between bacterial populations in the different water samples from the various study areas were calculated as population similarity (Sp) coefficients. Clustering of correlations and Sp coefficient were performed according to the unweighted-pair group method using average linkages (UPGMA) method. The phenotypic diversity (Di) of the bacterial population in each water sample was calculated as Simpson's index of diversity. All data handling, including optical readings, calculations of correlation coefficients, diversity indices, and Sp values, as well as clustering and printing of dendograms were performed using the software (BioSys inova, Stockholm) (Kuhn and Mollby, 1993).

D. Bacterial Flora of Fish from Cultured Ponds and Open System

Five live tilapias were collected from each pond or open system every month. Samples were transported to the laboratory where analysis was done on the bacteria presence on the skin and gills and in the gut, muscles and blood. The gills, gut, and muscle were separately homogenized in sterile phosphate buffered saline of pH 7.2 to achieve 10% wt/vol suspension of fish. One millilitre of each homogenized tissue as well as that of the blood and suspension of swabbing of the skin surface were separately cultured on general media, namely, Blood agar and Trypticase Soy agar, and on selective media, namely SS agar, Neomycin blood agar, and TCBS. Cultures on these media were randomly selected and re-cultured to obtain pure strains. Selected colonies were subjected to further tests as described under Section C above. Forty colonies were selected and identified to the generic level in each case.

E. Bacterial Populations of Fish Feed Types and Organic Fertilizers

Diets offered for commercial fish production could contain bacteria potentially harmful to man and to the fish. Eleven different fish feeds and four different organic manures commonly used by most fish farmers as inputs into their ponds were, therefore, tested for bacteriological contamination. The feeds tested were banana (waste), biscuit (waste), bread (waste), brewery spent grain, cassava (waste), corn

bran, groundnut bran, fufu (waste), rice bran, termites (dried) and wheat bran. The manures tested were blood from abattoir (dry), cow manure (dry), pig manure (dry) and poultry manure (dry). The dry manures were prepared by drying fresh manure under room condition for 10 days.

An amount of 10g of each sample was transferred to a sterile blender (Moulinex, EC) containing 90ml of 0.1% (w/v) peptone water and blended at high speed for two minutes. A duplicate sample was prepared for each test. The heterotrophic bacterial population was assessed using the pour plate method and standard plate count agar. The Colony Forming Units were counted after incubation of the plates at 37°C for 48 hours. MacConkey broth was used for the MPN estimation of Enterobacteriaceae. Faecal coliforms were confirmed by separate loop transfers from the positive total coliform tubes to EC medium and incubated at $44 \pm 0.5^\circ\text{C}$. Sodium azide broth was used for estimation of presumptive faecal streptococci and confirmation tests were also made with fresh sodium azide broth.

F. Survival of Selected Bacterial Pathogens Introduced into Organic Manures Used in Fertilizing Fish Ponds.

Since the results of the studies of section E revealed the presence of bacteria pathogenic to the fish and human, it was considered necessary to investigate as a sequel the longevity of such species in organic manures. Five organic manures commonly used to fertilize the fish ponds, namely, poultry droppings, piggery waste, cow droppings, blood from abattoir, and sewage water, were selected for this investigation.

Pond water (10L), from farms each solely fertilized with a particular organic matter was collected into aquarium tanks and taken to the laboratory. The water was sterilized by exposing it to ultra violet light (P.W. Allen & Co, Type A 425) for 48 hours. The duration of 48 hours was found to be effective in a preliminary test. The pond water was kept aerated throughout the experiment.

The following bacterial strains were used to separately inoculate each water sample: *Pseudomonas* sp. KI-MTC-001K, *Shigella* sp. KI-MTC-002K, *Enterobacter* sp. KI-

MTC-003K, *Klebsiella* sp. KI-MTC-004K, *Citrobacter* sp. KI-MTC-005K, *Proteus* sp. KI-MTC-006K, *Salmonella* sp. KI-MTC-007K, and *Vibrio parahaemolyticus* KI-MTC-008K.

Samples were taken immediately after inoculation and at 3, 6, 24, 48, 72, 96 and 120 hours after inoculation. An amount of 100ml of the inoculated water was filtered and plated on blood agar and the plates were incubated at 37°C for 48 hours, for estimation of the bacterial population.

G. Case Study of Akuse Fish Ponds: Bacteria-Fish Relationship in Sewage Treatment plant Wastewater.

The Akuse fish ponds as constructed serve two purposes - sewage treatment ponds as well as fish culture ponds. They could, therefore, present peculiar problems as wastewater, although satisfactory as a source of nutrients is often toxic to fish due to the presence of heavy metals and human pathogenic bacteria. The Akuse farm was treated as a special case study in which the four ponds formed a series with different environments, as the wastewater flowed from one treatment pond to the other. The physico-chemical characters and bacterial populations of the water and fish bacterial load were separately investigated for each of the four ponds. This was done to enable comparison of conditions in these four different environments and between conditions of the sewage treatment ponds and those of non-sewage-fed ponds.

H. Health Status of the Fish Farmers and Some Consumers of Fish

Although fish is reared in domestic wastewater as routine practice in various parts of the world, there could be a potential public health hazard. This supposition was investigated. Stool samples were collected from both fish farmers and persons living around the farms who regularly consumed fish cultured in ponds of the Aduabenba, Akuse, ARDEC, Boadi, Boahen, Frimpong and Sagoe farms, and the open system of Weija for examination.

The stool samples were collected separately from each individual into sterile 50ml plastic cups with lids, stored in thermo-insulated container at below 10°C and transported to the Public Health Reference Laboratory, Korle Bu.

Stool samples were streaked directly on MacConkey agar, Blood agar, Thiosulphate citrate-bile salts-sucrose agar and SS agar and incubated at 37°C for 48 hours. Morphological studies and biochemical tests listed in Section C were then made for identification of the isolates.

CHAPTER FOUR

RESULTS

A. Physico-Chemical Parameters of Water of the Cultured Ponds and Open System

1. Cow manure Fertilized Ponds

Aduabenba farm

The mean monthly values for the study period for each parameter are presented in Table 2a. The bacterial population counts made at the same time are appended. The Pearson product moment correlations between pairs of the physico-chemical and microbiological parameters showed significant and positive correlation between the following pairs of variables; acidity and faecal coliform (FC) count, acidity and pH, air and water temperatures, calcium and sulphate ions, chloride ion and pH, FC and pH, total hardness and water temperature, nitrite ion and silicon dioxide, and, total heterotrophic bacteria (THB) and turbidity. Pairs of variables which showed significant and negative correlation included acidity and alkalinity, air temperature and alkalinity, air temperature and ammonium ion, air temperature and total coliform (TC) count, biochemical oxygen demand (BOD) and suspended solids (SS), chloride ion and turbidity, and, conductivity and nitrate ion.

Ten homogenous groups were identified by the Duncan's range tests:

1. Sulphate, nitrite, phosphate, nitrate, ammonium, silicon dioxide, FC, FS, magnesium and pH.
2. FS, magnesium, pH, BOD and DO.
3. BOD, DO and calcium.
4. Turbidity, air temperature and water temperature.
5. Acidity and suspended solids (SS).
6. TC and total hardness.
7. Chloride and alkalinity.
8. Total hardness.
9. Conductivity
10. Total dissolved solids (TDS).

TABLE 2a

Physico-chemical parameters and bacterial population level of Aduabenba Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.00	29.00	30.30	31.00	29.83	31.00
Water Temperature (°C)	29.17	30.90	31.33	32.25	31.83	32.17
pH	7.07	6.98	6.99	7.04	7.09	7.07
Acidity (mg/l ¹)	39.63	36.73	39.17	40.40	41.76	40.62
Alkalinity (mg/l ¹)	82.53	83.83	78.90	77.40	76.23	76.50
Calcium ion (mg/l ¹)	13.78	16.33	14.60	16.45	15.34	13.63
Total hardness (mg/l ¹)	35.63	63.83	64.87	73.45	66.63	60.57
Chloride ion (mg/l ¹)	81.43	68.90	73.32	75.95	78.43	88.00
Magnesium ion (mg/l ¹)	6.88	5.87	6.63	5.87	6.05	5.99
Phosphate ion (mg/l ¹)	0.11	0.09	0.09	0.09	0.11	0.09
Ammonium ion (mg/l ¹)	0.16	0.14	0.14	0.12	0.15	0.12
Nitrate ion (mg/l ¹)	0.10	0.09	0.11	0.10	0.11	0.10
Nitrite ion (mg/l ¹)	0.04	0.05	0.08	0.04	0.10	0.11
Sulphate ion (mg/l ¹)	0.00	0.01	0.00	0.01	0.00	0.00
Silicon dioxide (mg/l ¹)	1.08	1.10	1.09	1.09	1.12	1.12
Dissolved oxygen (mg/l ¹)	8.88	9.17	8.63	8.61	8.95	9.00
Biochemical oxygen demand (mg/l ¹)	8.62	8.36	8.79	8.87	8.72	8.12
Total dissolved solids (mg/l ¹)	125.73	131.53	170.33	138.75	129.13	140.37
Suspended solids (mg/l-1)	44.83	52.50	42.97	36.80	40.20	51.17
Turbidity (NTU)	26.43	28.80	27.67	25.80	26.67	24.87
Conductivity (Scm ⁻¹)	122.17	144.87	119.90	126.75	120.87	130.00
Total coliform count x 10 ³ (ml ⁻²)	65.00	63.33	53.00	54.00	58.33	55.00
Faecal coliform count x 10 ³ (ml ⁻²)	1.31	1.14	1.23	1.30	1.53	1.53
Faecal streptococci count x 10 ³ (ml ⁻²)	2.53	2.17	2.37	2.05	1.80	2.13
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	101.33	110.00	112.67	81.00	90.00	83.33

Boateng farm

The mean monthly values of the physico-chemical parameters and bacterial population levels are presented in Table 2b. The Pearson product moment correlations between pairs of the physico-chemical and microbiological parameters showed significant and positive correlation between air and water temperatures, BOD and chloride ion, conductivity and hardness of the water, conductivity and turbidity, FC and faecal streptococci (FS) counts, nitrate ion and suspended solids (SS), and pH and total dissolved solids (TDS).

Significant but negatively correlated variables were acidity and TDS, alkalinity and FC, BOD and conductivity, BOD and turbidity, calcium ion and FC, calcium ion and FS, chloride ion and SS, chloride ion and turbidity and FC and phosphate ions.

Eight homogenous groups were identified by the Duncan's range tests:

1. Sulphate, ammonium, nitrite, nitrate, phosphate, silicon dioxide, FC, FS, BOD, turbidity, magnesium, pH, DO and calcium.
2. FS, BOD, turbidity, magnesium, pH, DO, calcium and suspended solids (SS).
3. Calcium, suspended solids (SS) and chloride.
4. Acidity, air temperature and water temperature.
5. Total dissolved solids (TDS).
6. Total hardness and TC.
7. Alkalinity and conductivity
8. Total heterotrophic bacteria (THB).

2. Poultry manure Fertilized Ponds

Agyeman farm

The mean monthly values for this farm is presented in Table 2c. The Pearson product moment correlations showed positive and significant correlation between air and water temperatures, alkalinity and SS, ammonium ion and turbidity, calcium ion and DO, calcium ions and total dissolved solids (TDS), FC and FS, pH and silicon dioxide, and TC and total heterotrophic bacteria (THB). Significant but negatively correlated pairs of variables were air temperature and FC, alkalinity and conductivity, BOD and

TABLE 2b

Physico-chemical parameters and bacterial population level of Boateng Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.67	29.83	30.17	30.25	30.17	30.00
Water Temperature (°C)	29.00	30.67	31.00	30.75	31.50	30.67
pH	6.99	7.00	7.00	6.95	6.74	6.71
Acidity (mg/l ¹)	28.33	25.00	27.67	30.00	30.00	33.33
Alkalinity (mg/l ¹)	116.33	114.00	106.00	104.00	72.67	112.67
Calcium ion (mg/l ¹)	10.69	10.70	10.57	10.75	10.50	10.77
Total hardness (mg/l ¹)	61.00	61.33	63.33	62.50	60.33	59.00
Chloride ion (mg/l ¹)	19.60	19.47	19.19	19.05	19.00	19.47
Magnesium ion (mg/l ¹)	6.19	6.05	6.08	6.09	6.20	6.03
Phosphate ion (mg/l ¹)	0.25	0.25	0.23	0.25	0.23	0.24
Ammonium ion (mg/l ¹)	0.01	0.03	0.03	0.03	0.02	0.01
Nitrate ion (mg/l ¹)	0.12	0.12	0.13	0.13	0.13	0.13
Nitrite ion (mg/l ¹)	0.09	0.19	0.09	0.10	0.08	0.18
Sulphate ion (mg/l ¹)	0.00	0.00	0.00	0.00	0.00	0.00
Silicon dioxide (mg/l ¹)	1.17	1.25	1.24	1.04	1.25	1.21
Dissolved oxygen (mg/l ¹)	7.64	7.46	7.48	7.92	8.05	6.12
Biochemical oxygen demand (mg/l ¹)	5.85	5.81	5.33	5.16	5.27	5.95
Total dissolved solids (mg/l ¹)	45.47	45.73	44.93	45.30	44.40	44.20
Suspended solids (mg/l ¹)	11.27	11.20	12.07	13.35	12.67	12.20
Turbidity (NTU)	5.40	5.67	5.87	6.00	5.93	5.33
Conductivity (Scm ⁻¹)	119.60	109.67	113.33	115.00	110.93	107.80
Total coliform count x 10 ³ (ml ⁻²)	88.00	92.00	38.33	45.50	91.67	65.33
Faecal coliform count x 10 ³ (ml ⁻²)	1.03	1.27	1.70	1.01	2.07	1.09
Faecal streptococci count x 10 ³ (ml ⁻²)	1.38	1.90	2.07	1.12	2.47	1.17
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	126.00	161.00	81.33	123.50	135.00	140.00

TABLE 2c

Physico-chemical parameters and bacterial population level of Agyeman Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.67	29.83	30.13	29.75	30.27	29.00
Water Temperature (°C)	28.83	31.33	32.00	31.75	31.17	30.80
pH	6.91	6.96	6.96	6.98	6.99	7.00
Acidity (mg/l ¹)	29.93	29.13	30.20	31.60	29.67	32.00
Alkalinity (mg/l ¹)	76.13	89.33	89.33	83.30	74.00	78.00
Calcium ion (mg/l ¹)	11.80	11.80	11.99	11.80	11.75	11.53
Total hardness (mg/l ¹)	28.83	25.00	32.00	30.00	25.00	24.83
Chloride ion (mg/l ¹)	13.60	12.81	15.47	13.55	15.33	12.75
Magnesium ion (mg/l ¹)	2.18	1.88	2.03	1.77	1.63	1.62
Phosphate ion (mg/l ¹)	0.52	0.43	0.53	0.56	0.49	0.52
Ammonium ion (mg/l ¹)	0.28	0.21	0.22	0.19	0.23	0.30
Nitrate ion (mg/l ¹)	0.14	0.14	0.13	0.10	0.12	0.12
Nitrite ion (mg/l ¹)	0.04	0.04	0.05	0.06	0.05	0.05
Sulphate ion (mg/l ¹)	13.87	12.41	13.83	11.60	12.55	13.05
Silicon dioxide (mg/l ¹)	17.48	17.77	18.57	18.40	18.67	19.27
Dissolved oxygen (mg/l ¹)	7.00	6.47	8.13	6.35	6.77	6.03
Biochemical oxygen demand (mg/l ¹)	6.20	6.23	5.23	5.73	4.95	4.53
Total dissolved solids (mg/l ¹)	101.47	103.33	102.60	100.00	98.77	94.87
Suspended solids (mg/l-1)	94.67	107.33	112.20	110.30	95.33	106.20
Turbidity (NTU)	95.67	84.67	80.00	68.30	84.00	96.00
Conductivity (Scm ¹)	142.20	120.67	127.07	127.10	152.87	148.53
Total coliform count x 10 ³ (ml ²)	39.67	44.67	47.33	28.50	42.67	44.00
Faecal coliform count x 10 ³ (ml ²)	93.33	79.69	78.00	77.00	76.33	86.00
Faecal streptococci count x 10 ³ (ml ²)	103.33	94.67	91.00	89.00	93.00	93.33
Total heterotrophic bacteria x 10 ³ (ml ²)	79.33	76.67	86.67	63.00	80.67	72.00



silicon dioxide, FS and water temperature, FS and nitrite ion, FS and water temperature, magnesium ion and pH, and, nitrate and nitrite ions.

Eleven homogenous groups were identified by the Duncan's range tests:

1. Nitrite, nitrate, ammonium, phosphate, FC, FS, magnesium and BOD.
2. Magnesium, BOD, DO and pH.
3. DO, pH and calcium.
4. Calcium, sulphate and chloride.
5. Sulphate, chloride and silicon dioxide.
6. Total hardness, air temperature, acidity and water temperature.
7. Total coliform (TC).
8. Total heterotrophic bacteria (THB).
9. Alkalinity and turbidity.
10. Total dissolved solids (TDS) and suspended solids (SS).
11. Conductivity.

ARDEC 20

The mean monthly values for the 25 parameters are presented in Table 2d. Pearson product moment correlations showed significant and positive correlation between alkalinity and calcium ion, alkalinity and silicon dioxide, BOD and DO, calcium ion and silicon dioxide, chloride ion and total dissolved solids (TDS), nitrate ion and pH, silicon dioxide and turbidity, and TC and THB. Pairs of parameters which showed significant but negative correlation were chloride and magnesium ions, FC and sulphate ion, magnesium ion and TDS, nitrate ion and turbidity, and, sulphate ion and THB.

Ten homogenous groups were identified by the Duncan's multiple range tests:

1. Nitrite, nitrate, phosphate, ammonium, FC, FS, magnesium, BOD, sulphate, pH, DO and calcium.
2. FC, FS, magnesium, BOD, sulphate, pH, DO, calcium and silicon dioxide.
3. Calcium, silicon dioxide and chloride.
4. Chloride, acidity and SS.
5. Acidity, SS, water temperature, air temperature and total hardness.
6. Water temperature, air temperature, total hardness and turbidity.
7. Turbidity and TC.

TABLE 2d

Physico-chemical parameters and bacterial population level of ARDEC 20 Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.33	30.50	29.17	30.75	29.67	30.00
Water Temperature (°C)	29.67	28.50	28.17	31.00	30.33	30.17
pH	6.80	6.76	6.39	6.92	6.60	6.60
Acidity (mg/l ¹)	28.67	24.00	22.00	23.00	33.00	22.33
Alkalinity (mg/l ¹)	89.33	75.33	91.67	76.00	90.00	61.33
Calcium ion (mg/l ¹)	8.53	7.87	9.87	7.60	10.53	6.27
Total hardness (mg/l ¹)	22.67	25.67	35.33	36.00	40.33	29.00
Chloride ion (mg/l ¹)	14.67	19.17	17.50	13.75	18.52	16.14
Magnesium ion (mg/l ¹)	3.56	4.00	4.73	6.89	5.55	4.79
Phosphate ion (mg/l ¹)	0.22	0.24	0.31	0.30	0.24	0.61
Ammonium ion (mg/l ¹)	0.68	1.90	1.17	0.49	0.45	1.16
Nitrate ion (mg/l ¹)	0.18	0.34	0.09	0.44	0.18	0.21
Nitrite ion (mg/l ¹)	0.01	0.02	0.03	0.04	0.44	0.35
Sulphate ion (mg/l ¹)	4.90	11.13	3.83	3.95	8.85	3.44
Silicon dioxide (mg/l ¹)	12.49	8.53	16.47	10.45	15.61	9.29
Dissolved oxygen (mg/l ¹)	11.13	6.79	6.96	8.91	5.07	7.43
Biochemical oxygen demand (mg/l ¹)	8.92	5.45	4.58	6.56	3.39	4.50
Total dissolved solids (mg/l ¹)	87.43	84.33	78.20	58.70	78.47	71.03
Suspended solids (mg/l-1)	30.67	26.33	46.67	32.50	45.00	36.67
Turbidity (NTU)	40.33	27.30	46.67	11.00	28.00	12.47
Conductivity (Scm ¹)	141.67	170.07	156.67	117.55	173.67	136.60
Total coliform count x 10 ⁴ (ml ²)	31.33	28.20	47.67	41.50	51.00	49.67
Faecal coliform count x 10 ³ (ml ²)	3.30	2.90	4.07	4.70	2.77	3.83
Faecal streptococci count x 10 ³ (ml ²)	3.77	5.33	4.90	5.95	3.60	4.27
Total heterotrophic bacteria x 10 ³ (ml ²)	63.33	37.67	81.67	80.00	72.67	86.67

8. Total heterotrophic bacteria (THB) and TDS.
9. TDS and alkalinity.
10. Conductivity.

Asare farm

The mean monthly values of the physico-chemical parameters and the bacterial population levels are presented in Table 2e. The Pearson product moment correlations showed significant and positive correlations between acidity and phosphate ion, acidity and SS, air temperature and sulphate ion, air and water temperatures, alkalinity and turbidity, ammonium ion and phosphate ion, chloride ion and DO, chloride ion and total hardness, DO and total hardness, FC and FS, FC and THB, FS and THB, nitrate ions and pH, nitrate ions and silicon, pH and silicon dioxide, and, sulphate ion and water temperature. Pairs of variables which were significantly and negatively correlated were ammonium and nitrite ions, calcium ion and TC, FC and nitrate ion, FC and silicon dioxide, nitrate and THB, nitrite and phosphate ions, silicon dioxide and THB, silicon dioxide and turbidity, sulphate ion and TDS.

Nine homogenous groups were identified by the Duncan's range tests:

1. Sulphate, ammonium, nitrate, nitrite, phosphate, FC, silicon dioxide, FS, magnesium, pH, BOD, DO and calcium.
2. Air temperature, water temperature, SS and acidity.
3. Water temperature, SS, acidity and turbidity.
4. Total hardness and alkalinity.
5. Total coliform (TC).
6. Chloride ion.
7. Total heterotrophic bacteria (THB).
8. Total dissolved solids (TDS).
9. Conductivity.

Frimpong farm

The monthly mean values for the 25 parameters are presented in Table 2f. Pearson product moment correlation showed significant and positive correlation between acidity and DO, acidity and TDS, air and water temperatures, ammonium ion and

TABLE 2e

Physico-chemical parameters and bacterial population level of Asare Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.00	29.83	30.17	31.00	30.50	29.67
Water Temperature (°C)	28.17	30.55	31.50	32.25	31.33	31.67
pH	6.89	6.92	6.74	6.50	6.88	6.71
Acidity (mg/l ¹)	34.93	41.67	32.40	35.00	34.27	36.80
Alkalinity (mg/l ¹)	56.20	57.60	57.60	60.30	52.87	50.80
Calcium ion (mg/l ¹)	12.93	12.63	12.87	11.55	11.43	13.87
Total hardness (mg/l ¹)	56.87	59.20	58.33	55.20	49.60	53.20
Chloride ion (mg/l ¹)	106.67	109.73	109.40	104.50	100.00	110.20
Magnesium ion (mg/l ¹)	5.80	6.41	6.19	6.10	6.00	6.01
Phosphate ion (mg/l ¹)	0.10	0.32	0.09	0.09	0.09	0.10
Ammonium ion (mg/l ¹)	0.08	0.04	0.07	0.07	0.09	0.10
Nitrate ion (mg/l ¹)	0.07	0.07	0.07	0.05	0.07	0.05
Nitrite ion (mg/l ¹)	0.10	0.12	0.10	0.10	0.09	0.10
Sulphate ion (mg/l ¹)	0.00	0.01	0.01	0.01	0.01	0.01
Silicon dioxide (mg/l ¹)	2.03	2.06	2.05	1.90	2.06	1.83
Dissolved oxygen (mg/l ¹)	8.91	9.03	9.20	8.90	8.41	8.87
Biochemical oxygen demand (mg/l ¹)	7.74	8.82	8.50	7.19	7.32	7.84
Total dissolved solids (mg/l ¹)	163.33	118.47	128.87	139.30	128.43	158.27
Suspended solids (mg/l-1)	29.63	34.63	27.77	32.20	29.93	34.40
Turbidity (NTU)	42.53	40.83	40.50	47.50	36.80	45.20
Conductivity (Scm ⁻¹)	160.10	166.73	139.40	152.75	166.50	166.63
Total coliform count x 10 ³ (ml ⁻²)	38.33	64.00	41.67	84.00	78.33	97.33
Faecal coliform count x 10 ³ (ml ⁻²)	1.41	1.03	0.21	2.72	0.76	0.78
Faecal streptococci count x 10 ³ (ml ⁻²)	2.75	2.65	0.58	4.10	1.10	1.10
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	115.00	118.00	78.33	175.00	104.00	136.67 !

TABLE 2f

Physico-chemical parameters and bacterial population level of Frimpong Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.50	27.33	30.00	30.25	28.33	28.83
Water Temperature (°C)	30.17	29.50	30.83	30.75	29.50	30.33
pH	7.01	7.11	6.96	6.74	7.11	7.00
Acidity (mg/l ^l)	36.67	36.60	29.13	45.60	30.60	28.67
Alkalinity (mg/l ^l)	65.80	90.93	94.67	84.50	49.93	61.23
Calcium ion (mg/l ^l)	11.83	11.83	11.48	11.61	11.47	11.17
Total hardness (mg/l ^l)	39.67	35.33	51.93	40.50	35.33	39.67
Chloride ion (mg/l ^l)	125.00	153.33	135.00	132.50	130.00	133.33
Magnesium ion (mg/l ^l)	5.06	5.83	5.87	6.75	6.64	6.27
Phosphate ion (mg/l ^l)	0.19	0.20	0.17	0.22	0.17	0.20
Ammonium ion (mg/l ^l)	0.12	0.13	0.11	0.14	0.08	0.12
Nitrate ion (mg/l ^l)	0.85	0.16	0.15	0.08	0.13	0.15
Nitrite ion (mg/l ^l)	0.07	0.15	0.09	0.12	0.07	0.13
Sulphate ion (mg/l ^l)	0.02	0.01	0.02	0.01	0.01	0.27
Silicon dioxide (mg/l ^l)	1.05	1.80	1.05	1.47	1.28	1.01
Dissolved oxygen (mg/l ^l)	8.80	8.47	8.07	9.45	6.73	7.73
Biochemical oxygen demand (mg/l ^l)	6.67	7.33	6.47	8.60	5.01	6.13
Total dissolved solids (mg/l ^l)	129.73	74.33	77.37	138.30	71.67	73.80
Suspended solids (mg/l ^l)	19.40	18.93	20.33	24.75	13.27	10.70
Turbidity (NTU)	6.47	6.67	6.00	6.80	5.13	5.67
Conductivity (Scm ^l)	157.67	130.67	136.47	160.25	131.30	131.00
Total coliform count x 10 ³ (ml ⁻²)	56.00	45.87	28.83	29.75	37.40	51.33
Faecal coliform count x 10 ³ (ml ⁻²)	0.43	1.22	0.36	0.26	0.43	0.59
Faecal streptococci count x 10 ³ (ml ⁻²)	1.87	2.00	1.12	0.87	1.79	1.24
Total heterotrophic bacteria x 10 ³ (ml ⁻²)	68.00	78.00	40.67	52.00	60.00	80.67

BOD, ammonium ion and DO, ammonium and phosphate ions, ammonium ion and turbidity, BOD and DO, BOD and SS, BOD and turbidity, chloride ion and FC, conductivity and TDS, DO and SS, DO and turbidity, FS and pH, and TC and THB.

There were nine homogenous groups identified based on the Duncan's range tests:

1. Sulphate, nitrite, ammonium, phosphate, nitrate, FC, silicon dioxide, FS, magnesium, turbidity, BOD, pH, DO and calcium.
2. Magnesium, turbidity, BOD, pH, DO, calcium and SS.
3. Air temperature, water temperature and acidity.
4. Water temperature, acidity and total hardness.
5. Acidity, total hardness and TC.
6. Total heterotrophic bacteria (THB).
7. Alkalinity.
8. Total dissolved solids (TDS).
9. Chloride and conductivity.

3. Pig manure Fertilized Ponds

(Boadi farm)

The mean monthly values are presented in Table 2g. The Pearson product moment correlation showed significant and positive correlation between acidity and alkalinity, acidity and FS, air temperature and chloride ion, air temperature and SS, alkalinity and FS, ammonium ion and TC, FC and phosphate ion, FC and TC, total hardness and magnesium ion, nitrate ion and turbidity, SS and TC, SS and THB, TC and THB. Variables which showed significant but negative correlations were acidity and nitrite ion, calcium and total hardness, total hardness and water temperature, and phosphate and silicon dioxide.

Eight homogenous groups were identified through the Duncan's range tests:

1. Nitrite, phosphate, nitrate, ammonium, FC, BOD, magnesium, pH, sulphate, DO, calcium and FS.
2. BOD, magnesium, pH, sulphate, DO, calcium, FS, chloride and silicon dioxide.
3. Sulphate, DO, calcium, FS, chloride, silicon dioxide and SS.
4. Chloride, silicon dioxide, SS, air temperature and water temperature.

TABLE 2g

Physico-chemical parameters and bacterial population level of Boadi Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.50	29.67	33.00	30.50	30.83	30.33
Water Temperature (°C)	30.00	31.67	31.83	31.75	31.17	30.83
PH	6.83	6.84	6.87	6.90	6.81	6.87
Acidity (mg/l ¹)	34.20	34.13	32.83	36.00	36.00	57.53
Alkalinity (mg/l ¹)	63.07	84.00	83.67	83.75	83.20	86.33
Calcium ion (mg/l ¹)	8.73	8.88	8.75	9.10	8.87	8.62
Total hardness (mg/l ¹)	43.00	39.87	39.47	38.40	40.33	43.33
Chloride ion (mg/l ¹)	17.53	18.07	19.67	17.80	19.10	18.33
Magnesium ion (mg/l ¹)	5.83	5.32	4.01	4.30	3.89	6.53
Phosphate ion (mg/l ¹)	0.08	0.10	0.13	0.13	0.05	0.07
Ammonium ion (mg/l ¹)	1.49	1.64	2.28	2.16	1.75	2.40
Nitrate ion (mg/l ¹)	0.24	0.39	0.38	0.11	0.10	0.15
Nitrite ion (mg/l ¹)	0.05	0.05	0.06	0.05	0.04	0.03
Sulphate ion (mg/l ¹)	8.83	8.95	9.13	5.69	9.03	8.76
Silicon dioxide (mg/l ¹)	18.55	16.93	15.60	16.30	29.40	18.87
Dissolved oxygen (mg/l ¹)	8.10	10.21	9.00	9.40	6.93	7.32
Biochemical oxygen demand (mg/l ¹)	4.03	4.90	4.80	4.15	4.49	3.62
Total dissolved solids (mg/l ¹)	87.53	82.80	85.00	100.00	84.80	98.00
Suspended solids (mg/l ¹)	20.87	18.27	27.00	24.00	24.00	23.37
Turbidity (NTU)	72.67	73.33	79.67	65.00	64.67	68.00
Conductivity (Scm ¹)	129.33	124.67	130.20	122.00	128.67	120.80
Total coliform count x 10 ³ (ml ⁻²)	69.00	51.33	138.33	101.50	68.67	111.00
Faecal coliform count x 10 ³ (ml ⁻²)	1.90	2.20	3.88	2.80	1.51	2.43
Faecal streptococci count x 10 ³ (ml ⁻²)	5.13	3.27	5.33	3.85	2.47	3.95
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	111.67	70.87	180.67	193.50	130.00	148.00

5. Air temperature, water temperature, acidity and total hardness.
6. Turbidity.
7. Alkalinity, TDS and TC.
8. Conductivity and THB.

K.K. farm

The mean monthly values for the 25 parameters are presented in Table 2h. Pearson product moment correlation showed significant and positive correlations between acidity and total hardness, air and water temperatures, ammonium and phosphate ions, conductivity and DO, FC and total hardness, FS and phosphate ion, nitrate ion and DO, nitrite ion and pH, phosphate ion and TDS, silicon dioxide and THB, and, SS and TDS.

Nine homogenous groups were identified by the Duncan's range tests:

1. Sulphate, nitrite, nitrate, ammonium, silicon, FC, phosphate, BOD, FS, magnesium, DO, pH and calcium.
2. Magnesium, DO, pH, calcium and SS.
3. Calcium, SS and chloride.
4. Chloride, air temperature and water temperature.
5. Total hardness, turbidity and acidity.
6. Total dissolved solids (TDS) and TC.
7. Total coliform (TC) and alkalinity.
8. Conductivity.
9. Total heterotrophic bacteria (THB).

Pacific farm

The mean monthly values for the 25 parameters are presented in Table 2i. The Pearson product moment correlation showed significant and positive correlations between air temperature and THB, air and water temperatures, alkalinity and BOD, calcium ion and water temperature, chloride ion and pH, FC and FS, total hardness and phosphate ion, magnesium and phosphate ions, and TC and THB. Parameters which showed significant but negative correlation were acidity and phosphate ion, ammonium ion and FC, calcium and magnesium ions, calcium ion and silicon dioxide, FC and nitrite ion, total hardness and water temperature, magnesium ion and

TABLE 2h

Physico-chemical parameters and bacterial population levels of K.K. Farm Cultured Pond water

Parameter	Mean values per month (1996 - 1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.50	29.17	30.50	30.75	31.17	30.50
Water Temperature (°C)	29.83	30.00	32.00	32.25	32.33	31.50
pH	6.96	7.14	7.02	7.13	7.05	7.07
Acidity (mg/l ¹)	53.50	57.00	53.50	60.05	50.50	49.00
Alkalinity (mg/l ¹)	89.67	93.17	73.33	99.00	80.13	83.17
Calcium ion (mg/l ¹)	11.35	12.27	11.83	12.05	12.13	12.95
Total hardness (mg/l ¹)	45.83	50.50	46.47	49.05	42.73	38.87
Chloride ion (mg/l ¹)	18.67	35.73	23.07	19.50	20.20	27.07
Magnesium ion (mg/l ¹)	7.05	6.33	6.46	6.25	5.20	7.31
Phosphate ion (mg/l ¹)	1.71	1.90	1.63	1.17	1.65	1.51
Ammonium ion (mg/l ¹)	0.55	0.37	0.28	0.95	0.66	0.63
Nitrate ion (mg/l ¹)	0.23	0.31	0.51	0.39	0.53	0.56
Nitrite ion (mg/l ¹)	0.22	0.04	0.14	0.06	0.04	0.13
Sulphate ion (mg/l ¹)	0.02	0.03	0.03	0.02	0.00	0.01
Silicon dioxide (mg/l ¹)	0.99	1.06	1.04	0.98	1.04	0.87
Dissolved oxygen (mg/l ¹)	6.03	7.09	7.29	7.20	7.17	6.57
Biochemical oxygen demand (mg/l ¹)	3.01	3.13	3.06	3.01	3.27	3.33
Total dissolved solids (mg/l ¹)	72.27	54.20	69.60	90.35	81.97	73.30
Suspended solids (mg/l ¹)	16.80	18.80	16.60	16.00	16.43	16.37
Turbidity (NTU)	52.40	50.47	54.17	52.25	57.33	53.50
Conductivity (Scm ¹)	115.13	96.13	87.13	86.90	93.67	107.00
Total coliform count x 10 ³ (ml ²)	72.33	79.33	75.67	89.00	79.00	85.33
Faecal coliform count x 10 ³ (ml ²)	1.30	0.33	1.37	1.20	1.43	1.57
Faecal streptococci count x 10 ³ (ml ²)	3.43	3.33	3.40	3.95	3.47	3.33
Total heterotrophic bacteria x 10 ³ (ml ²)	92.00	103.33	98.00	113.00	112.33	205.33

TABLE 2i

Physico-chemical parameters and bacterial population levels of Pacific Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	27.67	28.67	29.17	30.50	28.67	28.83
Water Temperature (°C)	29.67	30.33	30.67	31.25	29.57	30.17
pH	6.88	7.08	6.89	6.88	6.88	6.98
Acidity (mg/l ¹)	47.33	52.00	51.67	50.00	48.67	48.00
Alkalinity (mg/l ¹)	203.33	280.00	250.00	235.00	243.33	247.67
Calcium ion (mg/l ¹)	13.33	13.33	14.67	15.00	13.00	13.67
Total hardness (mg/l ¹)	45.00	40.00	40.00	39.50	44.67	41.67
Chloride ion (mg/l ¹)	133.33	148.33	135.00	130.00	130.00	135.00
Magnesium ion (mg/l ¹)	6.10	6.03	5.56	5.40	6.75	6.45
Phosphate ion (mg/l ¹)	8.90	8.70	8.65	8.65	8.92	8.91
Ammonium ion (mg/l ¹)	8.08	8.13	8.14	8.15	7.99	8.27
Nitrate ion (mg/l ¹)	0.59	0.66	0.59	0.62	0.67	0.62
Nitrite ion (mg/l ¹)	0.32	0.30	0.29	0.28	0.24	0.31
Sulphate ion (mg/l ¹)	0.05	0.04	0.00	0.12	0.04	0.07
Silicon dioxide (mg/l ¹)	2.30	2.57	2.04	1.90	2.25	2.21
Dissolved oxygen (mg/l ¹)	9.33	9.68	10.09	9.40	9.90	9.67
Biochemical oxygen demand (mg/l ¹)	8.03	8.80	8.73	8.65	8.67	8.81
Total dissolved solids (mg/l ¹)	256.67	252.33	265.33	248.00	264.67	266.67
Suspended solids (mgM)	2.76	2.30	2.67	4.00	1.00	2.00
Turbidity (NTU)	7.33	5.67	6.33	6.50	6.00	7.67
Conductivity (Scm ¹)	14880.00	10950.00	14333.33	15460.00	16700.00	18260.00
Total coliform count x 10 ³ (ml ²)	63.00	76.90	49.33	132.00	62.33	45.33
Faecal coliform count x 10 ³ (ml ²)	0.54	0.64	0.76	0.44	1.54	0.33
Faecal streptococci count x 10 ³ (ml ²)	0.84	0.89	2.71	0.78	3.53	0.78
Total heterotrphic bacteria x 10 ³ (ml ²)	113.33	138.00	117.00	230.00	124.00	116.00

SS, magnesium ion and water temperature, phosphate ion and water temperature, and TC and TDS.

Two homogenous groups were identified by the Duncan's range tests:

1. Sulphate, nitrite, nitrate, FC, FS, silicon dioxide, SS, magnesium, turbidity, pH, ammonium, BOD, phosphate, DO, calcium, air temperature, water temperature, total hardness, acidity, TC, chloride, THB, alkalinity and TDS.
2. Conductivity.

4. Blood waste fertilized Pond (Boahen farm)

The mean monthly values are presented in Table 2j. The Pearson product moment correlation showed significant and positive correlations between alkalinity and FC, alkalinity and magnesium ion, alkalinity and nitrite ion, ammonium ion and DO, DO and phosphate ion, FC and magnesium ion, FS and pH, FS and TDS, total hardness and magnesium ion, magnesium and nitrite ions, pH and TDS, and turbidity and water temperature. Significant but negative variables were acidity and silicon dioxide, acidity and TC, air temperature and FC, air temperature and magnesium ion, ammonium and chloride ions, total hardness and turbidity, and silicon dioxide and water temperature.

Ten homogenous groups were identified by the Duncan's range tests:

1. Sulphate, nitrite, nitrate, ammonium, FC, phosphate, FS, BOD, silicon dioxide, magnesium, calcium, pH, and DO.
2. FC, phosphate, FS, BOD, silicon dioxide, magnesium, calcium, pH, DO and SS.
3. SS and chloride.
4. Chloride and acidity.
5. Acidity, air temperature and water temperature.
6. Total hardness, turbidity and alkalinity.
7. Turbidity, alkalinity and TDS.
8. Total coliform (TC).
9. Total heterotrophic bacteria (THB).
10. Conductivity.

TABLE 2j

Physico-chemical parameters and bacterial population levels of Boahen Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.83	29.83	29.33	31.30	30.67	30.83
Water Temperature (°C)	31.50	31.33	29.50	32.00	30.00	32.10
pH	6.95	7.11	7.03	7.05	6.92	7.00
Acidity (mg/l ¹)	21.83	21.00	20.70	24.40	21.40	23.00
Alkalinity (mg/l ¹)	52.67	51.27	52.00	46.50	42.73	48.33
Calcium ion (mg/l ¹)	6.17	5.47	6.83	6.30	5.23	6.10
Total hardness (mg/l ¹)	41.33	38.67	56.00	37.00	38.00	37.50
Chloride ion (mg/l ¹)	17.27	17.30	17.97	16.00	16.93	17.53
Magnesium ion (mg/l ¹)	6.60	5.99	7.27	4.81	4.70	5.27
Phosphate ion (mg/l ¹)	2.02	1.99	1.96	2.11	1.87	1.60
Ammonium ion (mg/l ¹)	0.86	0.74	0.74	1.02	0.88	0.69
Nitrate ion (mg/l ¹)	0.27	0.22	0.15	0.25	1.10	0.78
Nitrite ion (mg/l ¹)	0.27	0.27	0.30	0.25	0.19	0.26
Sulphate ion (mg/l ¹)	0.07	0.09	0.09	0.06	0.06	0.04
Silicon dioxide (mg/l ¹)	3.73	4.78	4.73	3.50	5.10	3.70
Dissolved oxygen (mg/l ¹)	7.25	7.11	6.88	8.15	6.85	6.50
Biochemical oxygen demand (mg/l ¹)	4.03	3.67	3.80	3.85	3.93	3.97
Total dissolved solids (mg/l ¹)	51.00	67.67	60.67	62.00	54.00	51.33
Suspended solids (mg/l-1)	15.20	10.80	10.20	9.15	10.80	11.40
Turbidity (NTU)	51.67	53.13	13.33	61.50	50.30	63.00
Conductivity (Scm ¹)	147.00	144.00	146.67	135.00	146.80	123.00
Total coliform count x 10 ³ (ml ²)	70.67	87.33	71.33	48.00	75.00	70.00
Faecal coliform count x 10 ³ (ml ²)	1.57	1.70	1.77	1.00	1.03	1.32
Faecal streptococci count x 10 ³ (ml ²)	1.99	2.73	2.67	2.95	2.20	2.40
Total heterotrphic bacteria x 10 ³ (ml ²)	116.33	145.67	97.67	71.00	87.67	125.67

5. Chemically Fertilized Ponds

Aheto farm

The mean monthly values for Aheto farm are presented in Table 2k. Pearson product moment correlations between pairs of the physico-chemical and bacterial parameters showed significant and positive correlations between the following; alkalinity and THB, chloride and magnesium ions, conductivity and total hardness, FC and SS, FC and TDS, nitrite ion and SS, and phosphate ion and silicon dioxide. Variables which were significant but negatively correlated included acidity and conductivity, alkalinity and phosphate ion, ammonium and nitrate ions, BOD and conductivity, calcium and nitrite ions, chloride ion and pH, FC and nitrate ion, magnesium and sulphate ions, phosphate ion and THB, and sulphate ion and turbidity.

Nine homogenous groups were identified based on the Duncan's range tests:

1. Sulphate, ammonium, nitrite, nitrate, phosphate, FC, silicon, FS, turbidity, BOD, magnesium and pH.
2. FC, silicon dioxide, FS, turbidity, BOD, magnesium, pH and DO.
3. Turbidity, BOD, magnesium, pH, DO and calcium.
4. Calcium and SS.
5. SS and chloride.
6. Air temperature, acidity and water temperature.
7. TDS, total hardness and TC.
8. Conductivity and THB.
9. Alkalinity.

Sagoe farm

The mean monthly values for the 25 parameters are presented in Table 21. The Pearson product moment correlation showed significant and positive correlation between air temperature and alkalinity, air temperature and TC, air and water temperatures, alkalinity and TC, ammonium and nitrite ions, ammonium and phosphate ions, BOD and DO, BOD and THB, FC and FS, total hardness and sulphate ions, nitrite and phosphate ions, TDS and water temperature. Significant but negatively correlated variables were acidity and TDS, acidity and water temperature, air temperature and silicon dioxide, alkalinity and silicon dioxide, FS and phosphate ion, magnesium and sulphate ions, and silicon and water temperature.

TABLE 2k

Physico-chemical parameters and bacterial population levels of Aheto Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.17	29.50	30.33	30.25	31.17	29.83
Water Temperature (°C)	29.17	30.67	31.33	32.00	31.50	31.33
pH	7.05	6.85	7.10	7.01	6.87	7.00
Acidity (mg ^l ⁻¹)	31.00	33.33	31.67	32.50	26.67	29.33
Alkalinity (mg ^l ⁻¹)	110.17	115.00	117.33	94.00	102.00	126.67
Calcium ion (mg ^l)	12.18	11.25	11.54	11.25	10.47	10.79
Total hardness (mg ^l ⁻¹)	51.67	43.67	45.33	47.50	53.50	60.00
Chloride ion (mg ^l ⁻¹)	19.43	20.03	18.30	19.10	20.60	18.83
Magnesium ion (mg ^l ⁻¹)	6.33	6.37	5.66	6.37	6.80	6.07
Phosphate ion (mg ^l ⁻¹)	0.27	0.28	0.27	0.31	0.27	0.25
Ammonium ion (mg ^l)	0.03	0.00	0.01	0.05	0.01	0.02
Nitrate ion (mg ^l ⁻¹)	0.13	0.18	0.15	0.10	0.15	0.11
Nitrite ion (mg ^l ⁻¹)	0.09	0.11	0.10	0.12	0.12	0.14
Sulphate ion (mg ^l ⁻¹)	0.00	0.00	0.01	0.00	0.00	0.01
Silicon dioxide (mg ^l ⁻¹)	2.03	1.76	1.91	2.24	1.80	1.50
Dissolved oxygen (mg ^l ⁻¹)	7.90	9.03	8.93	8.85	8.13	8.53
Biochemical oxygen demand (mg ^l ⁻¹)	5.60	6.10	7.10	7.00	5.77	5.17
Total dissolved solids (mg ^l ⁻¹)	42.70	41.20	49.30	55.85	44.47	51.27
Suspended solids (mg ^l ⁻¹)	9.87	13.83	12.57	27.00	13.57	29.60
Turbidity (NTU)	6.00	6.67	5.33	6.00	5.83	5.33
Conductivity (Scm ⁻¹)	91.37	62.33	53.33	60.00	101.50	103.20
Total coliform count x 10 ³ (ml ⁻²)	43.00	66.87	67.07	46.50	65.67	52.00
Faecal coliform count x 10 ³ (ml ⁻²)	0.98	0.90	0.96	1.18	0.86	1.21
Faecal streptococci count x 10 ³ (ml ⁻²)	3.09	2.87	2.70	2.90	1.62	4.03
Total heterotrophic bacteria x 10 ³ (ml ⁻²)	85.33	90.00	102.00	56.50	76.00	48.67

TABLE 21

Physico-chemical parameters and bacterial population levels of Sagoe Farm Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.33	29.67	29.83	30.00	30.67	30.67
Water Temperature (°C)	30.00	31.00	31.50	31.50	31.67	32.67
pH	7.00	6.94	6.92	6.95	6.97	6.95
Acidity (mg ^l ⁻¹)	35.43	29.37	27.63	28.30	29.20	26.43
Alkalinity (mgr ^l ⁻¹)	71.67	70.27	71.33	76.45	76.73	77.07
Calcium ion (mg ^l ⁻¹)	17.65	17.03	17.58	17.17	17.87	17.67
Total hardness (mg ^l ⁻¹)	36.66	36.83	36.37	41.00	36.40	34.43
Chloride ion (mg ^l ⁻¹)	20.73	21.47	19.27	21.20	22.03	19.53
Magnesium ion (mg ^l ⁻¹)	0.02	0.03	0.06	0.00	0.03	0.02
Phosphate ion (mgr ^l ⁻¹)	0.52	0.55	0.60	0.62	0.68	0.53
Ammonium ion (mg ^l ⁻¹)	1.67	1.76	1.75	2.01	2.00	1.77
Nitrate ion (mg ^l ⁻¹)	0.04	0.02	0.06	0.07	0.04	0.04
Nitrite ion (mg ^l ⁻¹)	0.01	0.01	0.03	0.04	0.04	0.01
Sulphate ion (mg ^l ⁻¹)	6.56	6.67	5.63	8.12	6.61	6.13
Silicon dioxide (mg ^l ⁻¹)	20.03	19.10	19.28	18.35	18.43	18.33
Dissolved oxygen (mg ^l ⁻¹)	5.01	5.68	5.14	5.20	5.25	5.91
Biochemical oxygen demand (mg ^l ⁻¹)	1.81	2.07	1.60	1.96	2.02	2.32
Total dissolved solids (mg ^l ⁻¹)	71.07	77.63	80.13	76.65	78.77	83.70
Suspended solids (mg ^l ⁻¹)	25.30	31.87	30.33	22.10	23.33	27.03
Turbidity (NTU)	42.27	38.67	38.80	38.60	38.63	43.57
Conductivity (Scm ⁻¹)	157.47	156.33	148.33	167.50	142.00	155.07
Total coliform count x 10 ³ (ml ⁻²)	31.67	31.67	30.00	35.50	39.33	42.00
Faecal coliform count x 10 ³ (ml ⁻²)	0.98	1.10	0.72	1.05	0.42	1.20
Faecal streptococci count x 10 ³ (ml ⁻²)	1.36	1.20	0.73	1.15	0.75	1.50
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	78.00	71.00	54.00	67.00	75.33	91.33

Twelve homogenous groups were identified by the Duncan's range tests results:

1. Nitrite, magnesium, nitrate, phosphate, FC, FS, ammonium and BOD.
2. Ammonium, BOD and DO.
3. DO, sulphate and pH.
4. Calcium, silicon dioxide and chloride.
5. Suspended solids (SS), acidity and air temperature.
6. Acidity, air temperature and water temperature.
7. Water temperature and TC.
8. TC and total hardness.
9. Total hardness and turbidity.
10. THB and alkalinity.
11. Total dissolved solids (TDS).
12. Conductivity.

6. Pond without any form of Fertilizer (ARDEC 3)

The mean monthly values are presented in Table 2m. Pearson product moment correlations showed significant and positive correlations between ammonium and calcium ions, calcium ion and conductivity, calcium ion and total hardness, calcium ion and THB, total hardness and THB, magnesium ion and water temperature, and silicon dioxide and TDS. The only pair of variables which showed significant but negative correlation was DO and hardness. Calcium and total hardness both had their highest values in March.

Thirteen homogenous groups were identified among the 25 parameters:

1. Nitrite, phosphate, ammonium, nitrate, FS, FC, sulphate, magnesium, BOD, DO and pH.
2. Sulphate, magnesium, BOD, DO, pH and calcium.
3. BOD, DO, pH, calcium and silicon dioxide.
4. Calcium, silicon and chloride.
5. Silicon, chloride and SS.
6. Chloride, SS and acidity.
7. SS, acidity and turbidity.
8. Turbidity, air temperature and water temperature.
9. Air temperature, water temperature and total hardness.

TABLE 2m

Physico-chemical parameters and bacterial population levels of ARDEC 3 Cultured Pond water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	30.33	31.17	30.50	30.00	30.33	29.83
Water Temperature (°C)	29.50	31.83	30.00	33.00	31.67	32.17
pH	6.85	6.63	6.75	6.82	6.83	6.71
Acidity (mg/l ¹)	21.00	21.33	17.67	24.00	28.00	16.33
Alkalinity (mg/l ¹)	65.33	68.67	67.67	69.00	71.00	66.00
Calcium ion (mg/l ¹)	9.14	11.07	9.20	8.40	10.53	9.47
Total hardness (mg/l ¹)	33.00	41.00	29.67	33.00	36.33	33.67
Chloride ion (mg/l ¹)	17.83	18.00	13.07	11.00	14.62	18.14
Magnesium ion (mg/l ¹)	3.17	5.00	3.27	5.98	4.58	4.67
Phosphate ion (mg/l ¹)	0.11	0.08	0.02	0.00	0.19	0.26
Ammonium ion (mg/l ¹)	0.33	0.77	0.24	0.03	0.73	0.26
Nitrate ion (mg/l ¹)	0.05	0.68	0.66	0.03	0.84	0.12
Nitrite ion (mg/l ¹)	0.02	0.03	0.01	0.00	0.10	0.03
Sulphate ion (mg/l ¹)	2.93	2.63	6.71	2.15	6.50	4.81
Silicon dioxide (mg/l ¹)	13.21	12.54	16.48	11.45	11.70	12.97
Dissolved oxygen (mg/l ¹)	6.67	4.03	9.87	6.60	5.91	5.25
Biochemical oxygen demand (mg/l ¹)	2.53	1.62	4.55	3.68	2.14	2.72
Total dissolved solids (mg/l ¹)	58.70	53.43	85.13	34.17	42.70	63.37
Suspended solids (mg/l ⁻¹)	19.27	8.13	8.33	18.00	26.11	23.67
Turbidity (NTU)	31.40	15.67	21.33	19.50	23.80	33.47
Conductivity (Scm ¹)	112.30	130.70	113.80	102.65	123.23	129.67
Total coliform count x 10 ³ (ml ²)	36.33	52.67	60.33	58.00	44.33	45.00
Faecal coliform count x 10 ³ (ml ²)	1.03	1.01	1.34	1.10	0.80	0.97
Faecal streptococci count x 10 ³ (ml ²)	0.63	0.56	0.99	0.90	0.67	0.90
Total heterotrphic bacteria x 10 ³ (ml ²)	63.33	96.67	68.33	72.50	80.00	77.33

10. TC and total dissolved solids (TDS).
11. Alkalinity.
12. Total heterotrophic bacteria (THB).
13. Conductivity.

7. Open Systems

Kpong Headpond

The mean monthly values are presented in Table 2n. The Pearson moment correlations between pairs of the physico-chemical and bacterial parameters showed significant and positive correlation between ammonium ion and conductivity, ammonium ion and FS, ammonium ion and TDS, chloride and nitrite ions, chloride and pH, conductivity and FS, FS and TDS, total hardness and TC, nitrate and phosphate ions and nitrite ions and pH. Parameters which showed significant but negative correlation were acidity and silicon dioxide, conductivity and THB, FC and phosphate ion, FS and THB, magnesium ion and turbidity, phosphate and water temperature, and TDS and THB.

Five homogenous groups were identified by the Duncan's range tests:

1. Phosphate, nitrite, nitrate, ammonium, FS, sulphate, turbidity, SS, BOD, FC, magnesium, DO, pH, calcium, silicon and chloride.
2. Magnesium, DO, pH, calcium, silicon dioxide, chloride and acidity.
3. Water temperature, air temperature, total hardness and TDS.
4. Alkalinity, TC and THB.
5. Conductivity.

Volta River

The mean monthly values of the parameters are presented in Table 2o. The Pearson product moment correlation showed significant and positive correlations between alkalinity and nitrate ion, calcium ion and DO, chloride ion and FC, chloride ion and FS, chloride ion and silicon dioxide, conductivity and TDS, nitrate and nitrite ions, nitrate ion and turbidity, nitrite ion and turbidity, TC and THB, and THB and water temperature. Variables which showed significant but negative correlations were acidity and calcium ion, alkalinity and ammonium ion, alkalinity and conductivity,

TABLE 2n

Physico-chemical parameters and bacterial population levels of Kpong Headpond Open System

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.17	26.33	32.17	27.00	29.50	32.83
Water Temperature (°C)	28.33	29.17	29.67	27.75	29.17	30.33
pH	6.63	6.81	7.07	7.43	7.11	6.85
Acidity (mg/l ¹)	14.67	16.67	12.67	11.00	13.33	11.33
Alkalinity (mg/l ¹)	44.33	46.00	48.00	46.00	43.00	45.33
Calcium ion (mg/l ¹)	6.67	7.73	6.93	7.60	7.60	6.93
Total hardness (mg/l ¹)	56.33	27.00	20.33	30.00	24.67	32.00
Chloride ion (mg/l ¹)	9.00	9.67	10.33	12.00	10.33	10.50
Magnesium ion (mg/l ¹)	3.85	4.69	3.26	5.59	4.32	5.81
Phosphate ion (mg/l ¹)	0.07	0.01	0.03	0.07	0.00	0.00
Ammonium ion (mg/l ¹)	0.27	0.34	0.23	0.21	0.48	0.86
Nitrate ion (mg/l ¹)	0.64	0.14	0.29	0.54	0.19	0.16
Nitrite ion (mg/l ¹)	0.01	0.03	0.03	1.00	0.13	0.01
Sulphate ion (mg/l ¹)	0.43	0.37	0.07	13.40	2.45	1.35
Silicon dioxide (mg/l ¹)	7.30	6.10	8.18	11.75	9.96	11.44
Dissolved oxygen (mg/l ¹)	6.19	0.72	7.11	5.04	8.16	6.56
Biochemical oxygen demand (mg/l ¹)	2.40	4.24	2.61	2.96	2.35	2.10
Total dissolved solids (mg/l ¹)	35.63	32.10	33.80	34.75	35.23	40.00
Suspended solids (mg/l-1)	3.33	2.37	2.33	1.33	3.33	2.67
Turbidity (NTU)	2.00	0.30	3.22	0.17	2.10	1.00
Conductivity (Scm ¹)	67.67	65.47	67.67	69.35	70.60	80.67
Total coliform count x 10 ³ (ml ²)	76.67	35.67	31.00	33.50	50.00	48.38
Faecal coliform count x 10 ³ (ml ²)	2.37	3.50	2.40	1.90	4.37	3.83
Faecal streptococci count x 10 ³ (ml ²)	1.10	0.77	0.84	0.71	0.85	2.08
Total heterotrophic bacteria x 10 ⁴ (ml ²)	52.33	85.00	55.33	46.00	81.00	92.00

TABLE 2o

Physico-chemical parameters and bacterial population levels of Volta River Open System

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.83	28.00	29.50	26.75	20.17	28.33
Water Temperature (°C)	28.50	27.83	29.17	27.00	28.83	30.33
pH	6.70	6.84	7.57	7.48	7.14	6.86
Acidity (mgr ^l)	20.00	14.67	12.67	11.00	13.33	11.33
Alkalinity (mg ^l ⁻¹)	44.33	48.67	50.00	46.00	43.33	44.67
Calcium ion (mg ^l ⁻¹)	6.70	7.73	8.00	7.60	7.87	7.73
Total hardness (mg ^l ⁻¹)	43.00	31.67	24.67	30.00	27.67	32.67
Chloride ion (mg ^l ⁻¹)	9.33	9.33	9.33	12.00	10.33	11.00
Magnesium ion (mg ^l ⁻¹)	5.53	5.82	3.24	5.59	5.26	6.20
Phosphate ion (mg ^l ⁻¹)	0.07	0.01	0.07	0.02	0.04	0.00
Ammonium ion (mg ^l ⁻¹)	0.30	0.15	0.17	0.21	0.41	0.25
Nitrate ion (mg ^l ⁻¹)	0.15	0.33	1.33	0.30	0.07	0.12
Nitrite ion (mg ^l ⁻¹)	0.00	0.04	0.38	0.05	0.01	0.01
Sulphate ion (mg ^l ⁻¹)	0.33	1.03	3.26	0.43	2.68	1.09
Silicon dioxide (mg ^l ⁻¹)	7.70	3.83	7.52	11.60	6.64	11.05
Dissolved oxygen (mg ^l ⁻¹)	6.24	8.87	8.16	8.08	8.69	7.25
Biochemical oxygen demand (mg ^l ⁻¹)	3.48	3.92	1.61	2.80	2.37	2.19
Total dissolved solids (mg ^l ⁻¹)	36.30	32.27	35.63	35.35	38.80	39.23
Suspended solids (mg ^l ⁻¹)	2.67	3.00	2.67	2.50	1.33	4.00
Turbidity (NTU)	1.67	1.33	3.73	1.00	1.00	2.00
Conductivity (Scm ⁻¹)	71.40	65.23	67.47	70.85	77.67	77.27
Total coliform count x 10 ³ (ml ⁻²)	49.66	101.00	59.33	22.50	129.67	399.00
Faecal coliform count x 10 ³ (ml ⁻²)	3.50	5.10	2.83	7.00	6.36	6.50
Faecal streptococci count x 10 ³ (ml ⁻²)	2.37	1.03	1.02	4.32	3.71	2.98
Total heterotrophic bacteria x 10 ³ (ml ⁻²)	133.33	150.00	143.33	60.00	223.33	250.00

calcium ion and total hardness, magnesium and nitrate ions, magnesium and nitrite ions.

Four homogenous groups were identified by the Duncan's range tests:

1. Phosphate, nitrite, ammonium, nitrate, sulphate, turbidity, FS, SS, BOD, FC, magnesium, pH, calcium, DO, silicon dioxide, chloride, acidity, air temperature, water temperature, total hardness and TDS.
2. FC, magnesium, pH, calcium, DO, silicon dioxide, chloride, acidity, air temperature, water temperature, total hardness, TDS and alkalinity.
3. TDS, alkalinity and conductivity.
4. Total coliform (TC) and THB.

Weija dam

The mean monthly values for the study period for each parameter are presented in Table 2p. The Pearson product moment correlations showed significant and positive correlations between acidity and air temperature, ammonium ion and TDS, BOD and DO, chloride ion and TC, FC and silicon dioxide, FC and TC, FS and TC, FS and THB, total hardness and magnesium ion, magnesium ion and TDS, nitrate and pH, nitrate ion and SS, nitrite ion and SS, silicon dioxide and TC, silicon dioxide and THB, sulphate ion and THB and TC and THB. Parameters which showed significant but negative correlations were acidity and nitrate ion, acidity and SS, alkalinity and silicon dioxide, alkalinity and THB, ammonium ion and total hardness, ammonium and magnesium ions, calcium ion and water temperature, chloride ion and FC, chloride ion and silicon, magnesium ion and TDS and phosphate ion, and phosphate ion and water temperature.

Five homogenous groups were identified for the 25 parameters based on the Duncan's range tests:

1. Phosphate, nitrite, ammonium, nitrate, turbidity, FS, silicon dioxide, BOD, pH, DO, acidity, FC, sulphate, SS, magnesium, calcium, water temperature, air temperature and chloride.
2. DO, acidity, FC, sulphate, SS, magnesium, calcium, water temperature, air temperature, chloride and total hardness.
3. Chloride, total hardness and alkalinity.
4. Total hardness, alkalinity and TC.
5. THB, TDS and conductivity.

TABLE 2p

Physico-chemical parameters and bacterial population levels of Weija Dam Open System

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	33.17	31.50	30.17	29.50	30.67	34.67
Water Temperature (°C)	29.67	31.83	29.83	26.75	29.33	31.67
pH	7.00	7.10	7.90	8.20	7.50	7.53
Acidity (mg/l ¹)	11.33	9.33	7.33	8.00	11.67	13.00
Alkalinity (mg/l ¹)	119.33	132.00	131.33	113.50	118.67	110.00
Calcium ion (mg/l ¹)	16.00	15.73	15.20	19.00	16.93	13.73
Total hardness (mg/l ¹)	90.67	98.00	81.33	82.00	65.33	84.00
Chloride ion (mg/l ¹)	47.00	50.67	50.33	41.50	40.67	45.33
Magnesium ion (mg/l ¹)	18.17	16.74	14.12	15.34	11.50	15.94
Phosphate ion (mg/l ¹)	0.07	0.02	0.07	0.10	0.02	0.01
Ammonium ion (mg/l ¹)	0.24	0.21	0.54	0.45	0.77	0.30
Nitrate ion (mg/l ¹)	0.19	0.19	1.67	1.54	0.16	0.18
Nitrite ion (mg/l ¹)	0.08	0.21	0.61	0.18	0.11	0.02
Sulphate ion (mg/l ¹)	6.57	3.70	10.12	12.35	12.66	17.03
Silicon dioxide (mg/l ¹)	4.07	2.68	2.60	11.08	10.72	8.89
Dissolved oxygen (mg/l ¹)	7.51	11.04	10.08	8.32	10.64	8.55
Biochemical oxygen demand (mg/l ¹)	5.53	8.59	7.95	6.44	9.04	6.91
Total dissolved solids (mg/l)	220.10	236.67	602.00	245.50	145.20	149.10
Suspended solids (mg/l-1)	8.33	9.40	18.33	13.50	6.33	8.00
Turbidity (NTU)	6.00	5.67	5.33	2.50	6.33	6.33
Conductivity (Scm ¹)	450.50	471.33	231.00	491.50	291.27	313.67
Total coliform count x 10 ³ (ml ³)	67.67	67.33	81.33	265.50	253.00	203.33
Faecal coliform count x 10 ³ (ml ²)	7.06	7.60	7.30	16.65	14.03	9.57
Faecal streptococci count x 10 ³ (ml ²)	3.50	4.87	5.53	6.60	6.90	6.67
Total heterotrphic bacteria x 10 ³ (ml ²)	101.00	134.67	148.33	460.00	421.33	570.67

B. Isolation of Pure Cultures and Identification of Bacterial Flora of Water of the Cultured Ponds and Open System.

Twenty-five genera were identified by the results of the various tests tabulated in Table 3. The identified genera belonged to the **Spiral and curved bacterium** (*Campylobacter* sp.), **Gram-negative aerobic rod** (*Pseudomonas* sp.), **Gram-negative facultatively anaerobic rods** (*Actinobacillus* sp., *Aeromonas* sp., *Citrobacter* sp., *Edwardsiella* sp., *Enterobacter* sp., *Escherichia* sp., *Flavobacterium* sp., *Hafnia* sp., *Klebsiella* sp., *Pasteurella* sp., *Proteus* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Vibrio* sp. and *Yersinia* sp.), **Gram-negative anaerobic bacterium** (*Bacteroides* sp.), **Gram-positive cocci** (*Micrococcus* sp., *Staphylococcus* sp. and *Streptococcus* sp.), **Endospore-forming rods** (*Bacillus* sp and *Clostridium* sp.) and **Actinomycetes related organism** (*Corynebacterium* sp). Plates 5a - 51 are photomicrographs of some of the isolates.

1. Cow manure-Fertilized Ponds

Aduabenba farm

Seventeen genera of bacteria were isolated from this pond as shown in Table 4a. Putting the values for the three years together *Bacillus* sp. was found to occur most frequently (16.18%) throughout the study period. This organism was followed by *Pseudomonas* sp. (15.59%), *Corynebacterium* sp (10.44%), *Flavobacterium* sp. (10.44%), *Micrococcus* sp. (10.15%), *Staphylococcus* sp. (9.71%), *Proteus* sp. (8.82%), and *Streptococcus* sp. (8.24%) and *Escherichia* sp. (3.97%). Eight species, *Aeromonas* sp., *Bacteroides* sp., *Campylobacter* sp., *Enterobacter* sp., *Pasteurella* sp., *Salmonella* sp., *Serratia* sp. and *Shigella* sp. were in low occurrence.

Boateng farm

The data in Table 4b indicated that 19 bacterial genera were identified from the Boateng farm. Species representing more than 4.00% of the total numbers of colonies were, in descending order of magnitude: *Pseudomonas* sp. (18.38%), *Corynebacterium* sp. (12.35%), *Micrococcus* sp. (11.47%), *Flavobacterium* sp. (10.44%), *Escherichia* sp. (10.15%), *Bacillus* sp. (10.00%), *Streptococcus* sp. (8.24%) and *Proteus* sp. (5.44%). The remaining 11 species representing less than 4.00% in each case were, *Actinobacillus* sp., *Aeromonas* sp., *Campylobacter* sp.,

TABLE 3

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species	Characteristics of Cultures on Agar	Morphology of cell	Crum stain	Kudos pore formation	Indole production
<i>Actinobacillus sp.</i>	Rough and sticky. Colony surrounded by greenish tinge on blood agar. Colony on BUI agar had star-like centre	Spherical, oval or rod-shaped cells, 0.4 x 1.0 µm. Longer forms up to 6µm.			
<i>Aeromonas sp.</i>	Small beta-haemolytic colony on blood agar. Yellow colony TCBS.	Straight rods, rounded ends. 0.3 - 1.0µm in diameter and 1.0 - 3.5µm in length. Occurred singly, in pairs or short chains.			+
<i>Bacillus sp.</i>	Gray white, irregular colony with wavy margin on blood agar. Non-haemolytic or slightly haemolytic	Rod shaped and straight 0.5 - 2.5 x 1.2 - 10µm. In pairs or short chains. Rounded or squared ends. Endospores oval, round or cylindrical.	+	+	
<i>liacteroides sp.</i>	Gray, non-haemolytic, 1-3mm glistening colony on Neomycin blood agar. Microaerophilic/Anaerobic	Rod shaped. 0.5 x 2.0 - 3.0µm. Pleomorphic and show terminal or central swellings. Vacuoles or filaments present.			
<i>Campylobacter sp.</i>	Gray to pinkish or yellowish gray, slightly mucoid-looking. Droplet-like colony on blood agar. Non-haemolytic. Microaerophilic.	Slender vibrioid cell 0.2 - 0.5µm wide and 0.5 - 5.0µm long. Spirally curved cell appearing S-shaped			
<i>Citrobacter sp.</i>	Gray, shiny, entire, convex and opaque colony on blood agar.	Rod-shaped. Straight, 1 µm in diameter and 2 - 6µm in length. Occurred singly or in pairs.			+
<i>Clostridium sp.</i>	Circular, 3-8mm in diameter, opaque centre, rhizoid margin, translucent, gray, matt to semi-glossy surface on Neomycin blood agar. Large beta-haemolytic. Anaerobic.	Rod-shaped, 0.3 - 2.0 x 1.5 - 20 µm, in pairs or short chain. Rounded or pointed ends. Pleomorphic. Endospore oval or spherical, distal cell.	+	+	
<i>Corynebacterium sp</i>	Opaque, white or gray, non-haemolytic or alpha haemolytic on blood agar. Anaerobic.	Rod-shaped. Pleomorphic, long thin and curved or short and enlarged at one end. In clusters. 0.3-0.8 x 1.0 - 8.0µm	+		

TABLE 3 (cont'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species*	Methyl Red test	Vogt's-Proskauer test	Catalase test	Oxidation test	Indole production	Nitrate reduction	Oxidation(O)/Fermentation(F)	Spore formation
<i>Actinobacillus</i> sp.		+		+		+	O	+/-
<i>Aeromonas</i> sp.	+	+/-	+	+	+	+	O	+
<i>Bacillus</i> sp.	I/-			+/-	I-	-IV-	I-	I-
<i>Bacteroides</i> sp.			+				F	
<i>Campylobacter</i> sp.				+	+	+		+
<i>Citrobacter</i> sp.	+		+		+	+	F	+
<i>Clostridium</i> sp.			+			+	I-	
<i>Corynebacterium</i> sp.	+					+	F	+

TABLE 3 (cont'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species	Production of hydrogen sulphide	Gelatin hydrolysis	Starch hydrolysis	Urease utilisation	Krtictose utilisation	Glucose utilisation	Mannitol utilisation
<i>Actinobacillus</i> sp.		+		+/-	A	A	A
<i>Aeromonas</i> sp.		+	+		AG	AG	A
<i>Bacillus</i> sp.		+/-	+		AG	AG	A
<i>Bacteroides</i> sp.	+	+/-		+/-			
<i>Campylobacter</i> sp.							
<i>Citrobacter</i> sp.		+		+	AG	AG	AG
<i>Clostridium</i> sp.		+/-			AC!	AG	
<i>Corynebacterium</i> sp.			+		A	A	A

TABLE 3 (cont'd)

Characteristics of the bacterial isolates from the Cultured Ponds and Open systems

Bacterial species	Characteristics of Culture on Agar	Morphology of cell	Cram stain	Kndosporc formation	Indole production
<i>Edwardsiella sp.</i>	Medium to large, shiny, gray colonies with green colour around sub-surface colony on blood agar	Straight rods with diameter 1.0µm and 2.0 - 3.0µm long			+
<i>Enterobacter sp.</i>	Medium to large colonies, slimy, grey on blood agar	Straight rods 0.6 - 1.0µm wide x 1.2 - 3.0µm long	-	~	■
<i>Escherichia sp.</i>	Colonies 1-4mm in diameter on blood agar, mucoid, haemolytic.	Rods 1.1-1.5µm x 2.0 - 6.0µm. Occurred singly or in pairs.			+
<i>Flavohacterium sp.</i>	Yellow colonies on blood tigr surrounded by lavender-green discoloration, 1 -2mm, translucent or opaque, circular, convex, smooth, shiny, entire edges	Long, thin, filamentous rods, swollen ends. Rounded ends 0.5 x 1.0 - 3.0µm.			
<i>Hafnia sp.</i>	Medium to large, shiny, gray colony on blood agar.	Straight rods, lum in diameter and 2.0 - 5.0µm in length.			
<i>Klebsiella sp.</i>	Large and mucoid on blood agar	Rod-shaped, capsulated, 0.7 - 1.0 µm in diameter and 0.6 - 6.0µm in length. Singly, pairs or short chains			
<i>Micrococcus sp</i>	Shades of yellow or red, circular, opaque, smooth colonies on blood agar. Butyrous.	Spherical cells, 0.5 - 2.0µm in diameter. Pairs, tetrads, or irregular clusters.	+		
<i>Pasteurella sp.</i>	Mucoid, smooth, or rough on blood agar. Non-haemolytic but produced brownish discoloration of the medium	Spherical, ovoid or rod-shaped 0.3 - 1.0µm in diameter and 1.0 - 2.0µm in length. Occurred singly, pairs or short chains.			
<i>Proteus sp.</i>	Spread on agar like waves. Gray, shiny, entire, convex and opaque. Non-lacose fermenting on SS agar. Distinctive smell.	Straight rods, 0.4 - 0.8µm in diameter and 1.0 - 3.0 µm in length.			
<i>Pseudomonas sp.</i>	Large or small, flat, haemolytic on blood agar. Yellow-green pigmentation produced. Colonies fluoresce green in IIV light.	Straight or slightly curved rods, 0.5 -1.0 x 1.5 -5.0µm. Cells singly,			

TABLE 3 (cont'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species	Methyl Red test	Voges-Proskauer test	Citrate utilisation	Oxidase test	Motility	NI Crat reduction	Oxidative(O)/ Fermentative(F)	Catalase test
<i>Edwardsiella</i> sp.	+				+	+	F	+
<i>Enterobacter</i> sp.		+	-h		+	+	F	+
<i>Escherichia</i> sp.	+				+	+	F	+
<i>Flavobacterium</i> sp.		+					O	+
<i>Hafnia</i> sp.	+/-	+			+	+	F	+
<i>Klebsiella</i> sp.	+/-	+	+			+	F	+
<i>Micrococcus</i> sp.	+			+			O	+
<i>Pasteurella</i> sp.				+		+	F	+
<i>Proteus</i> sp.	+	+/-	+/-		+	+	F	+
<i>Pseudomonas</i> sp.		+	+	+	+	+	O	+

TABLE 3 (cont'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species	Production of hydrogen sulphide	Gelatin hydrolysis	S larch hydrolysis	Urease utilisation	Fructose utilisation	Glucose utilisation	Mannitol utilisation
<i>Edwardsiella sp.</i>	+/-				A	AG	
<i>Rnterobacter sp.</i>					AG	AG	A
<i>Escherichia sp.</i>					AG	AG	AG
<i>Flavobacterium sp.</i>	+	+			AG	A	A
<i>Ilafnia sp.</i>	+/-				A	AG	A
<i>Klebsiella sp.</i>				H-	A	AG	A
<i>Micrococcus sp</i>					A	A	A
<i>Pasteurella sp.</i>	-i-		+		A	A	A
<i>Proteus sp.</i>	+	+	+	+	AG	AG	
<i>Pseudomonas sp.</i>		-i-			A	AG	AG

TAHUi 3 (conl'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial sppcies	Characteristics of Culture on Agar	Morphology of cell	Gram stain	Endospore formation	Indole production
<i>Salmonella</i> sp.	Non-laclose fermenting colony on SS agar. Blackening of colony (due to H ₂ S production) Pink colonics on Mact'conkey agar.	Straight rods, 0.7 - 1.5 x 2 - 5 pm.			
<i>Serratia</i> sp.	Medium to large, shiny, gray on blood agar. Haemolytic. Translucent on MacConkey agar	Straight rods, 0.5 - 0.8pm in diameter and 0.9 - 2.0pm in length.			
<i>Shigella</i> sp.	Medium lo large, shiny, gray on blood agar. Haemolytic. Translucnl on MacConkey agar.	Straight rods. 0.4 - 0.6 x 1.0 - 3.0pm			+/-
<i>Staphylococcus</i> sp.	Yellow to cream, white, 1-2mm in diameter on blood agar. Beta-haemolytic. Raised Smaller, non-lactose fermenting on MacConkey agar.	Cells spherical, 0.5 - 1.5pm in diameter. Occurred singly, pairs or irregular clusters.	+		
<i>Streptococcus</i> sp.	Ciray to while or colourless, dry or slimy and irregular in outline, less Hum 1 nun in diameter on blood agar. Haemolytic	Cells spherical or ovoid, 0.6 - 2.0 x 0.6 - 2.5pm. Occurred in pairs or short chains	+		
<i>Vibrio</i> sp.	Yellow colonics, 2-3mm in diameter on TCBS agar. Also green-blue colonics. Haemolytic on blood agar.	Curved rods, 0.5 - 0.ftpm in width and 1.4 -2.6pm in length.			+
<i>Yersinia</i> sp.	Small, shiny non-haemolytic on blood agar	Straight rods, approaching a spheriical shape, 0.5 - 0.Kpm in diameter and 1 - 3pm in length.			+/-

TABLE 3 (conl'd)

Characteristics of the Bacterial isolates from the Cultured Ponds and Open Systems

Bacterial species	Methyl Red test	Voges-Proskauer test	Citrate utilisation	Oxidase test	Motility	Nitrate reduction	Oxidative(O)/ Fermentative(F)	Catalase test
<i>Salmonella</i> sp.	+				+	+	F	+
<i>Serratia</i> sp.		+	+		+	+	F	+
<i>Shigella</i> sp.	+					+	H	+
<i>Staphylococcus</i> sp.	+					+	F	+
<i>Streptococcus</i> sp.	+		+				F	
<i>Vibrio</i> sp.	+/-	+	+/-	+	+	+	F	+
<i>Yersinia</i> sp.	+					+	F	+

TABLE 3 (cont'd)

Characteristics of the Bacterial isolates from Ibc (Polluted Ponds and Open Systems)

Uictrifli specie.s	Production (>r hydrogen .sulphide	Gelatin hydrolysis	Si inch hydrolysis	Urease utilisation	Fructose utilisation	Glucose utilisation	Mannitol utilisation
<i>Salmonella sp.</i>	1/-				A	AG	AC I
<i>Serratia sp.</i>		+			A	AG	A
<i>Shigella sp.</i>					A	A	A
<i>Staphylococcus sp.</i>	+	+		+	A	A	A
<i>Streptococcus sp.</i>				+	A	A	A
<i>Vibrio sp.</i>		+	+/-		A	A	A :
<i>Yersinia sp.</i>				1	A	A	A

Plate 5a. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Aeromonas* species cultured on TCBS agar.

Plate 5b. Photomicrograph [Nikon, 1 00x, oil immersion objective] of one of the *Bacillus* species showing endospores.

Plate 5c. Photomicrograph [Nikon, 1 00x, oil immersion objective] of one of the *Clostridium* species showing endospores.

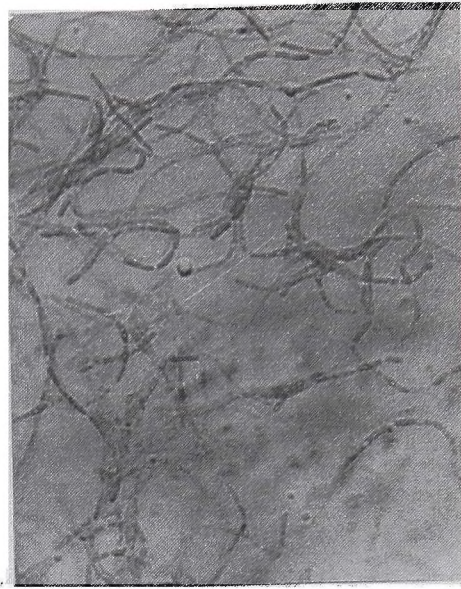
Plate 5d. Photomicrograph [Nikon, 1 00x, oil immersion objective] of one of the *Corynebacterium* species cultured on Blood agar.

Plate 5e. Photomicrograph [Nikon, 1 00x, oil immersion objective] of one of the *Escherichia* species cultured on Eosin Methylene Blue agar.

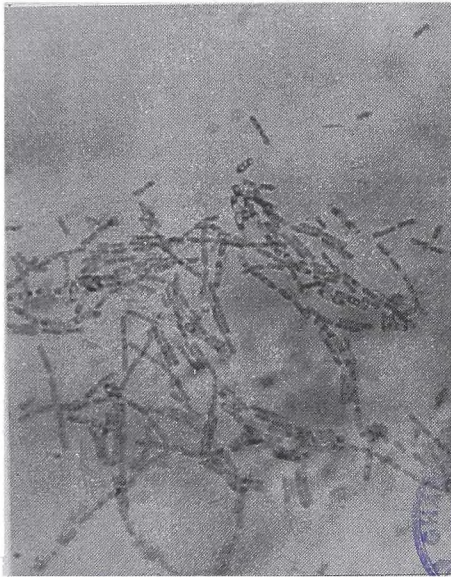
Plate 5f. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Flavobacterium* species cultured on Blood agar.



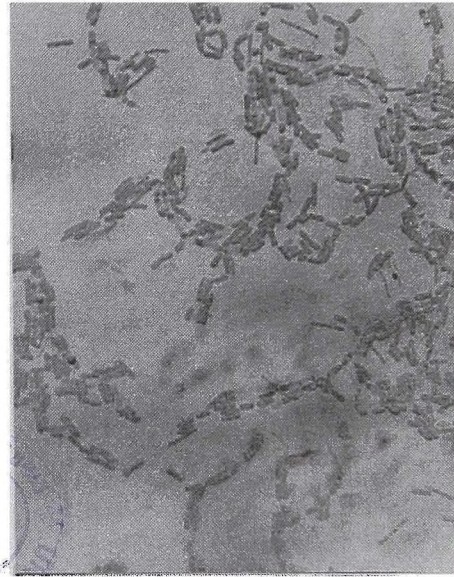
5a



5d



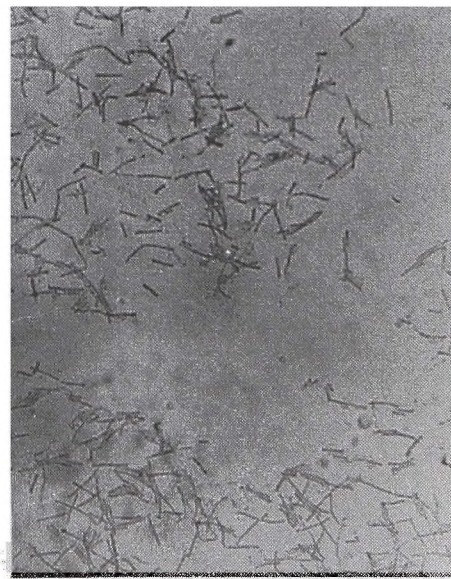
5b



5e



5c



5f

Plate 5g. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Klebsiella* sp. KI-MTC-004K cultured on MacConkey agar.

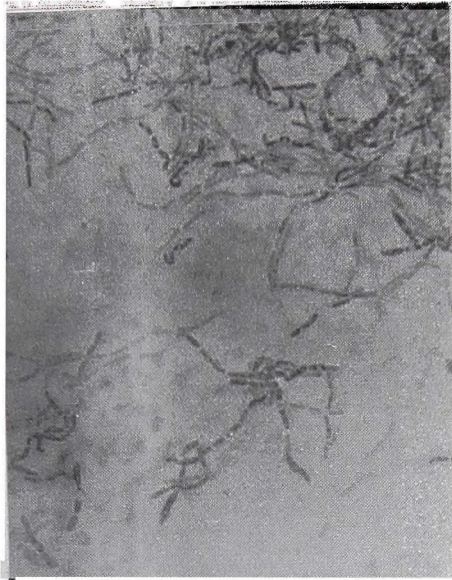
Plate 5h. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Staphylococcus* species.

Plate 5i. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Salmonella* sp. KI-MTC-007K cultured on Brilliant Green agar.

Plate 5j. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Serratia* species.

Plate 5k. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Micrococcus* species cultured on Blood agar.

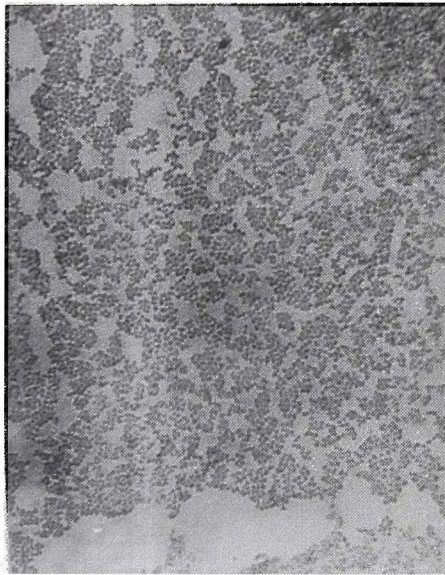
Plate 5l. Photomicrograph [Nikon, 100x, oil immersion objective] of one of the *Vibrio parahaemolyticus* KI-MTC-008K cultured on TCBS agar.



5g



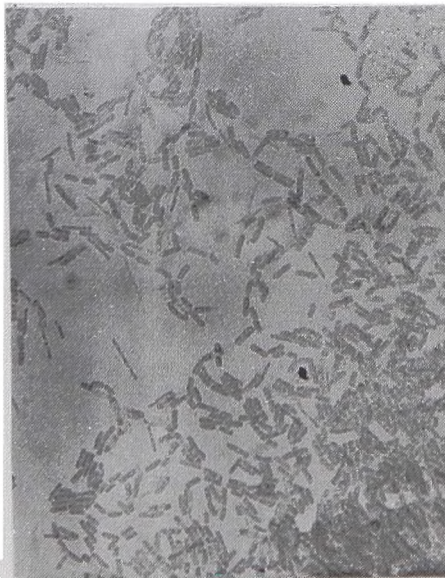
5j



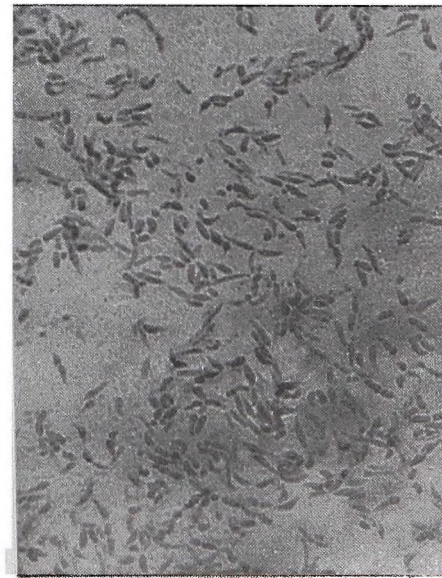
5h



5k



5i



5l

Citrobacter sp., *Clostridium* sp., *Enterobacter* sp., *Klebsiella* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp. and *Staphylococcus* sp.

2. Poultry manure-Fertilized Ponds

Agyeman farm

Twenty-two bacterial genera were identified in the pond of Agyeman farm during the study period as listed in Table 4c. *Pseudomonas* sp. was found to occur most frequently (12.14%) followed in descending order by *Escherichia* sp. (10.74%), *Streptococcus* sp. (8.82%), *Micrococcus* sp. (7.94%), *Citrobacter* sp. (7.65%), *Proteus* sp. (7.35%), *Enterobacter* sp. (6.76%), *Klebsiella* sp. (6.47%), *Aeromonas* sp. (4.56%) and *Corynebacterium* sp. (4.41%). Those with less than 4.00% occurrence were *Bacillus* sp., *Bacteroides* sp., *Campylobacter* sp., *Clostridium* sp., *Edwardsiella* sp., *Flavobacterium* sp., *Hafnia* sp., *Pasteurella* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp. and *Yersinia* sp.

ARDEC 20

The data in Table 4d showed that 18 bacterial genera were identified in the ARDEC 20 pond. They included *Salmonella* sp. (19.12%), *Pseudomonas* sp. (18.09%), *Streptococcus* sp. (15.88%), *Escherichia* sp. (15.74%), *Proteus* sp. (9.85%) and *Micrococcus* sp. (7.08%). The remaining twelve, *Aeromonas* sp., *Bacillus* sp., *Campylobacter* sp., *Citrobacter* sp., *Clostridium* sp., *Corynebacterium* sp., *Edwardsiella* sp., *Enterobacter* sp., *Flavobacterium* sp., *Klebsiella* sp. and *Yersinia* sp. were of low occurrence.

Asare farm

Eighteen bacterial genera were identified from the farm as shown in Table 4e. Those representing more than 4.00% of the colonies were *Pseudomonas* sp. (18.35%), *Escherichia* sp. (11.47%), *Streptococcus* sp. (10.88%), *Corynebacterium* sp. (10.00%), *Micrococcus* sp. (9.56%), *Bacillus* sp. (8.82%), *Flavobacterium* sp. (8.53%), *Staphylococcus* sp. (7.35%), and *Proteus* sp. (6.62%). The remaining nine genera, representing less than 4.00% of the colonies in each case were *Actinobacillus* sp., *Aeromonas* sp., *Bacteroides* sp., *Campylobacter* sp., *Citrobacter* sp., *Clostridium* sp., *Enterobacter* sp., *Klebsiella* sp. and *Serratia* sp.

TABLE 4c

Bacterial species isolated from Agyeman Farm Cultured Pond in 1996 -1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aeromonas sp.</i>	2.33	2.00	2.67	2.50	1.00	2.50
<i>Bacillus sp.</i>	0.33	3.00	0.33	0.00	1.50	1.50
<i>Bacteroides sp.</i>	0.67	0.33	0.67	0.00	0.00	0.00
<i>Campylobacter sp.</i>	1.33	2.00	0.67	2.00	2.00	1.00
<i>Citrobacter sp.</i>	2.67	2.67	3.33	4.50	2.00	3.00
<i>Clostridium sp.</i>	1.33	1.00	0.67	0.00	1.50	1.00
<i>Corynebacterium sp.</i>	1.33	2.33	1.33	1.00	2.50	2.50
<i>Edwardsiella sp.</i>	0.67	0.00	0.00	1.00	1.00	0.00
<i>Enterobacter sp.</i>	2.67	2.67	2.00	3.50	2.00	3.00
<i>Escherichia sp.</i>	5.33	2.33	5.33	3.50	4.00	5.00
<i>Flavobacterium sp.</i>	0.67	0.00	1.00	0.00	2.50	0.00
<i>Hafnia sp.</i>	0.00	1.00	0.00	0.00	0.00	1.00
<i>Klebsiella sp.</i>	3.67	2.33	2.33	3.00	1.50	2.50
<i>Micrococcus sp.</i>	3.33	4.00	3.67	4.00	2.50	3.00
<i>Pasteurella sp.</i>	0.00	0.00	1.33	0.00	0.00	1.00
<i>Proteus sp.</i>	3.00	1.67	3.33	4.00	3.00	3.50
<i>Pseudomonas sp.</i>	4.33	4.00	6.00	5.00	5.00	4.00
<i>Salmonella sp.</i>	0.00	4.33	0.00	0.00	3.00	0.00
<i>Serratia sp.</i>	1.33	0.00	1.33	2.00	0.00	1.00
<i>Shigella sp.</i>	0.00	1.33	0.33	0.00	2.00	0.00
<i>Staphylococcus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Streptococcus sp.</i>	4.33	3.00	3.00	4.00	3.00	4.00
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.67	0.00	0.67	0.00	0.00	0.50

Frimpong farm

The data in Table 4f showed that 24 bacterial genera were identified in the Frimpong farm of which each of the following represented more than 4.00% of the total colonies: *Salmonella* sp. (21.91%), *Pseudomonas* sp. (10.59%), *Streptococcus* sp. (10.44%), *Micrococcus* sp. (8.53%), *Escherichia* sp. (7.94), *Proteus* sp. (6.62%), *Bacillus* sp. (6.03%), *Shigella* sp. (4.85%) and *Enterobacter* sp. (4.56%). The remaining of lesser counts represented the remaining of the 25 genera except *Vibrio* sp. which was not encountered.

3. Pig manure-Fertilized Ponds

Boadi farm

As shown in Table 4g, 15 bacterial genera were identified. *Streptococcus* sp. occurred most frequently with a frequency of 24.71% for the study period. This was followed by *Clostridium* sp. (24.12%), *Pseudomonas* sp. (12.79%), *Escherichia* sp. (9.26%), *Micrococcus* sp. (9.12%), *Proteus* sp. (7.50%), *Yersinia* sp. (3.97%), *Corynebacterium* sp. (3.24%). Seven genera, *Aeromonas* sp., *Bacillus* sp., *Campylobacter* sp., *Citrobacter* sp., *Edwardsiella* sp., *Enterobacter* sp. and *Klebsiella* sp. occurred in lesser percentage.

KK farm

The genera encountered in KK farm are presented in Table 4h. Twenty genera were identified. The major ones were *Streptococcus* sp. (23.86%), *Clostridium* sp. (23.46%), *Pseudomonas* sp. (13.16%), *Escherichia* sp. (9.86%), *Proteus* sp. (7.40%), *Micrococcus* sp. (5.96%) and *Bacillus* sp. (4.96%); and the minor ones were *Aeromonas* sp., *Bacteroides* sp., *Citrobacter* sp., *Corynebacterium* sp., *Edwardsiella* sp., *Enterobacter* sp., *Flavobacterium* sp., *Klebsiella* sp., *Pasteurella* sp., *Salmonella* sp., *Shigella* sp., *Staphylococcus* sp. and *Yersinia* sp.

(c). Pacific farm

Twenty four bacterial genera were identified (Table 4i). The only genus which was not isolated from Pacific farm was *Flavobacterium* sp. The genera which occurred most frequently was *Streptococcus* sp. (23.24%). This was closely followed by *Clostridium* sp. (23.09%), The rest of the major species were *Pseudomonas* sp. (9.85%), *Escherichia* sp. (7.50%), *Micrococcus* sp. (6.91%), *Proteus* sp. (6.18) and

TABLE 4f

Bacterial species isolated from Frimpong Farm Cultured Pond in 1996 -1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.00	0.00	0.33	0.00	0.00	0.00
<i>Aeromonas sp.</i>	0.00	0.00	0.33	0.50	0.00	0.00
<i>Bacillus sp.</i>	2.00	4.00	1.67	1.00	3.00	4.00
<i>Bacteroides sp.</i>	0.67	0.00	0.00	0.00	1.00	0.00
<i>Campylobacter sp.</i>	0.33	0.00	0.00	2.00	1.00	0.00
<i>Citrobacter sp.</i>	0.67	0.67	1.00	0.50	1.00	0.50
<i>Clostridium sp.</i>	0.67	3.00	0.67	1.50	1.00	1.00
<i>Corynebacterium sp.</i>	1.67	1.00	1.67	0.50	2.50	0.00
<i>Edwardsiella sp.</i>	0.33	0.33	0.00	0.50	0.00	0.00
<i>Enterobacter sp.</i>	1.33	2.00	1.67	2.00	1.00	3.00
<i>Escherichia sp.</i>	3.00	2.33	5.00	2.50	3.50	3.00
<i>Flavobacterium sp.</i>	0.00	0.00	0.00	0.00	1.00	0.00
<i>Hafnia sp.</i>	0.33	0.00	0.33	0.00	0.00	0.00
<i>Klebsiella sp.</i>	0.33	0.00	1.67	3.00	1.00	0.00
<i>Micrococcus sp.</i>	4.67	2.33	4.33	2.50	2.00	4.00
<i>Pasteurella sp.</i>	0.00	0.00	0.00	1.00	0.00	0.00
<i>Proteus sp.</i>	2.33	2.67	2.67	2.50	2.50	3.00
<i>Pseudomonas sp.</i>	4.33	4.00	3.00	5.00	5.50	4.00
<i>Salmonella sp.</i>	10.00	9.33	8.67	8.50	7.50	9.00
<i>Serratia sp.</i>	0.67	0.33	2.00	1.00	1.00	0.50
<i>Shigella sp.</i>	1.67	1.67	1.67	2.50	1.50	3.00
<i>Staphylococcus sp. \</i>	0.00	1.00	0.00	0.00	0.00	0.00
<i>Streptococcus sp.</i>	5.00	5.00	3.33	3.00	4.00	5.00
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.00	0.33	0.00	0.00	0.00	0.00

TABLE 4g

Bacterial species isolated from Boadi Farm Cultured Pond in 1996 - 1999

SPECIES	Moan Number of Colony Forming Units ml ⁻¹ Isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aeromonas sp.</i>	0.33	0.00	0.00	0.00	0.50	0.00
<i>Bacillus sp.</i>	0.33	0.33	0.33	0.50	0.50	0.00
<i>Bacteroides sp.</i>	0.00	0.33	0.00	0.00	0.00	0.00
<i>Campylobacter sp.</i>	0.00	0.00	0.33	0.00	0.50	0.50
<i>Citrobacter sp.</i>	1.00	1.00	0.33	0.50	0.00	0.50
<i>Clostridium sp.</i>	9.33	9.67	9.33	10.00	9.50	10.00
<i>Corynebacterium sp.</i>	1.67	0.67	1.67	1.00	1.00	1.50
<i>Edwardsiella sp.</i>	0.00	0.00	0.00	0.00	0.50	0.00
<i>Entorobactor sp.</i>	0.67	0.67	0.33	0.50	0.00	0.00
<i>Escherichia sp.</i>	3.67	4.00	4.00	3.50	3.00	4.00
<i>Flavobacterium sp.</i>	0.33	0.00	0.00	0.00	0.00	0.00
<i>Hafnia sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Klebsiella sp.</i>	0.67	0.00	0.00	0.00	1.00	0.50
<i>Micrococcus sp.</i>	3.67	4.00	4.00	3.50	3.50	3.50
<i>Pasteurella sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Proteus sp.</i>	3.33	2.67	3.67	3.00	2.50	2.00
<i>Pseudomonas sp.</i>	4.67	4.67	5.00	5.50	5.50	6.00
<i>Salmonella sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Serratia sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Shigella sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Staphylococcus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Streptococcus sp.</i>	10.00	10.00	9.33	10.00	10.00	10.00
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.67	2.00	1.67	2.00	2.50	1.50

TABLE 4h

Bacterial species isolated from K.K. Farm Cultured Pond in 1996 - 1999

SPECIES	Mean Number of Colony Forming Units ml-1 isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.33	0.00	0.00	0.00	0.00	0.00
<i>Aeromonas sp.</i>	0.33	0.00	0.00	0.00	0.00	0.50
<i>Bacillus sp.</i>	2.67	2.67	3.00	0.00	3.00	1.50
<i>Bacteroides sp.</i>	0.00	0.33	0.00	1.00	0.00	0.00
<i>Campylobacter sp.</i>	0.33	0.33	0.33	0.00	0.00	0.00
<i>Citrobacter sp.</i>	1.33	0.67	0.67	0.50	0.00	1.50
<i>Clostridium sp.</i>	9.33	9.67	9.33	10.00	9.00	9.50
<i>Corynebacterium sp.</i>	0.33	0.33	0.33	2.00	0.50	0.00
<i>Edwardsiella sp.</i>	0.67	0.00	0.00	0.00	0.00	0.00
<i>Enterobacter sp.</i>	1.00	0.33	0.00	0.00	0.00	0.00
<i>Escherichia sp.</i>	3.00	3.67	3.67	3.50	3.00	5.50
<i>Flavobacterium sp.</i>	0.00	0.00	0.00	0.00	0.00	1.00
<i>Hafnia sp.</i>	0.00	0.33	0.00	0.00	0.00	0.00
<i>Klebsiella sp.</i>	0.67	0.00	0.00	0.00	0.00	0.00
<i>Micrococcus sp.</i>	2.33	2.33	3.00	2.50	2.00	2.00
<i>Pasteurella sp.</i>	0.00	0.00	0.00	0.00	0.00	0.50
<i>Proteus sp.</i>	2.67	2.33	3.33	2.50	2.50	3.50
<i>Pseudomonas sp.</i>	4.33	5.67	5.00	5.50	7.00	4.00
<i>Salmonella sp.</i>	0.67	0.67	0.00	0.00	1.00	0.00
<i>Serratia sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Shigella sp.</i>	0.00	0.00	0.00	0.00	1.00	0.00
<i>Staphylococcus sp.</i>	0.00	0.67	0.00	0.00	1.00	0.00
<i>Streptococcus sp.</i>	9.33	9.67	10.00	10.00	9.00	10.00
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.67	0.33	1.33	2.50	1.00	0.50

Bacillus sp. (3.82%).

4. Blood waste-Fertilized Ponds of Boahen farm

Twenty four bacterial genera were also identified from the Boahen farm (Table 4j), but the missing genus in this case was *Vibrio* sp. Genera with more than 3.00% of the total number of colonies were *Pseudomonas* sp. (15.74%), *Streptococcus* sp. (11.18%), *Bacillus* sp. (10.88%), *Micrococcus* sp. (10.29%), *Escherichia* sp. (8.68%), *Proteus* sp. (8.09%), *Edwardsiella* sp. (4.71%), *Corynebacterium* sp. (4.56%), *Enterobacter* sp. (3.68%) and *Staphylococcus* (3.60%).

5. Chemically Fertilized Ponds

Aheto farm

Table 4k shows the 21 bacterial genera identified from the farm. The most frequently occurring genus was *Pseudomonas* sp. (15.29%). The other major genera were *Escherichia* sp. (11.91%), *Streptococcus* sp. (10.88%), *Micrococcus* sp. (9.26%), *Citrobacter* sp. (6.76%), *Klebsiella* sp. (6.62%), *Aeromonas* sp. (5.44%), *Proteus* sp. (5.44%), *Corynebacterium* sp. (4.26%), *Enterobacter* sp. (3.68%) and *Bacillus* sp. (3.24%). The minor genera were *Bacteroides* sp., *Campylobacter* sp., *Clostridium* sp., *Edwardsiella* sp., *Flavobacterium* sp., *Hafnia* sp., *Pasteurella* sp., *Salmonella* sp., *Serratia* sp. and *Shigella* sp.

Sagoe farm

Twenty four bacterial genera with the exception of *Vibrio* sp. were identified in Sagoe farm (Table 4l). The major genera were *Pseudomonas* sp. (12.65%), *Micrococcus* sp. (8.97%), *Bacillus* sp. (7.65%), *Streptococcus* sp. (7.01%), *Proteus* sp. (6.62%), *Aeromonas* sp. (6.47%), *Citrobacter* sp. (5.88%), *Escherichia* sp. (5.59%), *Enterobacter* sp. (5.15%), *Corynebacterium* sp. (4.85%), *Klebsiella* sp. (4.12%) and *Campylobacter* sp. (3.82%), while *Actinobacillus* sp., *Bacteroides* sp., *Clostridium* sp., *Edwardsiella* sp., *Flavobacterium* sp., *Hafnia* sp., *Pasteurella* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Staphylococcus* sp. and *Yersinia* sp. occurred at very low percentage.

TABLE 4i

Bacterial species isolated from Pacific Farm Cultured Pond in 1996 1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.67	0.67	0.00	0.00	0.00	0.50
<i>Aommmnns sp</i>	1.00	1.00	0.00	0.00	0.00	0.00
<i>Bacillus sp</i>	1.33	1.67	2.33	1.50	2.00	1.00
<i>Bacteriodes sp</i>	0.00	0.67	0.00	0.00	0.00	0.00
<i>Campylobacter sp.</i>	0.33	0.00	0.00	1.00	0.00	1.00
<i>Cihobuctoi sp</i>	0.67	1.33	1.33	1.00	2.00	0.00
<i>Clostridium sp</i>	8.67	8.67	10.00	10.00	9.00	10.00
<i>Corynhoctoritim up.</i>	1.00	0.00	1.67	2.00	0.00	2.00
<i>Edwardsiella sp.</i>	0.00	0.67	0.00	0.00	0.00	0.00
<i>Enterohacter sp.</i>	0.67	0.67	0.00	0.50	0.00	0.50
<i>Escliorichki sp.</i>	2.07	2.07	2.33	3.50	4.00	3.00
<i>1 ft.ivohtwluouni up.</i>	0.00	0.00	0.33	0.00	0.00	0.00
<i>Hafnia sp.</i>	0.67	0.00	0.67	0.00	0.00	0.50
<i>Klebsiella sp.</i>	0.67	0.67	0.33	0.50	0.00	0.00
<i>Micrococcus sp</i>	3.33	3.33	3.67	0.50	1.50	3.50
<i>Pasteurella sp.</i>	0.33	0.00	0.00	0.00	0.00	0.00
<i>Proteus sp.</i>	2.33	2.00	2.67	2.50	3.00	2.00
<i>Pseudomonas sp.</i>	3.00	4.00	3.33	5.50	4.00	4.50
<i>Salmonella sp.</i>	0.67	0.33	0.67	0.00	1.00	0.00
<i>Serratia sp.</i>	0.67	1.33	0.00	0.00	1.00	0.00
<i>Shigella sp.</i>	0.00	0.00	1.67	0.00	0.00	0.00
<i>Staphylococcus sp.</i>	1.00	1.33	0.00	0.00	2.00	0.00
<i>Stieptococcus sp.</i>	9.33	9.00	8.67	10.00	9.50	10.00
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	1.00	0.00	0.33	1.50	0.50	1.50

Table at

Uacleiial sppcios isolated hum Bualion I aim Cullumd l'ond in 1000

1009

SPECIES	Moan Number of Colony Forming Units ml ⁻¹ isolatod in					
	February	April	Juno	August	October	December
<i>Actinnhncillus sp</i>	0 33	1 67	1 33	1 00	0 00	0 50
<i>Aeromonas sp.</i>	0.67	0.6/	0.6/	0.50	1.00	0.50
<i>Bacillus sp</i>	5.00	4.33	4.67	4.00	4.00	3.50
<i>Bacteroides sp</i>	0.67	0.67	0.00	0.00	0.00	0.50
<i>Campylobacter sp.</i>	0.33	1.33	1.33	0.00	0.00	0.00
<i>Cttmhttnlot . : 'i</i>	l :i:i	l) (!/	0 00	1 00	y 50	0) 50
<i>Cltir.hitliini . :p</i>	l no	0 00	0 00	0 00	1 00	0 00
<i>Coynubuctuilum up.</i>	1,0/	2.33	1,33	2.00	0,00	2.00
<i>Edwardsiella sp.</i>	1.33	1.67	3.33	2.00	1.50	0.50
<i>Enterobacter sp.</i>	0.33	1.67	1.33	1.50	1.50	2.00
<i>Escherichia sp.</i>	3.67	3.33	3.33	3.50	4.50	3.00
<i>Flavobnctorhim sp.</i>	0 67	0.00	0,67	1.50	0.00	0.00
<i>Hafnia sp.</i>	0.00	0.00	0,00	0.00	0.00	1.50
<i>Klebsiella sp.</i>	0,67	7.33	0,67	000	1.50	2.00
<i>Micrococcus sp</i>	5.00	4.00	4.33	4.00	3.50	4.00
<i>Pasteurella sp.</i>	0.00	0.00	0.67	0.00	0.00	1.00
<i>Protions sp</i>	3 33	3 00	? 67	3 r>o	/! 50	3 fio
<i>Psoudonwiinii up</i>	5 07	li 33	G 33	/ 00	7 GO	7 00
<i>Sulinanulln up</i>	(.) ;)3	0.(1/	0 00	o oo	0 00	0 00
<i>Sermtin sp</i>	0 33	1 00	1 33	0 hO	0 50	1 00
<i>Shigella sp.</i>	0.67	0.33	0.33	1.00	0.50	0.50
<i>Staphylococcus sp.</i>	1.67	1.33	1.33	2.00	1.00	0.00
<i>Stmplococcu; ; :p</i>	f) 00	.1 6 7	A 33	A 1.0	!> 00	4 50
<i>Vibrio sp.</i>	0.00	0.00	0 00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0,33	0.00	0.00	0.50	0.00	0.00

TABLE 41

Bacterial species isolated from Sagoe Farm Cultured Pond in 1996 - 1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	1.00	1.67	1.00	1.00	0.00	0.50
<i>Aeromonas sp.</i>	3.00	2.33	2.33	4.00	1.50	2.00
<i>Bacillus sp.</i>	2.33	2.67	3.33	4.50	3.00	3.00
<i>Bacteriodes sp.</i>	1.33	0.00	1.00	1.50	0.00	1.00
<i>Campylobacter sp.</i>	1.00	1.67	1.33	1.50	2.00	2.50
<i>Citrobacter sp.</i>	3.33	2.67	2.67	1.00	1.50	2.00
<i>Clostridium sp.</i>	1.00	0.00	1.00	1.00	1.00	0.00
<i>Corynebacterium sp.</i>	2.33	1.33	1.33	2.00	2.00	3.00
<i>Edwardsiella sp.</i>	0.33	0.33	0.33	1.00	1.00	0.50
<i>Enterobacter sp.</i>	2.00	3.33	1.33	2.50	1.50	2.50
<i>Escherichia sp.</i>	1.33	2.33	2.33	1.50	3.00	3.00
<i>Flavobacterium sp.</i>	1.33	0.33	0.33	1.00	0.50	2.00
<i>Hafnia sp.</i>	1.33	1.67	0.00	2.00	0.50	1.00
<i>Klebsiella sp.</i>	2.33	1.67	1.33	2.00	2.50	1.00
<i>Micrococcus sp.</i>	3.00	4.00	4.33	1.50	4.00	3.50
<i>Pasteurella sp.</i>	0.33	1.00	0.33	0.50	0.00	0.00
<i>Proteus sp.</i>	4.00	2.33	3.33	1.50	2.50	2.50
<i>Pseudomonas sp.</i>	4.33	5.00	6.00	5.50	5.00	3.50
<i>Salmonella sp.</i>	0.00	0.67	0.33	1.00	0.50	1.00
<i>Serratia sp.</i>	1.00	1.00	1.00	0.50	2.00	0.00
<i>Shigella sp.</i>	0.00	0.33	1.33	0.00	0.50	1.50
<i>Staphylococcus sp.</i>	0.00	0.00	0.67	0.00	0.00	0.50
<i>Streptococcus sp.</i>	2.67	3.67	2.00	3.00	3.50	2.50
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.67	0.00	1.00	0.00	2.00	1.00

6. Pond without any form of Fertilizer (ARDEC 3)

Twenty-three bacterial genera were isolated (Table 4m). *Pseudomonas* sp. occurred most frequently (14.12%), followed by *Escherichia* sp. (8.38%), *Proteus* sp. (7.65%), *Streptococcus* sp. (7.65%), *Aeromonas* sp. (7.21%), *Klebsiella* sp. (6.76%), *Corynebacterium* sp. (5.88%), *Citrobacter* sp. (5.59%), *Bacillus* sp. (5.44%), *Micrococcus* sp. (5.15%), *Enterobacter* sp. (4.56%), *Edwardsiella* sp. (3.82%), *Salmonella* sp. (3.68%) and *Campylobacter* sp. (3.38%). The remaining genera of low occurrence were *Actinobacillus* sp., *Bacteroides* sp., *Clostridium* sp., *Flavobacterium* sp., *Hafnia* sp., *Pasteurella* sp., *Serratia* sp., *Shigella* sp. and *Yersinia* sp.

7. Open Systems

Kpong Headpond

All the 25 genera were isolated from the Kpong Head Pond (Table 4n). The most frequently occurring genera were *Pseudomonas* sp. (9.56%), *Streptococcus* sp. (9.41%), *Escherichia* sp. (9.26%), *Micrococcus* sp. (8.82%), *Campylobacter* sp. (5.74%), *Bacillus* sp. (5.44%), *Klebsiella* sp. (4.26%), *Corynebacterium* sp. (4.26%), *Pasteurella* sp. (4.26%), *Shigella* sp. (3.82%), *Proteus* sp. (3.53%) and *Clostridium* sp. (3.38%). The percentage occurrence of the rest ranged from 0.52% to 2.94%.

Volta river

Table 4o contains a list of 24 bacterial genera identified. *Vibrio* sp. was not isolated. The most frequently occurring genera were *Pseudomonas* sp. (11.62%), *Escherichia* sp. (8.38%), *Streptococcus* sp. (8.09%), *Bacillus* sp. (7.50%), *Proteus* sp. (7.50%), *Citrobacter* sp. (6.47%), *Aeromonas* sp. (6.03%), *Corynebacterium* sp. (5.15%), *Klebsiella* sp. (5.59%), *Corynebacterium* sp. (5.15%), *Pasteurella* sp. (4.41%), *Micrococcus* sp. (4.12%), *Enterobacter* sp. (3.82%) and *Campylobacter* sp. (3.68%). The percentage occurrence of the remaining ten genera ranged from 0.59% to 2.65%.

(c). Weija dam

All the 25 bacteria genera were identified (4.2.7c). *Pseudomonas* sp. occurred most frequently with an overall percentage of 13.38%. The remaining major species were *Escherichia* sp. (8.97%), *Streptococcus* sp. (8.97%), *Proteus* sp. (7.06%), *Micrococcus* sp. (6.18%), *Bacillus* sp. (6.03%), *Citrobacter* sp. (5.59%), *Klebsiella*

TABLE 4m

Bacterial species isolated from ARDEC 3 Cultured Pond in 1996 - 1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ Isolated In					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.33	0.00	0.67	1.00	0.50	1.00
<i>Aeromonas sp.</i>	3.00	4.00	2.33	3.00	2.00	2.00
<i>Bacillus sp.</i>	2.67	2.00	2.00	1.50	3.00	2.00
<i>Bacteroides sp.</i>	0.33	0.00	0.00	0.00	0.50	0.50
<i>Campylobacter sp.</i>	0.67	2.00	1.00	2.00	1.50	1.00
<i>Citrobacter sp.</i>	2.33	1.67	2.67	1.50	2.00	1.50
<i>Clostridium sp.</i>	0.00	0.00	0.00	0.00	0.50	0.00
<i>Corynebacterium sp.</i>	2.33	2.00	3.00	3.00	2.00	1.50
<i>Edwardsiella sp.</i>	2.00	1.33	1.33	1.00	1.50	2.00
<i>Enterobacter sp.</i>	1.00	2.00	3.00	1.50	1.00	1.00
<i>Escherichia sp.</i>	4.00	3.00	3.33	3.50	4.00	3.00
<i>Flavobacterium sp.</i>	0.67	0.67	1.00	2.00	1.50	1.00
<i>Hafnia sp.</i>	0.67	0.00	0.00	0.00	0.00	0.00
<i>Klebsiella sp.</i>	3.33	2.67	2.67	2.50	2.00	3.00
<i>Micrococcus sp.</i>	1.67	2.67	2.33	1.50	2.50	1.00
<i>Pasteurella sp.</i>	0.67	0.00	0.67	0.00	1.50	1.00
<i>Proteus sp.</i>	2.33	3.33	3.00	3.00	3.00	5.00
<i>Pseudomonas sp.</i>	6.00	5.33	4.67	5.00	8.00	6.00
<i>Salmonella sp.</i>	1.00	1.67	1.67	2.00	1.00	2.00
<i>Serratia sp.</i>	1.33	0.67	1.33	0.50	0.00	0.00
<i>Shigella sp.</i>	0.33	1.00	0.67	1.00	0.50	2.00
<i>Staphylococcus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Streptococcus sp.</i>	3.33	3.33	2.67	4.50	1.50	3.50
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.00	0.67	0.00	0.00	0.00	0.00

TABLE 4n

Bacterial species isolated from Kpong Headpond Open System in 1996 - 1999

SPECIES	Moan Number of Colony Forming Units ml ⁻¹ isolated In					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.67	1.00	0.67	0.00	1.00	0.50
<i>Aeromonas sp.</i>	1.67	1.33	2.00	2.00	1.50	1.50
<i>Bacillus sp.</i>	1.67	3.00	2.33	2.50	1.50	2.00
<i>Bacteriodes sp.</i>	0.00	0.00	0.00	1.00	0.50	0.00
<i>Campylobacter sp.</i>	1.33	3.33	2.00	1.50	2.50	3.50
<i>Citrobacter sp.</i>	2.67	0.67	2.33	2.00	1.00	1.50
<i>Clostridium sp.</i>	0.67	2.67	0.67	1.00	0.50	3.00
<i>Corynebacterium sp.</i>	2.33	1.33	2.00	1.00	2.00	0.00
<i>Edwardsiella sp.</i>	0.67	0.67	1.33	1.50	0.00	1.00
<i>Enterobacter sp.</i>	2.00	1.33	1.33	0.00	4.50	2.50
<i>Escherichia sp.</i>	4.00	4.00	3.00	4.00	3.00	3.50
<i>Flavobacterium sp.</i>	0.00	0.67	0.00	0.00	0.00	0.00
<i>Hafnia sp.</i>	1.33	0.00	0.67	2.00	0.00	0.00
<i>Klebsiella sp.</i>	1.33	2.00	2.00	3.00	2.00	2.00
<i>Micrococcus sp.</i>	4.33	2.67	3.67	3.00	3.50	3.00
<i>Pasteurella sp.</i>	2.33	2.00	1.00	2.00	0.50	3.00
<i>Proteus sp.</i>	1.00	1.00	0.67	2.00	2.50	2.00
<i>Pseudomonas sp.</i>	3.00	4.67	3.67	4.00	4.50	2.50
<i>Salmonella sp.</i>	0.67	0.67	1.00	1.00	1.00	0.00
<i>Serratia sp.</i>	1.67	0.67	1.67	0.00	1.50	1.00
<i>Shigella sp.</i>	0.67	0.67	2.00	2.50	2.00	2.50
<i>Staphylococcus sp.</i>	0.67	0.33	0.00	0.00	1.00	0.00
<i>Streptococcus sp.</i>	4.33	4.33	3.67	4.00	3.00	3.00
<i>Vibrio sp.</i>	0.67	0.67	1.33	0.00	0.50	1.00
<i>Yersinia sp.</i>	0.33	0.33	1.00	0.00	0.00	1.00

TABLE 4o

Bacterial species isolated from Volta River Open System in 1996 - 1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	1.33	1.33	1.00	0.50	0.50	0.50
<i>Aeromonas sp.</i>	3.00	2.33	2.00	2.00	1.00	2.00
<i>Bacillus sp.</i>	2.67	3.67	3.00	3.00	2.50	3.00
<i>Bacteriodes sp.</i>	0.33	1.00	0.00	1.00	1.50	2.00
<i>Campylobacter sp.</i>	2.00	1.00	2.00	0.50	0.50	1.50
<i>Citrobacter sp.</i>	1.67	1.33	2.67	3.50	4.50	3.50
<i>Clostridium sp.</i>	1.67	1.00	0.00	1.50	1.50	1.00
<i>Corynebacterium sp.</i>	1.67	2.33	2.33	1.50	1.50	2.00
<i>Edwardsiella sp.</i>	0.00	1.00	1.00	1.50	0.00	1.00
<i>Enterobacter sp.</i>	1.33	1.33	1.33	2.00	2.00	0.00
<i>Escherichia sp.</i>	3.00	3.67	3.33	4.00	3.50	3.50
<i>Flavobacterium sp.</i>	0.67	1.00	1.33	1.00	1.00	0.50
<i>Hafnia sp.</i>	0.00	0.00	0.67	1.00	0.50	1.00
<i>Klebsiella sp.</i>	2.33	2.00	1.33	0.50	3.00	2.00
<i>Micrococcus sp.</i>	1.00	2.33	1.33	2.00	1.50	3.50
<i>Pasteurella sp.</i>	2.67	1.33	2.67	1.50	1.50	1.00
<i>Proteus sp.</i>	3.00	3.00	3.00	2.00	4.00	2.50
<i>Pseudomonas sp.</i>	4.67	4.33	4.33	4.50	4.50	5.00
<i>Salmonella sp.</i>	1.00	0.33	0.67	1.00	1.00	0.00
<i>Serratia sp.</i>	1.33	0.00	0.00	1.00	1.00	1.00
<i>Shigella sp.</i>	0.00	0.67	0.67	0.50	0.00	0.00
<i>Staphylococcus sp.</i>	0.00	0.67	0.67	0.00	0.00	0.00
<i>Streptococcus sp.</i>	3.33	3.00	3.33	3.00	3.00	3.50
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	1.33	1.33	1.33	1.00	0.00	0.00

sp. (5.59%), *Aeromonas* sp. (4.85%) and *Corynebacterium* sp. (4.56%). The percentage occurrence of the remaining 15 species ranged from 0.99% to 2.94%.

TABLE 4p

Bacterial species isolated from Weija Dam Open System in 1996 - 1999

SPECIES	Moan Number of Colony Forming Units ml ⁻¹ Isolated In					
	February	April	June	August	October	December
<i>Aeromonas sp.</i>	2.67	1.67	1.33	2.50	1.50	1.00
<i>Bacillus sp</i>	2.00	1.33	3.67	2.00	2.50	2.50
<i>Bacteriodes sp</i>	1.33	1.00	1.33	0.50	1.00	0.00
<i>Campylobacter sp.</i>	0.67	0.00	0.33	1.50	1.00	1.50
<i>Citrobacter sp</i>	2.67	1.67	2.33	3.00	2.50	1.50
<i>Clostridium sp</i>	1.00	1.00	0.67	0.00	0.00	0.00
<i>Corynebacterium sp.</i>	1.33	1.67	1.33	2.50	1.50	2.50
<i>Edwardsiella sp.</i>	0.67	0.00	0.67	1.00	1.50	1.50
<i>Enterobacter sp.</i>	2.00	2.00	1.33	0.50	0.00	1.50
<i>Escherichia sp.</i>	4.00	3.67	3.00	2.50	3.50	4.00
<i>Flavobacterium sp.</i>	1.33	0.00	2.00	1.00	0.00	0.00
<i>Hafnia sp.</i>	2.00	0.33	1.00	1.00	0.00	2.00
<i>Klebsiella sp.</i>	1.00	1.33	2.00	3.00	4.00	3.50
<i>Micrococcus sp</i>	3.00	3.33	3.67	1.50	0.50	1.50
<i>Pasteurella sp.</i>	0.00	0.67	0.67	1.00	2.50	1.00
<i>Proteus sp.</i>	2.33	3.67	2.00	2.50	2.50	4.00
<i>Pseudomonas sp.</i>	5.33	7.33	4.67	5.50	5.50	3.00
<i>Salmonella sp.</i>	0.00	2.00	0.00	1.00	1.00	1.00
<i>Serratia sp.</i>	0.00	0.67	1.33	1.00	0.50	0.00
<i>Shigollo sp.</i>	0.67	0.67	0.00	1.00	0.50	1.50
<i>Staphylococcus sp.</i>	0.00	0.33	0.67	0.50	1.00	0.00
<i>Streptococcus sp.</i>	3.33	3.00	3.07	3.00	4.00	5.00
<i>Vibrio sp.</i>	1.33	1.00	0.33	0.50	0.50	0.00
<i>Yersinia sp.</i>	0.33	1.00	0.67	0.00	1.50	0.00

C. Analysis of the diversities of the bacterial flora from the cultured ponds and the open systems

1. Cow manure-fertilized ponds

The diversities of the bacterial flora were high (more than 0.90) for both Aduabenba ponds and Boateng ponds (Table 5a), indicating that the bacterial populations in these ponds consisted of many different PhP types (Appendices 1a-1j). The PhP types for Aduabenba ponds ranged from 17 to 34, and the PhP types for Boateng ponds ranged from 50 to 59. The clustering of the bacterial isolates for the two farms are presented in Figs 2a - 2j. All the dendrograms had high co-phenetic correlation (above 0.80) indicating that each dendrogram corresponded to the similarity matrix from which it was created.

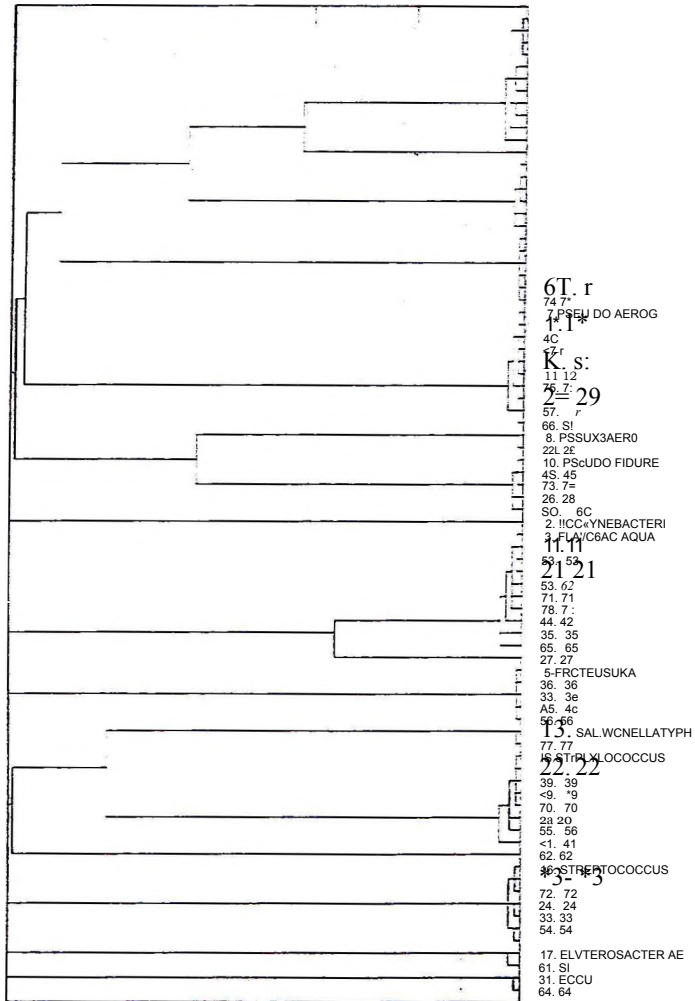
Table 5a. Diversities among bacterial flora in cow manure fertilized ponds

Sample name and no.	No. of isolates	Di value
Aduabenba 1	80	0.992
2	80	0.908
3	80	0.974
4	80	0.962
5	80	0.962
Boateng 1	80	0.989
2	80	0.978
3	80	0.987
4	80	0.978
5	80	0.987
Mean Diversity		0.972

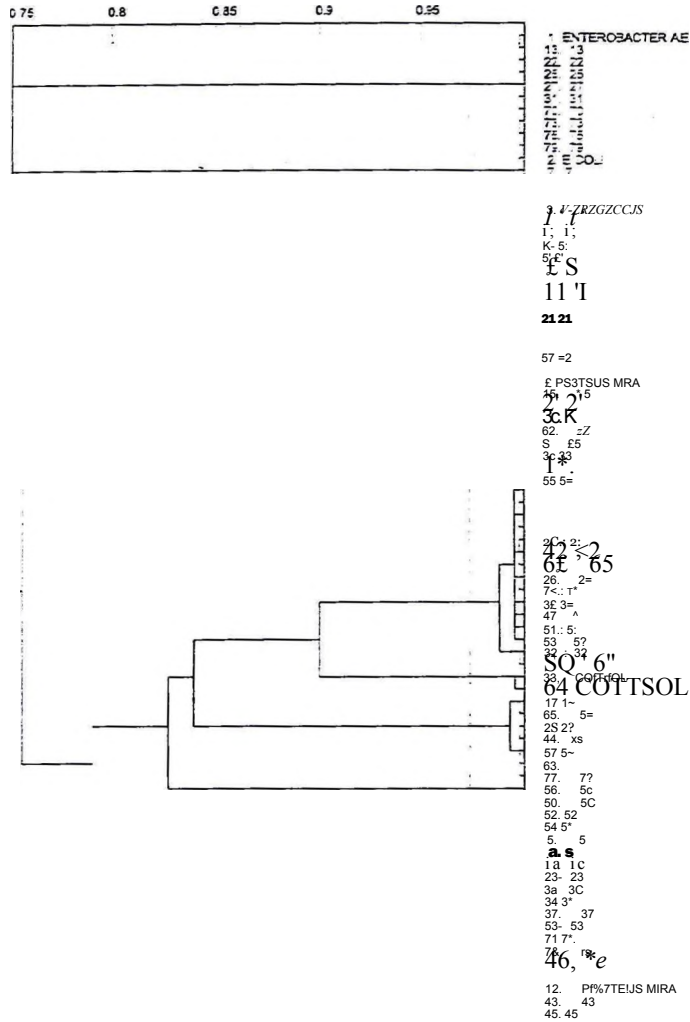
2. Poultry manure-fertilized ponds

The diversities of bacterial flora were high for Agyeman ponds, ARDEC 20, Asare ponds and Frimpong ponds (Table 5b) indicating many different PhP types in the bacterial populations present (Appendices 2a-2t). The PhP types for Agyeman ponds ranged from 31 to 64, those for ARDEC 20 from 43 to 53, Asare ponds from 56 to 63 and the PhP types for Frimpong were from 41 to 58. The clustering of the bacterial isolates to dendrograms (Figs. 3a - 3t) had high co-phenetic

No. of sampls: 80 No. of tess. 12 NKI. u.at u u*nownc aelafisn: 0&2S

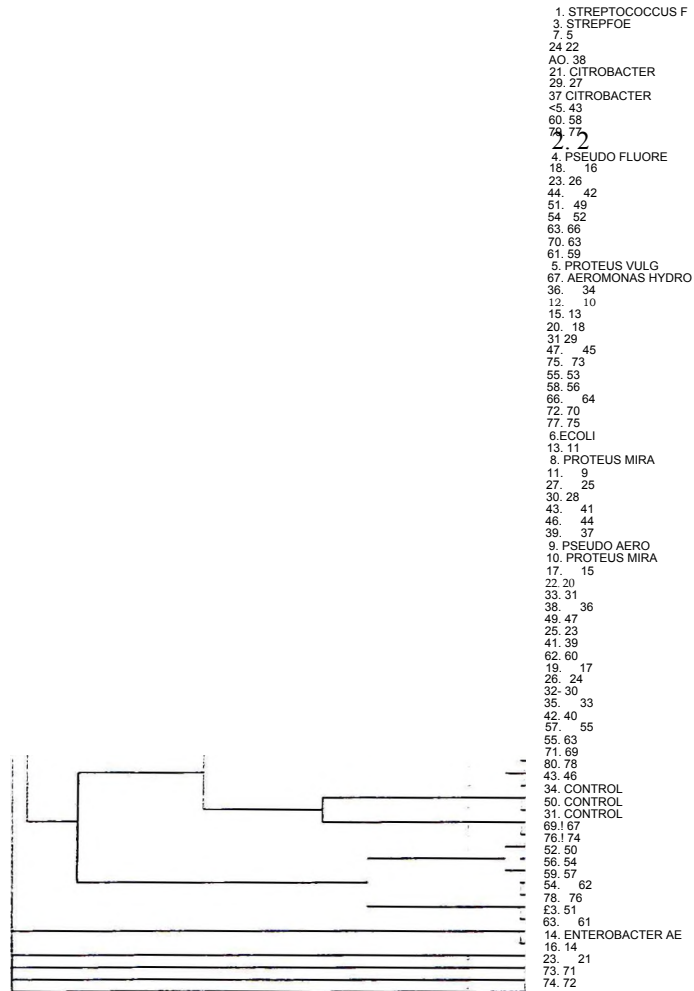


from A*ta*bafami uabec2) ID level: C.ff75 Co-fl*net*ic cocorelation: 0.93S
 No of sanies: 80 No. of tests: 12



No. of samples: 61 No. of tests: 12

ijhna..s.5 oo-poeneoccorateiorv 0.977



r i - v * . uenansgram snomng UPGMA cusienng of the bacterial tstoasesior August. iswo
 from Aduabenba ferm (AduzbenX). ID leiet 0.975 Co-phenetic correlation: 0.980
 Mo. of samples: &* No. of tests: 12

4

1. STREP FAEC
 10. 10
 36. 35
 19. 19
 2. STAP AUR
 44. 43
 22. 22
 15. 5
 26. 25
 14. 14
 21. 21
 7. PROTEUS OX
 17. 17
 8. PROTEUS MR*
 33. 33
 38. 37
 40. 39
 9. MICRO SP
 62. 61
 49. 43
 42. 41
 54. 53
 27. 25
 34. 33
 64. CONTROL
 30. 29
 56. 55
 59. 58
 63. 62
 32. 31
 51. 50
 3. STAPEVD
 31. 30
 60. 59
 58. 57
 52. 51
 12. 12
 5. PSEUDO =LLO=S
 20. 20
 4. SERMER
 13. 13
 16. 16
 6. PSEUDO AUR
 24. 24
 50. 49
 47. 46
 41. 40
 23. 23
 29. 28
 46. 45
 57. 56
 55. 54
 25. 25
 28. 27
 35. 34
 45. 44
 37. 36
 48. 47
 53. 52
 61. 60
 11. ENTEROBACTER CO
 15. 18
 39. 38
 43. 42

L

KM.C3 iui rtsuiuary. ltfst*
from Aduat>efefca ferrr Aduaben5). O tescei 0.975 Co-phenetic correlation: 0.933
No. of samples: 8C 'o. of tests: 12

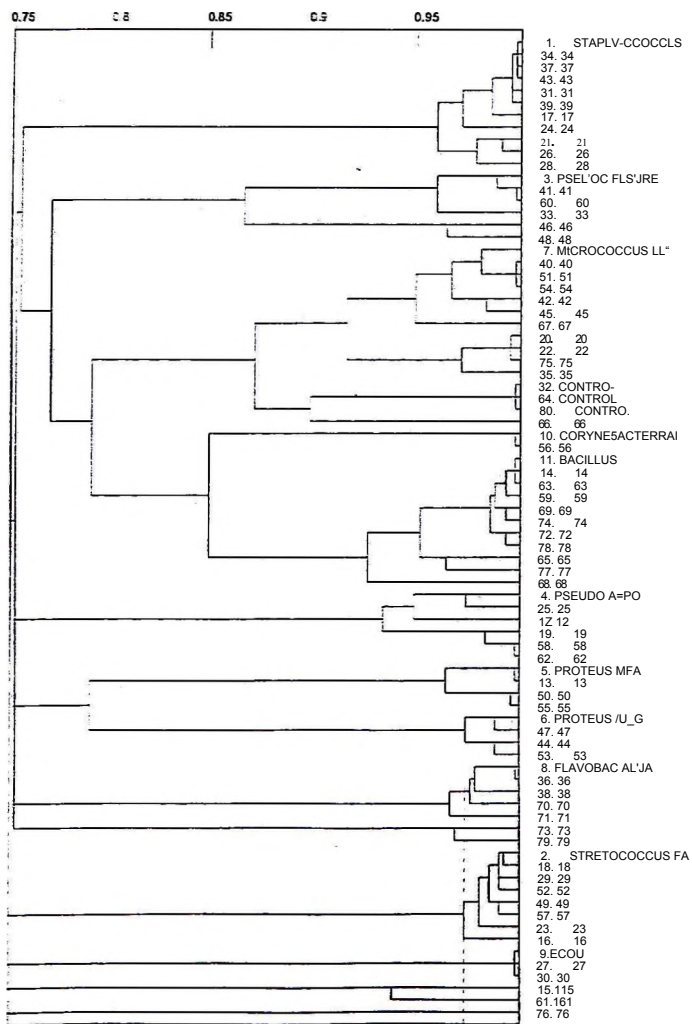
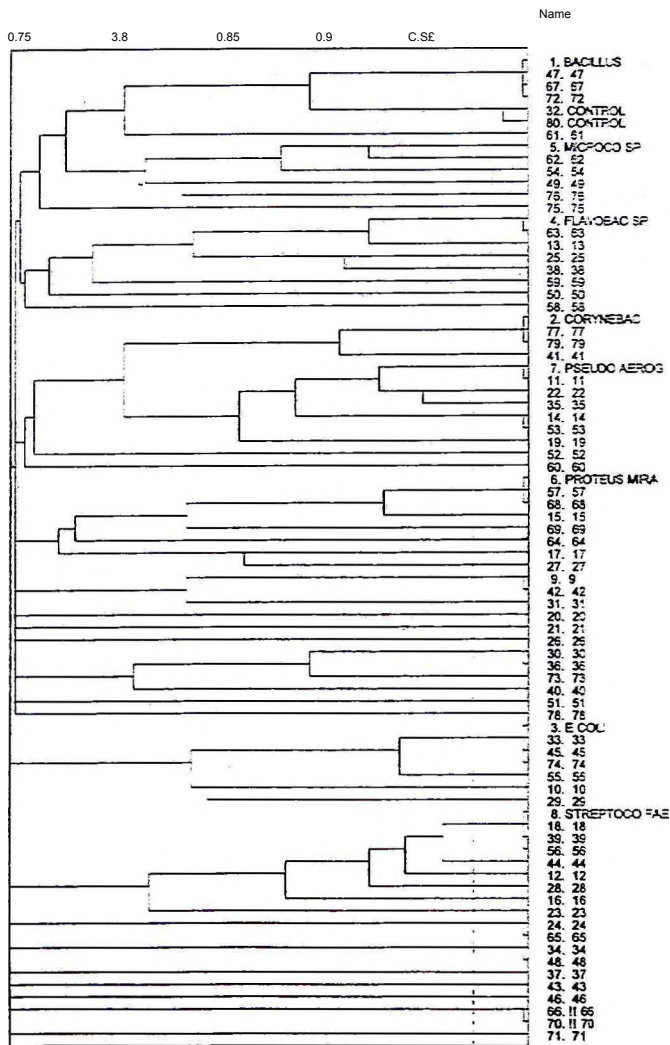


Fig. 1 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 19S7 from Boateng farm (Boaiengt). ID level: 0.975 Co-phenetic corretaSon: 0.871 No. of samples: 80 No of tests: 12



from Boaleng (Boateng2). ID level: 0.975 Co-phenetic correlation: 0.922
 No. of samples: 80 No. of tests: 12

n

1. BACILLUS
 9. 9
 40. CONTROL
 2. CORYNEBAC
 13. 13
 5. MICROCO SP
 4. FLAVOBAC
 20. 20
 12. 12
 75. 75
 7. PSEUDO AERO
 38. 38
 24. 24
 50. 50
 60. 60
 73.1 73
 3. E COU
 23. 23
 44. 44
 30. 30
 10. 10
 67. 67
 35. 35
 39. 39
 6. PROTEUS MIRA
 32. 32
 25. 25
 16. 16
 8. STREPTOCO FAE
 26. 26
 53. 53
 19. 19
 14. 14
 31. 31
 48. 48
 36. 36
 11. 11
 33. 33
 22. 22
 15. 15
 17. 17
 63. 63
 18. 18
 61. 61
 27. 27
 54. 54
 21. 21
 34. 34
 28. 28
 29. 29
 37. 37
 41. 41
 46. 46
 42. 42
 52. 52
 43. 43
 45. 45
 55. 55
 56. 56
 58. 58
 64. 64
 68. 68
 70. 70
 77. 77
 78. 78
 80. CONTROL
 47. 47
 49. 49
 51. 51
 57. 57
 59. 59
 62. 62
 72. 72
 65. 65
 66. 66
 69. 69
 71. 71
 74. 74
 76. 76
 79. 79

Fig - Z II Dendrogram showing UPGMA clustering of the bacterial isoates for February, 1998 from Boateng farm (Boateng3). ID level: 0.975 Co-phenetic correlation: 0.892
 No. of samples: 81 No. of tests: 12

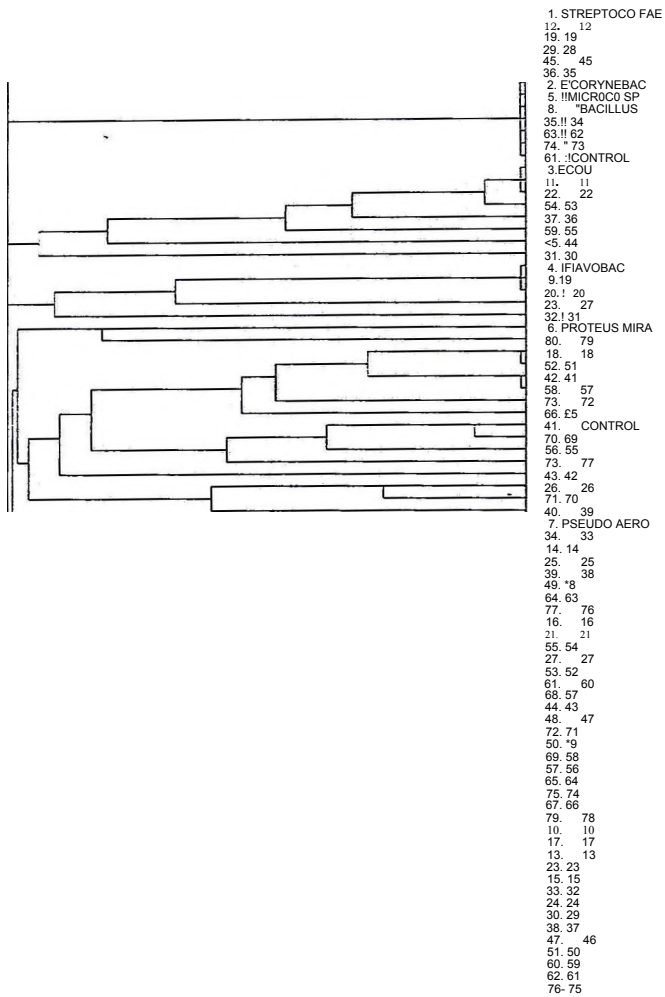


Fig. ^1 Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from Boateng (Boateng4). ID level: 0.975 Co-pheretic correlation: 0.925
No. of samples: 80 No. of tests: 12

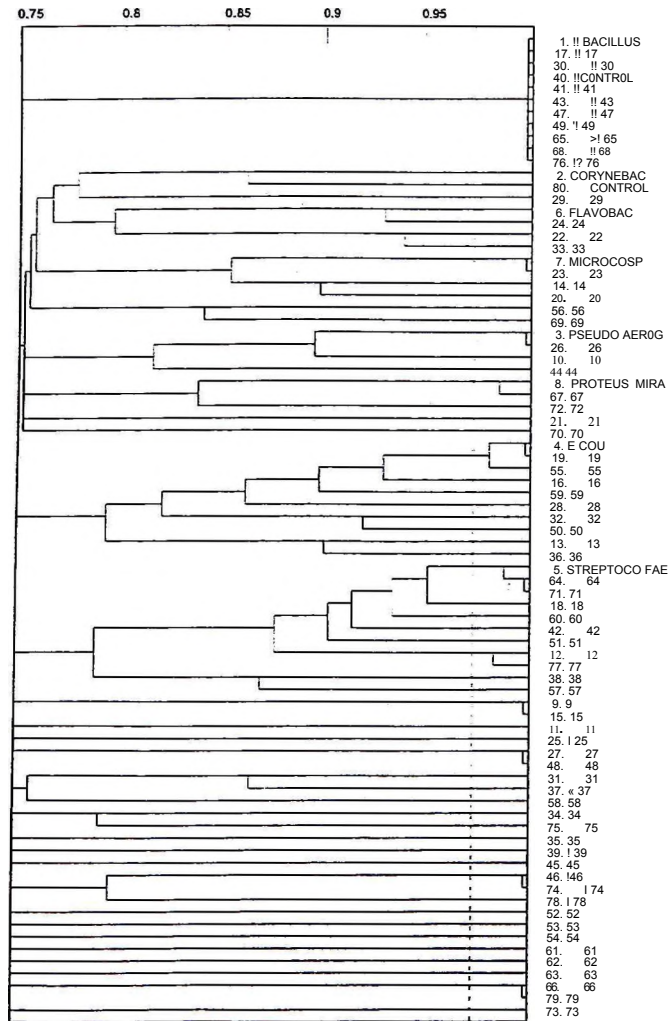


Fig. 2 | . Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from Boateng (Boateng5). ID level: 0.975 Co-phenetic correlation: 0.912 No. of samies: 81 No. of tests: 12

r-i

-a

```

1. PR07FJS MIRA
5. MICROCO SP
*2 41
31. 3C
14. 14
13. 13
52. 51
55. 54
75. 74
73. 72
53. 67
E5. 64
51. 60
26. 25
39. 38
51. 50
29. 28
71. 70
41. CONTROL
61. CONTRiOL
*3. 42
E3. 52
47. 46
73. 75
66. 65
64. 63
73. 78
72. 71
*3. 48
53. 58
63. 62
3. PSELOO AEROG
23. 22
30. 29
80. 79
50. 49
53. 57
70. 59
*0. 38
77. 76
74. 73
2. IIC0RYNEBAC
S. IBACaj_US
11!! 1C
35-!! 3*
56-!! 55
69-!! 66
4. ECOU
23. 27
AS. 45
60. 69
11 11
21. 20
32. 31
13. 18
67. 56
6. IFLA!0=AC
45. 44
7. STREET DCO FAE
15. 16
27. 26
33- 32
12. 12
36- 35
2. 9
15. 15
34. 33
38. 37
17. 17
19. 19
20. 19
37. 36
22. 21
24. 23
25. 24
44. 43
48. 47
67. 66
54. 53
62. 61
78. 77
    
```

correlation (above 0.80) indicating that each dendrogram corresponded to the similarity matrix from which it was created.

Table 5b. Diversities among bacterial flora in poultry manure fertilized ponds

<u>Sample name and no.</u>	<u>No. of isolates</u>	<u>Di val</u>
Agyeman 1	80	0.963
2	80	0.987
3	81	0.986
4	80	0.993
5	72	0.978
ARDEC 20 1	80	0.985
2	80	0.979
3	80	0.981
4	81	0.977
5	80	0.962
Asare 1	81	0.990
2	80	0.989
3	81	0.990
4	80	0.994
5	80	0.991
Frimpong 1	80	0.988
2	82	0.990
3	73	0.982
4	80	0.974
5	80	0.934
Mean Diversity		0.981

3. Pig manure-fertilized ponds

The diversities of bacterial flora from ponds fertilized with pig manure were generally high (more than 0.90) (Table 5c), indicating that the bacterial populations in the three different ponds, i.e. Boadi, KK and Pacific, consisted of many different PhP types (Appendices 3a-3o). The only exception was Pacific ponds, which at some sampling occasions contained bacterial populations with low diversity (less than 0.90), indicating selection and re-growth of one or few strains of bacteria

Fig. 3 a. Dendrogram showing UPGMA clustering of tie bacterial isolates for February, 1997 from Agyeman farm (Agyeman) ID level: 0.975 Co-plogenetic correlation: 0.974 No. of samples: 80 No. of tests: 12

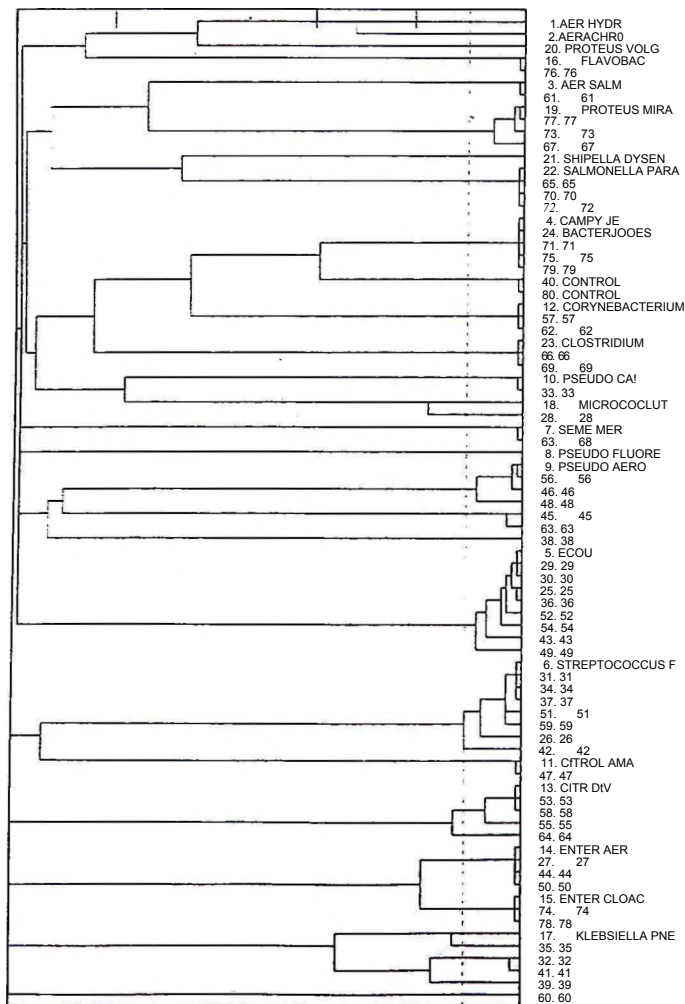


Fig. 3b Dendrogram showing UPGMA clustering of the bacterial Isolates for August, 1997 from Agyeman farm (Agyeman2) ID level: 0.975 Co-phenetic correlation: 0.874 No. of samples: 80 No. of tests: 12

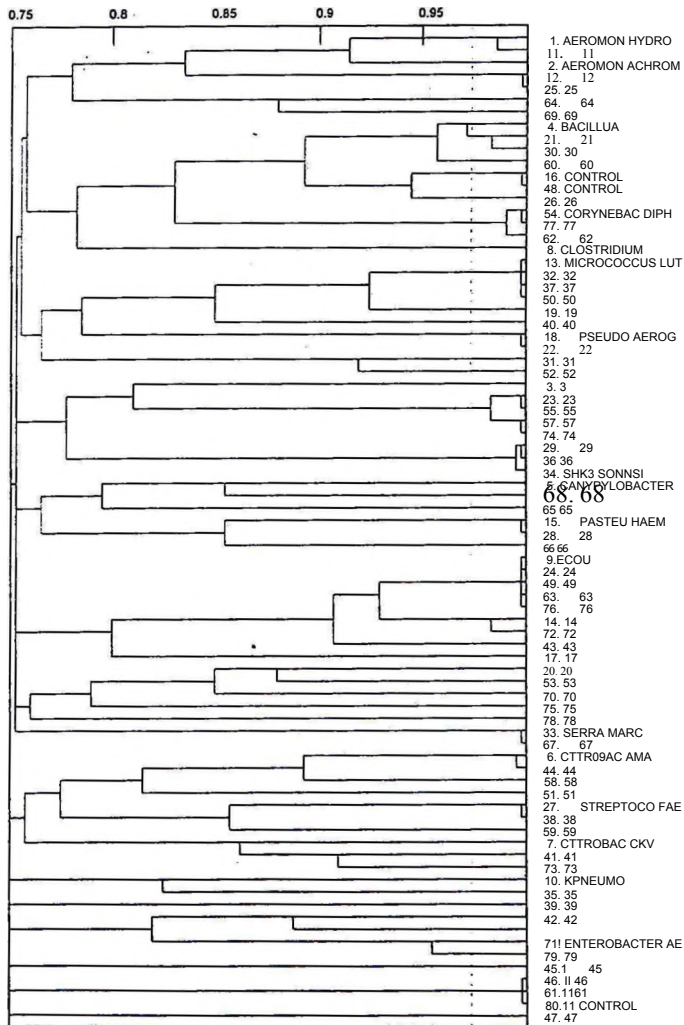


Fig. 3 C Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from Agyeman farm (AgyemanS) ID level: 0.975 Co-phenetic correlation: 0.920 No. of samples: 61 No. of tests: 12

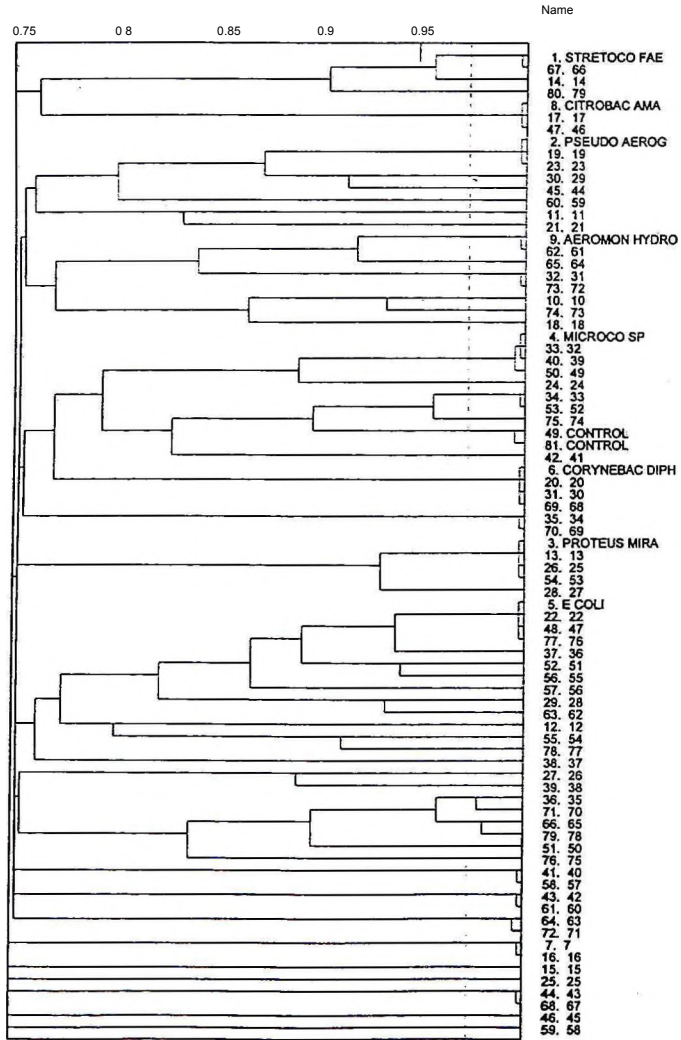
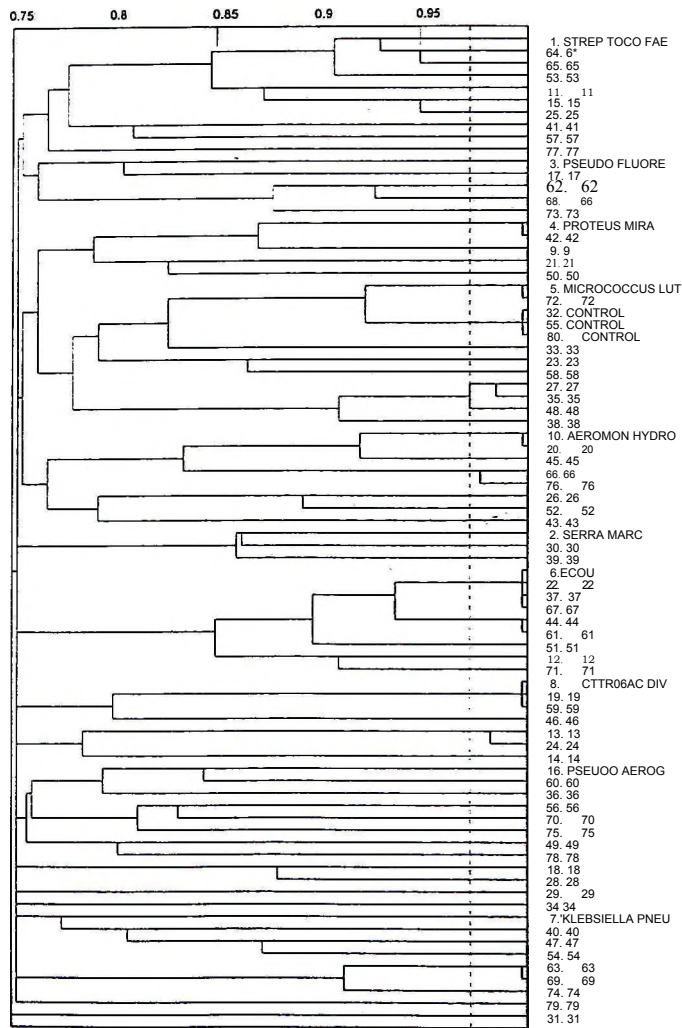


Fig. 3d Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from Agyeman farm (Agyeman4). ID level: 0.975 Co-phenetic correlation: 0.909 No. of samples: 80 No. of tests: 12



Mg. J Dendrogram showing UPGMA clustering of the bacterial isolates for from Agyeman (Agyeman5). ID level: 0.975 Co-phenetic correlation: 0.903 No. of samples: 72 No. of tests: 12

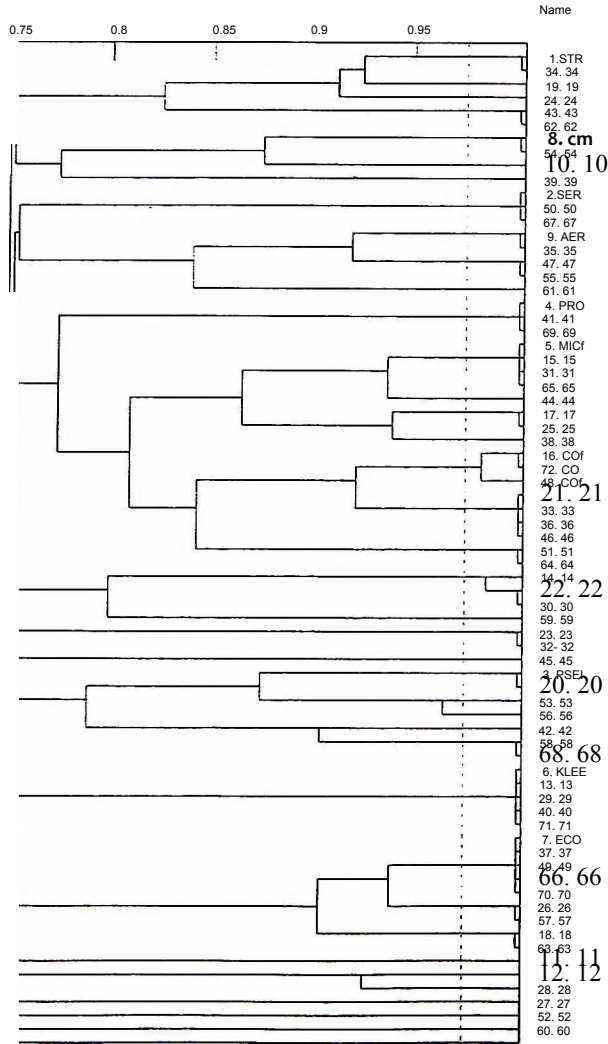


Fig. 3 f Dendrogram showing UPGMA clustering of the bacterial Isolates for February, 1997 from ARDEC 20 pond (Ardec201), ID level: 0.975 Co-phenetic correlation: 0.874 No. of samples: 80 No. of tests: 12

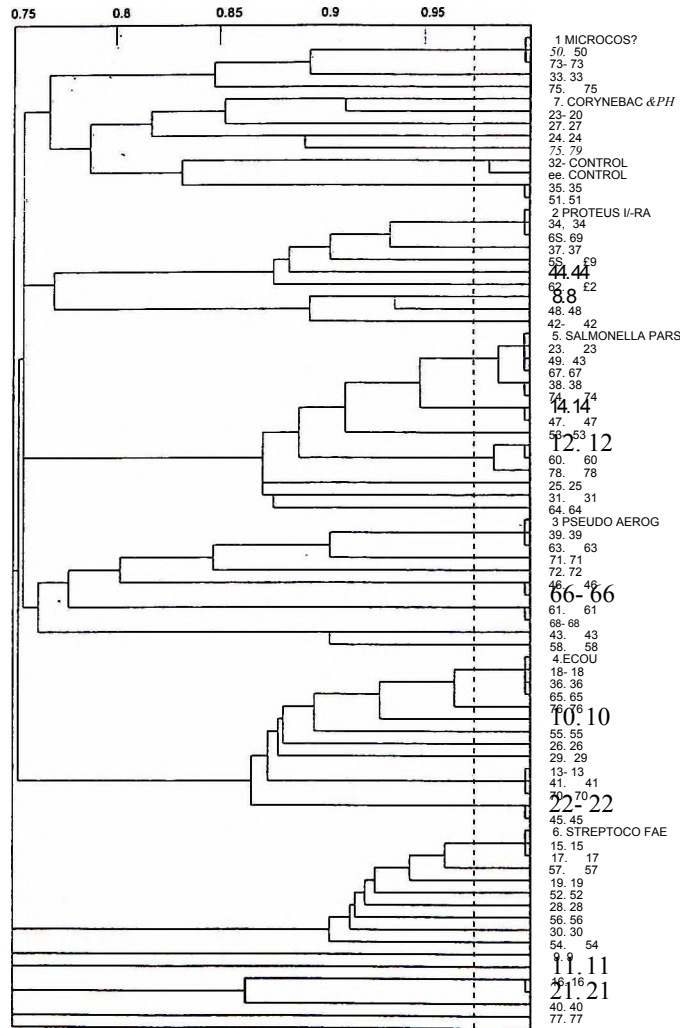


Fig- Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1997
 frax-n ARDEC 20 pond (Ardec202) ID level 0.975 Co-pfenebc correlatxi: 0.896
 No. of samples: 60 No. of tests: 12

0.75
 I—

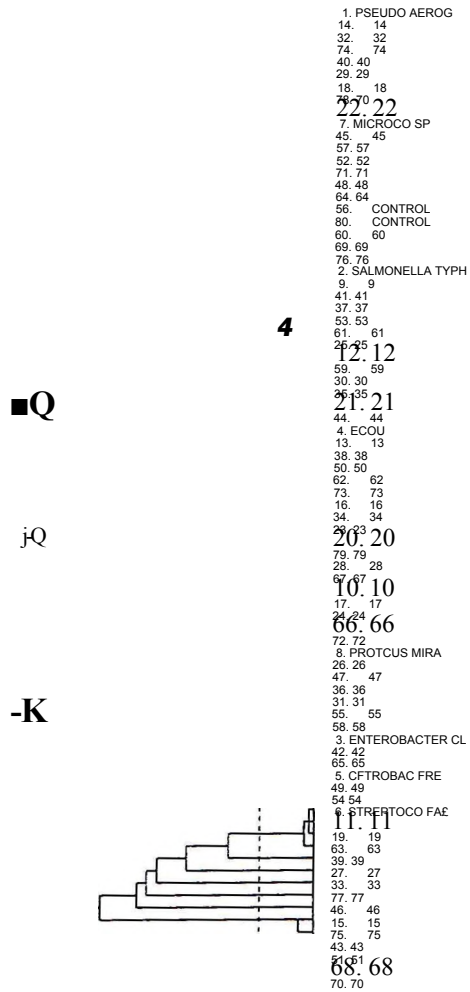
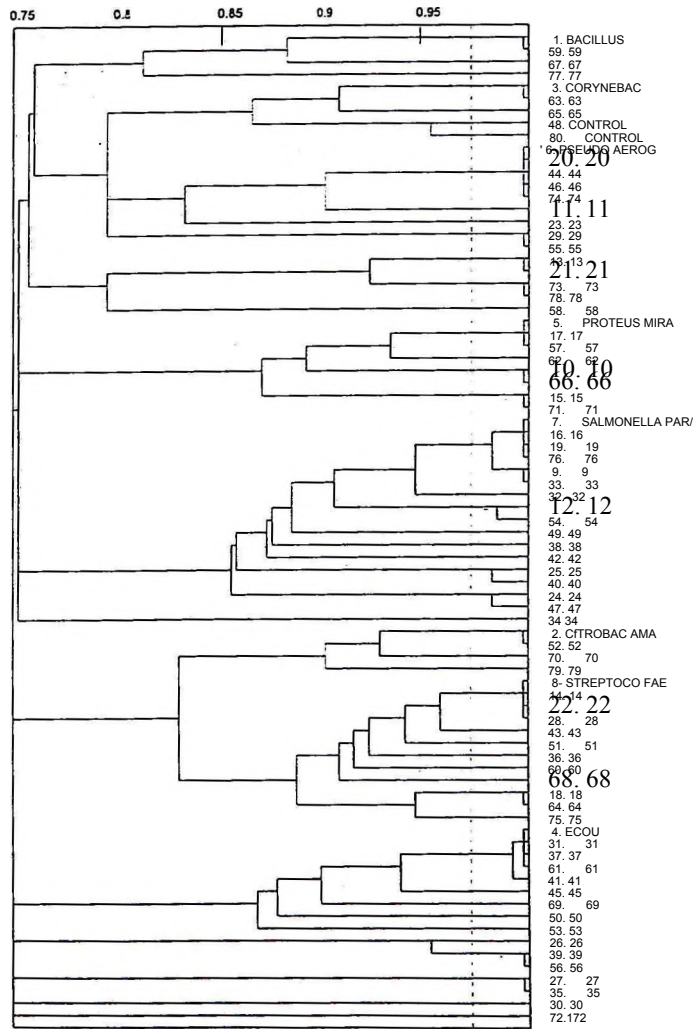


Fig. 3h Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from ARDEC 20 pood (Ardec203). ID level: 0.975 Co-pheneBc correlation: 0.846
 No. of samples: 80 No. of tests: 12



Hg, Ji Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from ARDEC 20 pond (Ardec204). ID level: 0.975 Co-phenetic correlation: 0.886 No. of samples: 81 No. of tests: 12

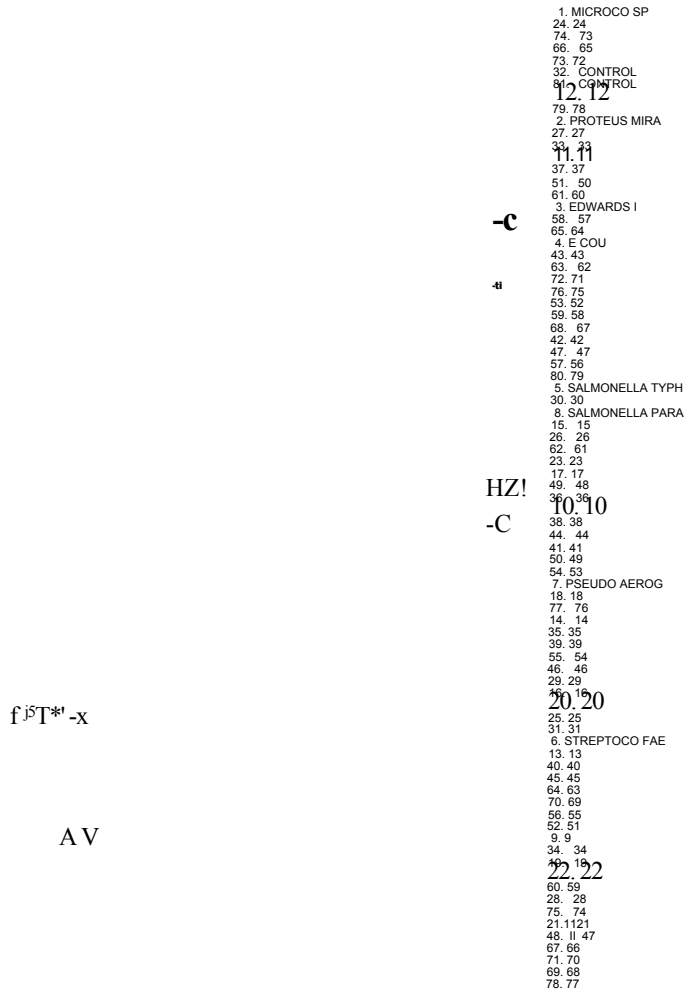
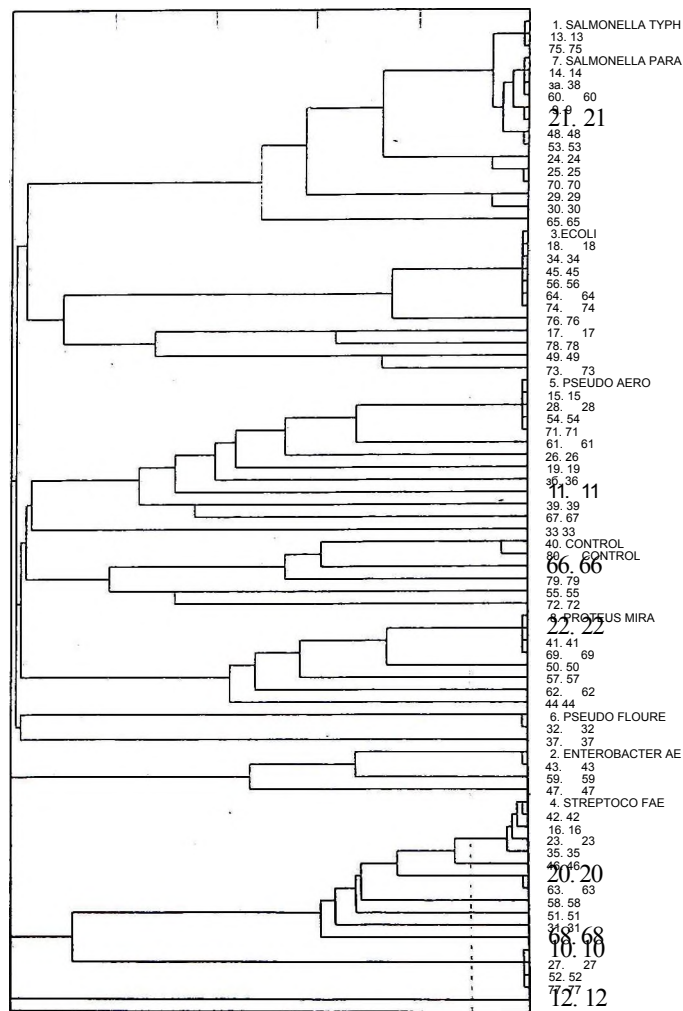


Fig. 3 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from ARDEC 20 pond (Ardec205). ID level: 0.975 Co-phenetic correlation: 0.912
 No. of samples: 80 No. of tests: 12

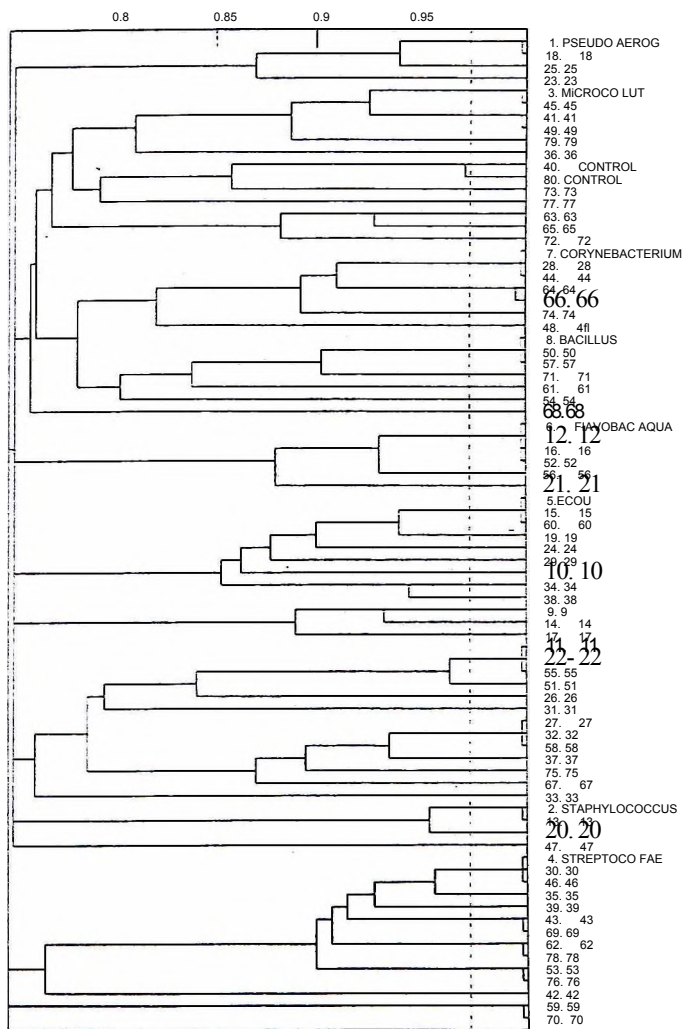


rdv. _>EV uenarogram snowtng UPGMA clustering of the bacterial Isolates for February, 1997
from Asare (Asarel). ID level: 0.975 Co-phenetic correlation: 0.8B2
No. of samples: 81 No. of tests: 12

-d

1. eccou
14. 14
70. 69
73. 72
28. 27
75. 74
77. 76
30. 29
2. FIABOBAC AQUA
21
22. 21
19. 19
39. 38
44. 43
37. 36
58. 57
47. 46
6. STAPHYLOCOCCUS
9. 9
35. 34
15. 15
18. 18
38. 37
4. PROTEUS MIRA
21
20
41. 40
61. 60
40. 39
8. MICROCO SP
10. 10
16. 16
36. 35
23. 22
32. 31
26. 25
33. CONTROL
81. CONTROL
60. 59
63. 62
51. 50
67. 66
53. 52
55. 54
7. PSEUDO AEROG
56. 55
66. 65
50. 49
72. 71
76. 75
42. 41
71. 70
79. 78
65. 64
52. 51
3. KLEBSIELLA PNEU
68. 67
24. 23
80. 79
13. 13
29. 28
43. 42
49. 48
59. 58
64. 63
1. STREPTOCO FAE
11
46. 45
25. 24
27. 26
54. 53
31. 30
57. 56
62. 61
20. 20
34. 33
48. 47
69. 68
74. 73

Fig. 31 Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1997 for Asare (Asare2). ID level: 0.975 Co-phenetic correlation: 0.883 No. of samples: 80 No. of tests: 12



F³C₃m Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1996
■ran Asare farm (Asare3). ID Iewel 0.975 Co-phenetic correlation: 0.861
**c. of sampfes: 81 No. of tests: 12

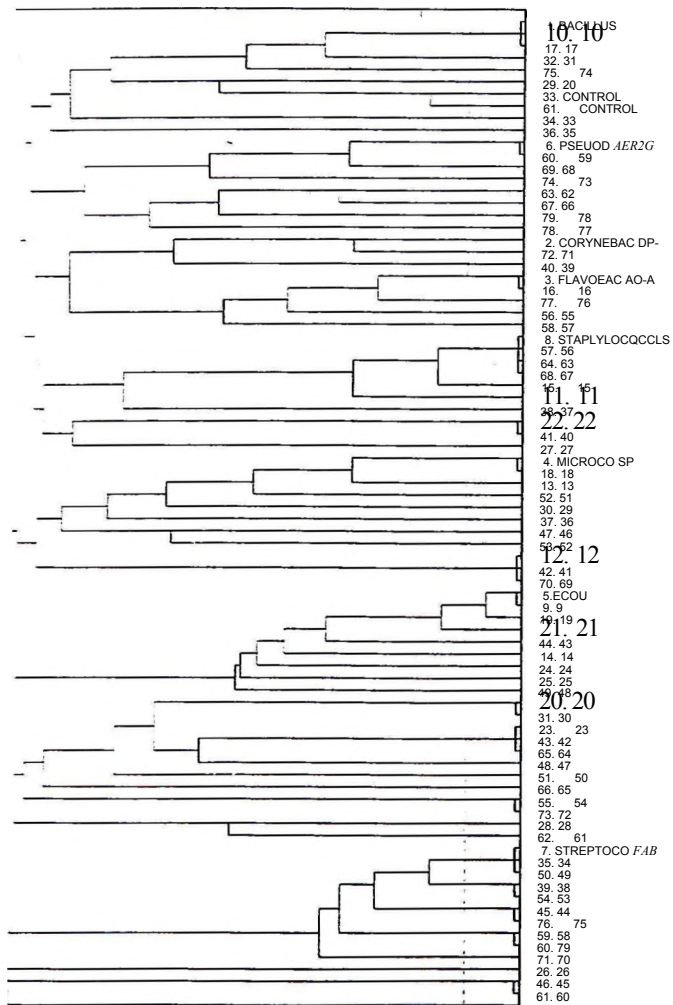


Fig. 3n Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from Asare farm (Asare4). ID levefc 0.975 Co-phenetic correlation: 0-853 No. of samples: 80 No. of tests: 12

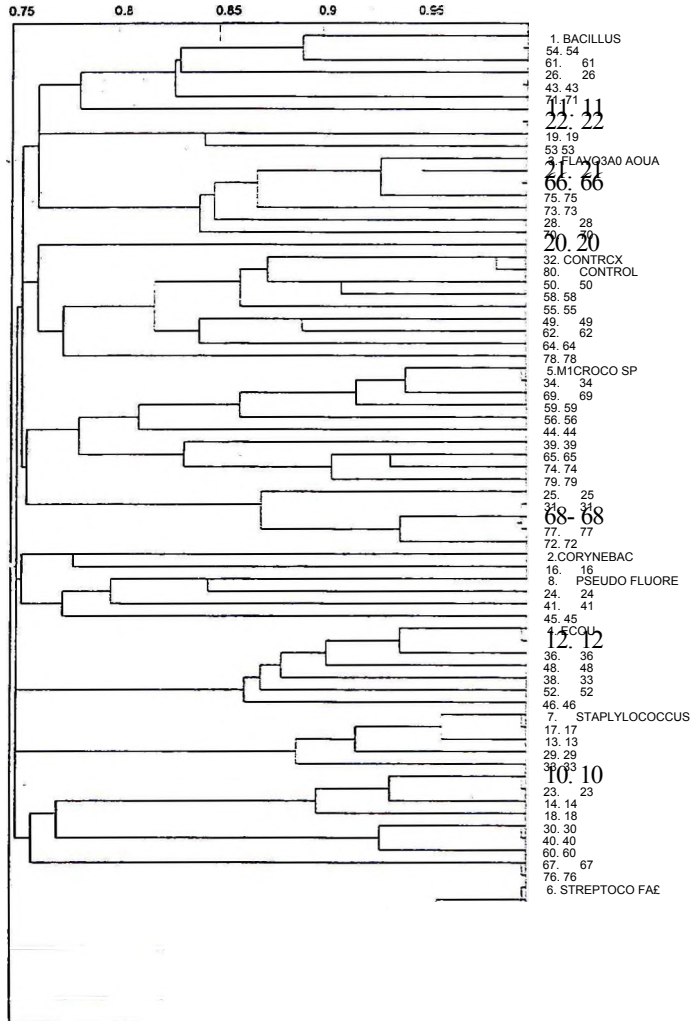


Fig. d0 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from Asare farm (Asare5). ID level: 0.975 Co-phenetic correlator: 0.864 No. of samples: 80 No. of tests: 12

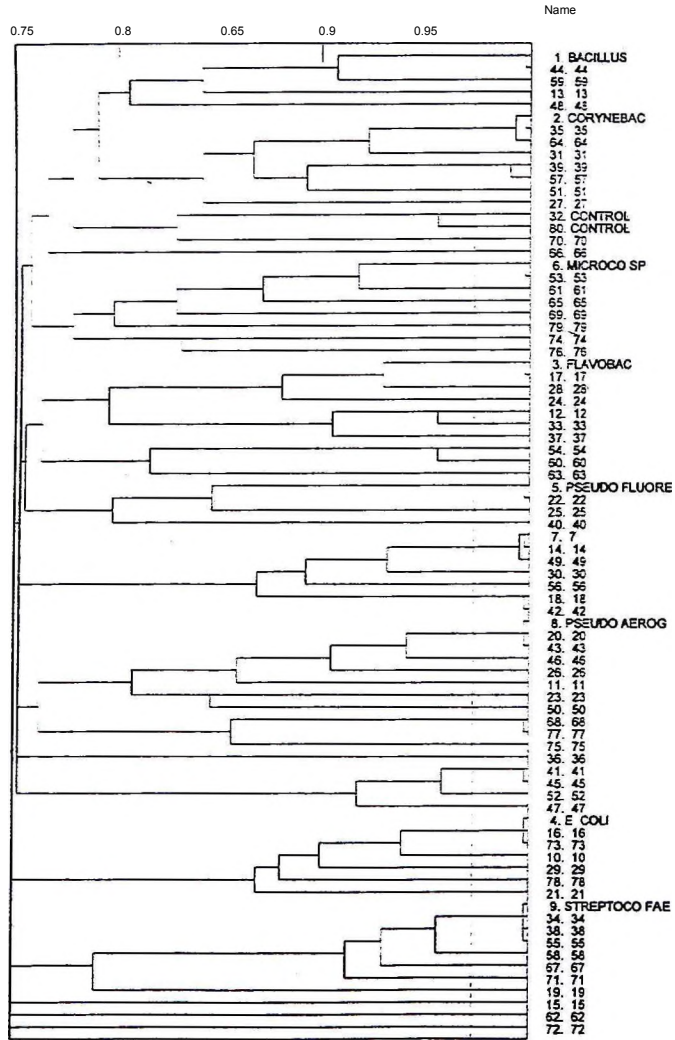


Fig 3p Dendrogram showing UPGMA clustering of the bacterial isolates *or t-eocuary. 19*37 from (fampon) ID level: 0.975 Co-phenetic com*iaSoc: 0.850 No. of samples: 80 No. of tesis: 12

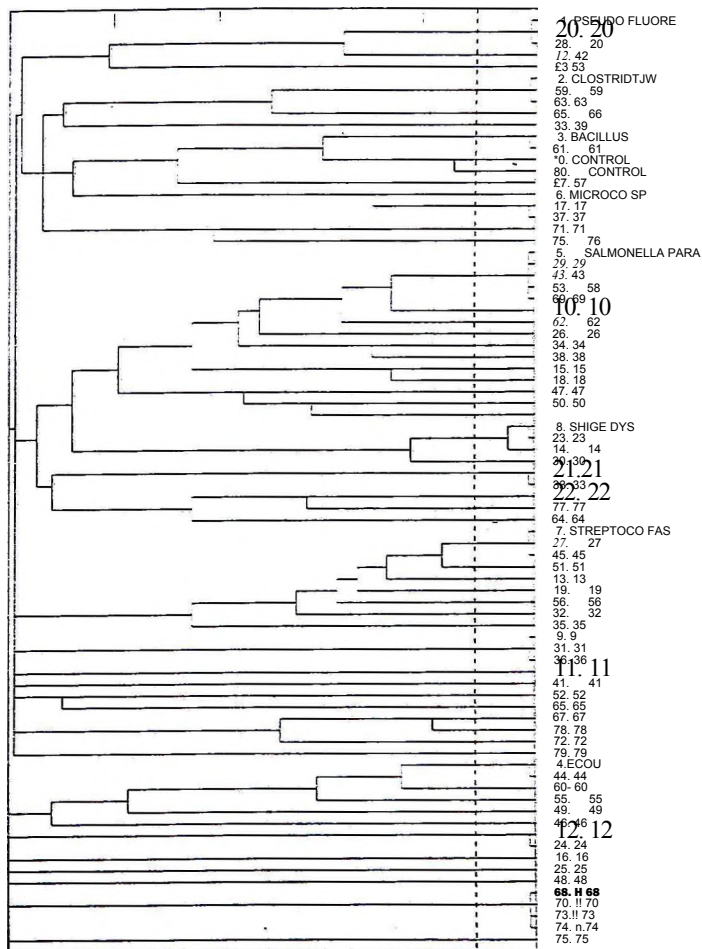


Fig. 3. Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1997 from Frimpong farm (frspon2). ID level: 0.975 Co-phenetic correlation: 0.803 No. of samples: 82 No. of tests: 12

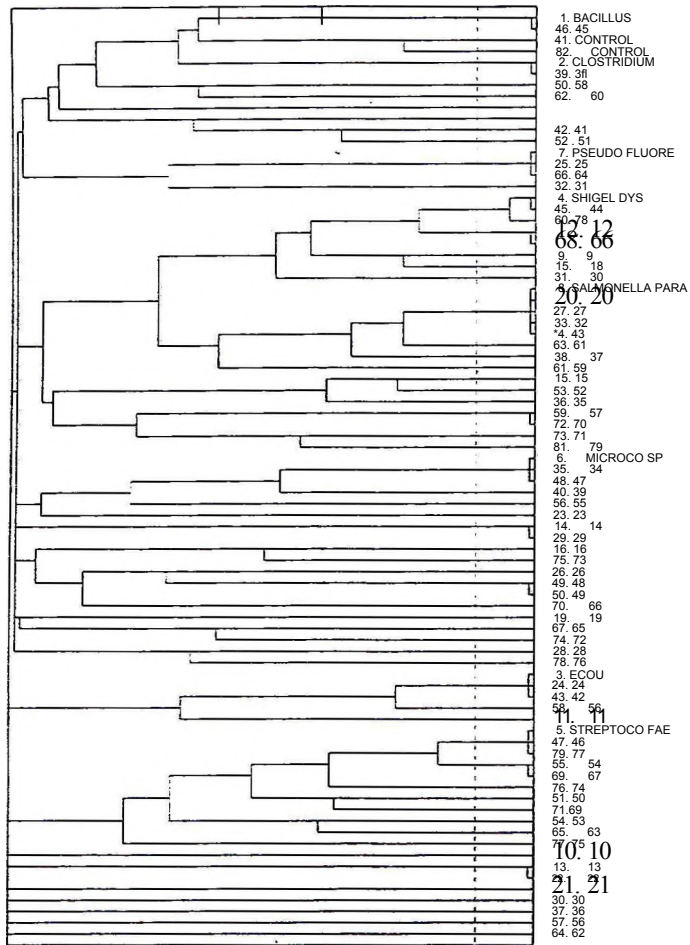


Fig. -3 T Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from Frimpong (frimpon3). ID level: 0.975 Co-phenetic correlation: 0.827
No. of samples: 80 No. of tests: 12

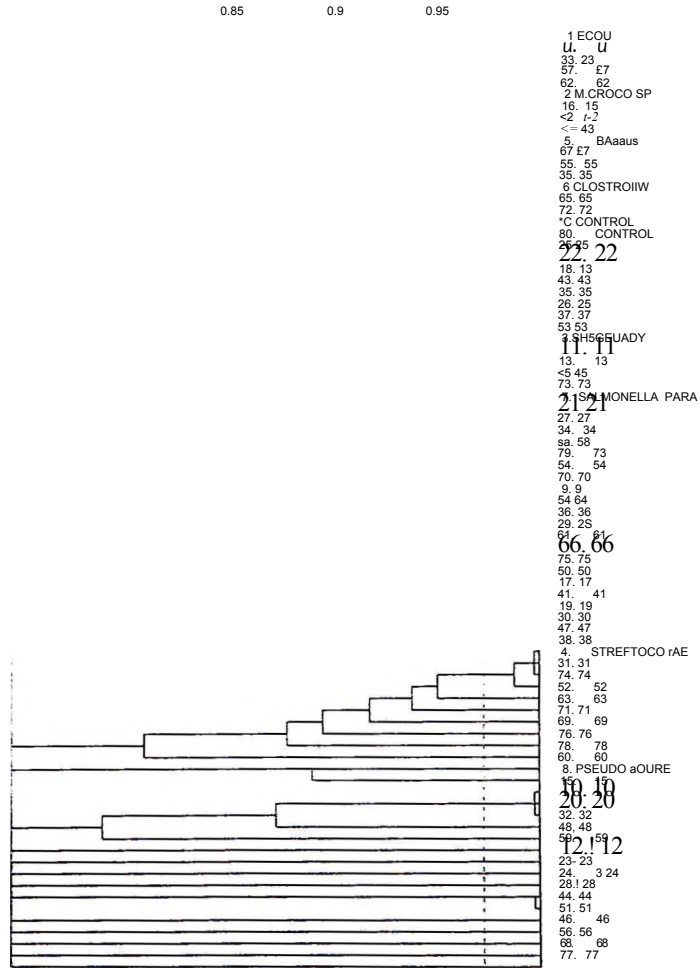


Fig. 3 S Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from Pnmpoog farm (frimpoo4). ID level: 0.975 Co-phenetic correlation: 0.944
 No. of samples: 73 No. of tes^s: 12

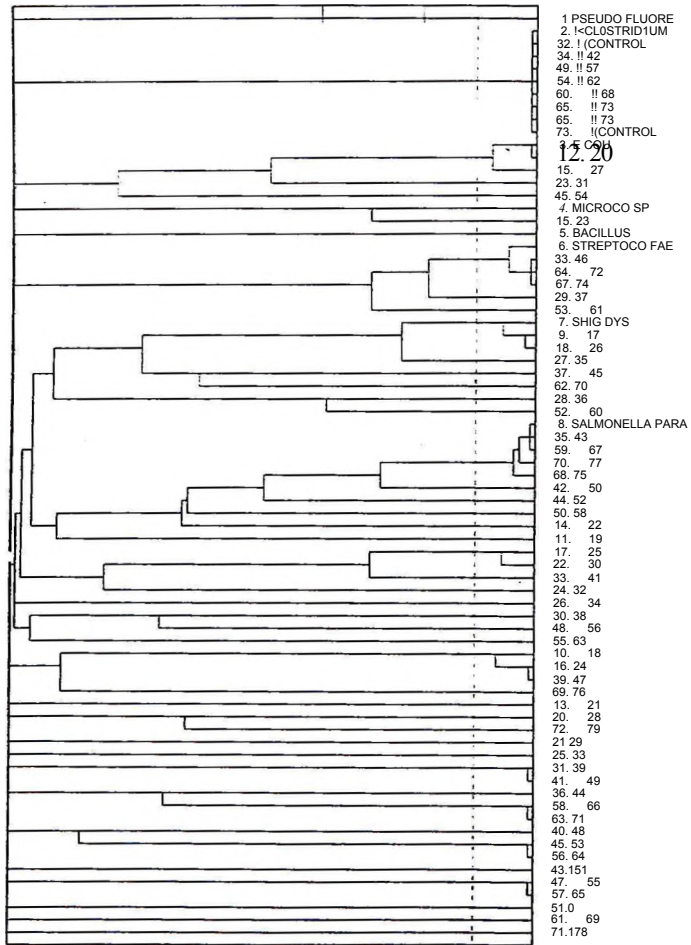
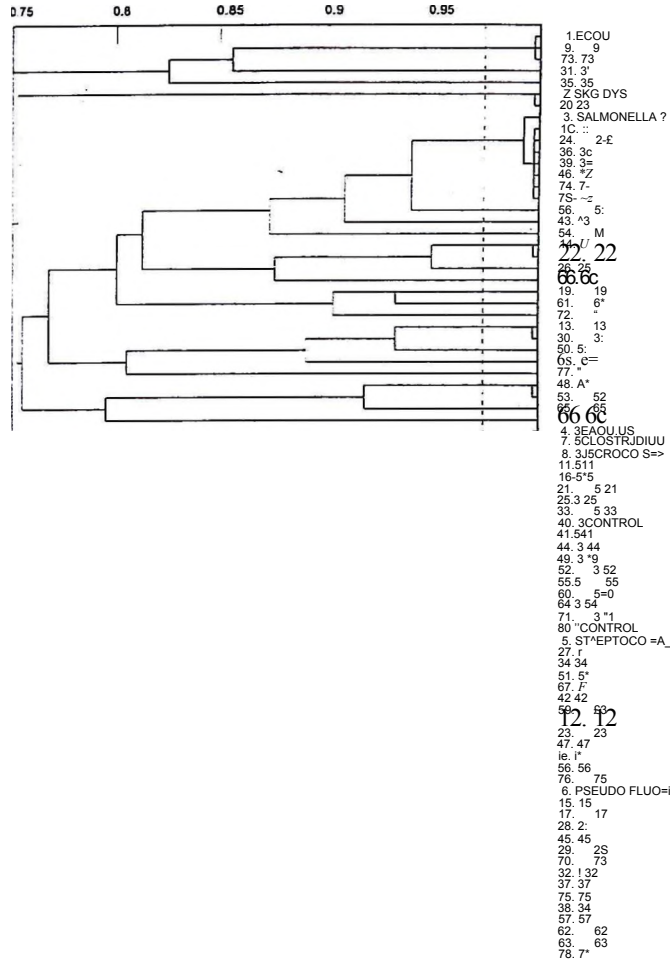


Fig. 3 1 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from Frimpong (frimponS). ID level: 0.975 Co-phenetic correlation: 0.932 No. of samples: 80 No. of tests: 12



in these samples. The PhP types for Boadi ponds ranged from 43 to 56. The PhP types for KK ponds ranged from 42 to 51, and those for Pacific ponds ranged from 27 to 41. The clustering of the bacterial isolates for the various sampling periods are presented in Figs 4a 4o. The dendrograms had high co-phenetic correlation (above 0.80), indicating that the dendrograms corresponded to the similarity matrix from which they were created.

Table 5c Diversities among bacterial flora in pig manure fertilized ponds

Sample name and no.	No. of isolates	Di values
Boadi	1	0.968
	2	0.971
	3	0.984
	4	0.974
	5	0.982
KK	1	0.959
	2	0.943
	3	0.924
	4	0.924
	5	0.915
Pacific	1	0.898
	2	0.908
	3	0.862
	4	0.928
	5	0.855
Mean Diversity		0.952

4. Blood waste-fertilized ponds

The diversities of bacterial flora were high (more than 0.90) for the blood waste fertilized pond (Boahen ponds) (Table 5d), indicating that the bacterial populations in these ponds consisted of many different PhP types (Appendices 4a - 4e). The PhP types for the ponds ranged from 46 to 63. The clustering of the isolates are presented in Figs 5a 5e. All the dendrogram had high co-phenetic correlation (above 0.80) indicating that the dendrograms corresponded to the similarities matrix from which they were created.

Fig. 4 a. Dendrogram showing UPGMA clustering of the bacterial bolacs for February, 1997 from Boacfi farm (Boadli), ID level: 0.975 Co-ptene6c correlation: CJ5S4
No. of samples: 80 No. of tests: 12

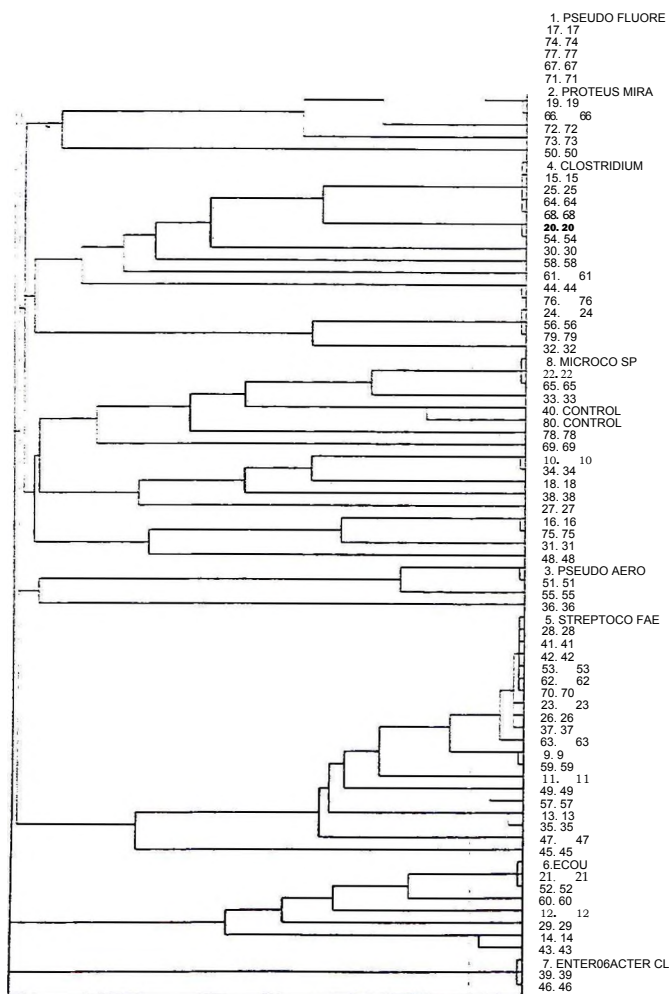


Fig. 4b Dendrogram showing UPGMA clustering of the bacterial isolates from Boadi farm (Boadi) in August 1997. CD level: 0.975 Co-phenetic correlation: 0.690 No. of samples: 81 No. of tests: 12

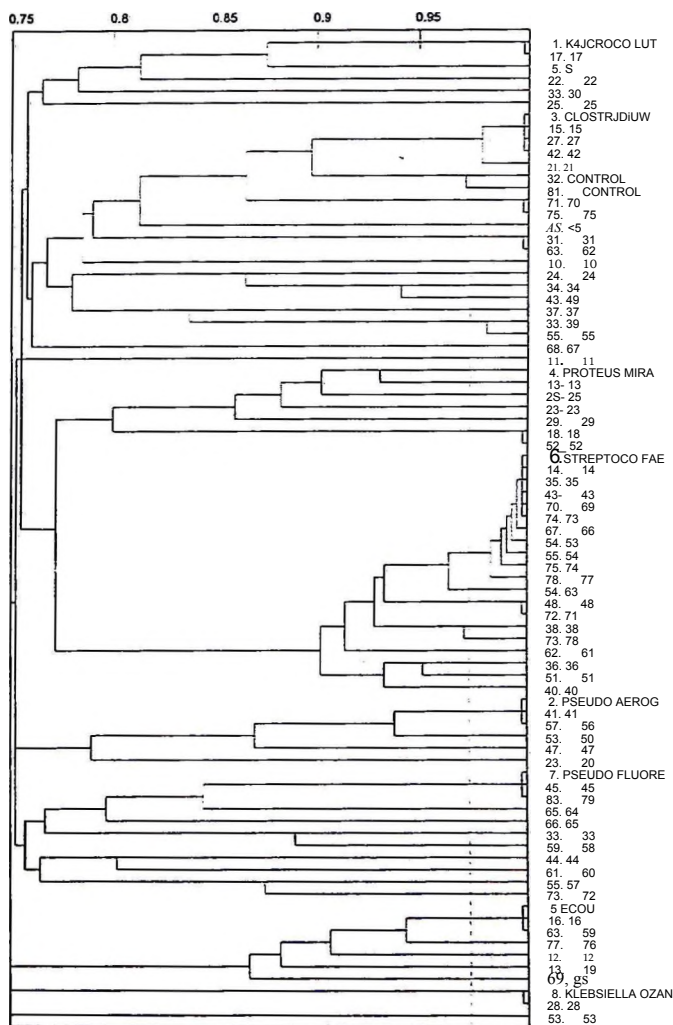
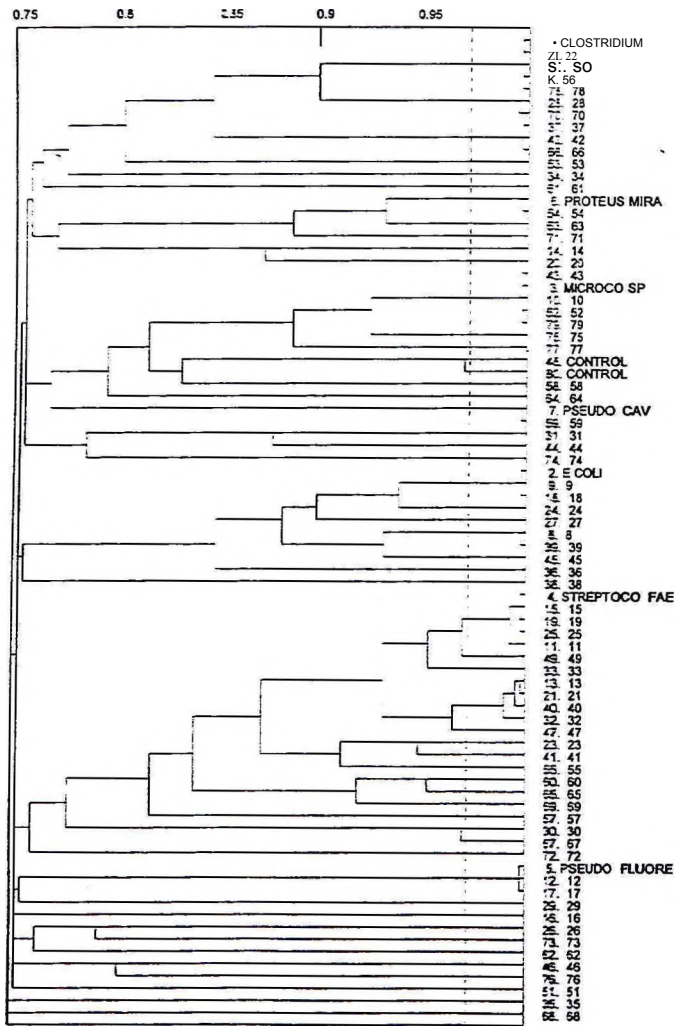


Fig 4 C - Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from BoatS fejn (Boa-f13). ID level: 0.975 Co-phenetic correlation: O-SOS No. of samplers 80 No. of fess: 12



Fi Ad Dendrogram sf-avring UPGMA ctostersg rf tie bacterial Isolates for August. 19S8
Enxn Boadi (Boadi4). iD teveE: 0.975 Co-pher'eEc cocorelation: 0.904
No. of samples: 80 No. of tests: 2

!: L "CE

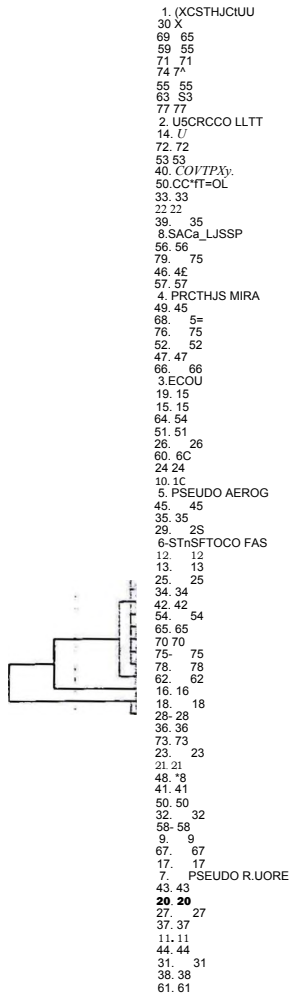


Fig. 4e j Dendrogram
 from BoacS farm (BoadB).
 No. of samples: 81 No. of tes^ai 12

UPGMA clustering of the bacterial isolates for February, 1999
 10 level 0.975 Co-phenetic correlation: 0.889

-d

n

- 1. STREPTOCOCCUS FAECIUM
- 18. 18
- 30. 30
- 35. 35
- 39. 39
- 42. 42
- 52. 51
- 56. 65
- 26. 26
- 50. 49
- 10. 10
- <5. 45
- 46. 45
- 33. 33
- 19. 48
- 55. 54
- 15. 15
- 62. 61
- 21. 21
- 59. 58
- 71. 70
- 51. 50
- 58. 57
- 3. CLOSTRIDIUM
- 9. 9
- 43. 43
- 75. 74
- 29. 29
- 53. 52
- 76. 75
- A4. 44
- X8. 47
- 16. 16
- 61. 60
- 7. 46
- 79. 78
- 37. 37
- 56. 55
- 54. 53
- 23. 23
- 34. 34
- 80. 79
- 64. 63
- 67. 66
- 73. 72
- 7a. 69
- 31. 31
- 72. 71
- 77. 76
- 5. MICROCOCCUS SP
- 8. MICROCOCCUS LU7
- Al. 41
- 81. CONTROL
- 32. 32
- 57. 56
- 38. 38
- 65. 64
- 5. PROTEUS MIRA
- 17. 17
- 25. 25
- 7. PSEUDOMONAS AERUGINOSA
- 13. 13
- 28. 28
- 74. 73
- 2. PSEUDOMONAS FLUORESCENS
- 7. 7
- 12. 12
- 68. 67
- 4. ECOLI
- 27. 27
- 36. 36
- 60. 59
- 63. 62
- 11. 11
- 22. 22
- 69. 68
- 19. 19
- 14. 14
- 24. 24
- 2a. 20
- 0.!! CONTROL

Fig.-<4f Dendrogram showing UPGMA clustering of the bacterial isoefies for Febraary, 1997 from KK 0*1)- ID level: 0.975 Co-phenetic corretalxki: 0.923 No. of samples: 60 No. of tests: 12

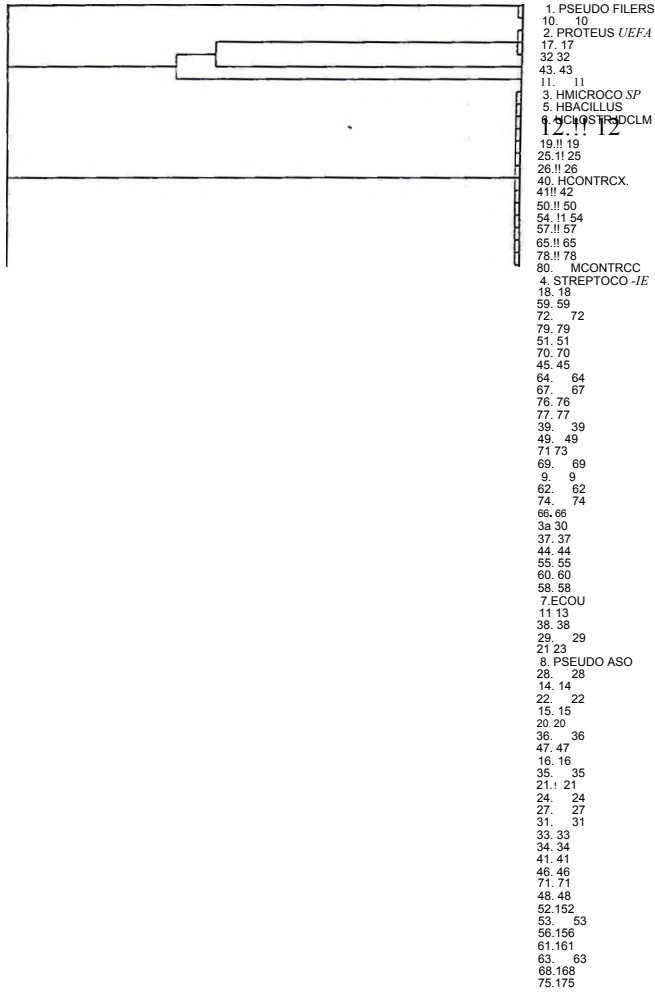


Fig. 4. g Dendrogram showing UPGMA clustering of the bacterial Isolates for August, 1997 from KK farm (kk2), to level: 0.975 Co-phenetic correlation: 0.941 No. of samples: 87 No. of tests: 12

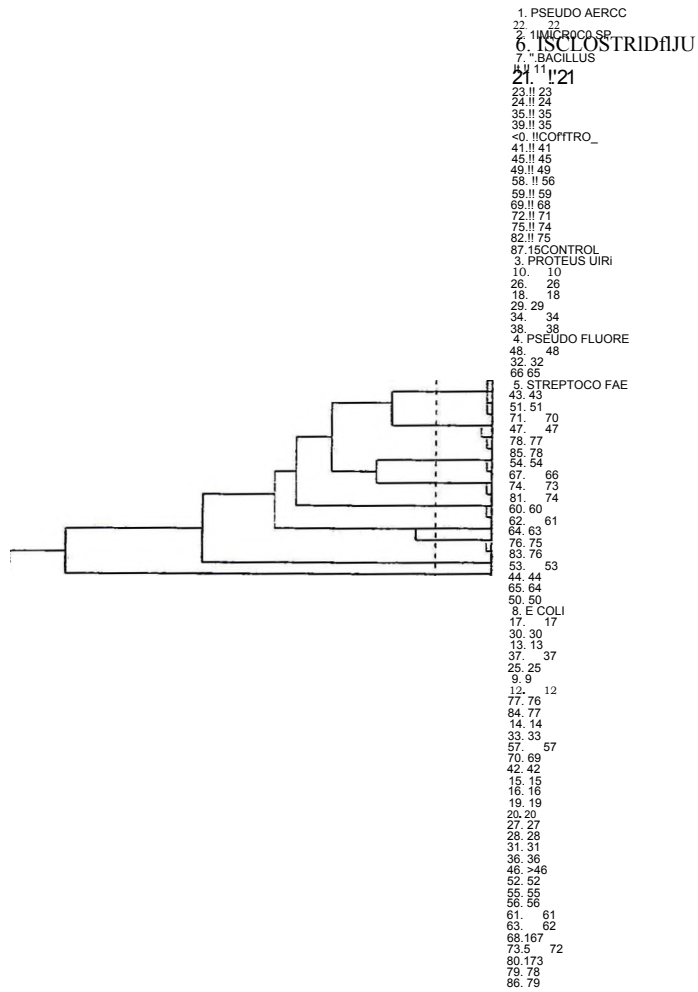


Fig. 4-4 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from KK fck3). ID level: 0.975 Co-phenetic correlation; 0.888 No. of samples: 81 No. of tests: 12

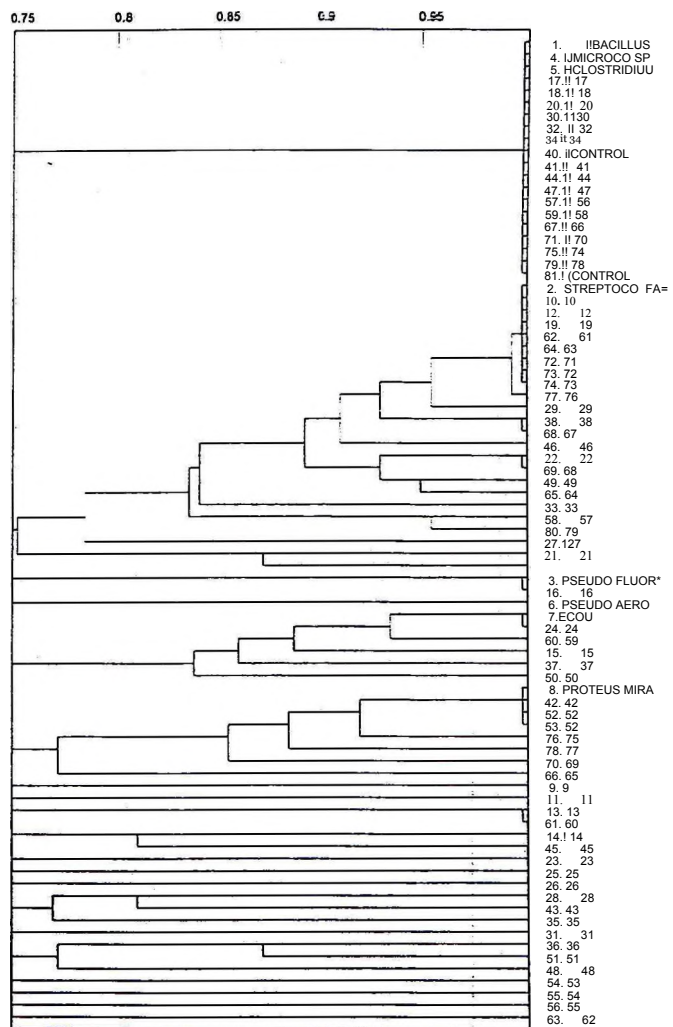


Fig. 4.1 ■ Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1SS8 from KK farm (kk4). ID level: 0.973 Co-phenetic correlation: 0.895
 No. of samples: 80 No. c< tests: 12

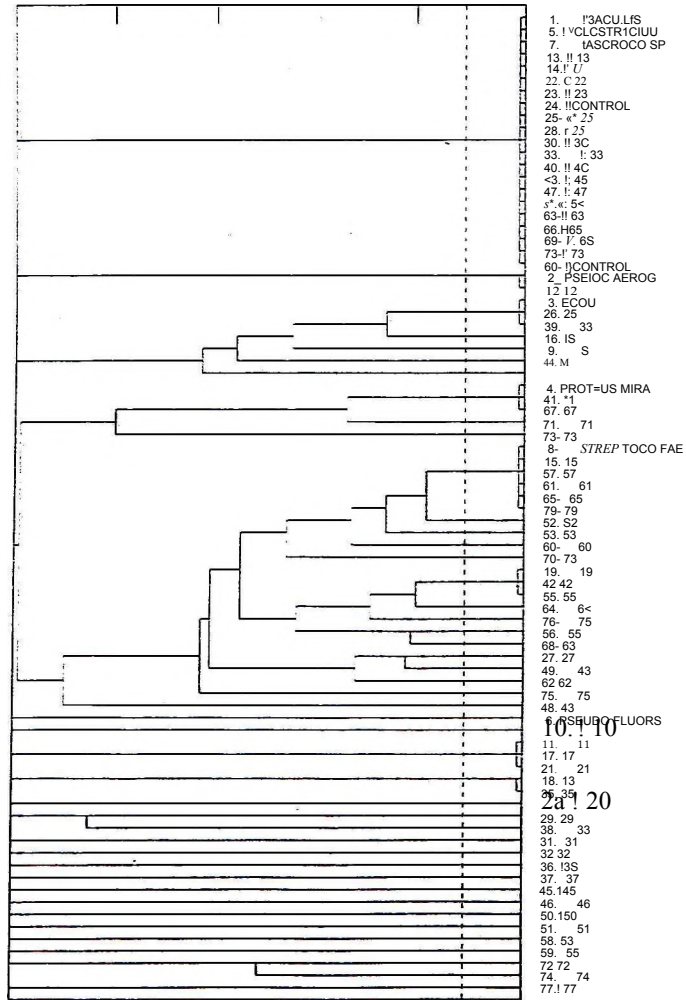


Fig 4 i . Dendrogram showing UPGMA clustering of *S. w* bacilferaf isolates for February, 1999 from Kktanm (kk5). ID level; 0.975 Co-pherteSconelaSon: 0.907
 No. of samptes. 81 No. of tests: 12

1.ECOU
 44. 43
 50. 49
 69. 66
 62. 61
 2. BACILLUS
 3. CLOSTRIDIUM
 7. MICROCOCOCCUS
 11. 11
 14. 14
 21. 20
 24. 23
 26. 25
 33. 32
 35. 34
 36. 37
 41. CONTROL
 43. 42
 45. 44
 46. 45
 51. 50
 53. 52
 57. 56
 63. 62
 71. 70
 76. 75
 81. CONTROL
 4. PROTEUS MIRA
 64. 63
 12. 12
 73. 72
 5. PSEUDO AERUGINOSA
 6. STREPTOCOCCUS
 10. 10
 42. 41
 65. 64
 80. 79
 52. 51
 56. 55
 77. 76
 46. 47
 63. 67
 75. 74
 13. 13
 23. 22
 28. 27
 72. 71
 70. 69
 1 PSEUDO FLUORESCENS
 39. 36
 9. 9
 20. 19
 15. 15
 40. 39
 79. 78
 16. 16
 19. 18
 17. 17
 18. 17
 37. 36
 22. 21
 25. 24
 29. 28
 27. 26
 30. 29
 31. 30
 47. 46
 74. 73
 32. 31
 59. 58
 34. 33
 36. 35
 49. 48
 54. 53
 55. 54
 58. 57
 60. 59
 61. 60
 66. 65
 67. 66
 78. 77

Fig. Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1997 from Pacific feon (pacat). ID level: 0.975 Co-phenetic: correaSon; 0.955 No. of samples: 80 No of tests: 12

```

1.ECOU
24. 24
36. 26
46. 45
53. 53
62. 62
2. HEAGIUS
5. HIAJROCO LUT
7. HIAJROCO LUT
It !! I!
21. 21
29. 29
33. JI 33
40. HCONTROL
44. 44
45. 45
51. 51
52. 52
56. 56
59. 53
60. 50
65. 55
66. 55
68. 53
74. 74
75. 75
78. 73
80. CONTROL
3. PROTEUS MIRA
19. 19
4. STREP TOCO FAE
47. 47
9. 9
54. 54
58. 53
53. 63
73. 73
18. 18
30. 30
79. 79
61. 61
64. 64
13. 13
23. 23
6. PSEUDO FIUORE
20. 20
67. 67
8. SER MAR
34. 34
10. 10
12. 12
39. 139
69. 69
48. 45
72. 72
14. 14
32. 32
22. 22
42. 42
16. 16
26. 26
17. 17
25. 25
31. 31
49. 49
41. 41
37. 37
58. 50
57. 57
55. 55
27. 27
43. 43
25. 28
70. 70
77. 77
35. 35
71. 71
76. 76
    
```

Fig. - 41 Dendrogram showing UPGMA clustering of *E. coli* Isolates for August, 1997 from Padfic farm (pad2)
 ID level: 0.975 Co-phenetic correlation: 0.902
 No. of samples: 80 No. of tests: 12

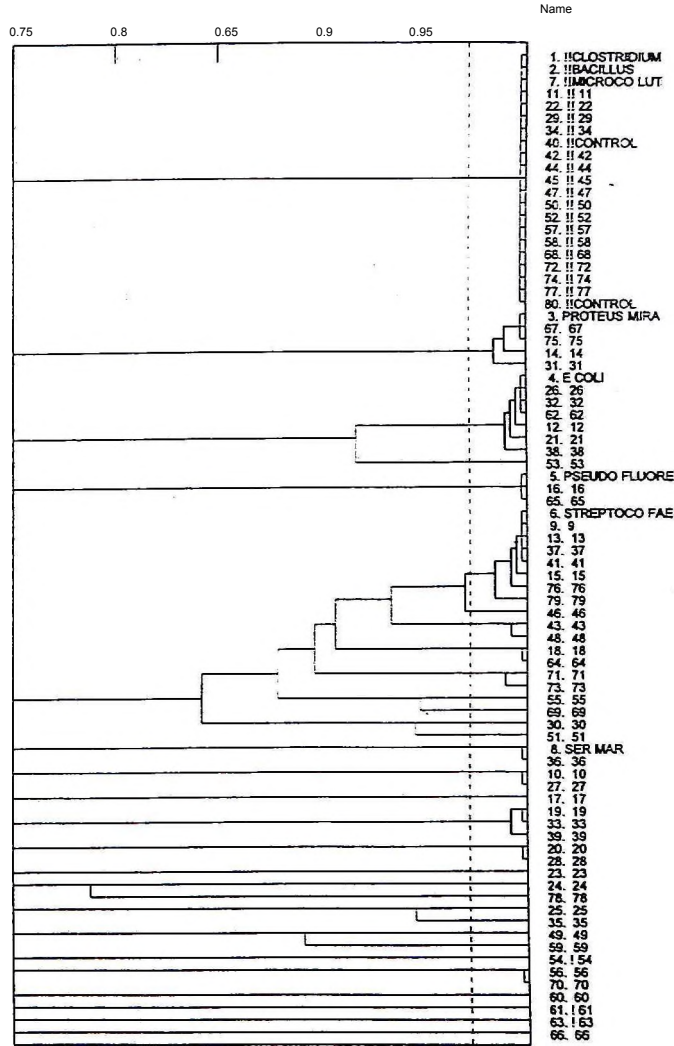


Fig. 4m Dendrogram showsrg UPGMA clustering of the bacteria isolate* for February, 1958 for Pacific fa/m (pact). -O level 0.975 Co-phenetic correlation: 0.896 No. of samples: 80 No. of tests: 12

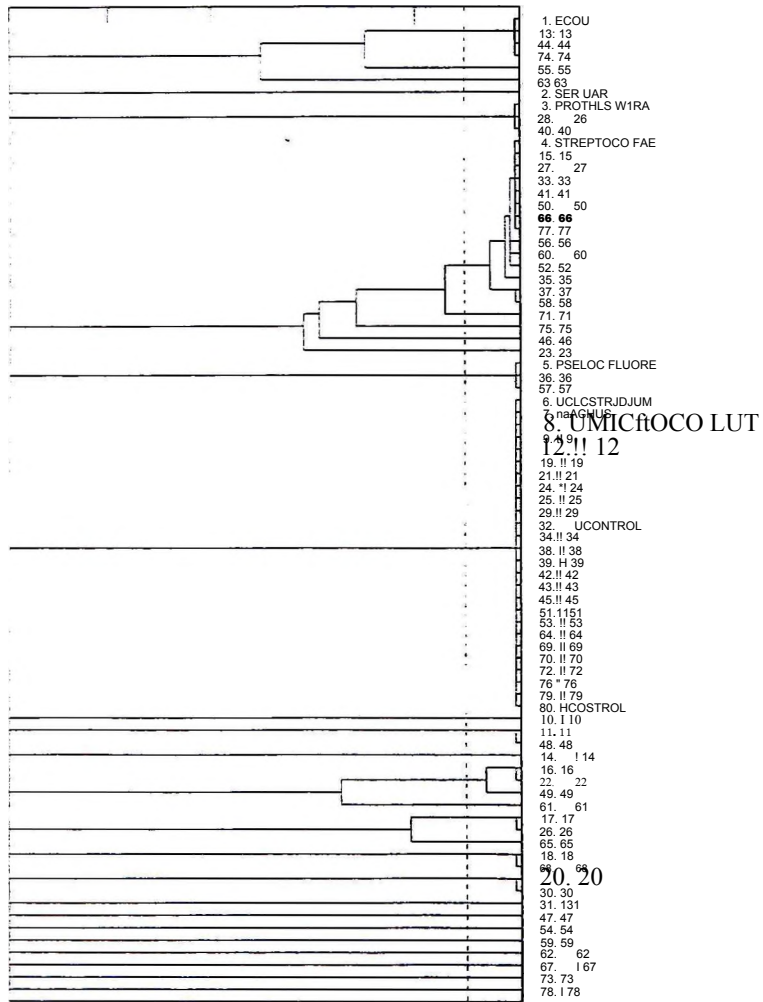


Fig. 4 n Dendrogram showing UPGMA clustering of the bacterial *isdata*s for August 1998 from Pacific farm (pactf). ID level: 0.975 Co-phenetic correlation: 0.8&S
 No. of samples: 82 No. of tests: 12

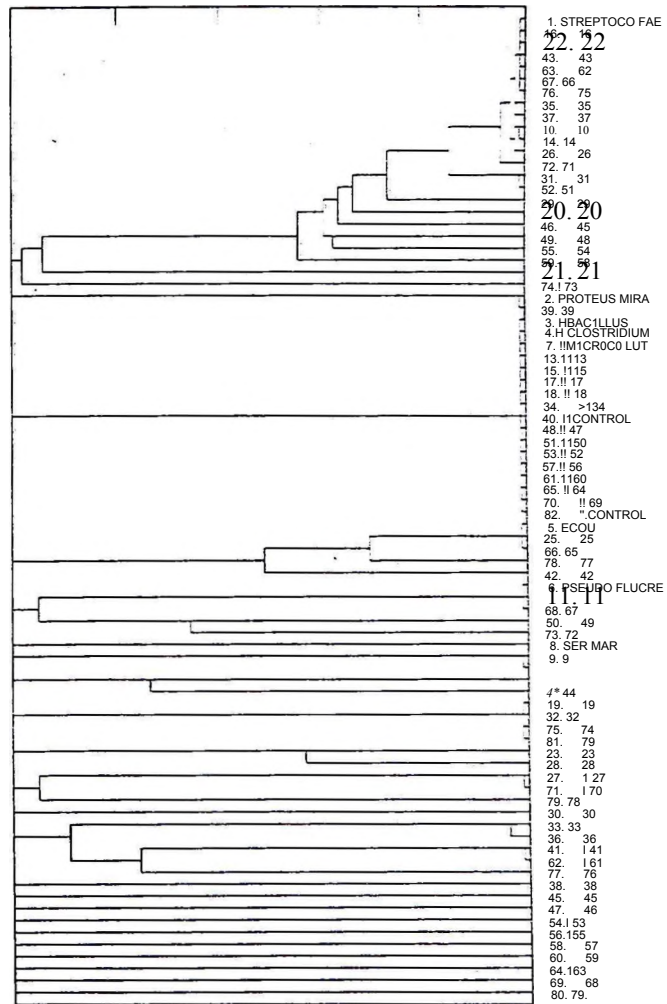


Table 5d. Diversities among bacterial flora in blood waste fertilized ponds

<u>Sample name and no.</u>	<u>No. of isolates</u>	<u>Divalues</u>
Boahen 1	79	0.991
2	80	0.992
3	80	0.990
4	82	0.990
5	80	0.984
Mean diversity		0.989

5. Chemically fertilized ponds

The diversities of the bacterial flora were high (more than 0.90) for both Aheto and Sagoe ponds (Table 5e), indicating that the bacterial populations in these ponds consisted of many different PhP types (Appendices 5a - 5j). The PhP types for Aheto ponds ranged from 59 to 64, and the PhP types for Sagoe ponds ranged from 34 to 43. The clustering of the bacterial isolates for the two farms are presented in Figs 6a - 6j. Most of the dendrograms had high co-phenetic correlation (above 0.80) indicating that each dendrogram corresponded to the similarity matrix from which it was created. The only exception was from Aheto ponds which had a dendrogram from a sampling period with a low co-phenetic correlation (less than 0.80), indicating that some data that could not be clustered might have shown up as clusters and care must be taken in interpreting such clusters.

Fig. -4 O Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from Pac-5c farm (pao5). ID level: 0.975 Co-pher-eilC correlation; 0.971 No of sampes: 86 No. of tests: 12

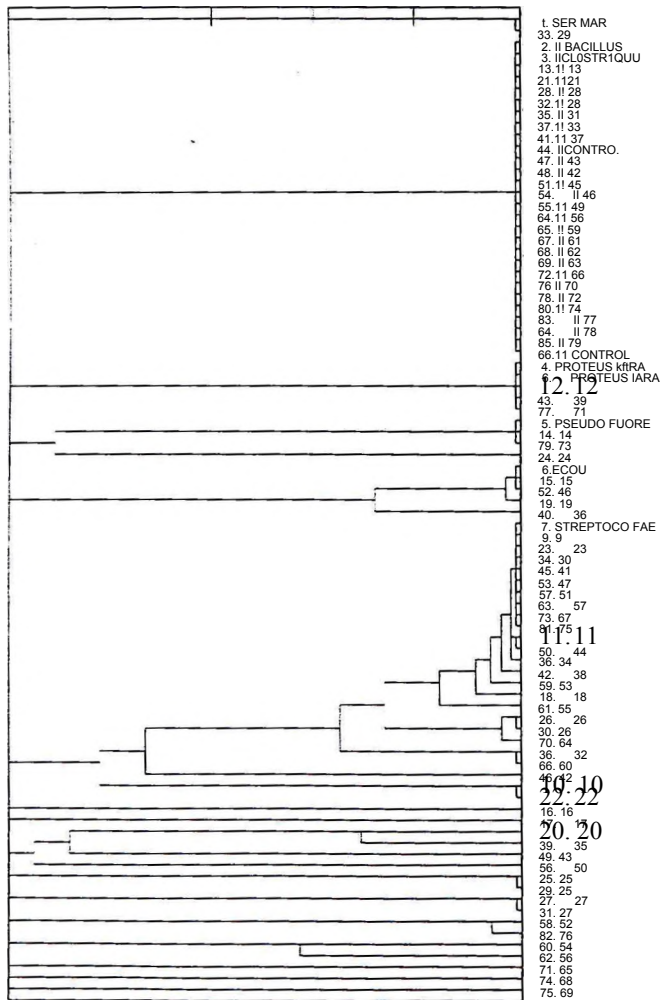


Fig. - 5 a Dendrogram shoeing UPGMA clustering of the bacterial isolates for February, 1997 from Boahen farm (boahent). ID tevefc 0.975 Co-phenetic cocrd&on: 0.B16
No. of samples: 79 No. of less: 12

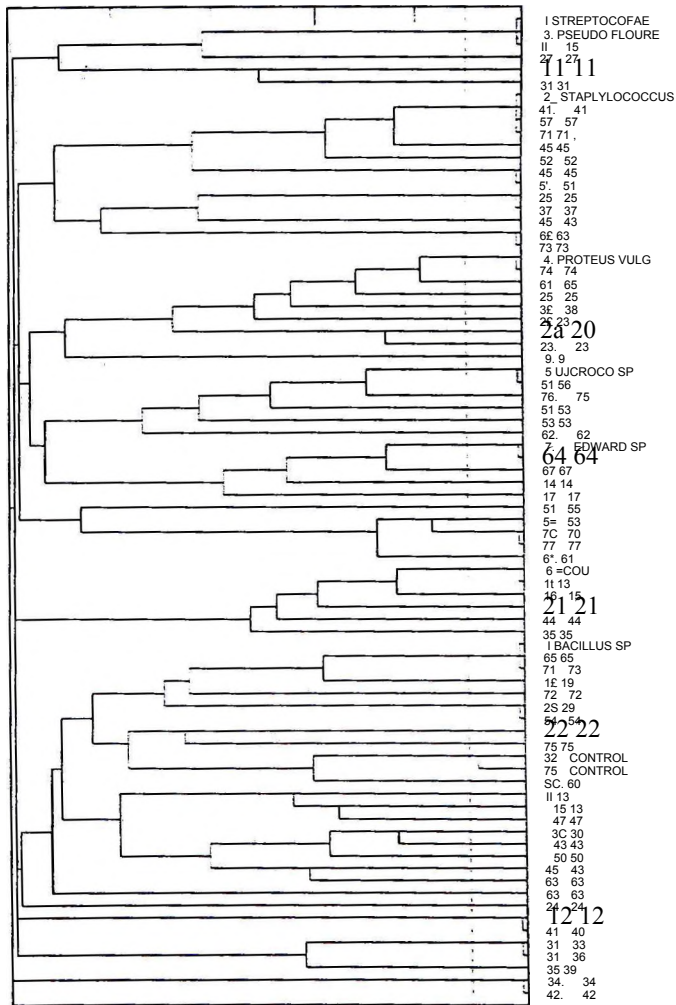


Fig. 5 b DctxSrcgraa showing UPGMA clustering of Ih* tadsma sctaiBS for August, 1997 from Beaten Sam (bcErien2). ID level: 0.975 Co-phenetic co-eLatioo: 0.826 No. ofsa-ripes: SC No. of tests: 12

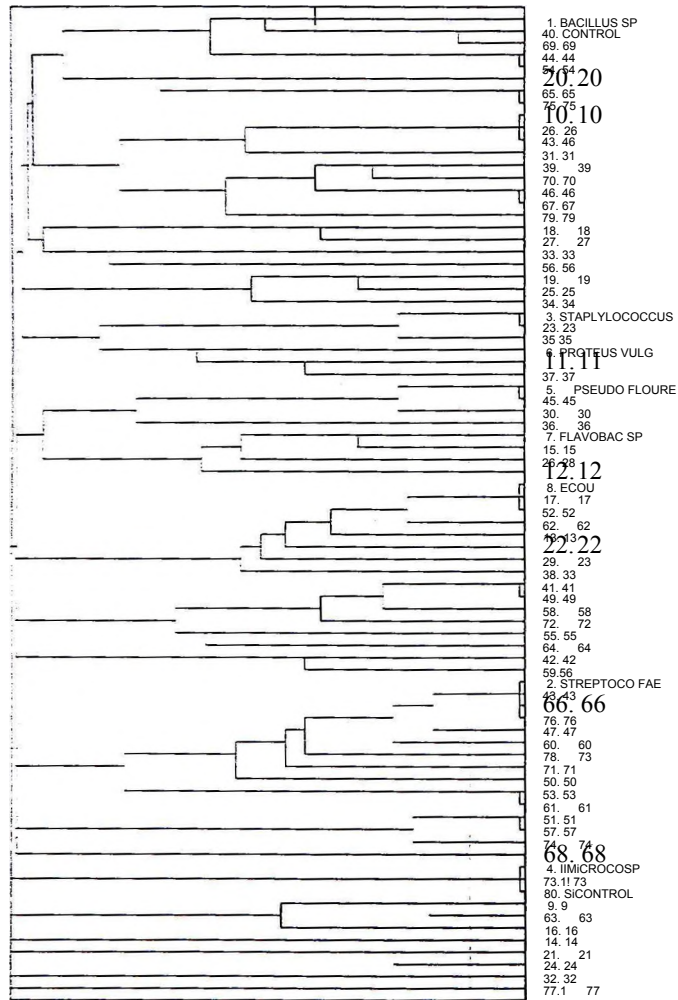


Fig. 5c Dendrogram showing UPGMA clustering of the bacterial Isolates for February, 1958 from Baoben farm (baobenS). E-toveJ: 0.975 Co-phenetic correlation: 0.09
 No. of samples: 00 No. of wa: 12

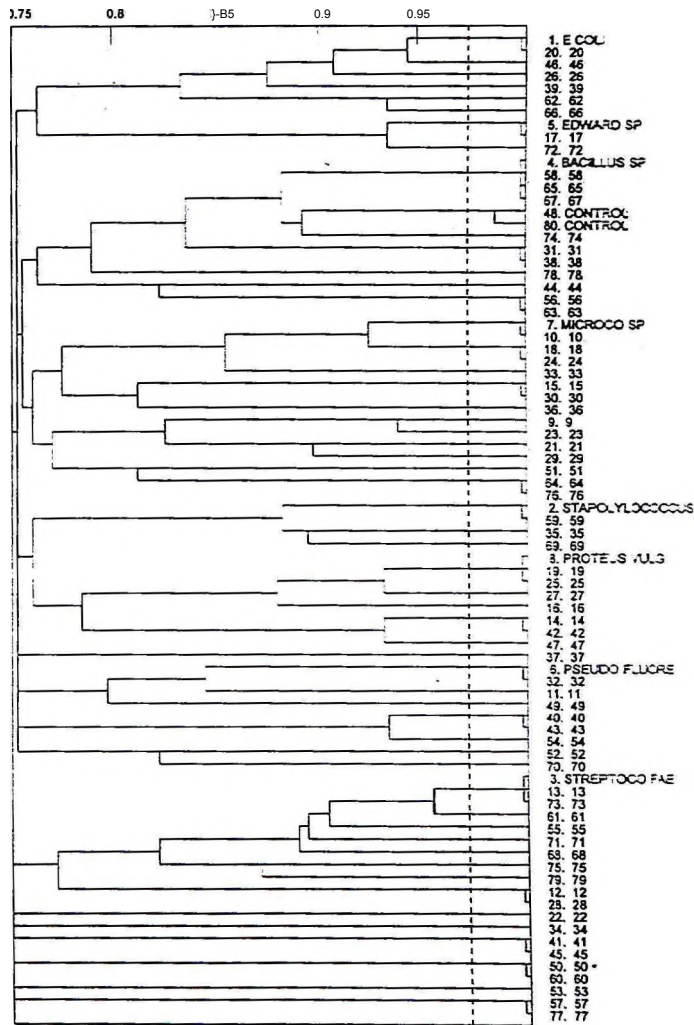


Fig. 3 d Dendrogram showing UPGVA *su/sssvtg* of *ta* *bacSenal* isolates for August, 1998 to Soafien fcurm_bcafn4). ID C. 975 Co-phenetic correlation: 0.839
n/samples: 62 S/o of tests: 12

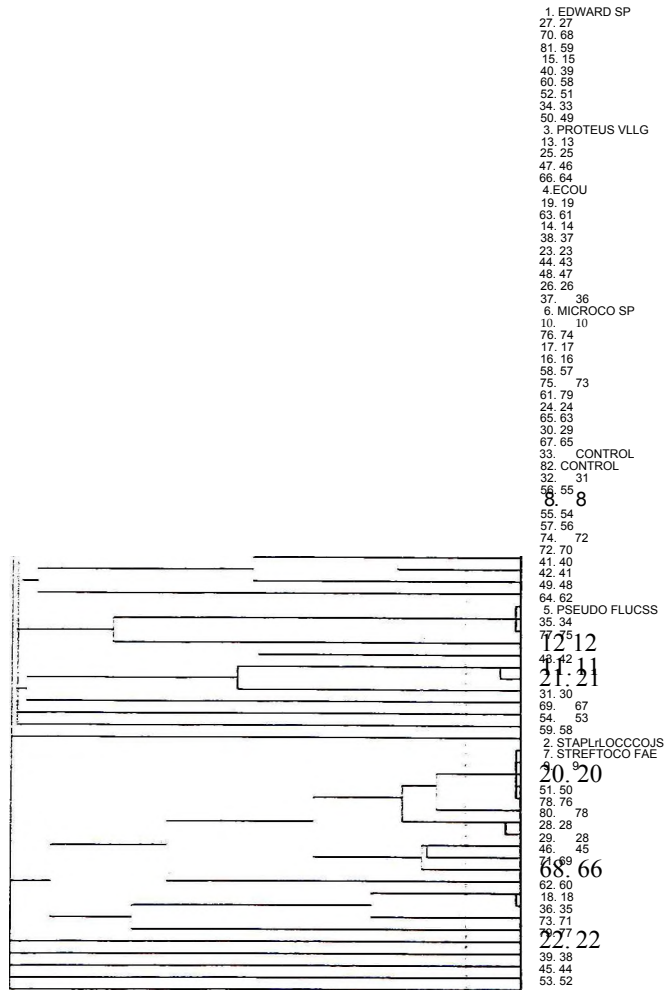


Fig. 5 e • Dendrogram showing UPGMA clustering of the bacterial Hotafes for Feorsasy, 1999 from Boahen atm. Cbaahen5). ID level: 0.975 Co-phenetic correftacitr 3.250 No. of samples: 80 No. of tests: 12

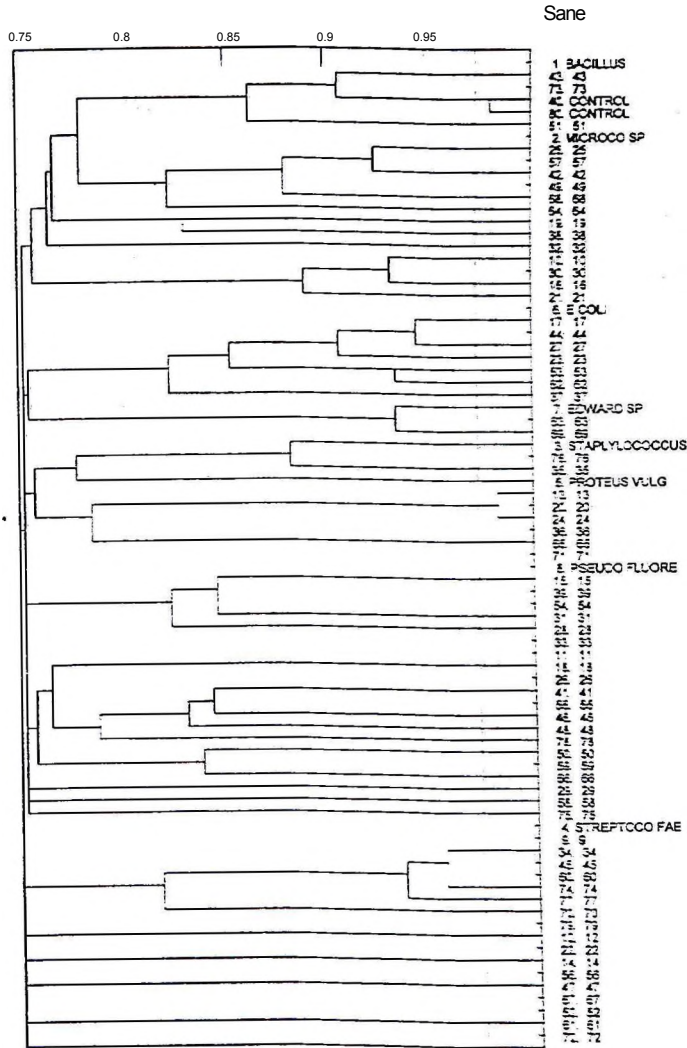


Fig. 6a Dendrogram showing UPGMA clustering of bacterial isolates from Fe&rsari, -507
Ahefo farm (Ahefo). ID Jewel: 0.975 Co-phenetic correlation: 0.812
No. of samples: 60 No. of less: 12

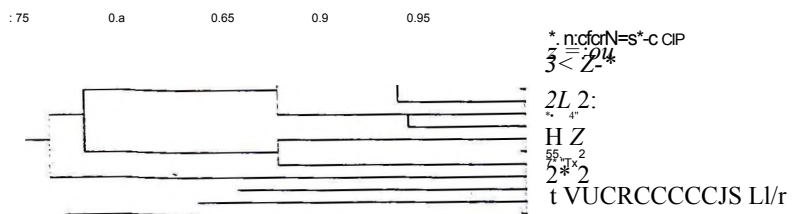


Fig. 6b Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1991 from Aheto farm (Aheto2). ID level: 0.973 G_{o-p}^{medc} sarstaSocr 0-787
No. of samples: 80 No. of tests: 12

1. MICROCOCCUS URR
45. 45
14. 14
25. 25
30. 30
32. 32
11. 11
16. CONTROL
80. CONTROL
40. CONTROL
17. 17
75. 75
57. 57
2. PSEUDO ASROG
46. 46
77. 77
21. 21
50. 50
61. 61
27. 27
55. 55
6. CORYNEBAC DIPH
60. 60
76. 76
51. 51
15. 15
63. 63
69. 69
19. 19
28. 28
5. E COU
24. 24
59. 59
73. 73
29. 29
54. 54
64. 64
12. 12
79. 79
43. 43
49. 49
65. 65
8. SERRA UASC
23. 23
34. 34
53. 53
38. 38
2. ERMON HYDRO
32. 32
33. 33
52. 52
10. ENTEROBACTER AE
48. 48
41. 41
56. 56
70. 70
42. 42
47. 47
78. 78
3. STREPTOCO FA=
37. 37
15. 15
71. 71
39. 39
4. CITROSAC DIV
62. 62
26. 26
13. 13
7. KLEBSIELLA RKIS
31. 31
58. 58
74. 74
67. 67
72. 72

Fig. 6g Dendrogram showing IGMVIAcfae1enBB cl-w bacterial testates for Febcua¹. 1B98 from Ahela farm (Aheto3). IOfewt 0975 Colbraic correlation: 0.863
No. of samples: 80 - No. of tests: 12

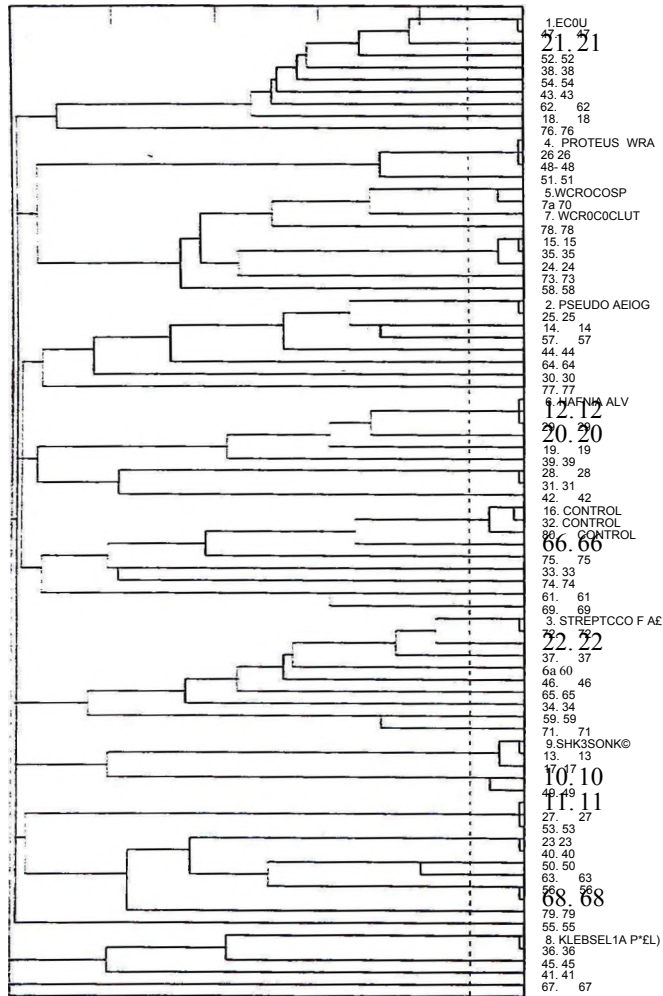
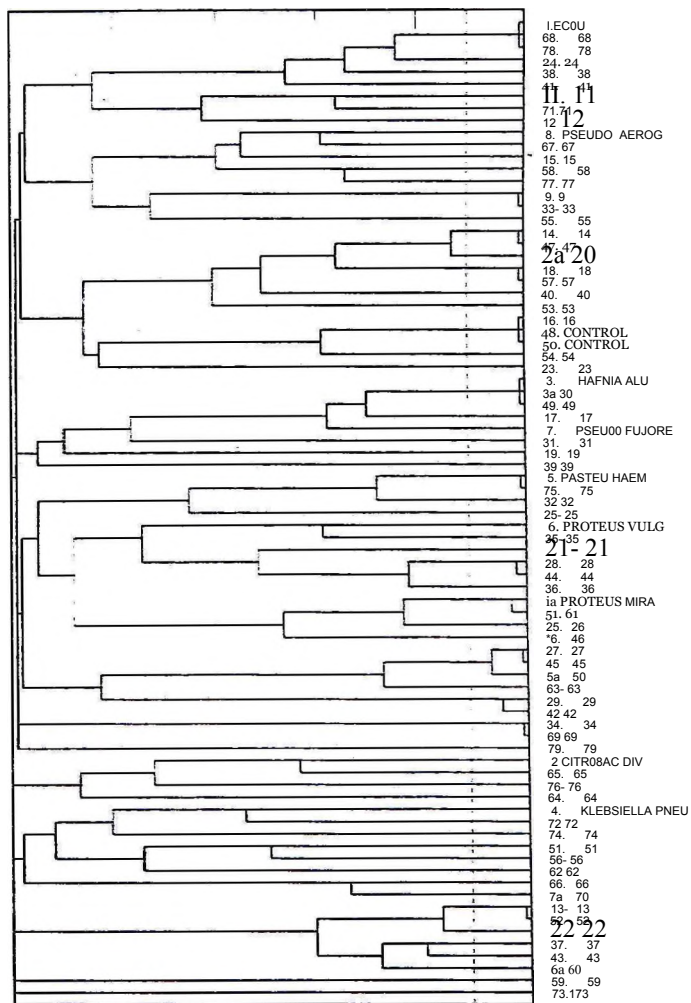


Fig. bd EmdrogrM showing UPGMA clustering of bacterial iscAaes for August, 1998 from Alwiti lens (Afaefc>4) DiawatO.S75 Co-pheneCcoorratatoo:0J532 No. ofsnp:80 No. of teste 12



«w wc- ucramgnrosnowina uruH Hosmg «« Notarial isolates for Febrauiy, 11
fionAbetofefin(A.J.Ns">5), ID lewet 057S Co-pftecoSc correlation: 0.850
Mo. of samples; 80 No. of (ests: 12

0.9 0.95

-ri

-rt

- 1. ECOU
- 35. 35
- 79. 79
- 56. 58
- 70. 74
- 66. 10
- 66. 66
- 18. 18
- 42. 42
- 52. 52
- 27. 27
- 3. CORYNE3AC DPH
- 44. 44
- 70. 70
- 51. 51
- 63. 63
- 7. MICROCOCCUS LUT
- 54. 54
- 77. 77
- 80. CONTROL
- 40. CONTROL
- 64. 64
- 31. 31
- 45. 45
- 8. PSEUDO AEROG
- 60. 60
- 71. 71
- 67. 67
- 14. 14
- 9. PSEUDO CAV
- 73. 73
- 46. 46
- 53. 53
- 24. 24
- 57. 57
- 5. PSEUOO FLUOFS
- 47. 47
- 11. 11
- 49. 49
- 43. 43
- 62. 62
- 30. 30
- 68. 68
- 2. KLEBSIELLA ?*EU
- 33. 33
- 61. 61
- 21. 15
- 21. 21
- 29. 29
- 6. PROTEUS VLLG
- 48. 48
- 60. 60
- 2. 12
- 20. 20
- 37. 37
- 17. 17
- 32. 32
- 19. 19
- 23. 23
- 25. 25
- 78. 78
- 4. STREP TOCO FAE
- 26. 26
- 65. 65
- 72. 72
- 34. 34
- 22. 22
- 38. 38
- 59. 59
- 76. 76
- 16. 16
- 28. 28
- 41. 41
- 50. 50
- 55. 55
- 75. 75

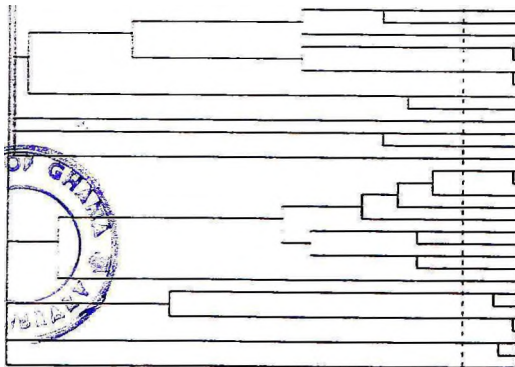


Fig. 01 Dendrogram showing UPGMA clustering of the bacterial genus *Urea* from Sagoo fan (aagool). ID limit 0.975 Co-phenetic crenation: OSea No. of samples: SO No. of #***: 12

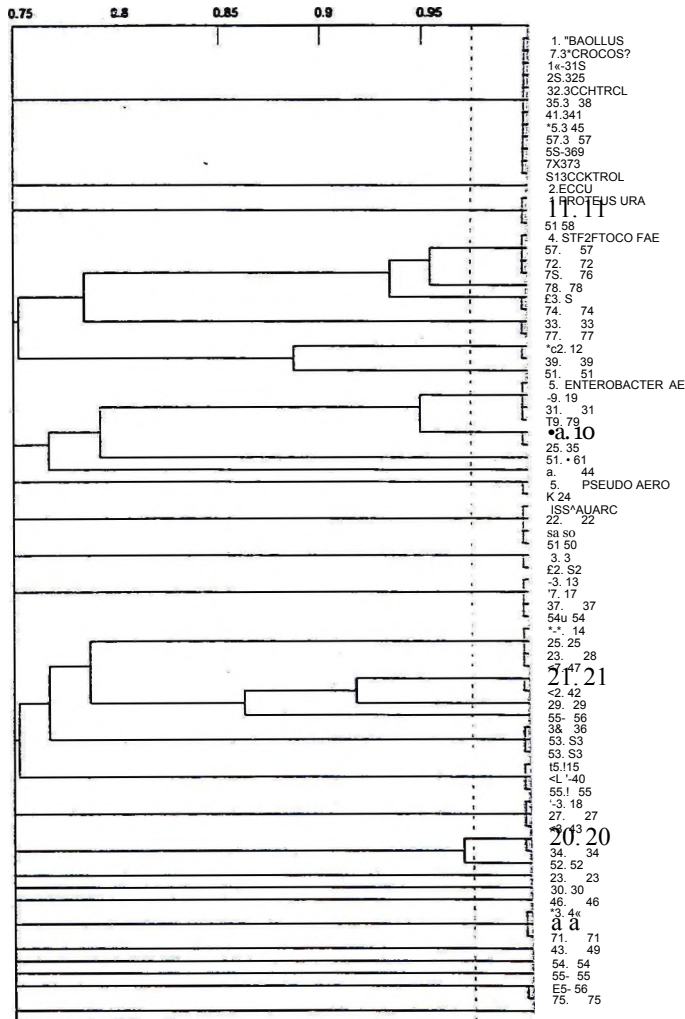
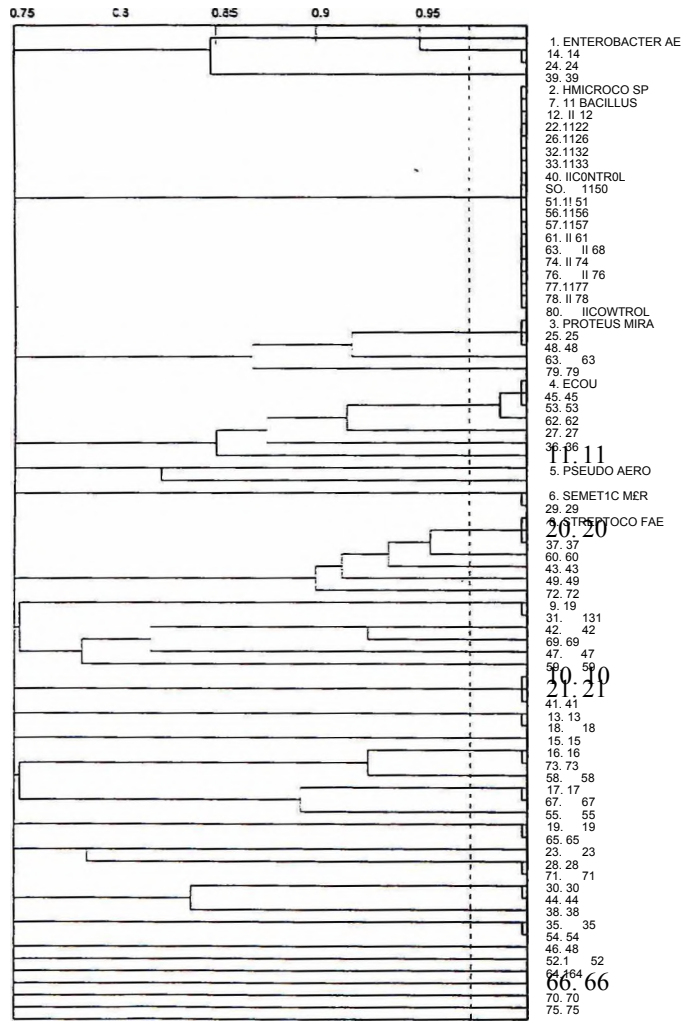


Fig. 6 g Dendrogram showing LFCSUA clustering of lbe bacterial Isolates for August, 1997 from Sagoe fens (sagoe2). ID e.ei 0.975 Co-phenetic correlation: 0.967 No. of samples: 30 No. of tests: 12



hig. on uenofx>gr^n etxiwng UKtIMA ausienng O1 me bacienal isolates kx f-etxuary. 1998
from Sago* farm (sagoe3). ID level: 0.975 Co-pienelic cofftetation: 0.991
No. of safnples: 80 Mo. of rests: 12

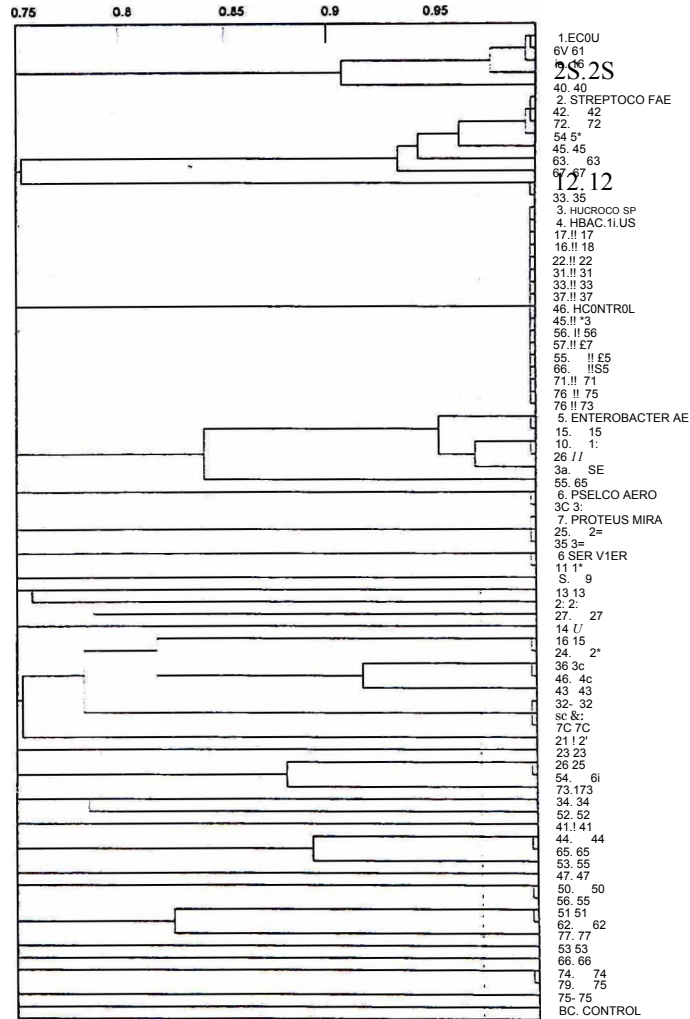


Fig. 6 | Dendrogram showing UPGMA clustering of the bacterial isolate* for August, 1998 from Sagoe farm (sagoe4).
 IO cvfcv 0.975 Co-phenetic conflation; 0.985
 No. of samples: 81 No. of genes: 12

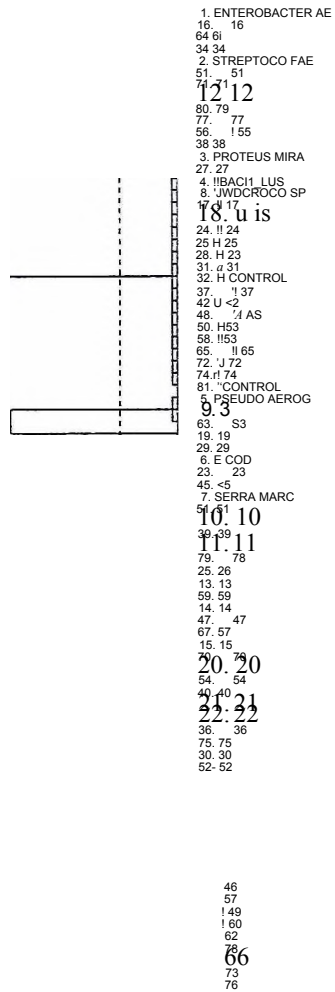


Fig. 6 j Dendrogram iiww-*eng* UPGMA clustering of the bacterial isolates for February, 1999 from Sago farm (sagoe5). ID level: 0.975 Co-phenetic correlation: D=7B
 No. of samples: 80 No. of tests: 12

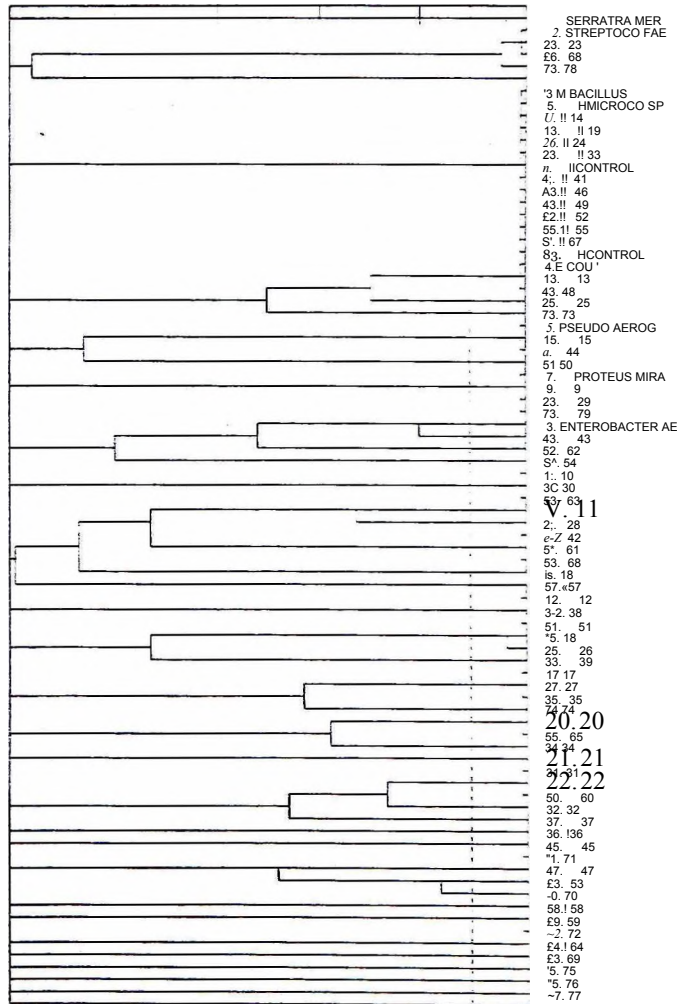


Table 5e. Diversities among bacterial flora in chemically fertilized ponds

Aheto	1	80	0.993
	2	80	0.995
	3	80	0.991
	4	80	0.993
	5	80	0.993
Sagoe	1	80	0.962
	2	80	0.937
	3	80	0.947
	4	81	0.944
	5	80	0.959
Mean Diversity			0.972

6. Non-fertilized ponds

The diversities of bacterial flora were high (more than 0.90) for the non-fertilized ponds (ARDEC 3) (Table 5f), indicating that the bacterial populations in these ponds consisted of many different PhP types (Appendices 6a - 6e). The PhP types for the ponds ranged from 55 to 66. The clustering of the isolates are presented in Figs 7a - 7e. All the dendrogram had high co-phenetic correlation (above 0,80) indicating the dendrograms corresponded to the similarities from which they were created.

Table 5f. Diversities among bacterial flora in non-fertilized ponds

	No. of isolates	Di values
ARDEC 3 1	80	0.992
2	80	0.992
3	81	0.989
4	82	0.993
5	81	0.994
Mean diversity		0.996

g. 7a Dendrogram showing UPGMA clustering of the raderial isolates for m ARDEC 3 pood (Ardec31). ID level: 0.975 Co-j3haneEc correlation: 0. >. of samples: 80 No. of tests: 12

5 0.5 0.55 0.9

i—c

ebuary. (9

Nam©

- 1 EO
- 46. 46
- 23. 23
- 26. 26
- 31. 11
- 27. 32
- 40. 40
- 51. 12
- 28. 28
- 53. 63
- 58. 56
- 69. 69
- 2. PSE
- 77. 77
- 52. 52
- 6. PSE
- 45. 45
- 76. 15
- 21. 21
- 43. 43
- 4. PSE
- 65. 65
- 74. 74
- 67. 67
- 71. 71
- 25. 25
- 70. 70
- 73. 73
- 79. 79
- 9. BAC
- 18. 18
- 24. COF
- 56. COF
- 80. CO*
- 59. 59
- 20. 22
- 44. 44
- 49. 49
- 51. 51
- 64. 64
- 3. KLE
- 47. 47
- 50. 50
- 54. 54
- 8. ENT
- 35. 35
- 16. 16
- 39. 39
- 17. 17
- 55. 55
- 27. 27
- 33. 33
- 37. 37
- 75. 75
- 40. 40
- 50. 60
- 53. 53
- 46. 46
- 41. 41
- 42. 42
- 5. STR
- 29. 29
- 36. 36
- 62. 62
- 60. 68
- 7. KLEI
- 19. 19
- 34. 34
- 36. 38
- 14. 14
- 57. 67
- 66. 66
- 76. 76
- 72. 72
- 78. 76

Fig / D Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1997 from AROEC 3 pond (Ardec3Z). ID level: 0.975 Co-phenetic correlation: 0.903 No. of samptos: 80 No. of tests: 17

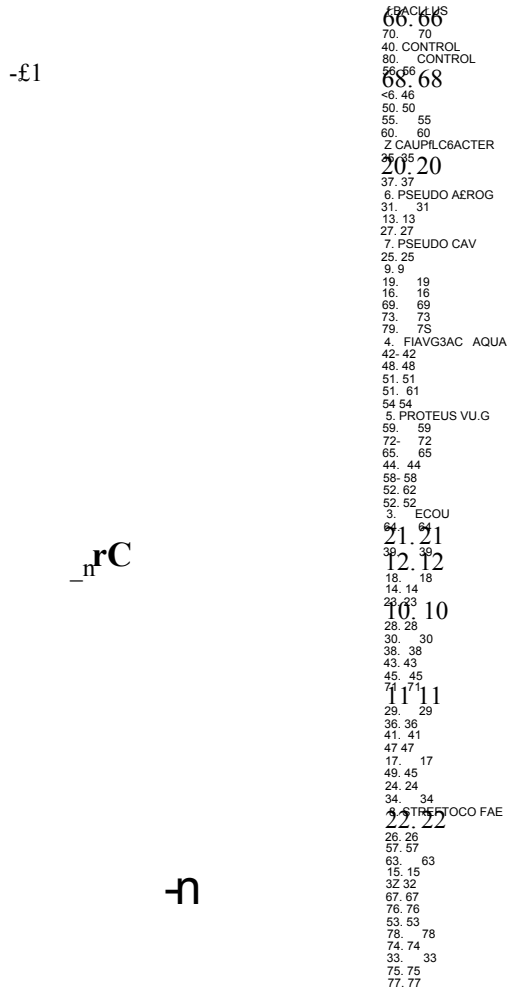


fig 7 C Ca* -rogram showing UFNSMA clustering of the bacterial isolates for February, 1998 from ARDEC 3 pond (Ardec33). 1C Sevel 0.975 Co-phenolic correlation: 0.892 S'a of sa.nptes: 51 No. of tests: 12

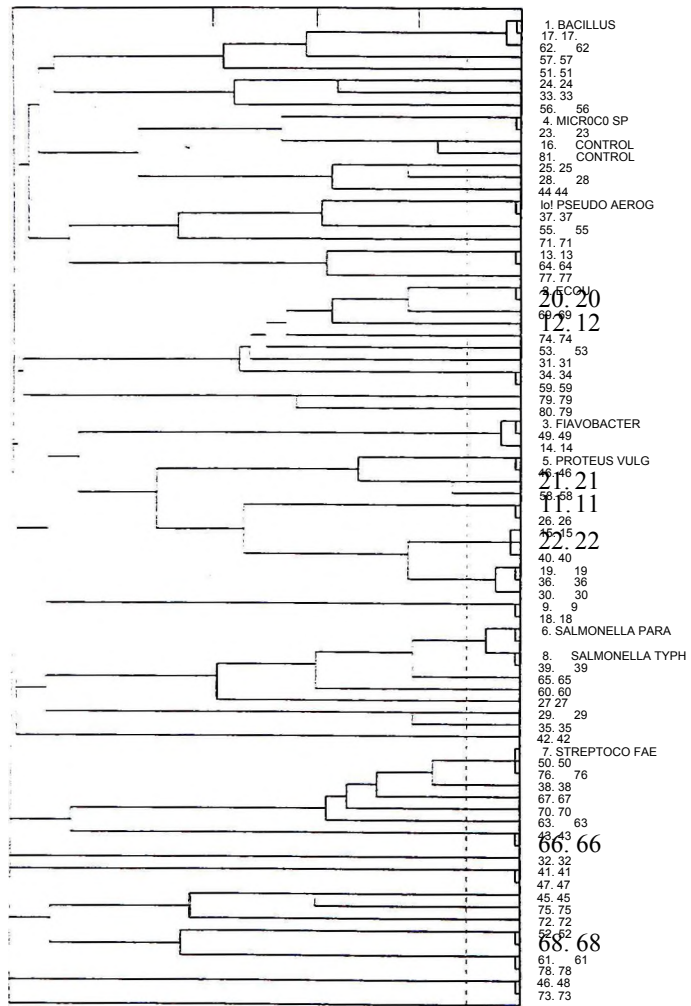
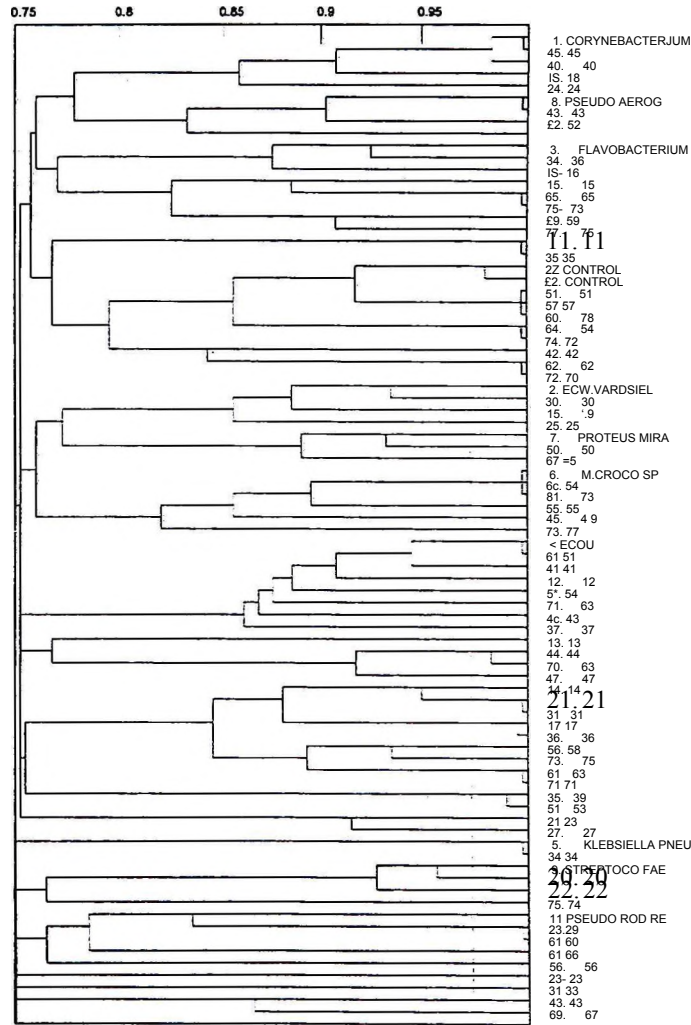


Fig.7 d. Dendrogram showing UPGMA clustering of the bacterial isolate for August, 1996 from ARDEC 3 pool (Ard*c34). O level: 0.975 Co-phenetic correlator: 0.840
 No. of samples: 82 No. of tests: 12



7. Open systems

The diversities of bacterial flora were generally high (more than 0.90) for samples from Kpong head pond, Volta river and Weija dam (Table 5g), indicating that the bacterial populations in the rivers consisted of many different PhP types (Appendices 7a-7o). The PhP types for Kpong Headpond ranged from 35 to 41. The PhP types for Volta river ponds ranged from 30 to 39, and those for Weija dam ranged from 29 to 41. The clustering of the bacterial isolates for the various sampling periods are presented in Figs 8a-8o. The dendrograms had high co-phenetic correlation (above 0.80), indicating that the dendrograms corresponded to the similarity matrix from which they were created.

Table 5g. Diversities among bacterial flora in the open systems

Sample name and no.	No. of isolates	Di values
Kpong	1	0.940
	2	0.955
	3	0.940
	4	0.961
	5	0.943
Volta	1	0.954
	2	0.938
	3	0.960
	4	0.942
	5	0.937
Weija	1	0.947
	2	0.950
	3	0.967
	4	0.968
	5	0.944
Mean Diversity		0.950

Fig. 7 e. 1 DEndrogram shewing UPGMA clustering of the bacterial isolates fro February, 1999 from ARDEC 3 pond (Ardeo35). ID level: 0.975 Co-phonetic correlation: 0.900 No. of samples: 81 No. of tests: 12

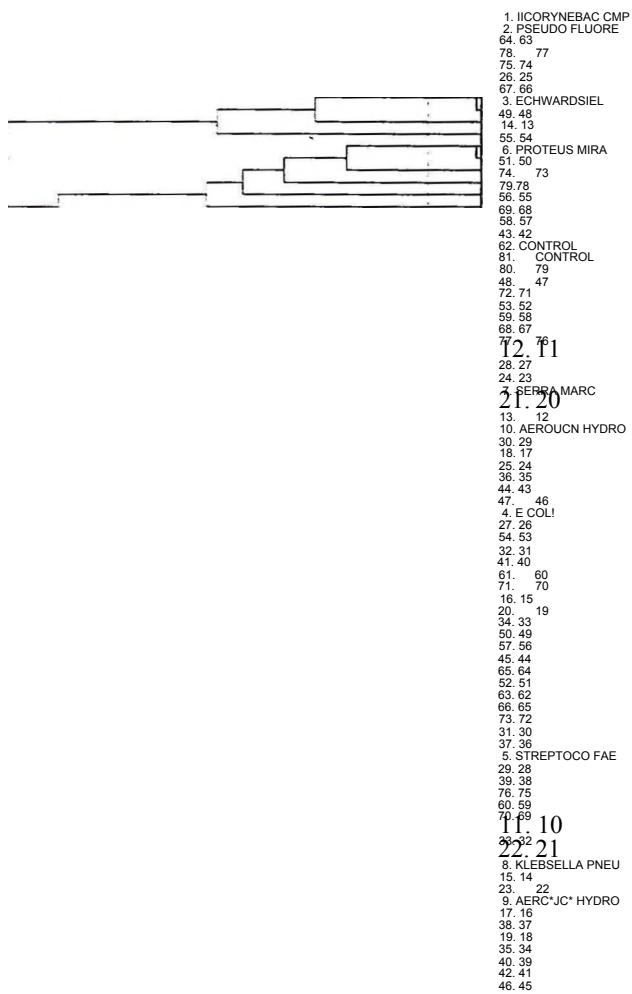


Fig. 8.2. dendrogram showing UPGMA clustering of the badenal adates for Fetorjary, 1997 from the Kpong headpond (kpong 1). ID level: 0.975 Co-pheneSc correlation: 0.578 No. of samples: 80 No. of tests: 12

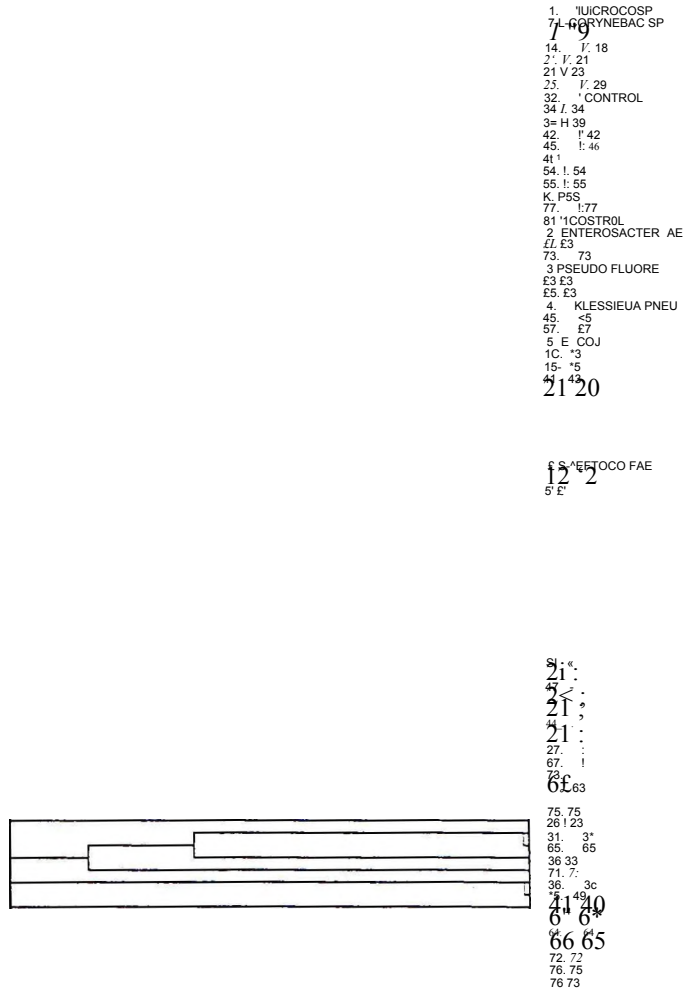


Fig. 8 b Dendrogram showing UPGMA clustering of (he bacterial isolates for August, 1997 from the Kpong head- pond (kpong2). ID level: 0.975 Co-phenetic correlation: 0.963 No. of samples: 82 No. of tests: 12

1. ECOU
 16. 16
 28. 28
 60. 60
 17. 17
 37. 37
 33. 33
 2. (MICROCO SP
 6. IICORYNEBAC
 35. !! 35
 39. !! 39
 40. ICONTROL
 43. !! 43
 46. 1146
 47. !! 47
 52. !! 52
 54. 1154
 63. !! 63
 64. 1164
 76. !! 74
 78. 11 76
 82. ICONTROL
 3. STREPTOCO FAE
 14. 14
 62. 62
 81. 79
 48. 48
 50. 50
 30. 30
 8. CITROBAC AMA
 4. PSEUDELLA PNEU
 56. 56
 65. 65
 69. 69
 71. 69
 5. PSEUDO FLUORE
 18. 18
 29. 29
 36. 36
 45. 45
 10. 10
 10. 10
 32. 32
 9. 9
 23. 23
 12. 12
 19. 19
 24. 24
 13. 13
 27. 27
 38. 38
 72. 70
 42. 42
 49. 49
 77. 75
 20. 20
 26. 26
 34. 34
 21. 21
 25. 25
 31. 31
 44. 44
 55. 55
 41. 41
 51. 51
 53. 53
 61. 64
 66. 66
 73. 71
 75. 73
 57. 57
 76. 77
 68. 68
 70. 68
 58. 58
 59. 59
 74. 72
 67. 67
 80. 178

Fig. 8 C / Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1998 from the Kpong headpond (kpong3). ID level: 0.975 Co-phenetic correlation: 0.966
No. of samples: 80 No. of tests: 12

1.C1TROBACUA
41. 41
4. STREPTOCO FAS
9. 9
15. 15
52. 52
62. 62
74. 74
63. 63
78. 78
75. 75
15. 15
12. 12
17. 17
30. 30
53. 53
38. 38
34. 34
19. 19
45. 45
3. !!UJOCROCO SP
8. !CORYNEBAC
36. 36
40. !!CONTROL
43. !! 43
53. !! 53
61. !! 61
64. !!64
65. !! 65
65. !!56
63. !! 59
70. !! 70
71. !! 71
72. !! 72
73. !! 73
77. !! 77
80. (!CONTROL
5. ENTEROBACTER. A=
43. 43
55. 55
14. .4
6. PSEUDO FLUOR.E
10. .3
7. KLEBSIELLA PNEL
11. 11
33. 33
20. 20
36. 25
15. 15
25. 25
49. <9
29. 29
59. 59
67. 67
44. 44
47. <7
54. 54
21. 13
21. 21
22. 22
25. 25
32. 32
60. 60
51. 51
23. 23
42. 42
24. 24
27. 27
57. 57
23. 23
33. 33
56. 56
37. 37
45. 45
50. 50
63. 63
75. 75
79. 79

Fig. 8a Dendrogram showing UPGMA clustering of fræe bacterial Isolates fee August '9S8 from the Kpong headpond (Kpong*). ID levefc 0 975 Co-phenetic cofrefeSorç 0 9*5 Ms. cf samples: 80 No of tests: 12

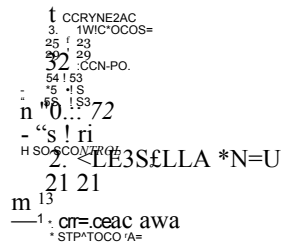


Fig. 8e Dendrogram showing UPGMA dusiefirtg c< re laceral isolates for February, 1999 from the Kpong headpond (kpong5). ID level: 0.STS C>-^erefc ccre-'afion: 0.973 No. of samples: 80 No. of tests: 12

1. STREPTOCO FA5
 11.11
 38.38
 70.76
 79.79
 23.23
 6. CITROBAC AMA
 2. UMICROCO SP
 7. ICORYNEBACTER1
 20.20
 22.22
 27.27
 30.30
 31.31
 34.1134
 37.37
 44.44
 48.1145
 48.1145
 48. UCONTROL
 53.53
 80. CONTROL
 3. ENTEROBACTER AE
 4. E COLI
 13.13
 43.43
 56.56
 19.19
 21.28
 52.52
 36.36
 12.12
 56.56
 77.77
 71.71
 73.73
 5. PSEUDO FLUORE
 21.21
 8. KLEBSIELLA PNEU
 10.10
 24.24
 40.40
 59.59
 51.61
 63.63
 64.68
 74.74
 78.78
 44.44
 49.49
 75.75
 14.14
 53.69
 39.39
 17.17
 32.32
 42.42
 55.55
 65.65
 47.47
 18.18
 25.25
 60.60
 26.26
 35.35
 29.29
 33.33
 51.51
 54.54
 58.158
 64.64
 67.67
 72.72
 70.70

Fig. 8f Denti-grani showing UPGMA clustering of the bacterial isolates for February, 1097 from the Volta river (votlal). ID level: 0.975 Co-phenetic correlation: 0.964 No. of samples: 60 No. of tests: 12

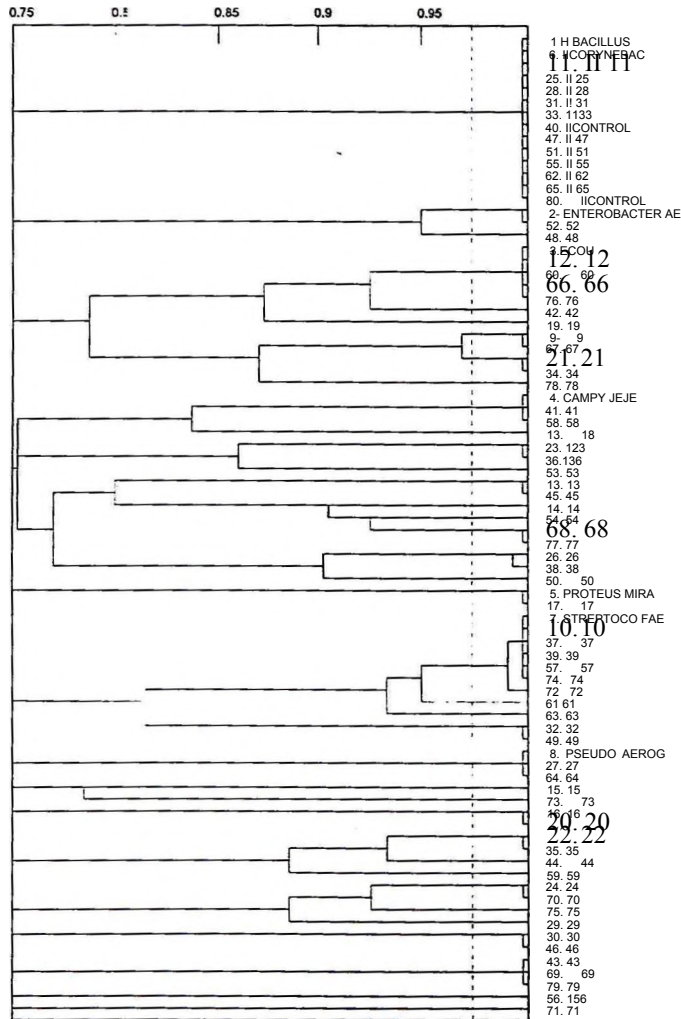
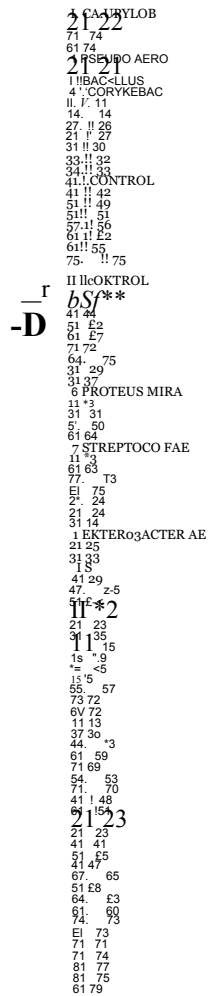
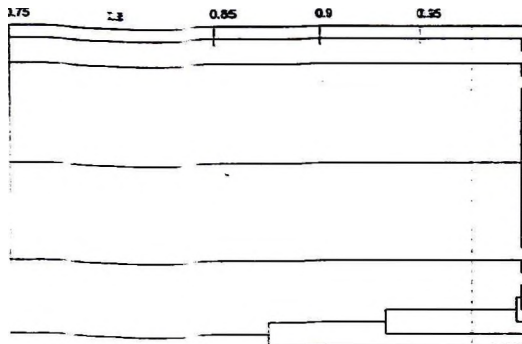


Fig. 8 B Dendrogram showing UPGMA clustering of the bacterial isolates for August 1997 from the voUa river (volta2). ID level: 0.975 Co-phenetic coaelation: 0.988 No. of samples: 89 No. of tests: 12



allowing UPGUA c
*ja3> ID met 0075
cm lto. of:luts 12

ifcr February. 18
c 0.979



- 1. ENTCS08ACTERAE
- 48. 48
- 2. PROTEUS MRA
- 25. 25
- 3. BACILLUS
- 6. *ICORF* & C
- 13. II 13
- 15. II 15
- 16. II 16
- 22. 1122
- 32. II 32
- 33. 1133
- 40. ICOTR3L
- 51. II 51
- 55. 1155
- 57. II 57
- 80. ICOKTOX
- 4. CAWYIOJE
- 49. 49
- 5. CSW
- 20. 20
- 40. 40
- 11. 11
- 43. 43
- 62. 62
- 7. PSELDO AEROG
- 18. 18
- 70. 70
- 8. STRSPTG00 FAE
- 74. 74
- 78. 78
- 27. 27
- 63. 63
- 72. 72
- 10. 10
- 9. 9
- 45. 45
- 29. 29
- 17. 17
- 66. 66
- 79. 79
- 14. 14
- 31. 31
- 58. 58
- 17. 17
- 19. 19
- 35. 35
- 28. 28
- 46. 46
- 60. 60
- 71. 71
- 47. 47
- 69. 69
- 65. 165
- 68. 168
- 73. 73
- 77. 177
- 23. 23
- 39. 39
- 24. 24
- 26. 26
- 44. 44
- 34. 34
- 50. 50
- 38. 38
- 75. 75
- 37. 37
- 61. 61
- 67. 67
- 76. 76
- 54. 54
- 38. 38
- 56. 56
- 41. 41
- 42. 142
- 52. 52
- 59. 59
- 53. 53
- 64. 164

HI

-Oz

Fig. S1 Dendrogram showing UPGMA clustering of the bacterial sequences from August 2010. O.M.: 0.075 Co-phonetic coarsening scale. No. of Bootstrap: 1000. No. of Sites: 12

- 1. IBAOLUS
- 2. JCORYNEBAC
- 20. T20
- 22. T22
- 31. I 51
- 32. ICOMTROC.
- 33. L S
- 31 I 38
- 30. tB
- 4a to
- 41 r 55
- 55. r 54
- 6a IS)
- 63. r
- 71. 19
- 82. ICOWTRO1
- 3. E*TB3Q3ACTER AE
- 25. 25
- 4. S**S*TOC0 FAE
- 13. 3
- 17. 7
- 7a «
- 23. 23
- 61 E2
- 71 < 75
- 46. *c
- 67. 55
- 28. a
- 73. 71
- 52. S
- 18. *1
- 3a X
- 35- 25
- 8a 71
- 53. 52
- 5. ECOLI
- ia. M
- 53. a
- 71
- S. PSUDO AEROG
- 7. CAMPTLOJE
- sa 5:
- 21. PROTEUS MIRA
- 43. 4S
- 51 5*
- 3. S
- 13. *e
- 81. 75
- 11. V
- 61. e:
- 61. X.
- 34. >
- 54. 53
- 64. E
- 24. 2*
- 23. 2=
- 21. 2E
- 27. T
- 42. C
- 62. 5*
- 71 7S
- 41. 4'
- 61 e
- 43. 10
- 44. 4i
- 51- 5'
- 47. -r
- 41 41
- 51 52
- 65. 6*
- 63. EF
- 72. 71
- 74. 71
- 79. 7-
- 71 73

Fig. 8 -i_ Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from the Votta river (votta5). ID level: 0.75 Co-phenetic correlation: 0.643 No. of samples: 50 No. of tests: 12

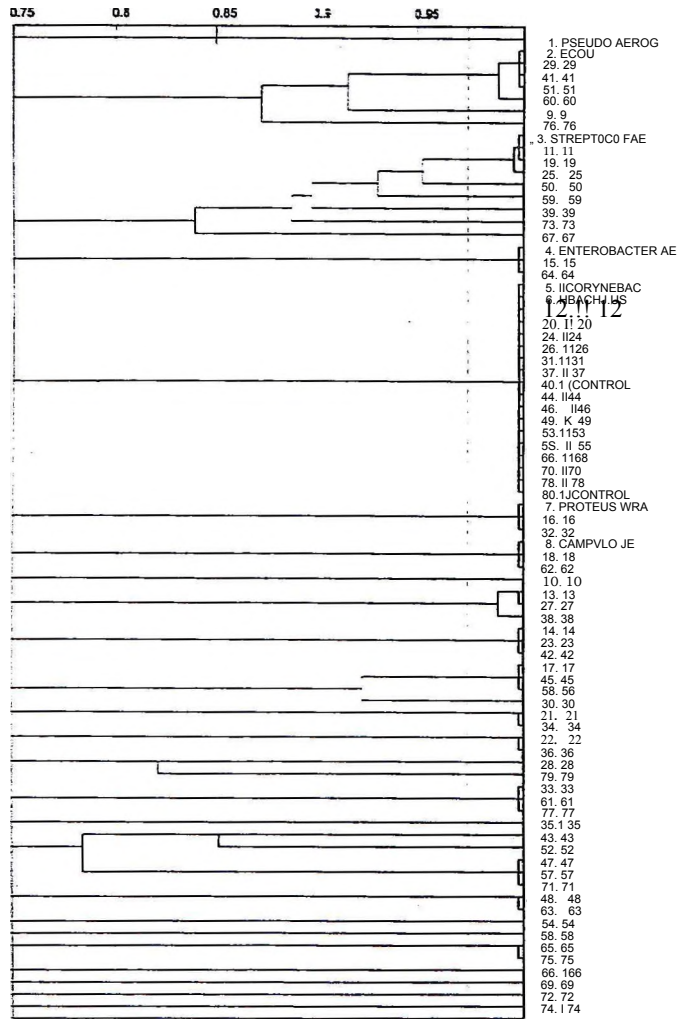


Fig. Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1997 from the We'a dan (wegal). ■> level 0.975 Co-phenetic correlation; 0-982 No. of samples: 80 Mo-erf tests: 12

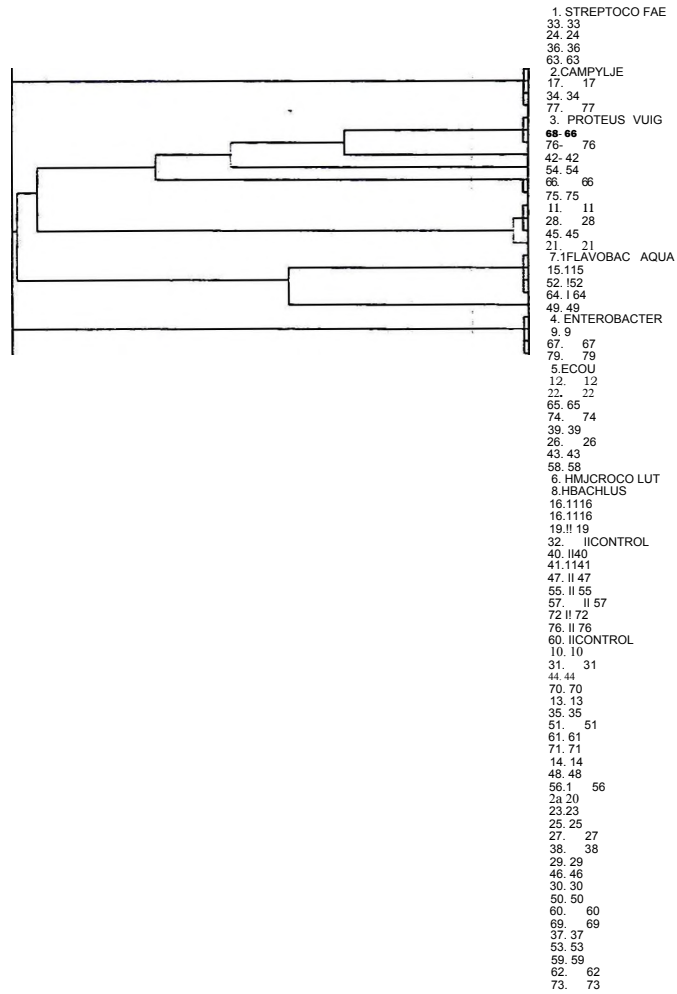


Fig. 2 x Dendrogram showing UPGMA clustering of (ha bacterial isolates for August, 1097 from the We'a dam (wefa2). ID levefc 0.975 Co-phenwBc correlation: 0.973 No. of samples: 80 No. of tests: 12

1. ENTEROBACTER CL
 24. 24
 2. HBACLUS
 6. HMICROCO LIT
 11. 11 11
 13. 1113
 15. 1115
 21. 1121
 26. 11 26
 27. 11 27
 39. 11 39
 40. 1 |CONTROL
 45. 11 45
 47. 11 47
 56. 11 56
 77. 11 77
 60. HCONTROL
 3. PROTEUS VULG
 18. 18
 44. 44
 12. 12
 30. 30
 37. 37
 54. 54
 63. 63
 20. 20
 43. 43
 67. 67
 76. 76
 4. IFLAV06AC AQUA
 14. 1 14
 35. 135
 52. 152
 59. 159
 53. 53
 74. 1 74
 5. ECOU
 16. 16
 65. 65
 29. 29
 7. ST REP TOCO FAE
 9. 9
 36. 36
 57. 57
10. 10
 32. 32
 46. 46
 73. 73
 6. CAMPY JE
 17. 17
 72. 72
 19. 19
 31. 31
 71. 71
 42. 42
22. 22
 34. 34
 58. 58
 23. 23
 38. 38
 25. 25
 79. 79
 28. 28
 33. 33
 50. 50
 41. 41
 76. 78
 46. 46
 49. 49
 60. 60
 51. 51
 61. 61
 55. 55
 62. 62
 64. 64
 69. 69
66. 66
 70. 1 70
 75. 1 75

Flo-Bti-Dendrogram showing UPGMA clustering of the bacteria isolates for August, 1998
 from the Weta dam (weta3). ID level 0.075 Co-phene Co-correlation: 0.976
 No. of samples: 80 No. of tests: 12

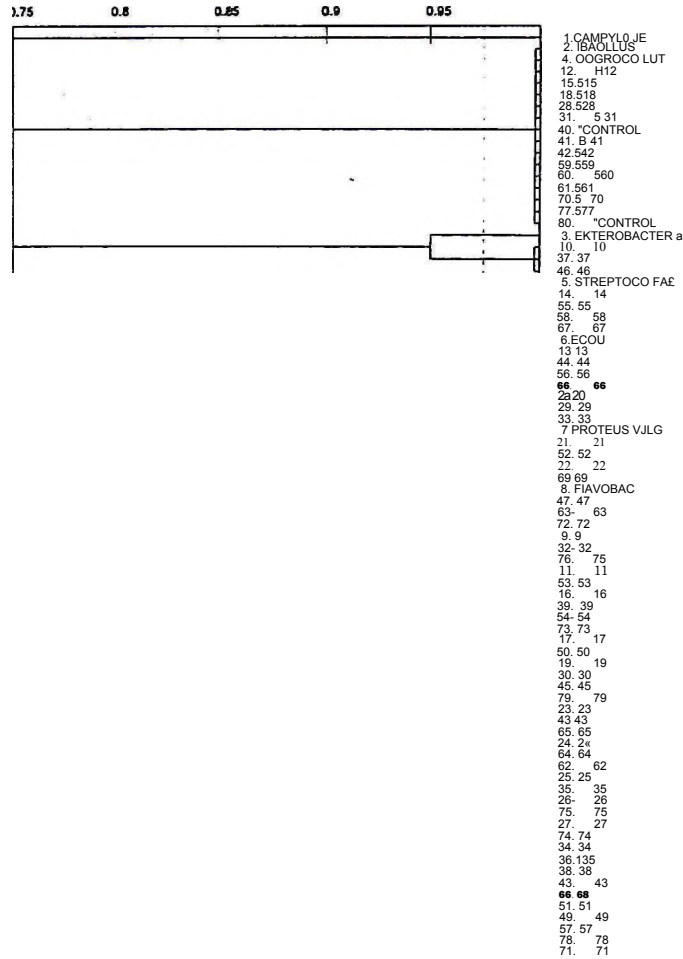
1. BACILLUS
 6. LOWBACCOLUT
 11. 11
 12. 112
 15. 1115
 21. 1121
 34. 1134
 35. 1135
 40. CONTROL
 64. 1164
 75. 1175
 80. CONTROL
 2. CALCPYLGB
 3. 1FLAVO6AC AQUA
 16. 116
 30-30
 8. PROTEUS VULG
 14. 14
 41. 41
 62. 62
 29. 29
 38. 38
 89. 89
 56. 64
 20. 20
 59. 59
 4. STREPTOCO FAE
 9. 9
 39. 39
 10. 10
 42. 42
 72. 72
 5. ECOU
 13. 13
 32. 32
 44. 44
 56. 56
 57. 57
 78. 78
 7. ENTEROBACTER CL
 17. 17
 36. 36
 49. 49
 16. 18
 37. 37
 53. 53
 19. 19
 39. 33
 22. 22
 23. 23
 31. 31
 71. 71
 43. 43
 58. 56
 24. 24
 46. 46
 64. 64
 66. 68
 25. 25
 55. 55
 26. 26
 27. 27
 47. 47
 28. 28
 48. 46
 70. 70
 74. 74
 45. 45
 63. 63
 50. 50
 66. 68
 51. 51
 52. 152
 60. 60
 65. 65
 67. 67
 79. 79
 73. 73
 76. 76

from the Wega dam (wey44), ID level: 0.975 Co-phenetic comatafon: 0-974
No. of samples: 80 to- cf tests: 12

as.

- 1. EMTEROBACTER CL
- 2. PROTEUS VULG
- 20. 20
- 41. 41
- 3. IBACILLUS
- S. ili/CROCO Litr
- 13. 1113
- 18. 1118
- 32. II 32
- 37. II 37
- 40. II CONTROL
- 51. 1151
- 67. II 67
- 72. II 72
- 80. II CONTROL
- 4. STREPTOCO FAE
- 19. 19
- 42. 42
- 65. 65
- 59. 59
- 79. 79
- 24. 24
- 74. 74
- 4. 4
- 64. 64
- 69. 69
- 73. 73
- 28. 28
- 17. 17
- 29. 29
- 63. 63
- 44. 44
- 6. CAMPYLO JE
- 16. 16
- 47. 47
- 7. IFLAVOBAC AQUA
- 33. 33
- 49. 49
- 10. 10
- 56. 56
- 11. 11
- 66. 66
- 76. 76
- 52. 52
- 21. 21
- 38. 38
- 12. 12
- 45. 45
- 77. 77
- 14. 14
- 35. 35
- 78. 78
- 15. 15
- 58. 58
- 23. 23
- 57. 57
- 68. 68
- 75. 75
- 25. 25
- 26. 26
- 43. 43
- 60. 60
- 27. 27
- 71. 71
- 39. 39
- 54. 54
- 30. 30
- 31. 31
- 62. 62
- 34. 34
- 36. 36
- 46. 46
- 48. 48
- 7a 70
- 50. 50
- 53. 53
- 55. 55
- 61. 61

Fig. 80 DenarodaiB#iow#MUPGMAeteterinaptBwbadarialledlatefcFebmai. 1999
 from the Weia dam 5) towet OJS75 Co-phcne6c correlation: 0.946
 No. of samples: 80 Mb. of lesac 12



D. Similarities between bacterial populations in the different samples.

The mean similarity was calculated as mean population similarity (Sp) coefficient and the results are presented in Table 6. Comparison between the different fertilization types, i.e. cow manure, poultry manure, pig manure, blood waste, chemical fertilizer, no fertilization and the open systems, showed Sp values all below 0.50. Similarly comparison between farms with same fertilization types showed Sp values below 0.50, an indication of related populations with high diversities of bacteria.

Table 6 Population similarities between the various study areas.

<u>Parameter</u>	<u>Population of Compared to Sp value</u>		
Cow manure	Aduabenba	Boateng	0.13
Poultry manure	Agyeman	ARDEC 20	0.14
	Agyeman	Asare	0.17
	Agyeman	Frimpong	0.13
	ARDEC 20	Asare	0.30
	ARDEC 20	Frimpong	0.20
	Asare	Frimpong	0.17
Pig manure	Boadi	KK	0.17
	Boadi	Pacific	0.27
	KK	Pacific	0.35
Open system	Kpong	Volta	0.55
	Kpong	Weija	0.45
	Volta	Weija	0.49
Fertilization types	cow manure	poultry manure	0.15
	cow manure	pig manure	0.18
	cow manure	blood waste	0.34
	cow manure	chemical	0.12
	cow manure	no fertilization	0.22
	cow manure	open systems	0.04
	poultry manure	pig manure	0.18
	Doultrv manure	blood waste	0.28

Table 6 (cont'd) Population similarities between the various study areas.

<u>Parameter</u>	<u>Population of</u>	<u>Compared to</u>	<u>Sn value</u>
Fertilization type poultry manure		chemical	0.33
	poultry manure	no fertilization	0.23
	poultry manure	open systems	0.28
	pig manure	blood waste	0.29
	pig manure	chemical	0.16
	pig manure	no fertilization	0.33
	pig manure	open systems	0.10
	blood waste	chemical	0.16
	blood waste	no fertilization	0.38
	blood waste	open systems	0.10
	chemical	no fertilization	0.17
	chemical	open systems	0.49
	<u>no fertilization</u>	<u>open systems</u>	<u>0.10</u>

Comparison between the populations of bacteria from Kpong Headpond and the Volta river, however, showed Sp value greater than 0.50. This is an indication that the related populations were of low diversity.

E. Bacterial Flora of Fish from Cultured Ponds and Open System

Tilapia caught from the various culture systems were found to harbour bacteria belonging to the twenty five genera of bacteria isolated from the different culture systems, in various tissues but at different magnitudes. The species included *Actinobacillus* sp., *Aeromonas* sp., *Bacillus* sp., *Bacteroides* sp., *Campylobacter* sp., *Citrobacter* sp., *Clostridium* sp., *Corynebacterium* sp., *Edwardsiella* sp., *Enterobacter* sp., *Escherichia* sp., *Flavobacterium* sp., *Hafnia* sp., *Klebsiella* sp., *Micrococcus* sp., *Pasteurella* sp., *Proteus* sp., *Pseudomonas* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Staphylococcus* sp., *Streptococcus* sp., *Vibrio* sp. and *Yersinia* sp.

1. Fish cultured in cow manure-fertilized ponds

Bacterial species isolated from the blood and muscle of fish from Aduabenba farm belonged to 16 and 21 genera, respectively, and those isolated from the skin, gills and gut belonged to 25, 25 and 23 genera, respectively.

Blood and muscle of fish from Boateng farm contained species belonging to 12 and 17 genera, respectively, and those from the skin, gills and gut belonged to 24, 25 and 10 genera, respectively (Table 7a)

The data indicated that certain species seemed to be associated more with certain tissues than with others. For example, counts of *Edwardsiella* sp. (5.3 and 5.3), *Pasteurella* sp. (7.7 and 13.0) and *Salmonella* sp. (11.7 and 10.3) were similar to muscle of fish of Aduabenba and Boateng farms, respectively. Examples for blood were *Corynebacterium* sp. ((8.3 and 8.3), *Flavobacterium* sp. (11.0 and 10.0) and *Pseudomonas* sp. (15.3 and 13.3). For the gills, gut and skin, the respective counts for Aduabenba and Boateng farm fishes were: *Bacillus* sp., 10.0, 21.3 and 12.7 compared to 22.3, 25.3 and 18.0; *Pseudomonas* sp., 11.0, 31.0 and 11.3 compared to 16.3, 44.0 and 13.3; *Streptococcus* sp., 8.3, 31.3 and 8.3 compared to 15.0, 24.3 and 16.0; and *Vibrio* sp., 13.0, 0.0 and 12.0 compared to 11.3, 0.0 and 13.0.

Analysis of variance determination showed significant difference at 95.0% confidence level between the means for the muscle, blood, gut, gill and skin of fish

Mean total number of bacterial isolates occurring in tissues of fish from cow manure-fertilized ponds

Bacterial species	Adiphenitit in					Dontuk firai				
	muscle	blood	gut	skin	skin	muscle	blood	gut	skin	skin
<i>Actinobacillus sp.</i>	0.0	0.3	2.3	0.7	2.3	0.0	0.0	1.7	0.0	1.7
<i>Aeromonas sp.</i>	0.0	4.7	6.3	0.0	6.0	1.7	1.0	1.10	1.0	12.1
<i>Bacillus sp.</i>	2.7	5.3	10.0	21.3	12.7	5.3	3.3	22.3	25.3	18.0
<i>Bacteroides sp.</i>	4.0	0.0	14.0	2.3	11.0	0.7	3.0	12.0	0.0	9.0
<i>Campylobacter sp.</i>	0.7	1.3	3.7	6.7	2.0	0.3	3.3	1.7	0.0	3.3
<i>Citrobacter sp.</i>	3.0	6.0	8.3	5.0	10.7	5.7	2.3	6.3	0.0	7.7
<i>Clostridium sp.</i>	3.7	0.0	8.0	6.3	7.7	2.3	0.0	7.0	0.0	11.0
<i>Corynebacterium sp.</i>	1.7	8.3	5.7	25.7	7.7	1.7	8.3	7.3	27.0	6.3
<i>Edwardsiella sp.</i>	5.3	1.0	12.0	1.3	17.0	5.3	0.0	17.0	0.0	13.0
<i>Enterobacter sp.</i>	1.0	0.7	<1.3	28.6	6.0	0.0	0.0	1.7	0.0	5.3
<i>Escherichia sp.</i>	1.7	0.0	8.7	2.7	6.0	0.0	0.0	7.0	21.0	0.3
<i>Flavobacterium sp.</i>	2.3	11.0	13.0	8.7	8.3	6.0	10.0	13.3	26.0	12.0
<i>Uqfin sp</i>	5.0	0.0	16.0	1.0	M.O	1	0.0	10.3	0.0	11.3
<i>Klebsiella sp.</i>	0.0	0.0	5.3	1.3	3.7	0.0	0.0	4.3	0.7	7.3
<i>Micrococcus sp.</i>	2.7	7.3	11.0	28.7	8.3	4.0	11.0	6.7	30.3	4.7
<i>Pasteurella sp.</i>	7.7	0.0	17.3	2.7	20.7	13.0	0.0	14.0	0.0	18.3
<i>Proteus sp.</i>	0.7	0.3	5.3	8.7	7.0	1.3	10.0	2.3	0.0	3.3
<i>Pseudomonas sp.</i>	5.0	15.3	11.0	11.0	11.3	11.0	13.3	16.3	44.0	13.3
<i>Salmonella sp.</i>	11.7	0.3	21.7	2.7	24.0	10.3	0.0	24.7	0.0	22.3
<i>Serratia sp.</i>	0.3	1.0	3.3	4.2	6.3	0.0	0.0	4.0	3.3	2.3
<i>Shigella sp.</i>	0.7	0.7	5.7	0.7	3.3	0.0	0.0	2.3	0.0	0.7
<i>Staphylococcus sp.</i>	2.0	3.3	3.7	9.0	7.0	3.7	2.3	3.0	24.3	3.0
<i>Streptococcus sp.</i>	2.3	0.0	8.3	31.3	8.3	6.0	0.0	15.0	24.3	16.0
<i>Vibrio sp.</i>	1.7	0.0	13.0	0.0	12.0	0.0	0.0	11.3	0.0	13.3
<i>Yersinia sp.</i>	0.0	0.0	2.7	0.7	1.3	0.0	0.0	0.7	0.0	0.0

from the two farms. Duncan's multiple comparison determination showed homogeneity between the means for the blood and muscles, and, among the means for the gill, gut and skin. Fig. 9a shows correlation between the means of the bacteria flora as found in the various tissues.

2. Fish cultured in poultry manure-fertilized ponds

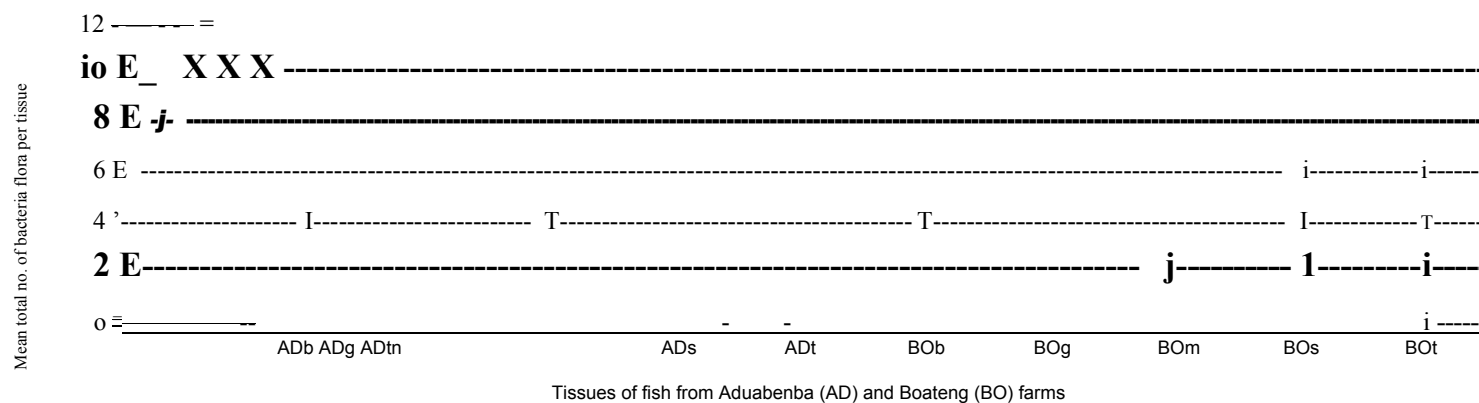
The data for fish from Agyeman farm showed the presence of 20 genera in the muscles, 19 in the blood flora, 25 in the gills and in the skin flora and 23 genera in the gut. The data for fish from ARDEC 20 showed the presence of 21 genera in the muscle, 20 genera in the blood, 25 genera in the gills and on the skin, and 22 genera in the gut. The data for fish from Asare farm showed the presence of 19 genera in the muscle, 11 in the blood, 25 each in the gills and on the skin and 16 in the gut, while data for fish from Frimpong farm showed 17 genera in the muscle, 12 in the blood, 24 each in the gill and on the skin, and 19 genera in the gut (Table 7b).

Generally more genera were encountered in the gills, gut and on the skin than in the blood and muscle. For fish from Agyeman farm, ARDEC 20, Asare farm and Frimpong farm, the most abundant isolate for the different tissues were:

- Muscle - *Salmonella* sp., *Pseudomonas* sp., *Bacillus* sp. and *Pasteurella* sp., and, *Pseudomonas* sp., respectively.
- Blood *Pseudomonas* sp., *Pseudomonas* sp., *Pseudomonas* sp. and *Micrococcus* sp., respectively.
- Gills - *Salmonella* sp., *Pseudomonas* sp., *Bacillus* sp. and *Salmonella* sp., respectively.
- Gut - *Salmonella* sp., *Escherichia* sp., *Pseudomonas* sp. and *Micrococcus* sp., respectively.
- Skin - *Salmonella* sp., *Pasteurella* sp., *Bacillus* sp. and *Salmonella* sp., respectively.

Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the flora of the blood, gills, gut, muscle and skin. Duncan's multiple comparison determination showed homogeneity between the means of the blood and muscles, and between the gill, gut and skin. Fig. 9b shows correlation between the means of the bacteria flora as found in the various tissues.

Fig. 9a Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from cow manure-fertilized ponds



ADb = Blood of fish from Aduabenba farm
 ADg = gills of fish from Aduabenba farm
 ADm = muscle of fish from Aduabenba farm
 ADs = skin of fish from Aduabenba farm
 ADt = gut of fish from Aduabenba farm

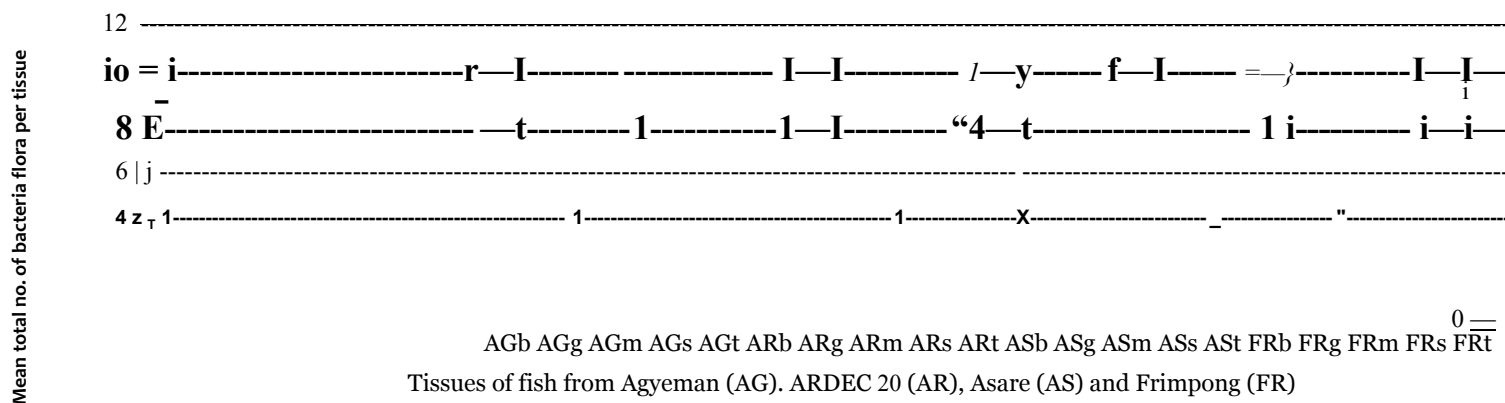
BDb = blood of fish from Boateng farm
 BDg = gills of fish from Boateng farm
 BDm = muscle of fish from Boateng farm
 BDs = skin of fish from Boateng farm
 BDt = gut of fish from Boateng farm

TABLE 7b

Mean total number of bacterial isolars occurring in tissues of fish from poultry manure-fertilized ponds

Bacterial species	Agyeman farm					ARDEC 20					Asare farm					Frimpong farm				
	muscle	blood	gill	gut	sldn	muscle	blood	gill	gut	sldn	muscle	blood	gill	gut	skin	muscle	blood	gill	gilt	sldn
<i>Actinobacillus</i> ~	0.0	0.0	1.7	0.0	1.0	0.0	C 0	1.7	2.7	1.7	0.0	0.0	3.0	0.0	43	C.O	10	3.3	0.0	2.0
<i>Aeromonas</i> -<tr>	0.3	2.3	8.7	2.3	8.0	■)	JT	10.7	1.3	8.3	1.7	0.0	10.3	0.0	14.3	C.3	2	14.3	0.0	12.7
<i>Bacillus</i> sp.	2.7	5.0	13.3	17.3	12.0	6."	f	16.0	20.0	14.3	11.7	4.0		21.3	20.3	-0	3.J	15.3	8.7	17.0
<i>Bacteroides</i> sp	3.7	1.7	10.0	3.3	9.0	5.3	CO	10.3	2.3	11.0	1.3	1.7	13.3	0.0	103	-3	5-	8.7	4.7	9.3
<i>Campylobacter</i> sp	0.3	1.7	4.3	5.7	5.3	0.0	2~	5.3	2.7	5.7	2.0	1.7	11.7	9.7	10.7			7.3	43	7.3
<i>Citrobacter</i> sp.	2.7	9.0	9.3	7.0	9.7	T"	6 0	11.3	2.7	9.3	1.0	10.7		0.0	70	5.3	13	11.7	3.7	9.7
<i>Clostridium</i> sp.	4.3	1.0	11.3	7.3	9.0	9.0	;-3	10.3	15.0	9.3	2.3	1.0	7.7	6.7	10.3	1.0	0.0	9.3	23	9.3
<i>Corynebacterium</i> sp.	1.0	4.0	5.7	13.0	4.3	2.3	53	8.7	7.0	10.0	2.3	10.7		24.0	6.0	2.3	12.0	6.3	20.7	9.7
<i>Edwardsiella</i> sp	4.3	1.3	8.3	1.7	10.7	7.0	C 7	12.0	0.7	12.3	8.3	0.0		1.3	9.7	6.3	0.0	9.7	0.0	11.0
<i>Enterobacter</i> sp	03	2.3	8.0	2.7	5.3	2.3	C "	4.0	0.0	2.3	2.0	0.0	5.7	0.0	2.0	C.O	0.0	1.0	0.7	03
<i>Escherichia</i> sp.	3.3	0.0	9.3	23.0	6.7	1.3	SO	8.0	29.3	9.3	0.7	2.3	10.3	24.0	5.0	C.O	0.0	6.7	20.C	53
<i>Flavobacterium</i> sp.	2.0	8.0	11.0	23.3	12.3	9.3	z-	13.7	10.7	10.7	2.0	8.3	14.3	21.0	10.7	6.0	93	14.0	173	12.3
<i>Hafnia</i> sp.	23	0.0	11.0	0.7	10.7	0.'	10	7.7	1.0	9.3	9.7	3.3	5.3	0.0	87	*3	0.0	10.0	03	10.3
<i>Klebsiella</i> sp.	0.0	1.0	5.7	1.3	2.7	1.0	C'	5.0	11.3	4.0	0.0	0.0	3.3	1.3	4.3	1.0	0.3	8.7	13.C	7.3
<i>Micrococcus</i> sp	4.3	7.0	10.7	26.3	13.3	3."	c -	15.3	26.7	14.7	3.3	14.3		26.7	12.7	6_3		13.3	2	13.7
<i>Pasteurella</i> sp	5.0	1.0	16.3	1.3	13.0	8.3	C 0	11.3	0.0	16.7	11.7	0.0	12.7	1.7	13.7	13.0	0.0	13.3	0.0	10.0
<i>Proteus</i> sp.	0.3	4.3	6.3	7.7	8.0	0.3		4.3	3.0	4.0	0.0	0.0	4.3	1.7	5.7	3.3	3.0	4.7	3	5.0
<i>Pseudomonas</i>	6.0	10.0	9.7	15.0	10.7	13.3	14. C	18.7	25.0	14.7	4.3	22.3	14.7	40.7	15.3	6."	o.-	13.0	25.-	11.7
<i>Salmonella</i> so.	10.3	1.0	18.7	29.7	20.7	113	2.7	13.7	24.0	17.0	5.0	0.0	18.7	1.0	14.7	4.7	2.0	16.0	223	19.3
<i>Serratia</i> sp.	0.0	2.3	11.7	4.3	14.0	1.7	C 7	5.7	1.7	11.3	0.0	0.0	1.0	1.3	1.7	2_3	0.0	8.3	123	10.0
<i>Shigella</i> sp.	1.0	0.0	7.0	4.0	5.7	0.0	C3	5.3	0.3	2.7	0.0	0.0	1.7	0.0	3.0	0.0	0.0	4.0	1.7	5.0
<i>Staphylococcus</i> sp.	0.3	0.3	3.3	9.0	4.0	0.7	C.3	6.0	9.7	4.3	3.3	0.0		21.7	4.7	0.0	0.0	3.3	12."	4.0
<i>Streptococcus</i> sp.	2.0	0.0	6.3	20.3	6.7	4.3	63	7.0	29.0	9.3	9.3	0.0	16.7	22.7	4.3	0.0	00	10.3	213	10.7
<i>Vibrio</i> sp.	0.0	0.0	11.7	0.0	10.7	6.7	C 0	li.O	0.0	10.0	2.3	0.0	11.7	0.0	15.0		00	13.7	0.0	13.7
<i>Yersinia</i> sp.	0.0	0.7	1.0	0.3	1.3	0.0	C 0	1.7	0.7	1.7	0.0	0.0	1.7	0.0	1.0	■5.0	O'	0.0	0.0	0.0

Fig. 9b Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from poultry manure-fertilized ponds



AGb = Blood of fish from Agyeman farm
 AGg = gills of fish from Agyeman farm
 AGm = muscle of fish from Agyeman farm
 AGs = skin of fish from Agyeman farm
 AGt = gut of fish from Agyeman farm

ARb = blood of fish from ARDEC 20 farm
 ARg = gills of fish from ARDEC 20 farm
 ARm = muscle of fish from ARDEC 20 farm
 ARs = skin of fish from ARDEC 20 farm
 ARt = gut of fish from ARDEC 20 farm

ASb = Blood of fish from Asare farm
 ASg = gills of fish from Asare farm
 ASm = muscle of fish from Asare farm
 ASs = skin of fish from Asare farm
 ASt = gut of fish from Asare farm

FRb = Blood of fish from Frimpong farm
 FRg = gills of fish from Frimpong farm
 FRm = muscle of fish from Frimpong farm
 FRs = skin of fish from Frimpong farm
 FRt = gut of fish from Frimpong farm

3. Fish cultured in pig manure-fertilized ponds

The muscle of fish caught from Boadi farm contained species from 19 genera while species isolated from the blood belonged to 13 genera. The species from the gills, gut and skin belonged to 24, 11 and 24 genera, respectively. The corresponding values for fish from KK farm were 21, 15, 25, 13 and 25 genera, respectively. Fish caught from Pacific farm showed the presence of 17 genera in the muscle, 14 genera in the blood, 25 genera from the gill, 12 genera in the gut and 24 genera from the skin (Table 7c).

Fish from all the three farms had smaller number of genera in the gut than in any of the other tissues. For fish from Boadi farm, KK farm and Pacific farm, the most abundant isolates for the different tissues were:

Muscle	<i>Pseudomonas</i> sp., <i>Pasteurella</i> sp. and <i>Salmonella</i> sp., respectively.
Blood -	<i>Pseudomonas</i> sp., <i>Micrococcus</i> sp. and <i>Pseudomonas</i> sp.,
Gills -	<i>Salmonella</i> sp., <i>Salmonella</i> sp. and <i>Salmonella</i> sp., respectively.
Gut -	<i>Streptococcus</i> sp., <i>Streptococcus</i> sp. and <i>Streptococcus</i> sp., respectively.
Skin	<i>Bacillus</i> sp., <i>Bacillus</i> sp. and <i>Bacillus</i> sp., respectively.

Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the values for the blood, gill, gut, muscle and skin flora. Duncan's multiple comparison determination showed homogeneity between the means of the blood and muscles, and between the gill, gut and skin. Fig. 9c shows correlation between the means of the bacteria flora as found in the various tissues.

4. Fish cultured in blood waste-fertilized pond

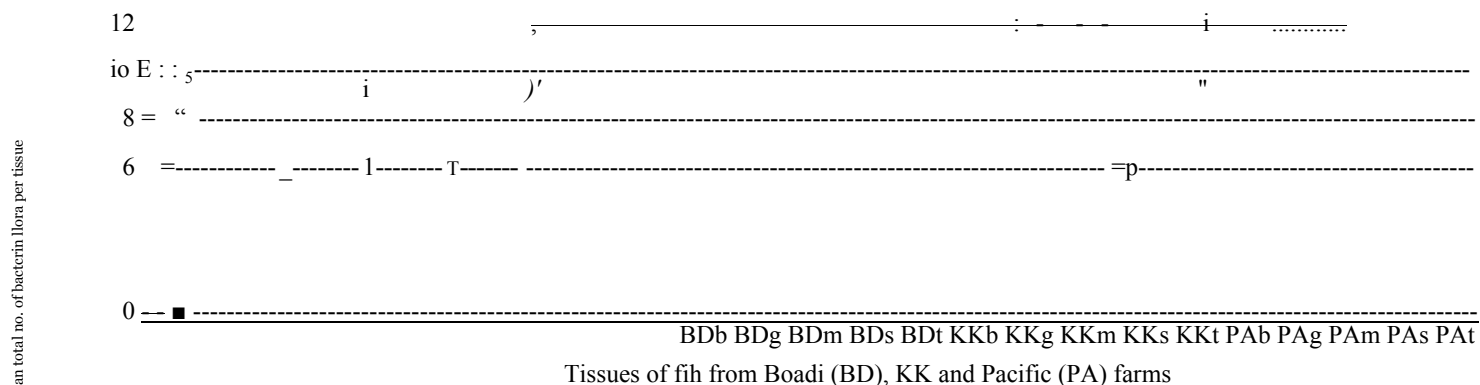
All the 25 genera were represented by isolates from gill and skin of fish from Boahen farm while 15, 14 and 22 genera were represented by isolates from the muscle, blood and gut, respectively. The dominant species of the muscle flora were *Pasteurella* sp., *Escherichia* sp. and *Salmonella* sp. The dominant species in the blood flora was *Micrococcus* sp., followed by *Campylobacter* sp. and then by *Aeromonas* sp. *Salmonella* sp. was the predominant species in the gill flora followed by *Bacillus* sp.

TABLE 7c

Mean total number of bacterial isolates occurring in tissues of fish from pig manure-fertilized ponds

Bacterial species	Boadi farm					KK farm					Pacific farm				
	muscle	blood	gill	gut	skin	muscle	blood	gill	gut	skin	muscle	blend	gill	gut	sldn
<i>Actinobacillus sp.</i>	0.0	0.0	3.3	0.0	2''	0.0	0.0	3.0	0.0	35	0.0	t:	2.7	0.0	3.3
<i>Aeromonas sp.</i>	0.0	0.0	14.7	0.0'	12 3	1.7	1.7	13.0	0.0	13.0	0.7	z~~	14.3'	0.0	14.'
<i>Bacillus sp.</i>	0.0	0.0	17.7	12.7	18 7	3.7	2.3	17.0	16.3	16.7	7.7	o.:	15.0	13.7	20r
<i>Bacteroides sp.</i>	0.0	0.3	10.7	0.0	11 T	6.7	6.0	7.7	0.3	8.7	2.3		11.3	0.0	11.'
<i>Campylobacter sp.</i>	2.3	2.0	4.0	0.3	6~	5.0	0.7	6.3	0.0	6.0	8.0	-L ~	4.0	3.3	65
<i>Citrobacter sp.</i>	9.0	4.3	11.3	0.0	105	2.3	8.7	9.7	0.0	13.0	3.0	2~	10.3	0.0	7.7
<i>Clostridium sp.</i>	4.3	0.0	14.3	46.0	11)	1.0	1.7	10.3	47.7	11.3	0.7	>:	11.0	34.7	11.*
<i>Corynebacterium sp.</i>	3.7	12.C	13.7	35	135	3.3	0.0	13.0	11.3	12.7	4.7	9.*	U.O	10.3	10.0
<i>Edwardsiella sp.</i>	4.3	1.0	4.7	0.0	4."	0.7	Z7	8.0	0.0	7.0	4.7	G> :	9.0	0.0	85
<i>Enterobacter sp.</i>	1.7	5.0	4.7	0.0	65	0.0	5.3	3.3	0.0	6.3	0.0	<u	5.7	0.3	55
<i>Escherichia sp.</i>	5.3	0.0	8.3	27.3	95	6.0	4.0	13.0	28.3	11.7	3.7		12.7	29.3	11.?
<i>Flavobacterium sp.</i>	5.0	16.5	13.3	9.7	117	0.0	7.3	13.3	12.7	10.7	4.7		12.0	2.7	11.'
<i>Hafnia sp.</i>	9.3	2.0	6.3	0.0	9.'	8.3	0.0	12.7	0.7	9.7	0.0	:	4.3	0.0	■-0
<i>Klebsiella sp.</i>	0.0	10	2.0	0.0		0.0	0.0	3.0	1.3	35	0.7	Q:	1.3	0.0	35
<i>Listeriacoccus sp.</i>	3.7	11 C	15.3	27.3	13)	3.7	14.0	15.0	24.0	11.0	5.7	195	9.3	29.3	125
<i>Pasteurella sp.</i>	6.7	0.0	10.7	0.0	12 7	10.0	0.0	9.3	0.0	8.7	14.7	G :	19.3	0.0	14.'
<i>Proteus sp.</i>	5.3	105	2.0	0.0	65	0.7	2.0	3.7	0.0	57	1.7		6.3	0.0	6.-;
<i>Pseudomonas sp.</i>	15.0	16. T	11.0	24.0	115	6.7	14.0	12.3	25.7	12.3	6.0	315	11.3	30.3	9.7
<i>Salmonella sp.</i>	10.7	0.0	20.7	0.0	175	93	0.0	17.7	0.0	15.0	16.3	9.-3	30.3	0.0	135
<i>Serratia sp.</i>	1.7	55	6.3	17.7	6.)	0.3	0.0	3.3	4.3	55	0.0	35	4.3	18.0	5.7
<i>Shigella sp.</i>	4.7	0.0	9.3	0.0	6."	0.7	0.0	7.7	0.0	9.3	7.0	a.3	11.3	0.0	10.0
<i>Staphylococcus sp.</i>	3.3	0.0	4.0	0.0	2.-	13	1.3	3.0	0.0	2.7	0.0	85	1.7	0.0	1.0
<i>Streptococcus sp.</i>	4.0	0.0	4.7	51.7	5.3	3.0	0.0	5.7	52.7	7.7	0.0	a;	3.7	53.0	4.7
<i>Vibriosp.</i>	0.0	0.0	13.7	0.0	110	5.0	0.0	13.0	0.0	12.0	0.0	Q':	12.0	0.0	14.0
<i>Yersinia sp.</i>	0.3	0.0	0.0	2.7	0.3	0.7	0.3	1.0	1.3	1.5	0.0	&;	0.7	1.7	0.0

Fig. 9c Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from pig manure-fertilized ponds



BDb = Blood of fish from Boadi farm
BDg = gills of fish from Boadi farm
BDm = muscle of fish from Boadi farm
BDs = skin of fish from Boadi farm
BDt = gut of fish from Boadi farm

KKb = blood of fish from KK farm
KKg = gills of fish from KK farm
KKm = muscle of fish from KK farm
KKs = skin of fish from KK farm
KKt = gut of fish from KK farm

PAb = blood of fish from Pacific farm
PAg = gills of fish from Pacific farm
PAm = muscle of fish from Pacific farm
PAs = skin of fish from Pacific farm
PAt = gut of fish from Pacific farm

and by *Vibrio* sp. *Micrococcus* sp. was found to be the predominant species in the gut. The next was *Escherichia* sp., and then *Streptococcus* sp. and *Flavobacterium* sp. *Salmonella* sp. dominated the flora of the skin, followed by *Bacillus* sp., and then *Flavobacterium* sp. (Table 7d).

Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the blood, gill, gut, muscle and skin flora. Duncan's multiple comparison determination showed homogeneity between the means for the blood and muscles, and between the gill, gut and skin. Fig. 9d shows correlation between the means of the bacteria flora as found in the various tissues.

5. Fish cultured in chemically fertilized ponds.

Bacterial species isolated from the muscle of fish caught from Aheto farm belonged to 13 genera. The blood was found to contain 12 of the genera, and the gut 19 genera. The gill and skin each showed 25 genera. Fish from Sagoe farm showed 18 genera from the muscle, 12 genera from the blood, 25 genera from the gill and skin flora, and 19 genera from the gut (Table 7e).

The blood contained the smallest number of bacterial genera in fish of both farms. For fish from the Aheto farm and Sagoe farm, the predominant species for the different tissues were:

Muscle - *Salmonella* sp. and *Pasteurella* sp., respectively.

Blood - *Corynebacterium* sp. and *Micrococcus* sp., respectively.

Gills *Salmonella* sp., and, *Bacillus* sp. and *Flavobacterium* sp., respectively.

Gut - *Pseudomonas* sp., and, *Escherichia* sp, *Flavobacterium* sp. and *Streptococcus* sp., respectively.

Skin - *Salmonella* sp., and, *Salmonella* sp. and *Vibrio* sp., respectively.

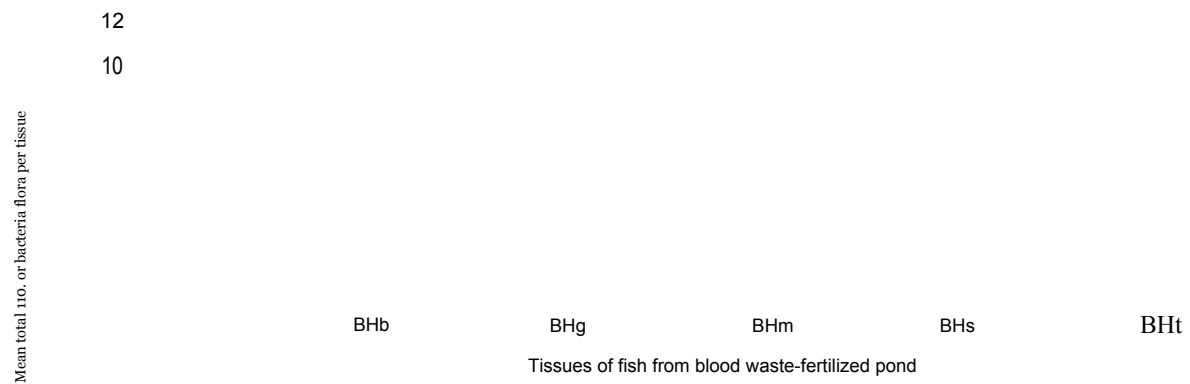
Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the tissues flora from the blood, gill, gut, muscle and skin. Duncan's multiple comparison determination showed homogeneity between the means for the blood and muscles, and between the gill, gut and skin. Fig. 9e shows correlation between the means of the bacteria flora found in the various tissues.

TABLE 7d

Mean (oiul immhci of buclci-iul isoluCcs occuning m (issues
of Mt l'iom htoiuI wank* h'ilili/cil penul Htinlicii Ini-iki

Bacterial species	niusclc	blood	gill	gul	skin
<i>Actinobacillus sp.</i>	0.0	0.0	3.3	3.0	3.3
<i>Aeromonas sp.</i>	1.7	7.3	12.0	1.3	9.7
<i>Bacillus sp.</i>	4.3	0.0	15.7	6.3	17.0
<i>Hacteroides sp.</i>	0.0	0.0	9.3	0.0	8.3
<i>Campylobacter sp.</i>	2.3	7.7	4.0	1 1.0	3.0
<i>Citrobacter sp.</i>	3.0	1.3	8.0	2.0	9.3
<i>Clostridium sp.</i>	1.3	1.3	11.0	2.7	10.0
<i>Corynehaclerlum sp.</i>	2.7	1.3	6.0	14 3	4.3
<i>Edwardsiella sp.</i>	0.0	0.0	11.7	0.7	10.3
<i>Enterobacter sp.</i>	0.0	5.3	9.3	2.7	6.7
<i>Escherichia sp.</i>	6.0	6.0	7.7	24.3	10.0
<i>Flavobacterium sp.</i>	1.0	5.0	12.7	19.3	13.3
<i>Hafnia sp.</i>	3.0	0.0	8.7	4.3	10.3
<i>Klebsiella sp.</i>	0.0	0.0	7.0	3.3	6.0
<i>MtrococL'is sp.</i>	3.0	1 8.0	10.0	41.3	12..1
<i>Pasteurella sp.</i>	9.7	0.0	11.3	2.3	12.3
<i>Proteus sp.</i>	0.0	3.7	3.0	13.0	2.3
<i>Pseudomonas sp.</i>	'1.3	7.0	13.3	33.0	11.3
<i>Salmonella sp.</i>	6.0	0.0	19.7	3.7	19.3
<i>Serratia sp.</i>	0.0	1.0	4.7	7.0	4.7
<i>Shigella sp.</i>	0.0	1.3	5.7	3.3	8.0
<i>Sinphylarmretis sp.</i>	0.0	0.0	4.0	0.0	5.7
<i>Streptococcus sp.</i>	3.0	7.0	8.0	23.3	7.3
<i>l 'tirlo sp.</i>	1.3	0.0	13.7	0.0	12.3
<i>Yersinia sp.</i>	0.0	0.0	2.7	4.3	3.3

Fig. 9d Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from blood waste-fertilized ponds



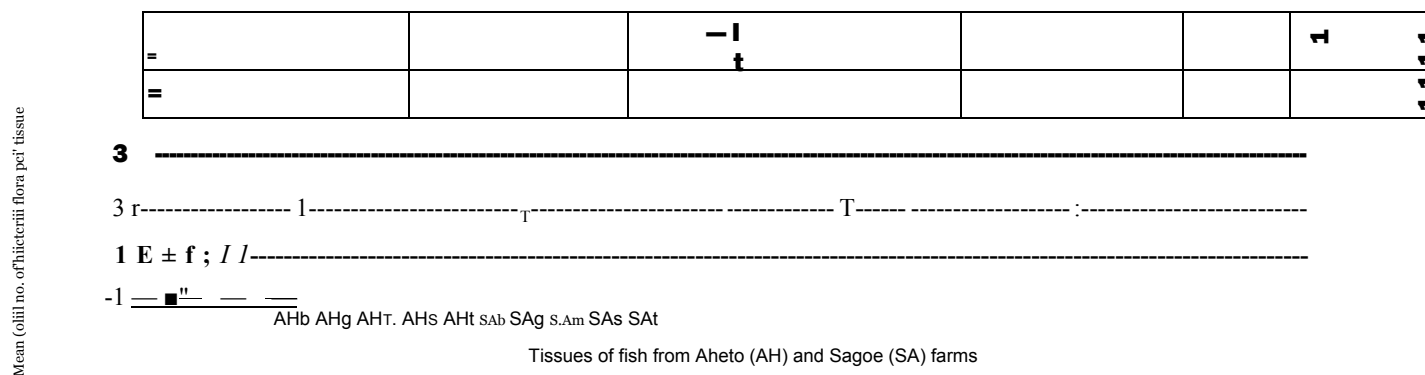
BHb = Blood of fish from Boahen farm
BHg = gills of fish from Boahen farm
BHm = muscle of fish from Boahen farm
BHs = skin of fish from Boahen farm
BHt = gut of fish from Boahen farm

TABUS 7c

Mean (olul numbei of'bucleiul isolulcs occurring in (issues <>'!lisl lioiu clieiiicilly-lei(ili/.eil poiuls

linrrrlnl	Alieli) i a mi					SIKHC fnnn				
	iniisrlc	hlootl	Kill	Kill	skin	inusilr	hlootl	Kill	Kill	Nkin
<i>AcitnbaclHus sp</i>	0.0	0.0	2.0	0.0	1.3	0.0	0.0	2.7	0.0	3.3
<i>Aeromonas sp.</i>	0.0	0.3	6.0	0.0	5.0	0.7	0.0	11.3	0.0	12.7
<i>Bacillus sp.</i>	1.0	6.0	9.7	25.3	9.3	1.3	8.3	14.7	14.3	18.0
<i>Bacteroides sp.</i>	4.3	0.0	12.0	2.0	12.7	5.7	0.0	12.7	2.0	11.7
<i>Campylobacter sp.</i>	0.0	0.0	6.0	0.0	6.0	2.3	1.0	8.0	11.0	9.0
<i>Citrobacter sp</i>	0.0	0.0	9.7	0.0	9.0	0.7	5.0	12.3	10.0	9.0
<i>Clostridium sp.</i>	0.0	0.0	12.0	6.3	8.7	5.0	0.0	7.7	0.0	7.7
<i>Corynehaclriiim sp.</i>	1.1	10.0	7.0	25.3	9.0	2.7	5.0	4.3	21.7	5.3
<i>Edwardsiella 'sp.</i>	<1.7	0.0	16.3	1.7	14.0	1.7	0.0	7.3	1.3	8.3
<i>Enterobacter sp.</i>	0.0	0.0	5.7	1.0	8.3	0.0	0.0	12.0	1.0	9.3
<i>Escherichia sp.</i>	0.0	0.0	10.0	23.7	6.7	2.3	5.7	13.0	27.0	8.7
<i>Flavobacterium sp.</i>	1.3	6.3	9.3	28.0	11.7	4.0	5.0	14.7	25.0	11.0
<i>Hafnia sp</i>	2.3	0.0	11.3	0.0	12.7	2.7	1.0	11.3	1.0	9.3
<i>Klebsiella sp.</i>	0.0	1.0	2.3	0.0	4.0	0.3	0.0	9.7	1.3	9.3
<i>Micrococais sp.</i>	5.0	7.0	12.3	31.3	9.0	3.0	14.3	9.0	27.0	11.0
<i>Pasteurella sp</i>	1.1	0.0	16.0	1.7	11.1	8.7	0.0	9.7	0.1	8.7
<i>Prntelis sp.</i>	0.0	0.0	6.7	3.0	9.0	0.0	1.3	6.0	12.7	7.3
<i>Pseudomonas sp.</i>	2.3	7.0	14.0	37.0	11.3	6.3	4.7	12.0	23.3	11.3
<i>Salmonella sp.</i>	6.0	1.7	19.7	0.3	22.3	2.3	0.7	12.7	8.7	13.3
<i>Serratia sp.</i>	0.0	0.7	3.3	0.7	6.3	0.0	4.7	6.7	8.0	7.7
<i>Shigella sp.</i>	0.3	1.3	4.3	1.7	2.7	5.0	0.0	5.3	0.0	6.3
<i>Staphylococcus sp.</i>	0.3	1.7	5.7	16.3	5.0	0.0	0.0	2.3	6.0	2.7
<i>Streptococcus sp.</i>	0.3	0.3	8.7	24.0	8.0	3.0	0.0	6.3	25.0	6.3
<i>Vibrio sp.</i>	0.0	0.0	10.0	0.3	11.0	0.0	0.0	11.7	0.0	16.3
<i>Yersinia sp.</i>	0.0	0.0	2.0	0.3	3.3	0.0	0.0	1.7	0.0	0.7

Fig. 9e Mean values and L.S.D (95%) intervals between the bacteria flora of fish tissues from chemically fertilized ponds



AHb = Blood of fish from Aheto farm
 AHg = gills of fish from Aheto farm
 AHm = muscle of fish from Aheto farm
 AHs = skin of fish from Aheto farm
 AHt = gut of fish from Aheto farm

SAb = blood of fish from Sagoe farm
 SAg = gills of fish from Sagoe farm
 SAm = muscle of fish from Sagoe farm
 SAs = skin of fish from Sagoe farm
 SAt = gut of fish from Sagoe farm

6. Fish cultured in ponds with no fertilization

The data in Table 7f showed that the bacterial species isolated from the muscle, blood, gills, gut and skin represented 20, 18, 24, 19 and 23 genera, respectively. The dominant species of the muscle flora were *Bacillus* sp., *Micrococcus* sp., *Pasteurella* sp and *Salmonella*. The dominant genera in the blood were *Micrococcus* sp, *Pseudomonas* sp. and *Proteus* sp.

Citrobacter sp., *Pseudomonas* sp. and *Salmonella* sp. were the predominant species in the gills. *Escherichia* sp., *Micrococcus* sp. and *Pseudomonas* sp. were the dominant species of the gut flora. *Bacillus* sp., *Pseudomonas* sp. and *Salmonella* sp. dominated the flora of the skin.

Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the values for the flora of the blood, gill, gut, muscle and skin. Duncan's multiple comparison determination showed homogeneity between the means of the blood and muscles, and between the gill, gut and skin. Fig. 9f shows correlation between the means of the bacteria flora as found in the various tissues.

7. Fish cultured in the open systems

Bacterial genera identified from the muscle, blood, gill, gut, and skin of fish caught from the Kpong Headpond were 18, 14, 22, 25 and 25, respectively (Table 7g). For the Volta river, they were 18, 15, 23, 24 and 25 genera, respectively, and for the Weija dam, 18, 14, 24, 25 and 25 genera, respectively.

The blood contained the smallest number of bacterial genera in fish of the three open systems. For fish from the Kpong Headpond, Volta River and Weija Dam, the predominant species for the different tissues were:

Muscle *Pasteurella* sp. and *Salmonella* sp.; *Salmonella* sp. and *Pasteurella* sp.,
respectively.

Blood *Micrococcus* sp. and *Pseudomonas* sp.; *Pseudomonas* sp., and,
Aeromonas sp., *Bacillus* sp. and *Micrococcus* sp., respectively.

IKI

Mean UMtil iminhei til Imclerriiil iriullHc* mimtiifj; in lisritim

ni li.sh li4»iii AUF .1 pond with no leiiii/.ation

lluclerriiil spi*cies	iniimk	blood	{ {ill	Kill	Nltiii
<i>Actinobacillus sp.</i>	0.70	0.00	1.70	1.70	3.70
<i>Ai'l'OHUhtS sp</i>	1.70	3.70	12.70	0.10	17.70
<i>IUtoiUm .vij</i>	9.70	1.00	10.00	21.70	17.30
<i>llacteroldes sp.</i>	6.70	1.00	1.1.00	2.70	11.70
<i>(ampylohactv. sp.</i>	0.00	0.00	6.10	10.70	6.70
<i>Citrobacter sp.</i>	3.00	9.00	15.30	1.00	10.00
<i>(hs/rit/inin sp.</i>	7. JO	0. JO	11 JO	1.70	M.00
<i>(orytwhacertuin .v/»</i>	1.10	7.70	5.70	»S.00	.to
<i>Edwardstella sp.</i>	10.00	0.00	11.70	0.00	12.70
<i>Lteivbacm»») .</i>	4. Uo	2. JO	*.7o	1.00	10.00
<i>Escherichia sp</i>	1.70	7.70	9.70	77.70	010
<i>b'lavohacertuin sp</i>	2.00	5.30	K.4.70	1.V00	12.00
<i>i_h/ii/ii a/a</i>	*1.70	0.00	10.10	0.00	H.OO
<i>Klebsiella sp</i>	0.00	7.70	4.00	s.00	S.70
<i>Micrococcus sp.</i>	9.70	11.30	11.70	29.00	10.70
<i>I'nteuvelhi sp</i>	»70	0.00	10.70	0.00	1.1.10
<i>PROUSA</i>	1.70	«> 70	£> 10	K.70	7.10
<i>i'svudonumas sp.</i>	1.1.00	12.00	1.1. JO	Jft.00	1. .VOC
<i>Salmonella sp.</i>	12.30	1.70	13.70	0.00	14.70
<i>Serratia sp.</i>	2.00	1.70	2.70	13.70	3.00
<i>Shly,eUa sp</i>	0.00	1.00	'1.10	0.00	1.70
<i>S/i tpU vlococi ITS sp.</i>	0.00	0.70	0.00	0.00	0.00
<i>Streptococcus sp</i>	1.70	1.70	7.30	75.70	S.10
<i>Vibrio s(> .</i>	ft.,JO	0.00	11. JO	0.00	12. JO
<i>Yersinia sp.</i>	0.00	0.00	0.30	0.30	0.00

Fig. 9f Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from non-fertilized ponds

Mean (total no. colbacteria Horn per 1 issue

AEb

AEg

AEm

AEs

AEt

Tissues of fish form non-fertilized oond

- AEb = Blood of fish from ARDEC 3 farm
- AEg = gills of fish from ARDEC 3 farm
- AEm = muscle of fish from ARDEC 3 farm
- AEs = skin of fish from ARDEC 3 farm
- AEt = gut of fish from ARDEC 3 farm

TABLE 7g

Mean total number of bacterial isolates occurring in tissues of fish from open systems

Bacterial species	Kpong licadpoutl					Volta river					Weija dam				
	muscle	blood	gill	gut	skin	niusclc	blood	gill	gut	skin	muscle	blood	gill	gut	skin
<i>Actinobacillus sp.</i>	0.0	0.0	1.7	1.7	2.3	2.3	0.0	0.0	0.3	0.3	0.0	0.0	3.3	0.7	2.3
<i>Aeromonas sp.</i>	2.3	11.3	9.7	7.0	10.7	3.3	9.3	8.0	13.3	10.3	2.7	11.0	10.3	3.0	12.0
<i>Bacillus sp.</i>	7.0	4.0	17.0	8.0	13.3	9.0	2.7	16.7	5.7	16.7	6.7	9.7	10.7	5.3	13.7
<i>Bacteroides sp.</i>	1.0	1.3	9.7	1.0	4.0	0.3	5.0	3.3	0.7	6.3	4.7	0.0	7.0	4.7	4.3
<i>Campylobacter sp.</i>	3.0	10.7	8.7	12.0	5.3	4.0	1.7	5.7	8.7	8.3	0.0	3.0	9.0	12.0	7.7
<i>Citrobacter sp.</i>	7.3	0.0	16.7	15.7	11.0	2.0	7.7	6.0	14.3	6.7	2.7	0.0	11.0	8.3	12.7
<i>Clostridium sp.</i>	0.0	0.0	12.7	0.0	11.0	4.3	0.0	11.0	0.3	11.0	0.7	0.0	8.7	5.0	10.7
<i>Corynebacterium sp.</i>	3.0	3.7	5.0	13.3	6.0	2.0	8.0	3.0	14.3	6.3	2.7	7.0	8.0	8.3	6.3
<i>Edwardsiella sp.</i>	0.0	4.0	6.7	8.0	11.0	4.7	1.0	10.3	1.7	12.3	4.0	2.7	12.3	9.3	9.3
<i>Enterobacter sp.</i>	9.0	6.0	8.0	12.7	5.3	0.0	0.0	0.0	1.7	0.3	5.0	0.0	10.3	5.3	8.3
<i>Escherichia sp.</i>	5.3	0.0	14.3	12.0	11.3	0.7	5.0	9.0	19.7	10.0	3.3	2.7	12.3	21.7	11.3
<i>Flavobacterium sp.</i>	3.0	12.0	7.3	14.7	5.0	5.3	7.3	16.7	19.3	16.0	3.7	4.0	13.7	12.3	12.7
<i>Hafnia sp.</i>	6.7	0.0	11.3	5.7	9.7	3.3	3.0	10.3	1.7	8.7	0.0	0.0	5.0	6.3	7.0
<i>Klebsiella sp.</i>	1.7	0.0	5.0	9.0	3.7	0.7	0.0	4.3	6.3	4.7	2.3	1.3	8.3	7.7	7.7
<i>Micrococcus sp.</i>	2.7	17.3	7.3	21.3	10.0	1.7	10.0	7.7	21.7	9.0	0.0	10.7	11.7	20.0	11.0
<i>Pasteurella sp.</i>	11.3	0.0	16.3	5.3	15.0	4.0	0.0	11.3	0.3	9.0	10.7	0.0	11.0	11.0	9.7
<i>Proteus sp.</i>	3.0	9.7	5.0	15.0	7.0	0.0	4.7	0.3	11.0	1.3	3.3	8.0	8.7	11.7	8.3
<i>Pseudomonas sp.</i>	4.3	21.0	14.3	27.7	20.0	9.7	21.0	19.3	38.3	17.0	6.3	8.0	13.0	26.7	16.7
<i>Salmonella sp.</i>	12.7	1.3	18.7	7.0	21.7	14.3	0.0	23.0	0.0	22.3	5.0	0.3	11.3	6.7	10.3
<i>Serratia sp.</i>	0.0	4.0	3.3	8.7	3.0	2.3	4.7	7.3	11.7	4.0	3.0	4.3	5.3	9.3	7.0
<i>Shigella sp.</i>	3.7	0.0	7.0	2.7	6.7	0.0	0.0	5.0	1.7	3.7	0.0	0.0	4.0	0.0	3.7
<i>Staphylococcus sp.</i>	0.0	1.0	1.0	2.3	2.3	0.0	0.0	3.0	1.3	3.0	0.0	2.7	6.0	4.7	3.7
<i>Streptococcus sp.</i>	1.7	0.0	5.0	16.0	12.7	0.0	0.0	18.0	24.3	13.0	2.3	0.0	11.0	22.7	13.7
<i>Vibrio sp.</i>	0.0	0.0	12.0	0.0	12.7	0.0	0.0	20.7	0.7	17.3	8.7	0.0	10.0	3.3	12.0
<i>Yersinia sp.</i>	0.0	0.0	1.3	0.0	1.0	0.0	0.7	3.0	7.7	3.7	0.0	0.0	4.0	0.7	3.3

Gills -*Citrobacter* sp., *Pasteurella* sp. and *Salmonella* sp.; *Bacillus* sp.,

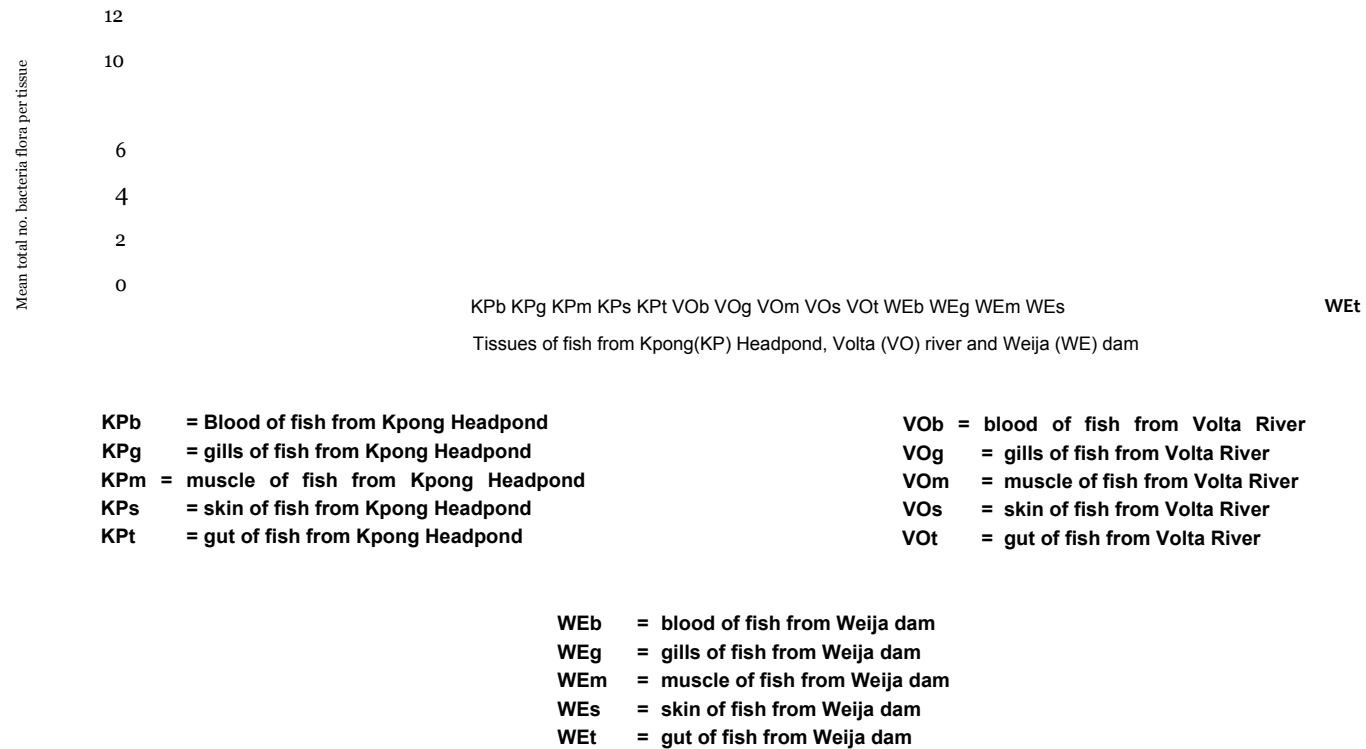
Flavobacterium sp., *Pseudomonas* sp. and *Vibrio* sp., and, *Edwardsiella* sp.,
Escherichia sp. and *Flavobacterium* sp., respectively.

Gut - *Micrococcus* sp. and *Pseudomonas* sp.; *Pseudomonas* sp., and, *Pseudomonas*
sp., respectively.

Skin *Pseudomonas* sp. and *Salmonella* sp.; *Salmonella* sp., and, *Pseudomonas* sp.,
respectively.

Analysis of variance determination showed significant difference at 95.0% confidence level between the means of the flora of the blood, gill, gut, muscle and skin. Duncan's multiple comparison determination showed homogeneity between the means of the blood and muscles, and between the gill, gut and skin. Fig. 9g shows correlation between the means of the bacteria flora as found in the various tissues.

Fig. 9g Mean values and L.S.D (95%) intervals between the bacteria flora of fish tissues from Open Systems



F. Bacterial Populations of Fish Feed Types and Organic Fertilizers

The results in Table 8 showed that all the eleven feed types and the four organic fertilizers tested had resident bacteria. The number of viable heterotrophic bacteria recorded for the eleven feed types varied from 2.15 to 3.48 log₁₀ CFU per gram of feed type. Banana waste recorded the least number of heterotrophic bacteria followed by wheat bran, corn husk and then rice bran. The rest, in ascending order, were spent grain, cassava, biscuit waste, termites, groundnut husk and fufu waste. The number of viable heterotrophic bacteria counts demonstrated in the four organic fertilizers varied from 6.17 to 6.86 log₁₀ CFU per gram. Cow manure had the least heterotrophic bacterial count followed by poultry manure, blood waste, and pig manure in ascending order. Enterobacteriaceae were detected in all the eleven feed types and the four organic fertilizers. The most probable number (MPN) estimates for total coliforms in the eleven feed types ranged from 1.04 to 3.04 log₁₀ CFU ml⁻², and from 5.04 to 5.97 log₁₀ CFU ml⁻² in the four organic fertilizers. The lowest value was determined in corn husk and the highest with pig manure.

Only three of the eleven feed types, biscuit waste, groundnut husk and termites contained faecal coliforms, and three out of the four organic fertilizers, cow manure, pig manure and poultry manure contained faecal coliforms. The counts were significantly higher for the organic manures than for the feed types (Table 8).

Only four out of the eleven feed types, viz. biscuit waste, cassava, groundnut husk and termites, and, all the four organic manures contained faecal streptococci (Table 8).

TABLE 8

The bacterial load present in Feed types and Organic manures used in the fish ponds

Sample Diet/Organic Manure	Heterotrophic Bacteria count (Log ₁₀ ml ⁻¹)	Most Probable Number (MPN) Log ₁₀ /10 grams.		
		Total coliform	Faecal coliform	Faecal streptococci
Banana waste	2.85	1.97	ND	ND
Biscuit waste	3.56	2.38	1.60	2.63
Bread waste	4.20	2.08	ND	ND
Brewery spent grain	3.45	2.08	ND	ND
Cassava waste	3.48	1.88	ND	1.60
Com husk	3.00	1.63	ND	ND
Fufu waste	4.28	3.04	ND	ND
Groundnut husk	3.85	1.88	1.00	2.30
Rice bran	3.15	1.04	ND	ND
Termites	3.78	2.66	1.60	2.60
Wheat bran	2.95	1.60	ND	ND
Blood waste	6.72	5.04	ND	1.60
Cow manure	6.17	5.59	4.04	4.36
Pig manure	6.86	5.97	4.15	4.63
Poultry manure	6.31	5.81	3.95	4.15

ND = Not Detected

G. Survival of Selected Pathogenic Bacteria Introduced into Organic Manures Used in Fertilizing Fish Ponds.

The five organic manures commonly used to fertilize the fish ponds, namely, blood waste from abattoir, cow manure, pig manure, poultry manure and sewage water, all supported growth of the eight pathogenic bacteria introduced into them but the pattern of survival varied with species and type of manure. Growth in water (control) was invariably poor. The eight bacterial strains used were *Pseudomonas* sp. KI-MTC-001K, *Shigella* sp. KI-MTC-002K, *Enterobacter* sp. KI-MTC-003K, *Klebsiella* sp. KI-MTC-004K, *Citrobacter* sp. KI-MTC-005, *Proteus* sp. KI-MTC-006K, *Salmonella* sp. KI-MTC-007, and *Vibrio parahaemolyticus* KI-MTC-008K. The results are presented in Tables 9a - 9h, and the values of population cited in sections 1 - 8 represent log₁₀ CFU ml⁻¹.

1. Survival of *Pseudomonas* sp. KI-MTC-001K

The greatest population growth occurred in sewage pond. From initial value of 1.08, a count of 9.26 was obtained after 96 hours and was maintained at 120 hours. The next most favourable medium to the bacterium was cow manure which supported an increase of count from 1.18 to a peak of 5.45 at 96 hours before declining to 4.78 at 120 hours. There was no difference for the growth of this bacterium in poultry manure, pig manure and blood waste. It was noteworthy that *Pseudomonas* sp. KI-MTC-001K multiplied in the tapwater used as control to a peak at 6 hours before the population started to decline (Table 9a).

2. Survival of *Shigella* sp. KI-MTC-002K

There was generally low growth of this strain in the manures. The highest growth was recorded in poultry manure with a count of 4.38 by 72 hours from an initial count of 1.34. The next most supportive medium was the pig manure which recorded 3.90 by 96 hours from an initial count of 1.26. There were no remarkable growth of this organism in cow manure, sewage and blood waste and, in fact, the cells were all dead after 96 hours in the blood waste and sewage medium. There was no growth in the control (Table 9b).

TABLE 9a

Growth of *Pseudomonas* sp. KI-MTC-001K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log_{10} CFU) ml^{-1} of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.45	2.38	2.38	3.58	4.15	3.38	3.26	3.15
Cow manure	1.18	2.15	2.64	3.15	3.26	5.38	5.45	4.78
Piggery manure	1.66	3.15	3.60	3.64	3.26	3.56	4.68	4.58
Poultry manure	1.75	3.38	3.00	3.78	4.08	4.26	4.79	4.85
Sewage	1.08	2.15	4.38	5.26	5.48	8.08	9.26	9.26
Tap water (Control)	1.15	3.38	1.48	1.00	1.00	1.00	0.78	-

TABLE 9b

Growth of *Shigella* sp. KI-MTC-002K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log_{10} CFU) ml^{-1} of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.62	2.08	1.92	1.91	1.79	1.53		
Cow manure	1.53	2.30	1.85	0.95	1.26	1.32	1.18	1.15
Piggery manure	1.26	2.08	2.89	3.26	2.95	3.15	3.90	1.15
Poultry manure	1.34	2.30	2.26	3.48	3.60	4.38	4.48	4.60
Sewage	1.38	1.15	1.48	1.51	1.26	0.60		
Tap water (Control)	1.18	-	-	-	-	-	-	-

TABLE 9c

Growth of *Enterobacter* sp. KI-MTC-003K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log_{10} CFU) ml^{-1} of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.56	2.15	2.15	4.08	4.41	5.08	5.43	6.08
Cow manure	1.34	2.15	2.38	2.26	1.98	2.08	2.26	2.20
Piggery manure	1.30	1.99	1.97	2.15	2.26	2.20	1.90	1.90
Poultry manure	1.58	2.62	2.08	2.78	2.90	2.48	1.78	1.60
Sewage	1.18	2.51	3.15	4.26	6.38	5.34	6.26	4.15
Tap water (Control)	1.34	0.78	0.60	0.70		0.00		

TABLE 9d

Growth of *Klebsiella* sp, KI-MTC-004K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log ₁₀ CFU) ml ⁻¹ of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.15	4.41	5.15	5.45	5.78	6.86	6.83	5.81
Cow manure	1.56	2.90	2.26	2.23	2.60	3.45	3.53	4.26
Piggery manure	1.59	2.20	2.15	3.26	3.26	3.45	2.90	2.20
Poultry manure	1.64	2.90	2.15	3.95	3.15	3.90	2.15	1.26
Sewage	1.63	2.20	2.20	4.45	4.51	4.45	4.56	4.26
Tap water (Control)	1.51	0.90	0.30	0.48	-	-	-	-

TABLE 9e

Growth of *Citrobacter* sp. KI-MTC-005K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log ₁₀ CFU) ml ⁻¹ of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.41	2.15	1.93	2.08	2.08	2.04	1.99	2.00
Cow manure	1.73	1.18	1.15	2.08	2.90	3.08	3.04	2.78
Piggery manure	1.08	2.04	2.08	2.08	1.99	2.15	2.04	1.89
Poultry manure	1.48	2.15	2.20	2.45	2.20	2.36	-	-
Sewage	1.34	2.43	2.15	2.20	2.08	2.15	1.15	1.15
Tap water (Control)	0.90	0.70	0.00	-	-	-	-	-

TABLE 9f

Growth of *Proteus* sp. KI-MTC-006K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log ₁₀ CFU) ml ⁻¹ of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.51	3.53	2.23	2.66	2.92	3.11	3.34	3.15
Cow manure	1.56	1.94	2.15	2.78	3.15	4.38	4.92	4.00
Piggery manure	1.41	2.60	2.90	3.30	4.60	5.62	5.92	5.78
Poultry manure	1.28	3.51	3.30	4.08	4.45	4.48	4.68	4.60
Sewage	1.20	3.36	3.26	4.23	6.38	7.26	8.34	4.15
Tap water (Control)	1.20	1.26	1.08	-	-	0.30	0.00	-

TABLE 9g

Growth of *Salmonella* sp. KI-MTC-007K. in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log ₁₀ CFU) ml ⁻¹ of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.15	2.08	2.08	3.30	3.81	3.81	3.76	2.66
Cow manure	1.38	1.93	2.15	1.56	1.73	1.32	1.11	0.60
Piggery manure	1.26	2.20	2.04	1.78	1.70	1.64	1.08	1.20
Poultry manure	1.52	2.15	2.45	3.08	3.54	3.66	4.51	4.48
Sewage	1.56	2.30	1.90	1.56	1.86	1.81	0.60	0.70
Tap water (Control)	1.15	0.30	-	-	-	-	-	-

TABLE 9h

Growth of *Vibriopara haemolyticus* K.I-MTC-008K in UV-sterilized pond water containing different types of organic matter

Organic matter	Population of pathogen (Log ₁₀ CFU) ml ⁻¹ of medium after following number of hours							
	0	3	6	24	48	72	96	120
Blood waste	1.30	1.64	1.62	1.18	0.90	1.04	0.48	
Cow manure	1.20	2.00	1.30	1.00	1.00	1.00	0.30	
Piggery manure	1.15	2.60	2.30	1.78	0.30	1.00		
Poultry manure	1.45	1.18	1.00	1.04	0.78			-
Sewage	1.66	1.08	0.90	1.00	0.90	0.78	0.70	
Tap water (Control)	1.26	-		-	-		-	

3. Survival of *Enterobacter* sp. KI-MTC-003K

The most supportive medium was the sewage followed by the blood waste. The sewage recorded a rise from an initial 1.18 to 6.38 after 48 hours. The blood waste showed an increase from 1.56 to 6.08 in 120 hours (Table 9c). There was comparatively lesser growth rate in cow manure, pig manure and poultry manure and the population started to decline after 72 96 hours. There was no growth in the control.

4. Survival of *Klebsiella* sp. KI-MTC-004K

The highest growth of 6.86 was recorded for blood waste after 72 hours from an initial count of 1.15. The next most supportive medium was the sewage which had an increase from initial 1.63 to 4.45 by 24 hours. Generally there was good growth of *Klebsiella* sp. KI-MTC-004K in cow manure, poultry manure and pig manure. There was no growth in the control (Table 9d).

5. Survival of *Citrobacter* sp. KI-MTC-005

The strain showed moderate growth in the organic matter. There was no marked difference between all the manures used. There was no growth of the bacterium in the control (Table 9e).

6. Survival of *Proteus* sp. KI-MTC-006K

The most supportive medium was the sewage which showed an increase to 8.34 by 96 hours from an initial 1.20. This decreased to 4.15 by 120 hours. The next most supportive medium was the pig manure which recorded 5.92 by 96 hours. Growth in the control occurred only in the initial 3 hours of incubation and the organism died out after 6 hours (Table 9f).

7. Survival of *Salmonella* sp. KI-MTC-007

The highest growth was recorded in poultry manure which showed 4.51 by 96 hours from an initial 1.52. Blood waste was the next supportive medium and recorded 3.81 by 72 hours. Generally there was less growth in pig manure, cow manure and sewage. There was no growth in the control (Table 9g).

8. Survival of *Vibrio parahaemolyticus* KI-MTC-008K

Generally growth of this strain in the various media was poor. After the initial recordings of growth in all the media there was gradual die-off in all the media and there was no viable cell by 120 hours. The organism did not survive 3 hours' incubation in tap water (Table 9h).

H. Case Study of Akuse Fisli Ponds: Bacteria-Fish Relationship in Sewage Treatment plant Wastewater.

1. Physico-chemical parameters

The mean monthly values for the four ponds of each of the parameters are presented in Table 10a 10d. The air temperature of the area and rainfall distribution pattern recorded by the Meteorological Department are presented in Appendix 9.

Correlation analysis of the various physico-chemical parameters indicated which parameters showed statistically significant non-zero correlations at the 95% confidence level. The Pearson product moment correlation showed that in Pond I physico-chemical and microbiological parameters which showed significant and positive correlations were acidity and magnesium ion, air and water temperatures, alkalinity and conductivity, alkalinity and DO, alkalinity and turbidity, ammonium ion and DO, BOD and phosphate ion, calcium ion and TC, calcium ion and TDS, chloride ion and THB, chloride ion and water temperature, conductivity and turbidity, FC and TC, and THB and water temperature. Parameters which showed significant negative correlations were acidity and THB, acidity and water temperature, air temperature and BOD, air temperature and phosphate ion, alkalinity and chloride ion, nitrate ion and TC, and TC and TDS.

Parameters of Pond II which showed significant and positive correlations were acidity and air temperature, acidity and FS, acidity and TDS, air temperature and FS, air and water temperatures, calcium and chloride ions, conductivity and FS, conductivity and turbidity, conductivity and water temperature, FS and turbidity, FS and water temperature, total hardness and SS, nitrate ion and silicon dioxide, and phosphate ion and THB. Parameters which showed significant and negative correlations were acidity and BOD and TDS, conductivity and DO, DO and FS, DO and water temperature, FC and total hardness, FC and SS, and nitrite ion and pH.

Parameters of Pond III which showed significant and positive correlations were air temperature and silicon dioxide, air and water temperatures, alkalinity and calcium ion, ammonium and chloride ions, ammonium ion and DO, calcium ion and FC, calcium ion and TC, chloride ion and DO, conductivity and turbidity, FC and TC, FC

TABLE 10a

Physico-chemical parameters and bacterial population levels of Akuse Pond I water

Parameter	Mean values per month (1996 -1999)					
	January	March	May	July	September	November
Air Temperature (°C)	28.50	30.17	30.17	31.25	30.00	30.17
Water Temperature (°C)	29.50	29.83	31.50	32.50	31.33	30.87
pH	6.95	6.98	7.03	7.00	6.93	6.80
Acidity (mg/l ¹)	63.33	60.00	52.00	53.00	51.67	55.60
Alkalinity (mg/l ¹)	96.00	90.00	89.67	63.67	92.33	96.33
Calcium ion (mg/l ¹)	12.83	12.23	11.67	13.00	13.83	12.00
Total hardness (mg/l ¹)	38.60	42.33	43.00	37.50	51.00	48.67
Chloride ion (mg/l ¹)	10.37	10.77	10.73	12.00	11.47	10.63
Magnesium ion (mg/l ¹)	6.47	6.17	4.76	5.59	4.56	5.63
Phosphate ion (mg/l ¹)	3.84	1.30	1.33	1.38	1.36	1.34
Ammonium ion (mg/l ¹)	2.73	3.33	3.19	1.95	2.61	3.08
Nitrate ion (mg/l ¹)	0.65	0.58	0.64	0.58	0.52	0.65
Nitrite ion (mg/l ¹)	0.23	0.33	0.34	0.33	0.29	0.23
Sulphate ion (mg/l ¹)	0.02	0.04	0.01	0.02	0.03	0.02
Silicon dioxide (mg/l ¹)	0.62	0.71	0.69	0.64	0.71	0.70
Dissolved oxygen (mg/l ¹)	17.51	18.22	19.20	14.60	17.47	18.87
Biochemical oxygen demand (mg/l ¹)	38.90	13.23	11.87	11.35	14.01	14.07
Total dissolved solids (mg/l ¹)	81.33	85.83	86.83	80.00	75.17	85.83
Suspended solids (mg/l-1)	19.37	20.33	20.27	18.95	19.27	19.23
Turbidity (NTU)	73.27	71.47	65.33	54.50	78.17	75.60
Conductivity (Scm ¹)	521.67	431.83	432.00	306.00	466.00	546.67
Total coliform count x 10 ³ (ml ²)	793.33	733.33	553.00	1380.00	1966.67	890.67
Faecal coliform count x 10 ³ (ml ²)	119.67	223.33	112.00	283.00	450.00	395.00
Faecal streptococci count x 10 ³ (ml ²)	2.03	1.70	2.80	1.20	1.97	1.37
Total heterotrphic bacteria x 10 ³ (ml ²)	466.67	7.05.33	3.260.67	5600.00	5366.67	1290.00

TABLE 10b

Physico-chemical parameters and bacterial population levels of Akuse Pond II water

Parameter	Mean values per month (1996 - 1999)					
	January	March	May	July	September	November
Air Temperature (°C)	30.33	30.33	29.83	29.50	30.83	30.67
Water Temperature (°C)	31.17	31.33	30.83	30.50	32.17	31.83
pH	6.99	6.98	6.81	6.92	6.95	6.96
Acidity (mg/l ¹)	46.67	46.67	45.00	30.00	48.33	46.67
Alkalinity (mg/l ¹)	71.00	77.33	79.50	84.50	84.00	80.33
Calcium ion (mg/l ¹)	14.00	14.97	13.63	13.25	13.30	14.00
Total hardness (mg/l ¹)	41.50	41.00	41.00	40.00	38.83	41.27
Chloride ion (mg/l ¹)	29.80	34.67	32.60	28.40	29.53	31.33
Magnesium ion (mg/l ¹)	7.15	6.82	6.95	6.85	6.88	7.03
Phosphate ion (mg/l ¹)	0.53	0.53	0.48	0.44	0.57	0.41
Ammonium ion (mg/l ¹)	0.28	0.03	0.29	0.14	0.06	0.09
Nitrate ion (mg/l ¹)	0.11	0.14	0.14	0.11	0.12	0.10
Nitrite ion (mg/l ¹)	0.13	0.15	0.21	0.17	0.16	0.18
Sulphate ion (mg/l ¹)	0.02	0.02	0.02	0.03	0.03	0.01
Silicon dioxide (mg/l ¹)	0.35	0.41	0.39	0.36	0.37	0.32
Dissolved oxygen (mg/l ¹)	14.17	14.30	13.87	15.40	13.50	13.17
Biochemical oxygen demand (mg/l ¹)	10.13	10.29	10.50	11.58	9.93	10.53
Total dissolved solids (mg/l ¹)	62.00	58.83	56.33	50.75	58.83	58.67
Suspended solids (mg/l-1)	8.67	9.13	8.30	7.80	5.33	8.40
Turbidity (NTU)	5.47	5.17	5.77	4.75	6.37	5.60
Conductivity (Scm ¹)	247.33	235.33	256.67	223.00	311.33	285.00
Total coliform count x 10 ³ (ml ²)	172.33	90.00	90.33	87.00	166.67	97.33
Faecal coliform count x 10 ³ (ml ²)	44.00	40.40	38.00	55.50	72.67	56.00
Faecal streptococci count x 10 ³ (ml ²)	1.17	1.14	1.26	0.66	1.43	1.47
Total heterotrophic bacteria x 10 ³ (ml ²)	533.33	318.00	3421.00	395.00	766.67	509.33

TABLE 10c

Physico-chemical parameters and bacterial population levels of Akuse Pond III water

Parameter	Mean values per month (1996 - 1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.67	29.00	30.67	29.50	29.67	33.83
Water Temperature (°C)	30.33	29.83	31.83	31.00	31.17	32.50
pH	6.86	6.91	6.72	6.75	6.68	6.67
Acidity (mgr ^l)	27.33	24.67	25.00	24.90	25.00	26.37
Alkalinity (mgr ^l)	53.33	56.67	60.00	58.50	64.53	56.00
Calcium ion (mg ^l ⁻¹)	8.67	8.87	8.87	9.10	9.83	9.17
Total hardness (mg ^l ⁻¹)	43.00	37.07	35.50	43.00	39.50	38.83
Chloride ion (mg ^l ⁻¹)	22.53	23.00	24.47	22.00	19.87	21.27
Magnesium ion (mg ^l ⁻¹)	7.77	7.78	6.70	5.09	6.09	7.13
Phosphate ion (mg ^l ⁻¹)	7.51	2.08	2.79	1.51	1.73	1.03
Ammonium ion (mg ^l ⁻¹)	0.97	0.59	0.92	0.54	0.03	0.29
Nitrate ion (mg ^l ⁻¹)	1.08	1.05	0.70	0.89	0.93	1.03
Nitrite ion (mg ^l ⁻¹)	0.07	0.05	0.07	0.04	0.05	0.06
Sulphate ion (mg ^l ⁻¹)	0.87	0.27	1.37	1.80	0.08	0.68
Silicon dioxide (mg ^l ⁻¹)	0.44	0.45	0.39	0.33	0.44	0.58
Dissolved oxygen (mg ^l ⁻¹)	9.99	9.70	9.81	9.19	8.73	9.42
Biochemical oxygen demand (mg ^l ⁻¹)	5.50	5.86	5.66	5.27	4.97	4.05
Total dissolved solids (mg ^l ⁻¹)	65.53	56.87	55.33	67.00	64.17	58.20
Suspended solids (mg ^l ⁻¹)	17.37	16.75	18.67	17.80	17.62	16.60
Turbidity (NTU)	53.47	46.20	47.33	57.20	52.13	54.20
Conductivity (Scm ⁻¹)	230.00	121.67	187.33	249.00	194.53	180.67
Total coliform count x 10 ³ (ml ⁻²)	38.00	39.67	26.33	63.50	71.33	57.67
Faecal coliform count x 10 ³ (ml ⁻²)	5.67	4.60	5.83	18.90	21.00	8.90
Faecal streptococci count x 10 ³ (ml ⁻²)	0.83	0.72	0.89	2.75	0.85	0.55
Total heterotrphic bacteria x 10 ³ (ml ⁻²)	155.67	12S.00	115.00	167.00	190.67	150.67

TABLE 10d

Physico-chemical parameters and bacterial population levels of Akuse Pond IV water

Parameter	Mean values per month (1996 - 1999)					
	January	March	May	July	September	November
Air Temperature (°C)	29.17	30.17	30.17	31.00	30.67	31.17
Water Temperature (°C)	30.00	30.85	31.33	32.50	31.83	32.00
pH	6.93	6.77	6.73	6.72	6.80	6.91
Acidity (mg/l ¹)	28.33	27.60	25.67	25.75	22.67	22.00
Alkalinity (mg/l ¹)	61.67	59.33	57.20	56.00	54.67	61.67
Calcium ion (mg/l ¹)	9.10	8.80	8.22	8.05	9.23	8.33
Total hardness (mg/l ¹)	45.67	46.67	42.67	37.80	36.93	44.67
Chloride ion (mg/l ¹)	16.20	14.87	17.53	17.50	16.73	16.00
Magnesium ion (mg/l ¹)	4.12	5.33	5.65	8.00	6.30	6.21
Phosphate ion (mg/l ¹)	4.50	1.16	1.47	1.60	6.10	1.60
Ammonium ion (mg/l ¹)	0.05	0.68	0.65	0.10	0.58	0.05
Nitrate ion (mg/l ¹)	0.35	0.38	0.02	0.53	1.19	0.60
Nitrite ion (mg/l ¹)	0.09	0.05	0.04	0.06	0.12	0.03
Sulphate ion (mg/l ¹)	0.05	0.23	0.04	0.02	0.05	0.04
Silicon dioxide (mg/l ¹)	0.34	0.29	0.08	0.18	0.34	0.40
Dissolved oxygen (mg/l ¹)	6.13	7.63	8.51	9.05	8.50	7.57
Biochemical oxygen demand (mg/l ¹)	3.26	3.67	3.84	3.50	3.76	3.63
Total dissolved solids (mg/l ¹)	55.33	53.53	52.67	49.20	57.00	52.00
Suspended solids (mg/l-1)	14.00	13.63	13.37	15.00	16.10	15.63
Turbidity (NTU)	50.53	51.93	47.33	48.30	51.07	51.33
Conductivity (Scm ¹)	80.07	87.47	80.33	44.63	138.00	93.47
Total coliform count x 10 ³ (ml ²)	22.33	17.67	16.37	19.65	13.07	15.90
Faecal coliform count x 10 ³ (ml ²)	2.13	1.67	1.47	2.68	1.40	2.33
Faecal streptococci count x 10 ³ (ml ²)	0.60	0.21	0.36	0.08	0.19	0.21
Total heterotrophic bacteria x 10 ³ (ml ²)	54.33	70.00	66.67	60.00	63.00	65.33

and THB, total hardness and TDS, total hardness and turbidity, and TC and THB. Parameters which showed significant and negative correlations were air temperature and BOD, ammonium and calcium ions, ammonium ion and TC, BOD and silicon dioxide, calcium and chloride ions, calcium ion and DO, chloride ion and TC, chloride ion and THB, DO, and FC, DO and TC, FC and magnesium ion, nitrate ion and SS, and TC and THB.

Parameters in Pond IV which showed significant and positive correlations were air temperature and magnesium ion, air and water temperature, alkalinity and total hardness, BOD and THB, calcium and phosphate ions, calcium ion and TDS, conductivity and TDS, DO and magnesium ion, DO and water temperature, FS and nitrite ion, magnesium and water temperature, nitrate ion and SS, and silicon dioxide and turbidity. Parameters which showed significant and negative correlations were acidity and SS, air temperature and FS, air temperature and nitrite ion, alkalinity and DO, ammonium ion and FC, BOD and TC, chloride and sulphate ions, chloride ion and turbidity, DO and nitrite ions, DO and pH, FS and magnesium ion, FS and water temperature, magnesium and nitrite ions, and phosphate and TDS.

The Duncan's range tests identified seven homogenous groups for Pond I. Seven homogenous groups were also identified for each of Pond II and Pond III, and eight homogenous groups for Pond IV.

The monthly mean values for the TC, FC, FS and THB counts for the four ponds are presented in Tables 10a-10d.

The Duncan's multiple range test identified two homogenous groups for the microbial parameters for Ponds I and II. FC, FS and TC formed one group and THB belonged to another group. Ponds III and IV on the other hand had three homogenous groups of FC and FS in one group, and a second and third group of TC and THB, respectively.

2. Bacterial Flora of the four Akuse Ponds

Tables 11a - 11d contain the mean monthly number of bacterial species recorded for the Akuse Ponds I-IV. *Pseudomonas* sp. was found to be clearly the

TABLE 11 d

Bacterial species isolated from Akuse Pond IV water in 1996 - 1999

SPECIES	Mean Number of Colony Forming Units ml ⁻¹ isolated in					
	February	April	June	August	October	December
<i>Actinobacillus sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Aeromonas sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Bacillus sp.</i>	2.33	1.33	2.00	1.00	2.00	2.50
<i>Bacteroides sp.</i>	0.67	0.33	0.67	1.00	0.50	0.50
<i>Campylobacter sp.</i>	0.67	1.33	0.33	0.50	1.00	1.00
<i>Citrobacter sp.</i>	0.67	1.33	1.67	1.50	1.50	2.00
<i>Clostridium sp.</i>	4.00	1.33	3.33	1.00	2.50	2.00
<i>Corynebacterium sp.</i>	0.67	1.67	0.00	0.00	0.00	1.00
<i>Edwardsiella sp.</i>	0.67	0.00	0.00	0.50	1.00	1.00
<i>Enterobacter sp.</i>	0.67	0.67	2.00	2.00	1.00	1.00
<i>Escherichia sp.</i>	4.67	4.00	3.67	5.50	4.00	5.00
<i>Flavobacterium sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Hafnia sp.</i>	0.00	0.00	0.00	1.00	0.00	0.00
<i>Klebsiella sp.</i>	3.67	5.67	5.00	5.00	5.00	4.50
<i>Micrococcus sp.</i>	1.00	1.33	2.00	4.00	2.50	1.00
<i>Pasteurella sp.</i>	0.00	0.67	0.67	0.00	0.00	0.00
<i>Proteus sp.</i>	3.67	3.33	4.33	3.00	3.00	4.50
<i>Pseudomonas sp.</i>	6.33	6.67	5.33	5.00	6.50	5.00
<i>Salmonella sp.</i>	4.33	4.00	3.67	3.00	3.50	4.50
<i>Serratia sp.</i>	0.00	0.67	0.00	0.00	0.00	0.00
<i>Shigella sp.</i>	0.33	0.00	0.00	0.00	0.00	0.00
<i>Staphylococcus sp.</i>	0.67	0.33	0.67	0.50	0.00	0.00
<i>Streptococcus sp.</i>	4.33	5.33	4.67	5.00	6.00	4.50
<i>Vibrio sp.</i>	0.00	0.00	0.00	0.00	0.00	0.00
<i>Yersinia sp.</i>	0.67	0.00	0.00	0.50	0.00	0.00

predominant strain in all the four sewage ponds. The species isolated from each pond, numbering 11, 18, 17 and 23 from Pond 1, 2, 3 and 4, respectively, in descending order of frequency of occurrence (per cent) are as follows:

POND I

<i>Pseudomonas</i> sp. 22.59	<i>Escherichia</i> sp. 10.74	<i>Corynebacterium</i> sp. 1.03
<i>Staphylococcus</i> sp. 13.82	<i>Micrococcus</i> sp. 10.59	<i>Citrobacter</i> sp. 0.88
<i>Klebsiella</i> sp. 12.50	<i>Salmonella</i> sp. 9.56	<i>Enterobacter</i> sp. 0.74
<i>Clostridium</i> sp. 11.47	<i>Shigella</i> sp. 6.18	

POND II

<i>Pseudomonas</i> sp. 18.09	<i>Micrococcus</i> sp. 9.85	<i>Edwardsiella</i> sp. 1.62
<i>Klebsiella</i> sp. 14.12	<i>Bacillus</i> sp. 5.29	<i>Staphylococcus</i> sp. 1.18
<i>Escherichia</i> sp. 12.06	<i>Enterobacter</i> sp. 4.71	<i>Serratia</i> sp. 0.59
<i>Streptococcus</i> sp. 9.85	<i>Clostridium</i> sp. 4.41	<i>Corynebacterium</i> sp. 0.44
<i>Proteus</i> sp. 7.65	<i>Citrobacter</i> sp. 3.53	<i>Campylobacter</i> sp. 0.29
<i>Salmonella</i> sp. 6.91	<i>Shigella</i> sp. 2.21	<i>Pasteurella</i> sp. 0.29

POND III

<i>Pseudomonas</i> sp. 15.88	<i>Micrococcus</i> sp. 7.65	<i>Shigella</i> sp. 2.21
<i>Escherichia</i> sp. 11.62	<i>Bacillus</i> sp. 6.47	<i>Corynebacterium</i> sp. 1.76
<i>Streptococcus</i> sp. 11.62	<i>Clostridium</i> sp. 4.12	<i>Campylobacter</i> sp. 1.08
<i>Klebsiella</i> sp. 10.59	<i>Citrobacter</i> sp. 2.97	<i>Edwardsiella</i> sp. 1.03
<i>Proteus</i> sp. 9.12	<i>Enterobacter</i> sp. 2.65	<i>Staphylococcus</i> sp. 0.88
<i>Salmonella</i> sp. 8.09	<i>Serratia</i> sp. 2.50	

POND IV

<i>Pseudomonas</i> sp. 14.71	<i>Micrococcus</i> sp. 4.71	<i>Pasteurella</i> sp. 0.59
<i>Klebsiella</i> sp. 12.06	<i>Citrobacter</i> sp. 3.68	<i>Serratia</i> sp. 0.69
<i>Streptococcus</i> sp. 11.91	<i>Enterobacter</i> sp. 3.24	<i>Yersinia</i> sp. 0.44
<i>Escherichia</i> sp. 11.03	<i>Campylobacter</i> sp. 1.91	<i>Hafnia</i> sp. 0.29
<i>Salmonella</i> sp. 9.56	<i>Corynebacterium</i> sp. 1.76	<i>Shigella</i> sp. 0.29
<i>Proteus</i> sp. 9.26	<i>Bacteroides</i> sp. 1.33	<i>Actinobacillus</i> sp. 0.18
<i>Clostridium</i> sp. 5.85	<i>Edwardsiella</i> sp. 1.03	<i>Aeromonas</i> sp. 0.15
<i>Bacillus</i> sp. 5.50	<i>Staphylococcus</i> sp. 0.88	

3 Analysis of the diversities of the bacterial flora

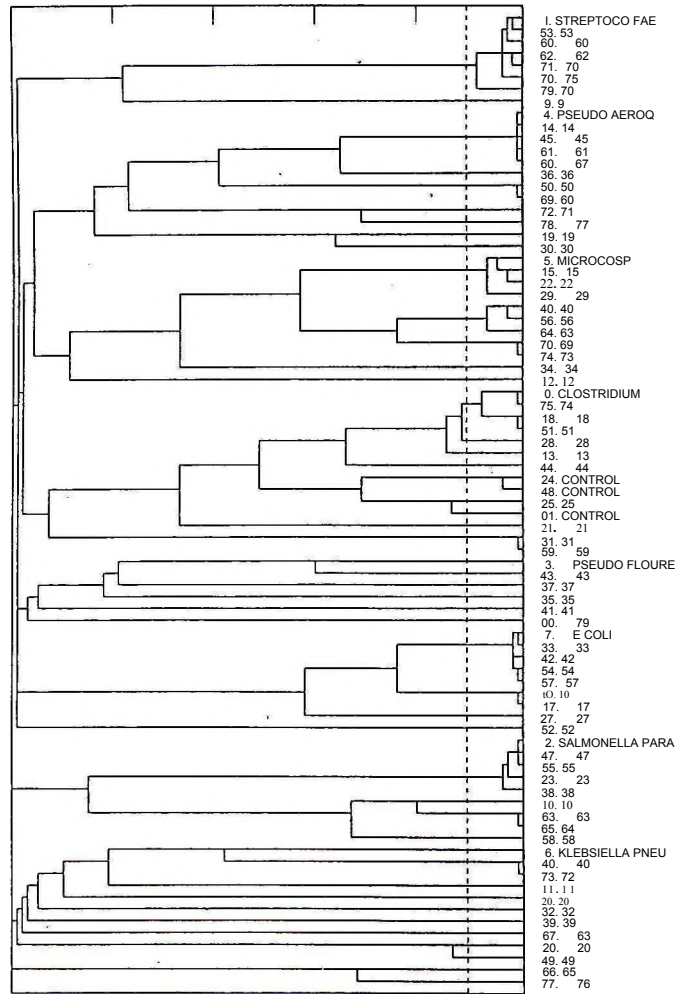
The diversities of the bacterial flora were generally high for each of the four sewage-fertilized ponds (Table 12) indicating that their populations consisted of many different types. The PhP types for pond I ranged from 38 to 54. The PhP types for pond II ranged from 48 to 62, and those for pond III ranged from 23 to 36. The PhP types for the pond IV ranged from 62 to 68 (Appendix 8a - 8t).

Table 12 Diversities among the bacterial flora of sewage fertilised ponds

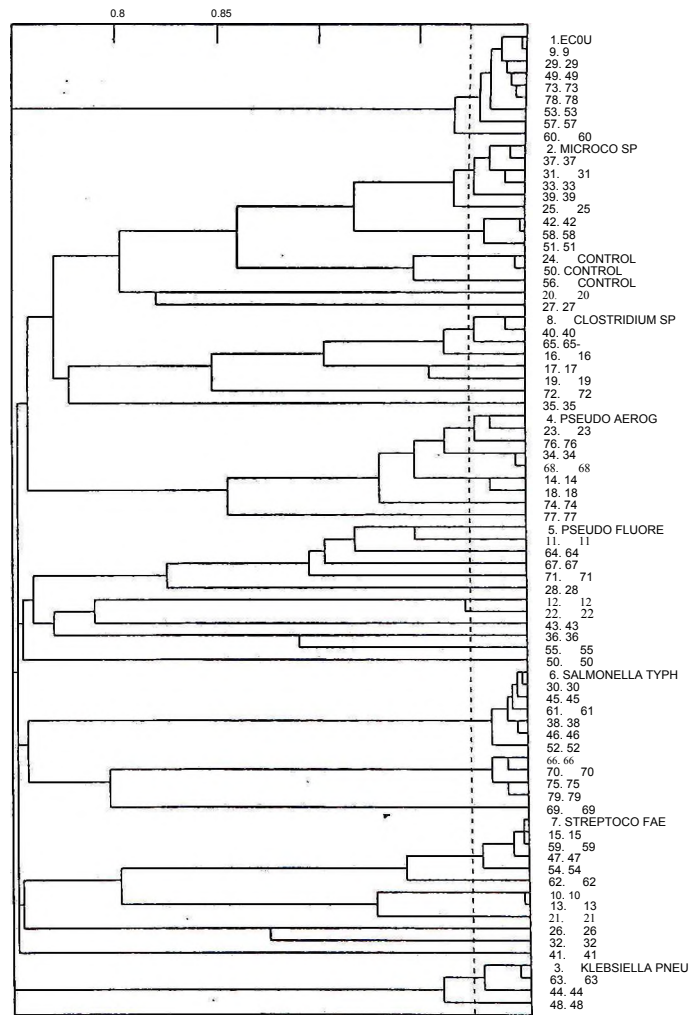
<u>Sample name and no.</u>	<u>No. of isolates</u>	<u>Pi values</u>
Akuse I 1	81	0.976
2	80	0.972
3	80	0.973
4	80	0.950
5	82	0.977
Akuse II 1	81	0.976
2	184	0.976
3	80	0.953
4	80	0.978
5	80	0.991
Akuse III 1	80	0.955
2	80	0.926
3	80	0.945
4	80	0.959
5	80	0.937
Akuse IV 1	80	0.989
2	80	0.995
3	102	0.989
4	78	0.995
5	80	0.994
Mean Diversity		0.971

The clustering of the bacterial isolates for the four ponds for five sampling periods are presented in Figs 10a-10t. The dendrograms had high co-phenetic correlation (above 0.80), indicating that the dendrograms corresponded to the similarity matrix

Fig. 1 OFIDemrogram showing UPGMA clustering of the bacterial isolates for February, 1907 for Akuse pond 1 (akuseit). ID level: 0.975 Co-phenetic correlation: 0.882 No. of samples: 81 No. of tests: 12



ngL.Ou Dendrogram showing UPGMA clustering of the bacterial isolates for August, 1997 from Akuso pond I (akusel2). ID level: 0.975 Co-phenetic correlation: 0.956 No. of samples; 80 No. of tests: 12



■ sa vu S-Gi.tu.yyiam oipwiiiy uruiw or ma Daclorial isolates for February, 1DD8
 from Akuse pond 1 (akusef3). ID level: 0.875 Co-phenetic correlation: 0.917
 No. of samples: 80 No. of tests: 12

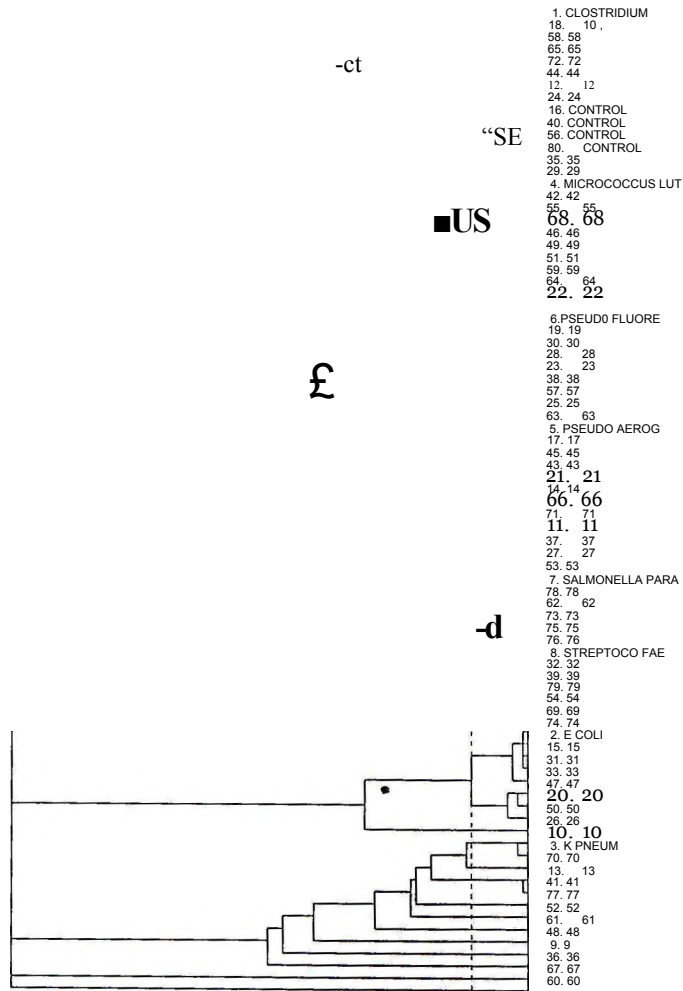


Fig. 0 d Dendrogram showing UPGMA of the bacterial isolates for August, 1998 from Akuse pond 1 (akuse14). IO level: 0.975 Co-phenetic correlation: 0.916 No. of samples: 80 No. of tests: 12

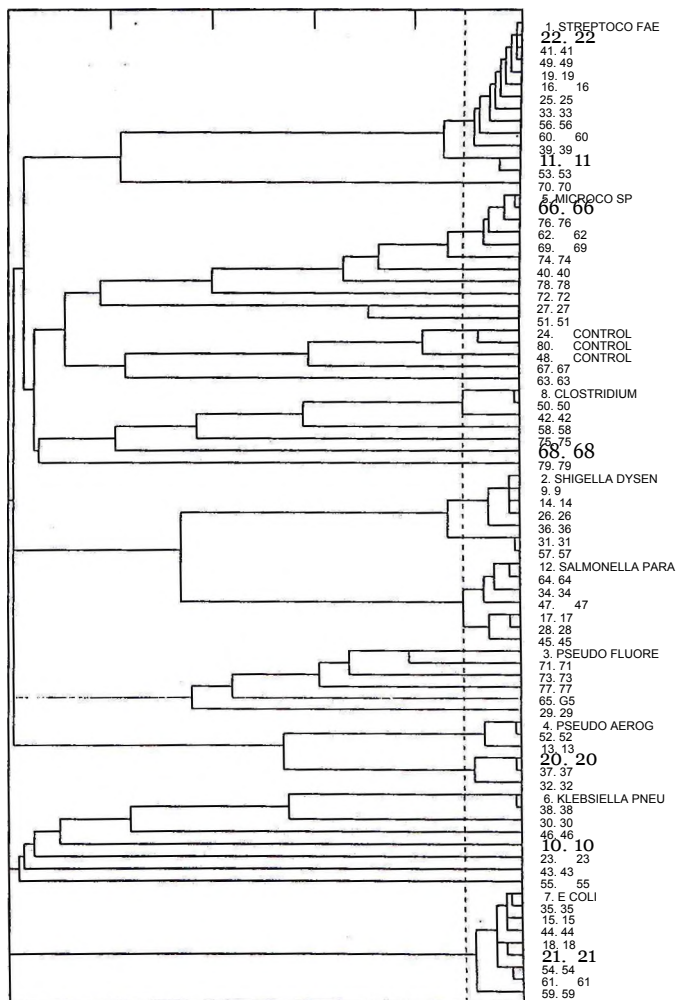
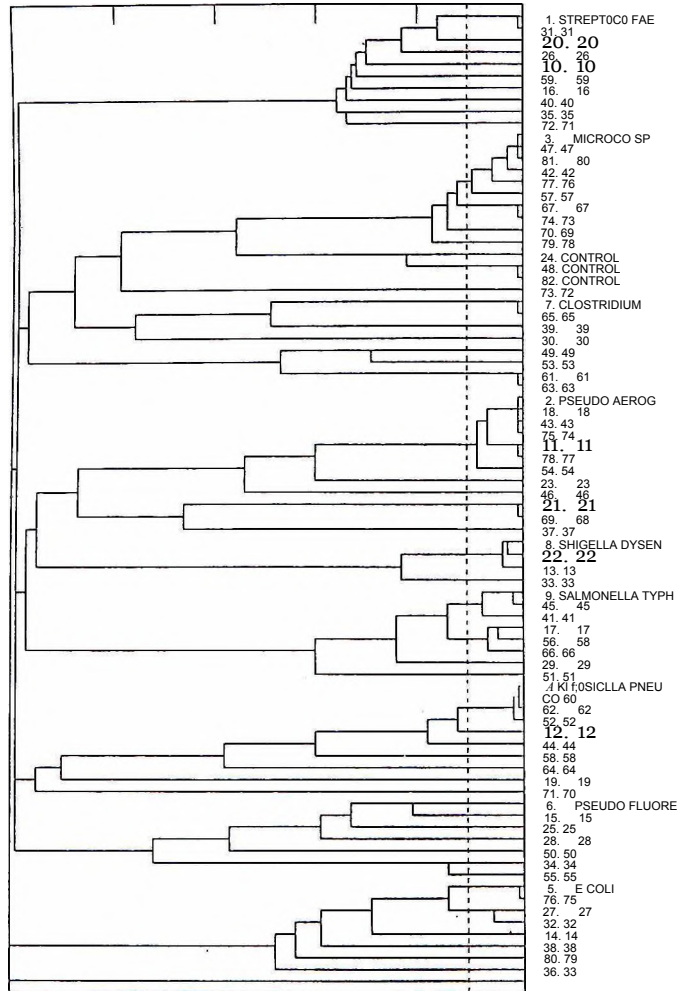
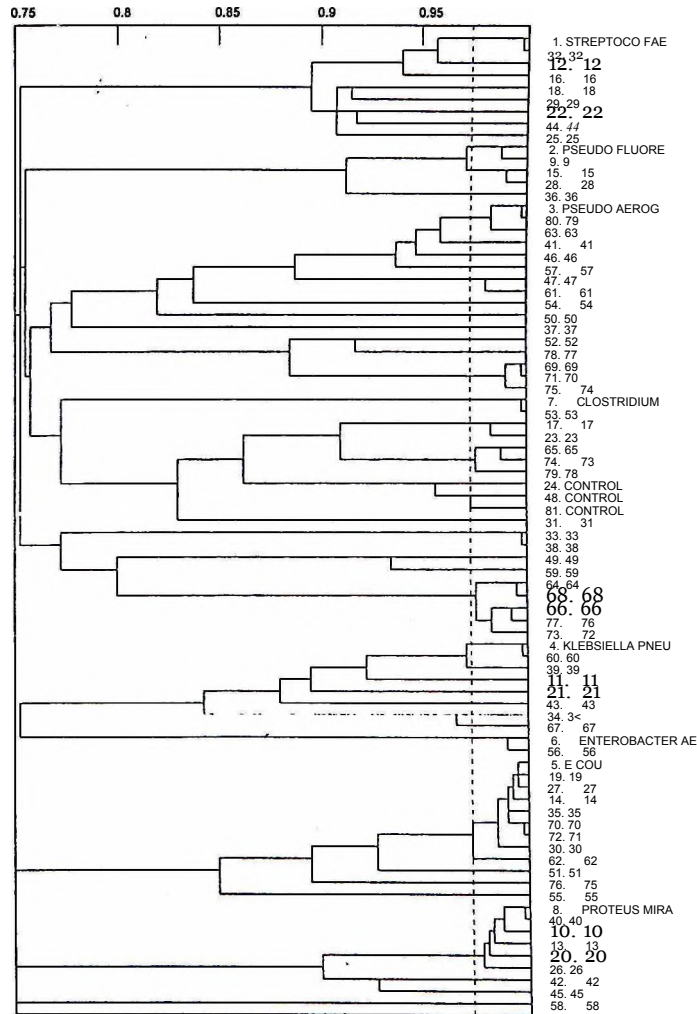


Fig. 1. OePantS^{am} showing UPGMA clustering of the bacterial isolates for February, 1099 from Akuse pond I (akuseI.S). ID level: 0.975 Co-phenetic correlation: 0.925 No. of samples: 82 No. of tests: 12



FJOLof Dendrogram showing UPGMA clustering of the bacterial Isolates for February, 1097 from Akuas pond II (akuselM). ID level: 0.075 Co-phenolic correlation; 0.003 No. of samples: 01 No. of tests: 12



F. Off. Oendrogram showing UPGMA clustering of the bacterial Isolates for August, 1997 from ARuse pond II (akusel2) Method: U ID level: 0.975 Co-phenetic correlation: 0.944 No. of samples: 184 No. of tests: 12

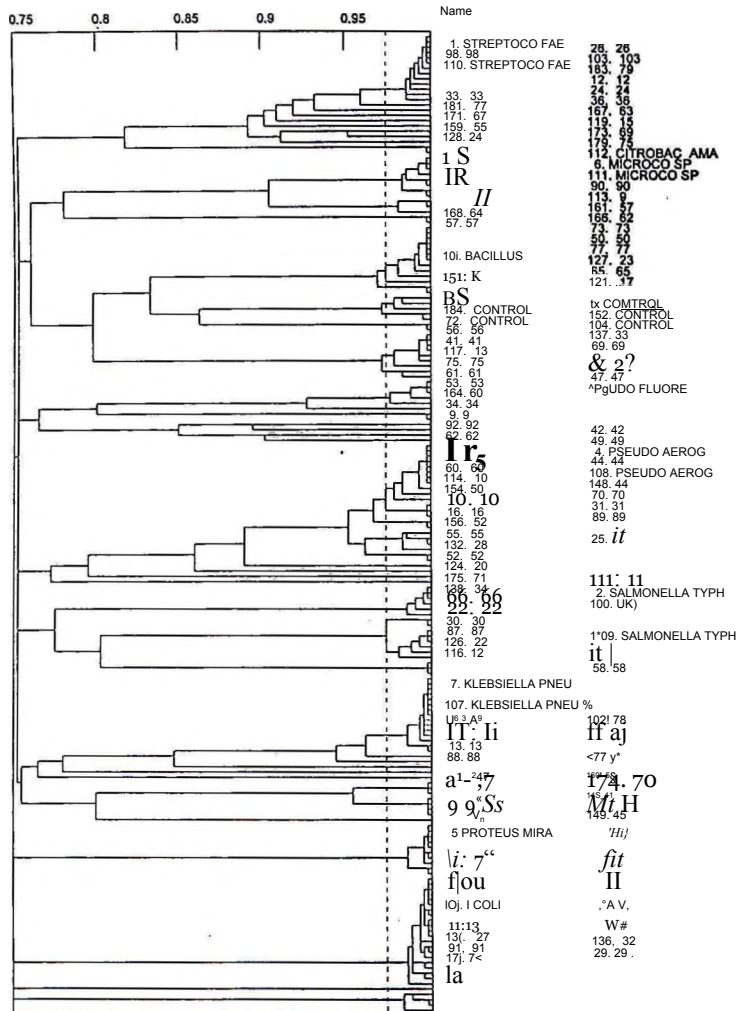
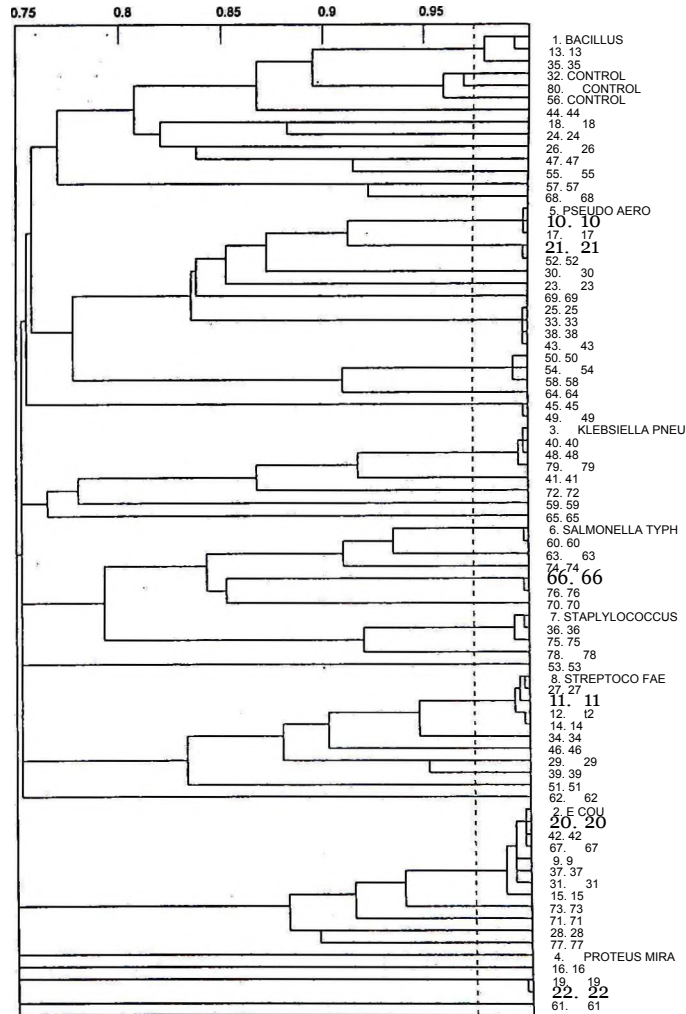
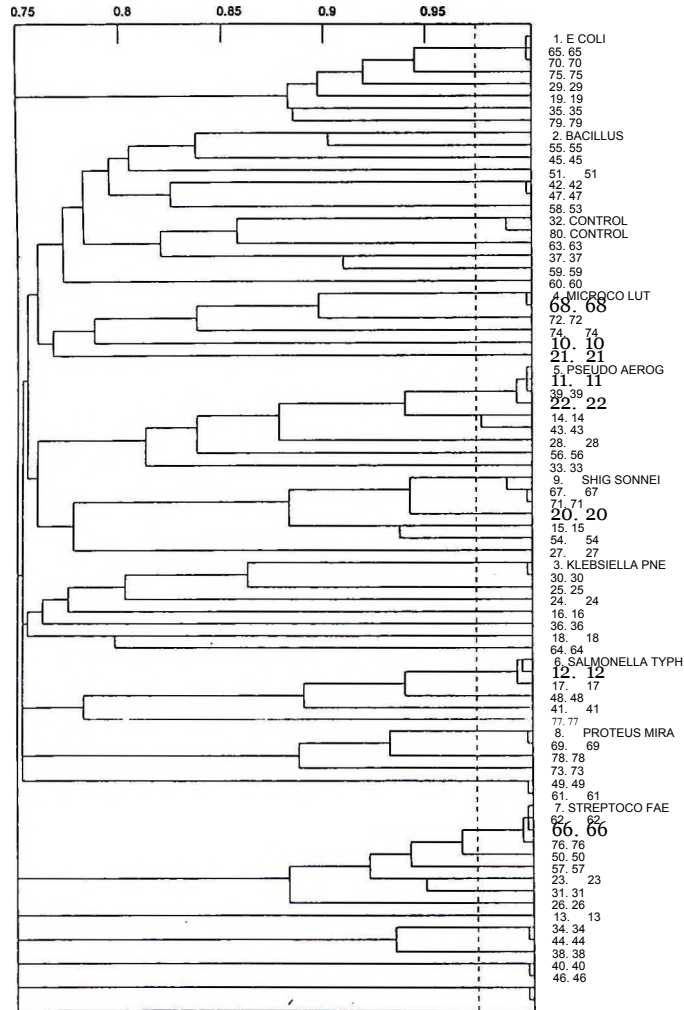


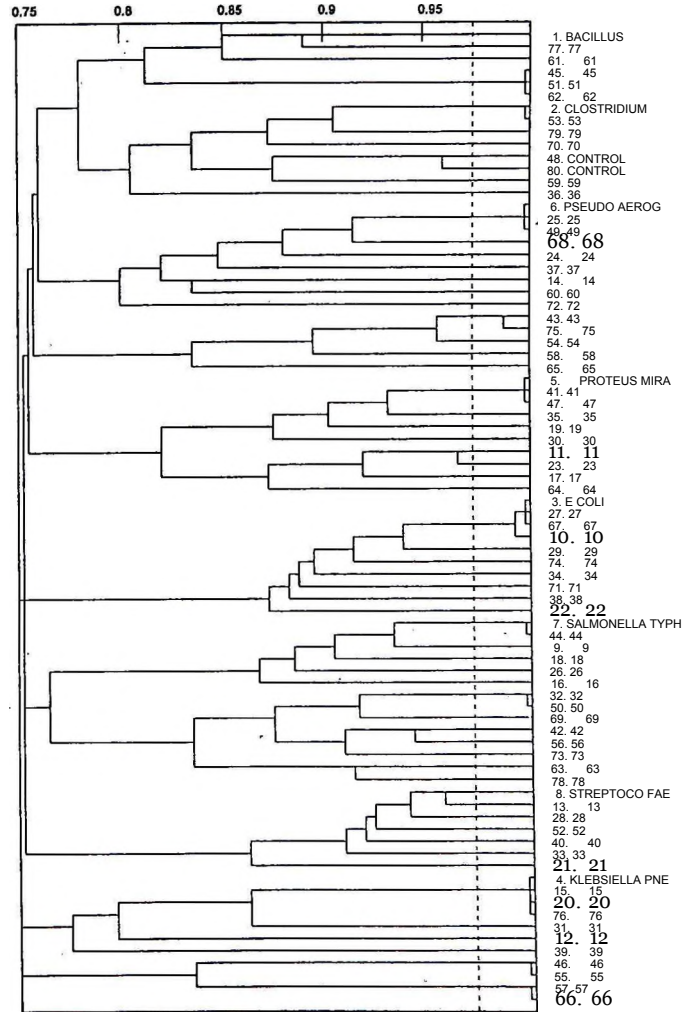
Fig. 1 OtiDendrogram showing UPGMA clustering of the bacterial Isoates for February, 1998 from Akue pond II (akusel3). ID level: 0.975 Co-phenetic correlation; 0.B90 No. of samples: 80 No. of tests; 12



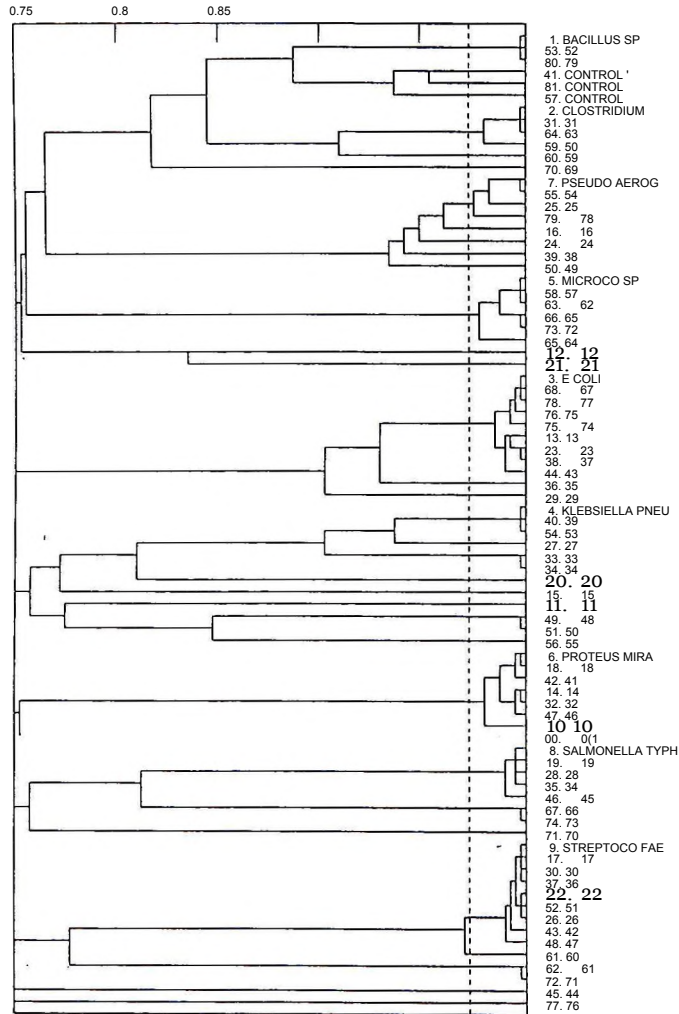
tram AKuse pond II (akuselM). ID level: 0.975 Co-phenetic correlation: 0.091
 No. of samples: 80 No. of tests: 12



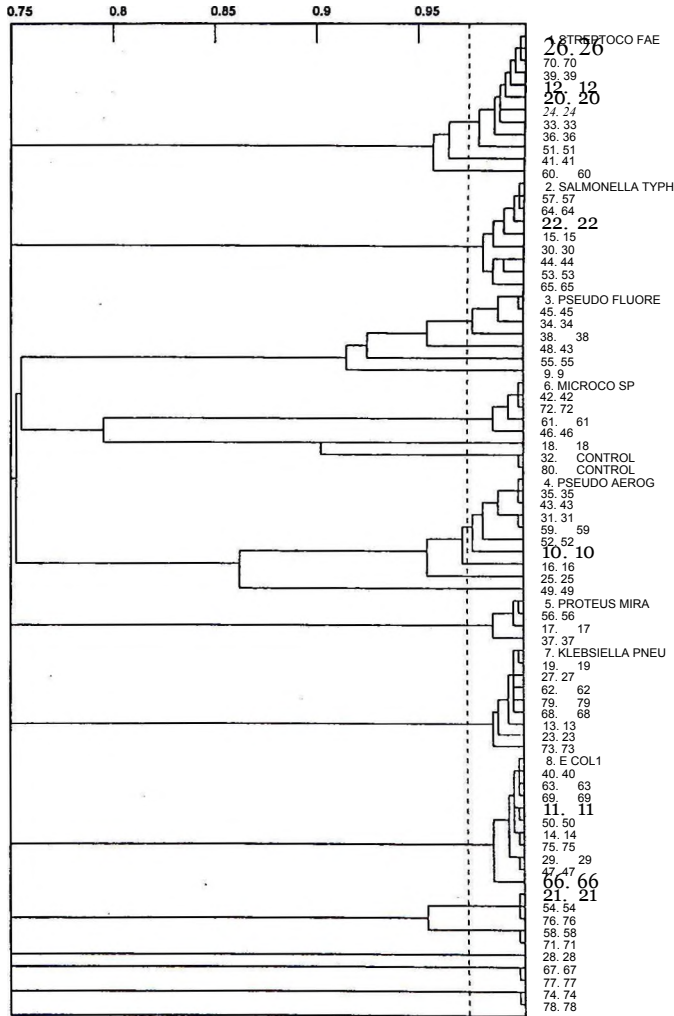
clustering of the bacterial isolates for February, 1999
 from Akuse pond II (akii>el5). ID level: 0.975 Co-phenetic correlation: 0.825
 No. of samples: 80 No. of tests: 12



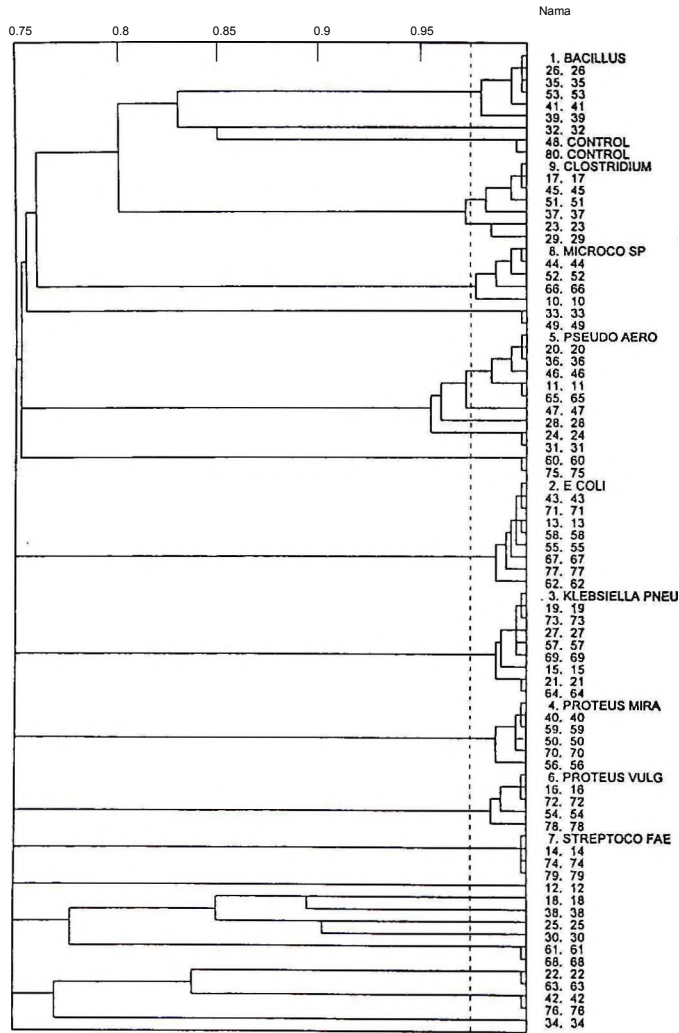
to, of samples: a i l t e s t s : 1 2



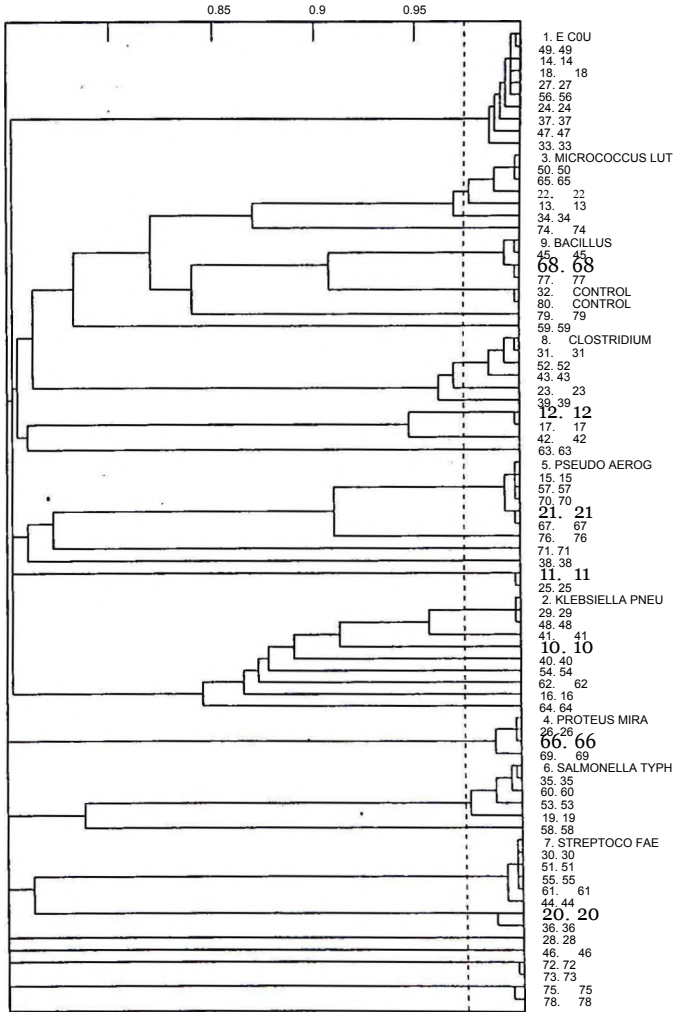
from AkuBB pond !!! (akuvo112). ID level: 0.975 Co-phonetic corrolallan: 0.9 82
No. of aampias: 80 No. of tests: 12



Uji t-tesis untuk uji homogenitas uji clustering or me oactional isolates Tor February, 1988
 from Akuse pond III (akusel 13). ID level: 0.975 Co-phenetic correlation: 0.972
 No. of samples: 80 No. of tests: 12



Fl&On Dendrogram showing UPGMA clustering of the bacterial isolates for August, 193B from Akuse pond III (akuse114). ID level: 0.075 Co-phenetic correlation: 0.959 No. of samples: 80 No. of tests: 12



rtm no uoluluyiulli anuwmy uruinn uaaleimyo o me oacienai isolates >or i-oDruoory, luyy
from Akuse pond III (akuse 115), ID level: 0.975 Co-phonetic correlation: 0.9GB
No. of samples: 80 No. of tests: 12

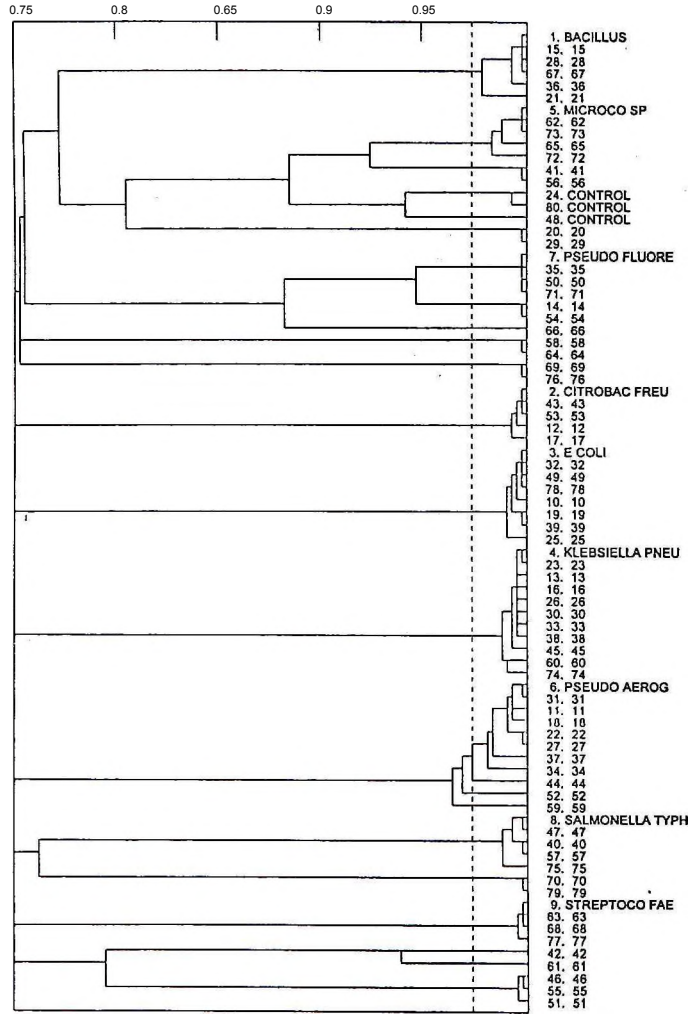


Fig1 Orp Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1897 from Akuse pond IV (akuselvi). ID level: 0.975 CorphehUc correlation: 0.879
 No. of samples: 80 No. of tests: 12

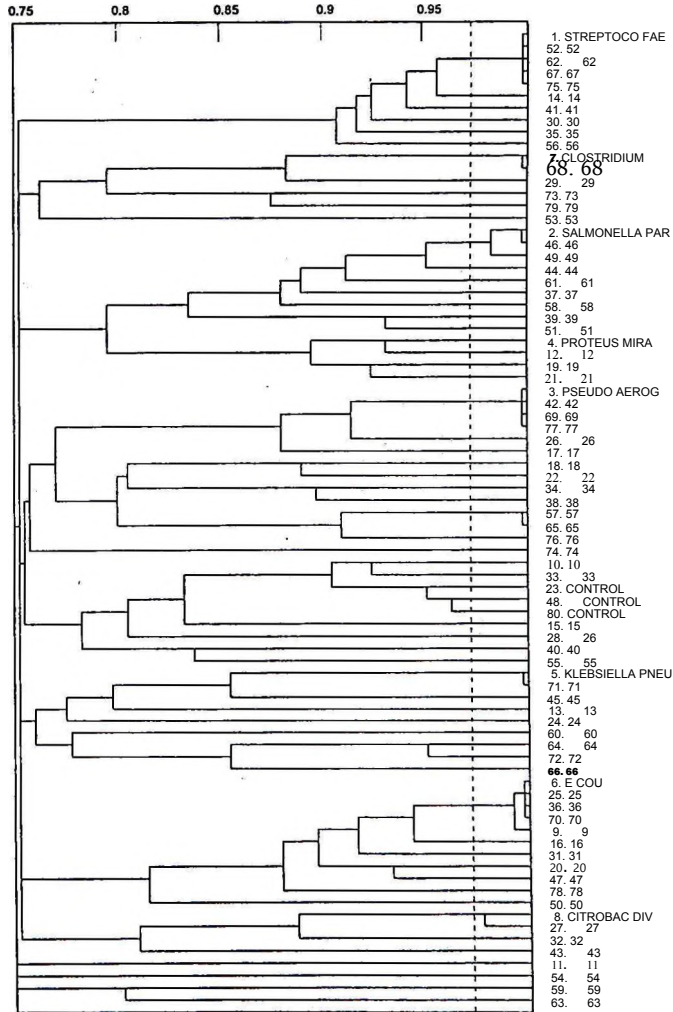


Fig. 1 QDondrogram showing UPGMA clustering of the bacterial isolotaa for August, 1997 from Akuse pond IV (akuseiv2). ID level: 0.975 Co-phenetic correlation: 0.831 No. of samples: 80 No. of tests: 12

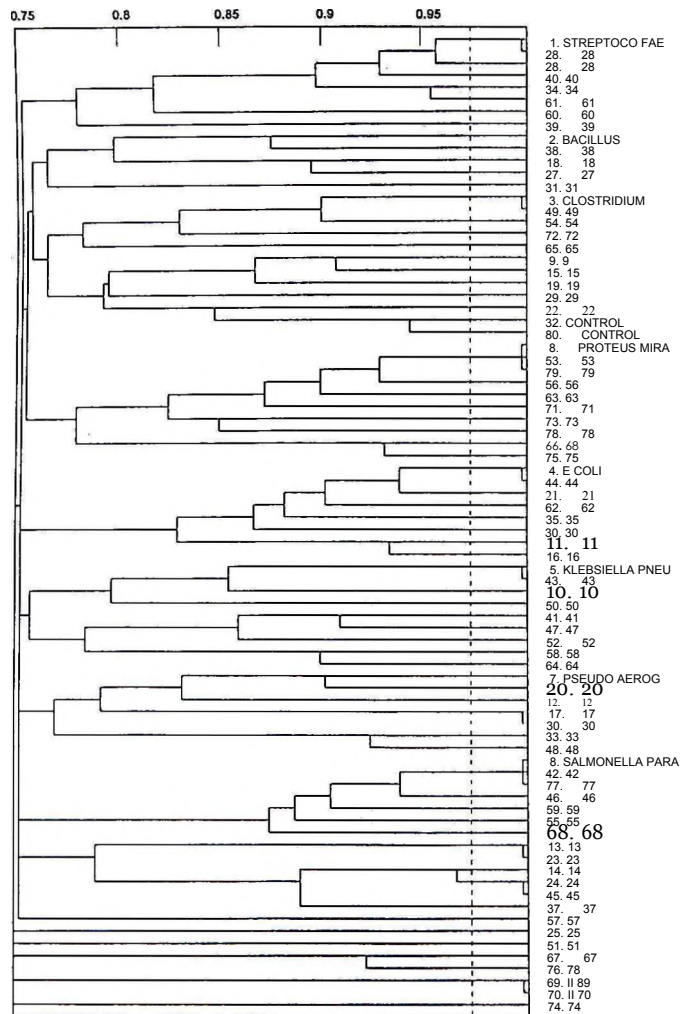


Fig.1Qr Dendrogram UPGMA clustering of the bacterial Isolates for February, 1998 from Akuse pond IV (akuseiv3). ID level: 0.975 Co-phenetic correlation: 0.907 No. of samples: 102 No. of tests: 12

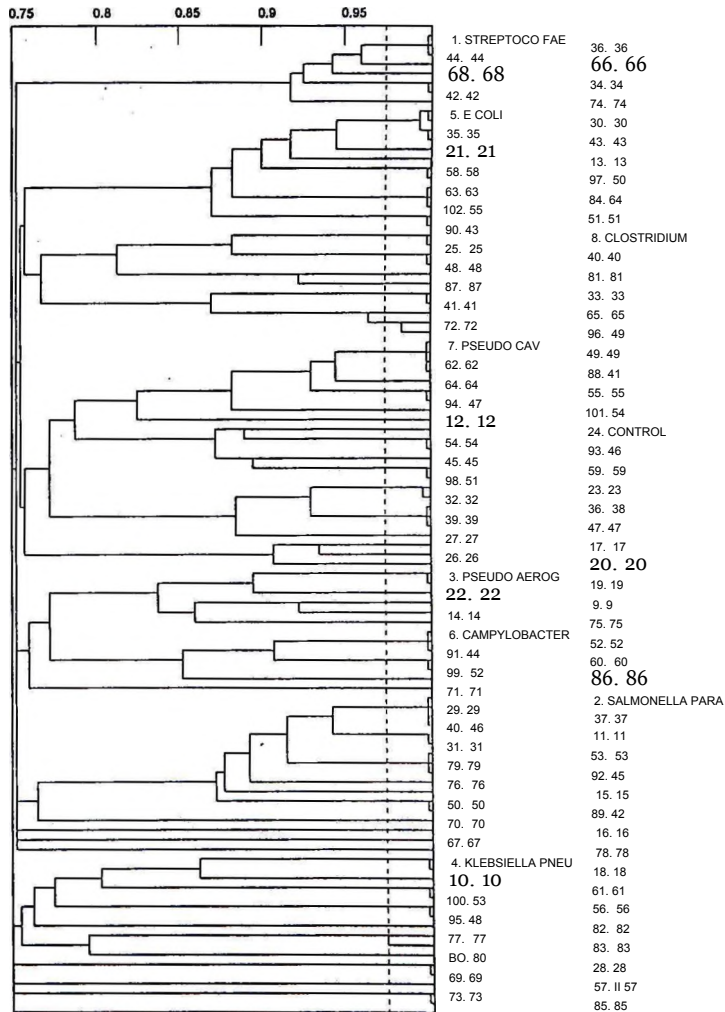


Fig-1 0 S'endrogram showing UPGMA clustering of the bacterial isolates for August, 1998 from Akuse pond IV (akuseiv4). ID level: 0.975 Co-phonetic correlation: 0.883 No. of samples: 78 No. of tests: 12

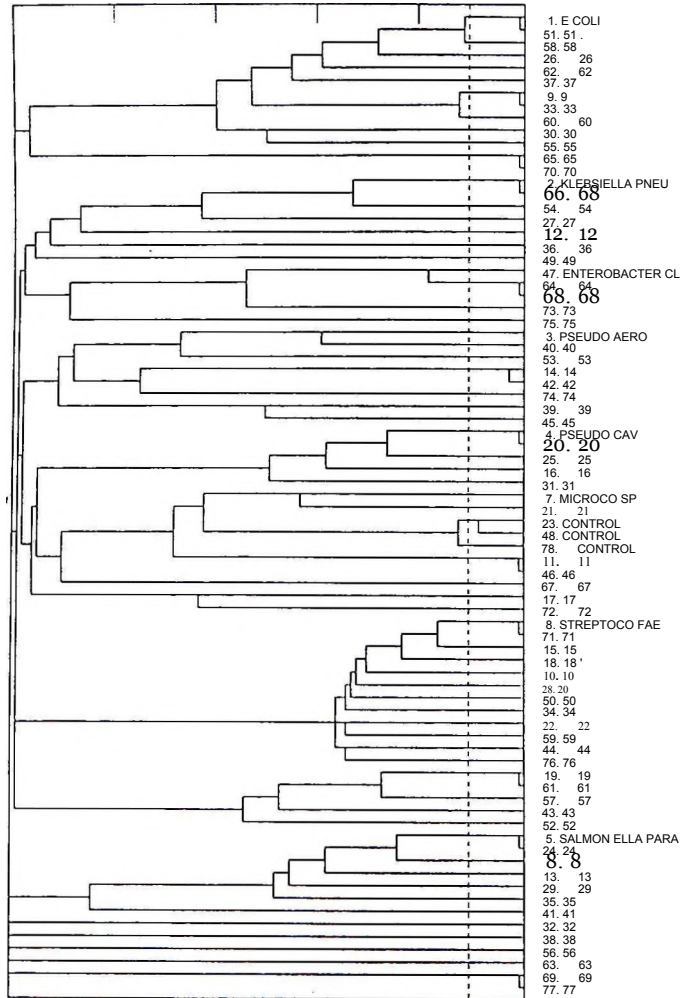
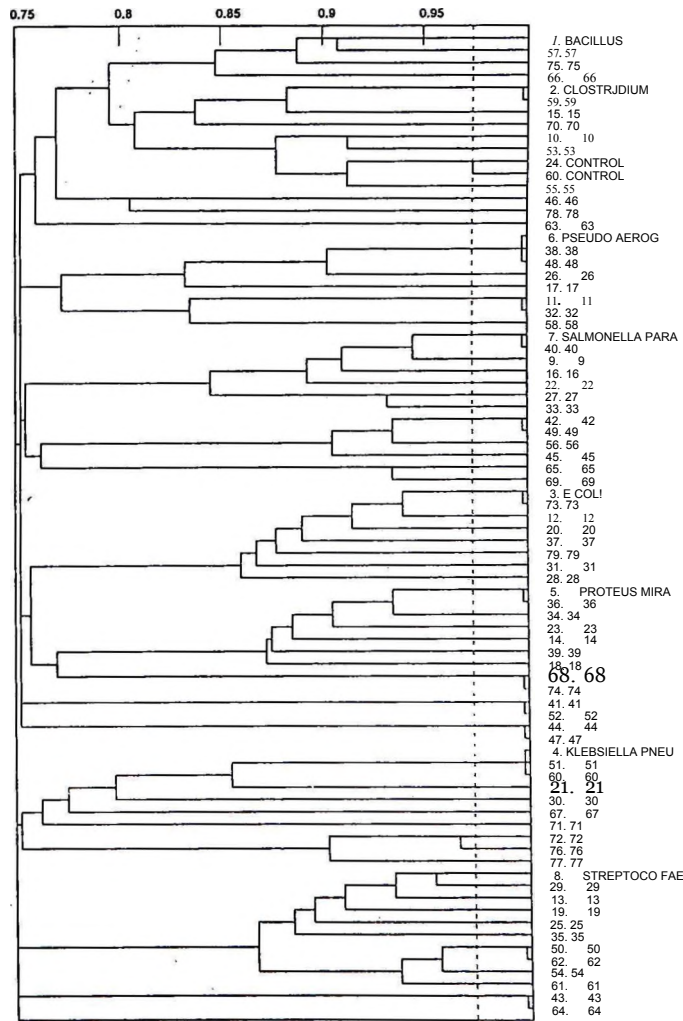


Fig. 10 Dendrogram showing UPGMA clustering of the bacterial isolates for February, 1999 from Axusa pond IV (akuselVS). ID level: 0.975 Co-phenetic correlation: 0.839
 No. of samples: 80 No. of tests: 12



from which they were created.

4. Similarities between the bacterial populations for the different ponds

The mean similarity was calculated as mean population similarity (Sp) coefficient and the results are presented in Table 13. Comparisons between the different ponds showed Sp values all below 0.50, indicating related populations in the different ponds all of which have high diversities of bacteria. Ponds I and III however showed some periods of unrelated populations (Sp values above 0.50)

Table 13. Population similarities between the Akuse Ponds.

<u>Population of</u>	<u>Compared to</u>	<u>Spvalue</u>
Pond I	Pond II	0.43
Pond I	Pond III	0.36
Pond I	Pond IV	0.20
Pond II	Pond III	0.53
Pond II	Pond IV	0.22
<u>Pond III</u>	<u>Pond IV</u>	<u>0.16</u>

5. Bacterial flora of fish cultured in sewage water

The data in Table 14 showed the identity of bacterial species isolated from tissues of the fish of the Akuse ponds. Fish from Pond I showed the presence of 18 genera in the muscles, 14 genera in the blood, 21 genera in the gill, 13 genera in the gut and 22 genera in the skin. The respective figures for fish from Pond II are 24, 22, 22, 22 and 24; 18, 19, 24, 22 and 25 for fish of Pond III, and 23, 20, 25, 25 and 21 for fish of Pond IV. The dominant species in the respective tissues could be easily identified for fish from each pond. The dominant flora were:

POND I

Muscle	<i>Clostridium</i> sp., <i>Corynebacterium</i> sp., <i>Pasteurella</i> sp. and <i>Salmonella</i> sp.
Blood	<i>Clostridium</i> sp., <i>Micrococcus</i> sp. and <i>Pseudomonas</i> sp.
Gills -	<i>Escherichia</i> sp., <i>Micrococcus</i> sp., <i>Pasteurella</i> sp., <i>Salmonella</i> sp. and <i>Serratia</i> sp.
Gut	<i>Clostridium</i> sp., <i>Escherichia</i> sp., <i>Micrococcus</i> sp. and <i>Pseudomonas</i> sp.
Skin	<i>Micrococcus</i> sp., <i>Pseudomonas</i> sp. and <i>Salmonella</i> sp.

TABLE 14

Mean total number of bacterial isolates occurring in tissues of fish from sewage-fertilized ponds

Bacterial species	Akuse pond I					Akuse pond II					Akuse pond III					Akuse pond IV				
	muscle	blood	gill	gut	skin	muscle	blood	gill	gut	skin	muscle	blood	gill	gut	skin	muscle	blood	gill	gut	skin
<i>Actinobacillus sp.</i>	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	2.3	0.7	1.7	0.0	0.0	2.7	0.3	2.0
<i>Aeromonas sp.</i>	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	1.7	0.0	0.0	7.0	1.0	7.0	1.3	9.7	7.0	2.0	11.3
<i>Bacillus sp.</i>	2.3	4.3	6.3	3.0	6.0	0.7	3.7	0.3	4.3	1.3	0.0	2.3	7.0	13.0	6.3	8.0	1.3	18.0	9.0	17.0
<i>Bacteroides sp.</i>	5.3	2.0	12.3	0.0	16.3	5.0	6.3	10.3	2.3	5.7	2.7	2.0	9.3	2.0	7.0	3.0	6.0	11.3	3.0	10.0
<i>Campylobacter sp.</i>	2.7	1.3	2.0	0.0	4.0	2.7	2.7	7.3	4.3	4.0	2.3	3.0	3.0	4.3	5.0	4.0	2.7	4.7	5.3	6.7
<i>Citrobacter sp.</i>	0.3	5.3	3.0	0.0	2.7	9.7	10.7	8.7	4.0	11.7	5.7	3.7	12.0	3.3	7.3	9.7	3.0	11.3	1.7	9.7
<i>Clostridium sp.</i>	12.7	15.7	9.7	30.7	11.7	9.3	8.3	14.3	30.3	6.7	4.7	2.0	12.0	17.7	12.7	5.7	0.3	13.3	16.0	14.0
<i>Corynebacterium sp.</i>	13.9	0.0	13.3	1.3	13.0	10.7	7.7	15.0	8.3	10.0	3.7	3.3	8.0	7.0	7.3	3.3	9.0	6.7	13.0	10.0
<i>Edwardsiella sp.</i>	1.3	0.0	1.7	0.0	3.0	6.0	1.3	14.0	4.7	12.0	6.3	3.3	6.7	2.3	6.0	8.0	1.3	7.0	0.7	6.7
<i>Enterobacter sp.</i>	0.0	0.0	3.7	1.0	5.0	1.3	2.7	4.7	8.3	9.3	4.0	0.0	8.3	1.3	10.0	2.0	0.0	4.7	8.0	3.7
<i>Escherichia sp.</i>	6.7	13.3	18.0	27.3	15.7	4.3	2.3	4.7	24.2	11.3	0.0	8.0	11.0	29.3	11.3	0.7	2.7	7.7	22.0	9.3
<i>Flavobacterium sp.</i>	6.3	0.0	14.7	0.0	14.7	3.3	5.3	13.7	5.0	15.7	4.7	1.0	13.3	1.3	12.7	3.3	9.0	11.3	8.3	11.3
<i>Hafnia sp.</i>	0.0	0.0	0.0	0.0	0.0	7.0	2.7	4.7	1.0	7.7	0.0	0.0	2.7	0.0	3.7	7.0	0.0	5.3	0.0	4.3
<i>Klebsiella sp.</i>	5.3	7.3	6.7	22.0	5.7	2.3	4.7	6.0	12.0	5.7	0.0	3.7	4.0	16.7	6.0	1.3	0.0	3.0	10.0	2.7
<i>Micrococcus sp.</i>	9.0	18.3	16.7	41.3	19.3	6.3	14.3	7.7	25.0	6.3	6.0	8.0	15.7	32.7	18.7	2.3	12.3	8.7	30.7	10.0
<i>Pasteurella sp.</i>	15.0	0.0	16.7	2.0	17.0	12.3	2.7	18.0	1.7	17.0	8.7	1.0	13.0	0.0	14.0	9.0	0.3	13.0	0.0	10.7
<i>Proteus sp.</i>	0.0	0.3	5.3	0.0	3.3	6.7	4.7	9.0	9.0	7.3	0.7	4.7	3.7	6.3	8.3	5.3	7.7	5.3	10.0	5.7
<i>Pseudomonas sp.</i>	6.7	23.0	15.7	36.7	20.0	6.3	9.7	12.3	33.0	15.7	5.0	8.7	13.7	31.7	13.3	6.0	15.0	12.3	25.0	14.3
<i>Salmonella sp.</i>	16.7	14.3	21.0	25.7	22.3	13.3	4.3	19.7	10.0	31.3	10.3	4.0	24.0	12.7	25.3	13.3	5.0	23.3	15.3	21.3
<i>Serratia sp.</i>	11.3	0.0	18.3	0.0	14.0	1.7	8.0	9.3	9.0	9.0	3.0	0.7	7.3	7.7	3.7	0.3	2.3	7.0	3.0	8.3
<i>Shigella sp.</i>	0.0	0.7	0.0	0.0	2.0	7.3	1.7	8.7	1.7	8.3	2.7	2.7	5.3	3.3	5.7	5.7	1.3	4.7	2.0	4.3
<i>Staphylococcus sp.</i>	1.3	1.0	5.3	2.7	3.7	2.7	30.0	5.7	7.0	6.7	3.3	1.4	6.0	0.7	5.7	1.3	5.7	5.3	10.7	5.7
<i>Streptococcus sp.</i>	3.3	12.7	14.0	32.0	10.0	2.3	13.0	14.3	29.3	10.7	2.3	6.0	13.3	31.0	10.0	5.3	4.3	12.3	30.7	10.3
<i>Vibrio sp.</i>	11.0	0.0	15.3	0.0	14.0	9.0	0.0	17.0	0.0	18.3	9.3	0.0	17.0	0.0	17.0	2.7	0.0	13.7	0.0	12.7
<i>Yersinia sp.</i>	0.0	0.0	1.7	1.0	1.7	0.0	1.7	0.0	1.0	1.0	0.0	0.0	0.0	0.7	1.0	0.0	0.3	3.3	0.0	2.3

POND II

Muscle	<i>Corynebacterium</i> sp., <i>Pasteurella</i> sp. and <i>Salmonella</i> sp.
Blood	<i>Staphylococcus</i> sp.
Gills	<i>Clostridium</i> sp., <i>Corynebacterium</i> sp., <i>Edwardsiella</i> sp., <i>Pasteurella</i> sp, <i>Salmonella</i> sp. and <i>Streptococcus</i> sp.
Gut	<i>Clostridium</i> sp., <i>Escherichia</i> sp., <i>Micrococcus</i> sp., <i>Pseudomonas</i> sp and <i>Streptococcus</i> sp.
Skin -	<i>Flavobacterium</i> sp., <i>Pseudomonas</i> sp., <i>Salmonella</i> sp. and <i>Vibrio</i> sp.

POND III

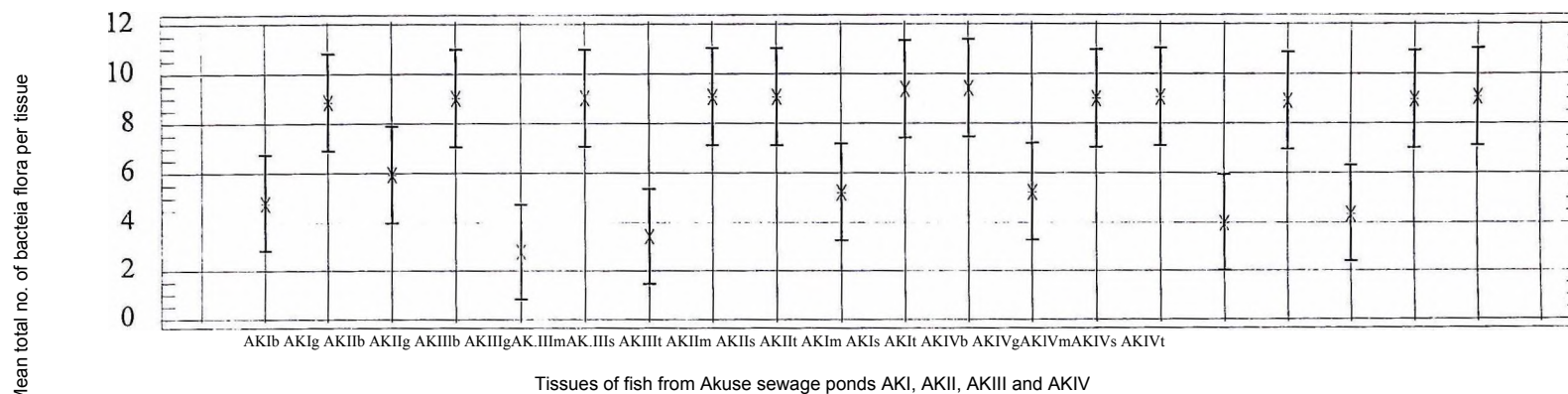
Muscle	<i>Pasteurella</i> sp. and <i>Salmonella</i> sp.
Blood	<i>Escherichia</i> sp., <i>Micrococcus</i> sp. and <i>Pseudomonas</i> sp.
Gills	<i>Flavobacterium</i> sp., <i>Micrococcus</i> sp. and <i>Pseudomonas</i> sp.
Gut	<i>Escherichia</i> sp., <i>Micrococcus</i> sp., <i>Pseudomonas</i> sp. and <i>Streptococcus</i> sp.
Skin	<i>Micrococcus</i> sp. and <i>Salmonella</i> sp.

POND IV

Muscle	<i>Citrobacter</i> sp. and <i>Salmonella</i> sp.
Blood	<i>Aeromonas</i> sp. and <i>Micrococcus</i> sp.
Gills	<i>Bacillus</i> sp. and <i>Salmonella</i> sp.
Gut	<i>Escherichia</i> sp., <i>Micrococcus</i> sp., <i>Pseudomonas</i> sp. and <i>Streptococcus</i> sp.
Skin	<i>Bacillus</i> sp. and <i>Salmonella</i> sp.

Analysis of variance determination showed significant difference at 95.0% confidence level. Duncan's multiple comparison determination showed homogeneity between the means of the blood and muscles, and between the gill, gut and skin. Fig. 11 shows correlation between the means of the bacteria flora as found in the various tissues.

Fig. 11 Mean values and L.S.D (95%) intervals between the bacteria flora offish tissues from Akuse sewage-fertilized ponds



AKIb = Blood of fish from Akuse Pond I
 AKIlg = gills of fish from Akuse Pond I
 AKIIm = muscle of fish from Akuse Pond I
 AKIs = skin of fish from Akuse Pond I
 AKIt = gut of fish from Akuse Pond I

AKIIb = blood of fish from Akuse Pond II
 AKIIlg = gills of fish from Akuse Pond II
 AKIIIm = muscle of fish from Akuse Pond II
 AKIIIs = skin of fish from Akuse Pond II
 AKIIIt = gut of fish from Akuse Pond II

AKIIIb = Blood of fish from Akuse Pond III
 AKIIIlg = gills of fish from Akuse Pond III
 AKIIIIm = muscle of fish from Akuse Pond III
 AKIIIIs = skin of fish from Akuse Pond III
 AKIIIIt = gut of fish from Akuse Pond III

AKIVb = blood of fish from Akuse Pond IV
 AKIVlg = gills of fish from Akuse Pond IV
 AKIVIm = muscle of fish from Akuse Pond IV
 AKIVIs = skin of fish from Akuse Pond IV
 AKIVt = gut of fish from Akuse Pond IV

I. Health Status of the Fish Farmers and Some Consumers of Fish

The results of the population of bacteria isolated from the stool of the fishermen are presented in Table 15. In all a total of twenty different bacterial species were isolated from the fishermen. Out of the twenty pathogens identified, fishermen working in, and consuming fish from cow manure-fertilized ponds (e.g. Aduabenba farm) carried 15 different pathogens. Those associated with poultry manure-fertilized ponds (e.g. Frimpong Farm) and pig manure-fertilized ponds (eg. Boadi farm) carried 13 and 15 different pathogens, respectively. Fishermen working in, and consuming fish from, Blood waste-fertilized ponds (e.g. Boahen farm) and sewage-fertilized ponds (Akuse farm), chemically fertilized ponds (eg. Sagoe farm) and unfertilized pond (e.g. ARDEC 3) carried 12, 14, 10 and 9 pathogens, respectively. Tests on fishermen working in, and consuming fish from, the open system (e.g. Weija dam) yielded 17 different pathogens. *Escherichia coli* was consistently the predominant species in all the eight locations.

The occurrence of pathogenic bacteria isolated from the fishermen and their families who work in, and consume fish from, the various fertilization type ponds is presented as histograms in Fig. 12. Bacterial species common in individuals sampled varied from one community to the other. For example, community of the cow-manure-fertilized ponds recorded the highest number of individuals harbouring *Citrobacter diversus*, *Klebsiella oxytoca*, *Enterobacter cloacae* and *Pseudomonas* sp. That of poultry manure-fertilized ponds recorded the highest number of individuals associated with *Klebsiella rhinoscleromatis*, *Salmonella* sp. and *Staphylococcus* sp. Strains, which were isolated from the largest number of individuals from pig manure-fertilized ponds farm were *Alcaescens dispar* and *Klebsiella ozanae*. The commonest species occurring in the community of the blood waste-fertilized pond and chemically fertilized pond was *Micrococcus* sp. and *Alcaescens dispar* respectively. The community of the non-fertilized pond recorded the highest number of individuals with *Klebsiella oxytoca* and *Streptococcus faecalis*.

TABLE 15

Bacterial species isolated from stool of fishermen associated with different fish culture sites.

Species	Number of isolates from Open water	Number of isolates from unfertilized pond	Number of isolates from cultured ponds fertilized with					
			Blood waste	Chemical	Cow manure	Pig manure	Poultry manure	Sewage
<i>Alcalescens dispar</i>	1	0	0	0	2	4	1	0
<i>Citrobacter amaloniticus</i>	8	7	4	5	4	6	5	7
<i>Citrobacter diversus</i>	2	0	2	2	4	3	1	0
<i>Citrobacter freundii</i>	2	0	1	0	2	0	0	1
<i>Klebsiella oxytoca</i>	0	1	0	1	1	0	0	0
<i>Klebsiella ozanae</i>	3	0	3	1	3	4	0	0
<i>Klebsiella pneumoniae</i>	6	4	3	2	3	4	2	6
<i>Klebsiella rhinosceromatis</i>	0	0	0	1	2	1	2	0
<i>Edwardsiella sp.</i>	0	0	0	1	0	1	0	0
<i>Enterobacter cloacae</i>	4	4	4	3	7	5	5	7
<i>Escherichia coli</i>	16	13	16	12	14	16	8	19
<i>Micrococcus sp.</i>	1	0	4	2	1	1	0	6
<i>Proteus mirabilis</i>	3	1	3	4	4	3	2	6
<i>Proteus vulgaris</i>	3	0	0	0	1	1	0	3
<i>Pseudomonas sp.</i>	7	3	7	6	9	8	7	9
<i>Salmonella sp.</i>	1	0	0	0	1	0	2	3
<i>Serratia sp.</i>	1	1	0	0	0	0	0	0
<i>Shigella sp.</i>	3	0	1	0	0	2	1	3
<i>Staphylococcus sp.</i>	2	0	0	1	0	0	2	4
<i>Streptococcus sp.</i>	5	8	5	5	7	6	7	8

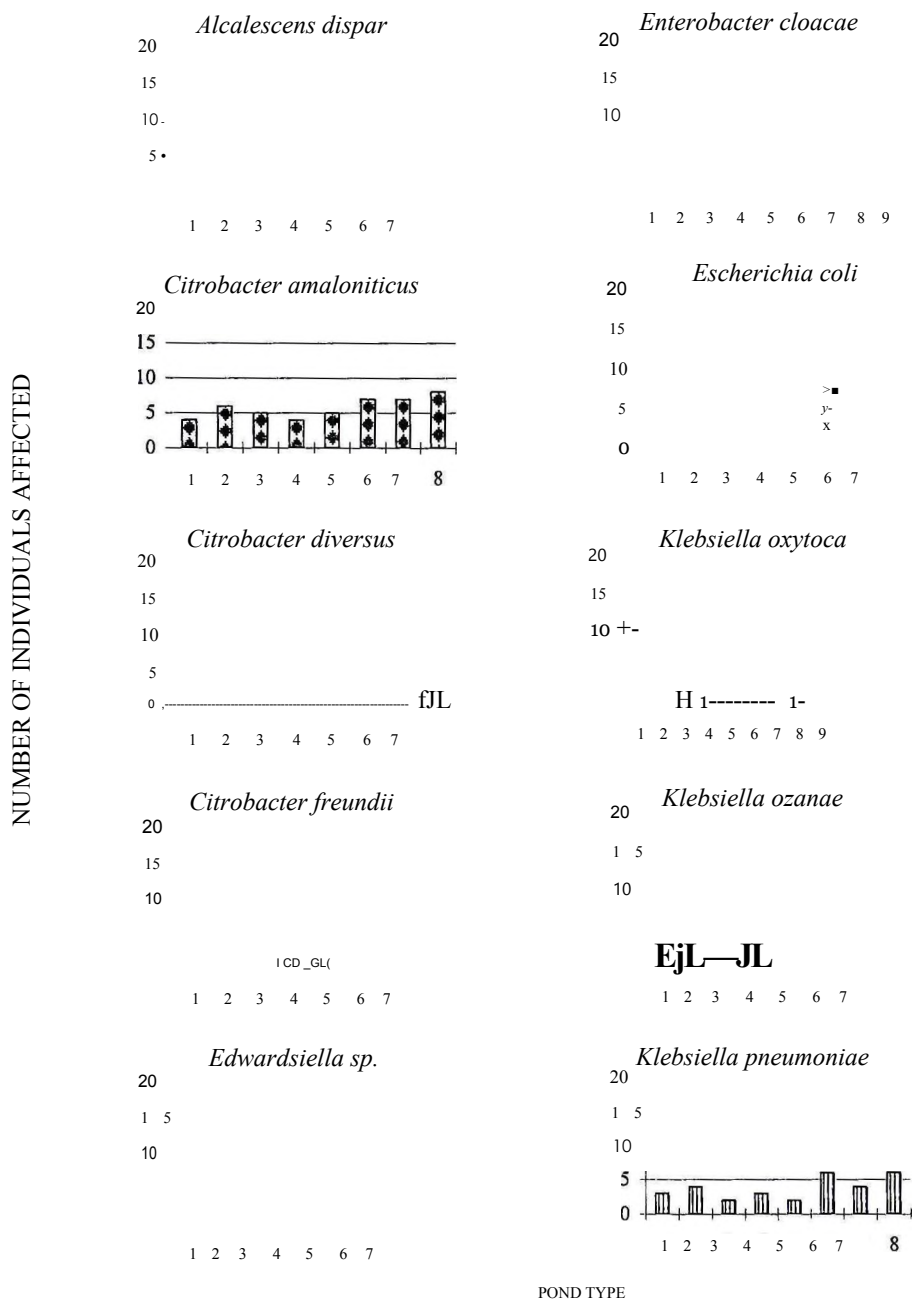


Fig. 12 Number of individuals of fishing communities associated with ponds treated with cow manure (1), pig manure (2), poultry manure (3), blood waste (4), chemical (5), sewage (6) and no manure (7), and open system (8), harbouring the indicated pathogenic bacteria

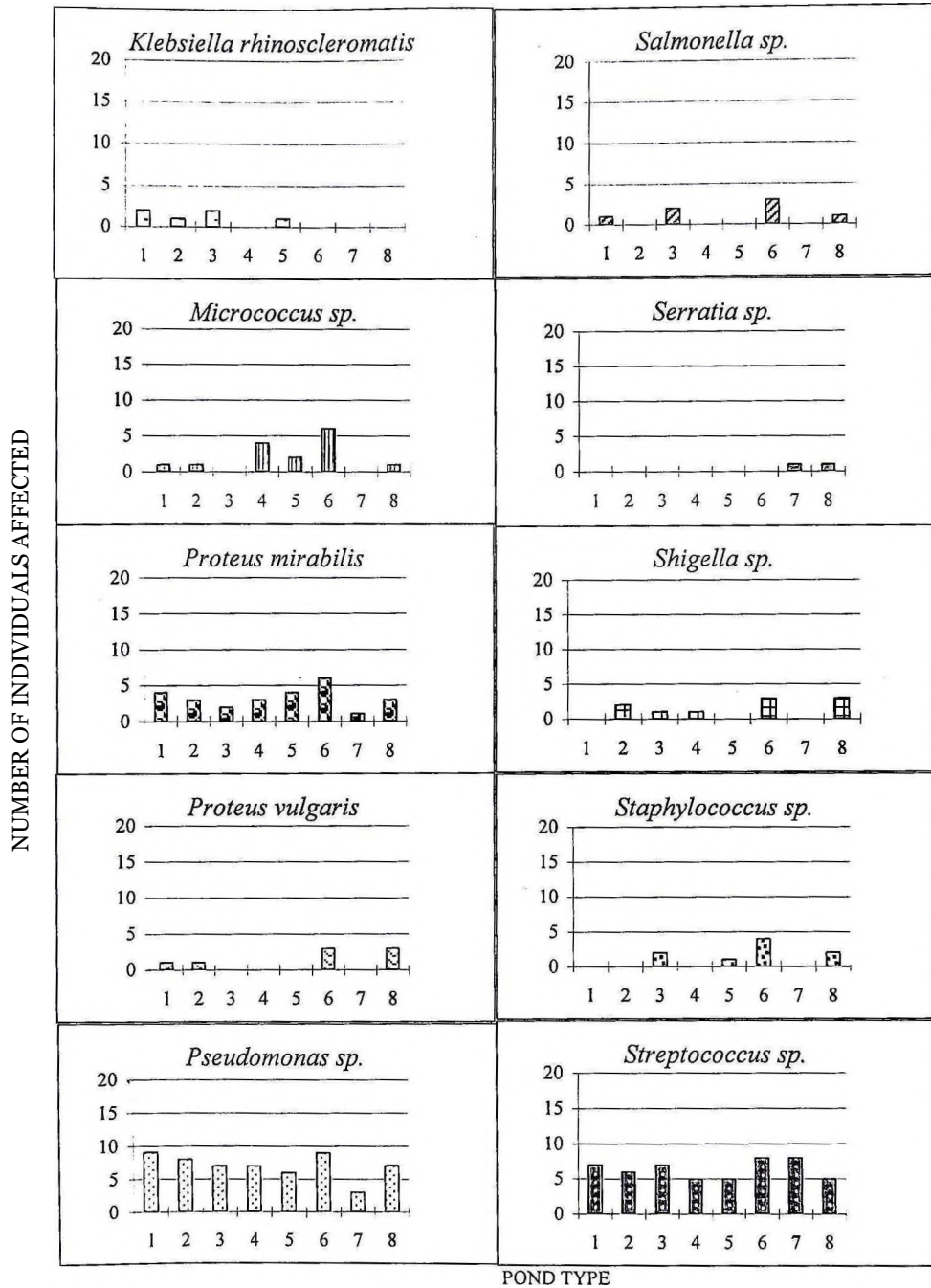


Fig. 12 Number of individuals of fishing communities associated with ponds treated with cow manure (1), (cont'd) pig manure (2), poultry manure (3), blood waste (4), chemical (5), sewage (6) and no manure (7), and open system (8), harbouring the indicated pathogenic bacteria.

CHAPTER FIVE

GENERAL DISCUSSION

All forms of fish culture are susceptible to outbreaks of diseases, as many pathogenic bacteria are normal inhabitants of the aquatic environment. In both culture and open systems, the occurrence of disease is a complex interaction between the host species, pathogens and the environment. Disease outbreaks are normally the results of a combination of hosts in a pre-disposed condition, virulent pathogens and adverse environmental conditions. Most aquacultural practices favour disease occurrence, because of the high stocking densities which increase stress in the stocks, the intensive feeding which provides abundant substrate for microbial growth and the sub-optimal environment of inadequate water exchange. On the other hand, disease outbreaks have been relatively less common in open water systems with less stressful environments, even though the pathogens and host species may be present. The present studies on the physico-chemical parameters and the occurrence and diversity of the bacteria of the culture ponds and open systems in Ghana would form the basis for a fairly accurate assessment of their fish-production potential, and more importantly, would direct the development of appropriate measures to increase their productivity.

The growth of aquatic bacteria is affected by a number of physical and chemical factors, the effects of which in diverse ways may be synergistic or antagonistic. They may influence not only the size and composition of bacterial populations but also the morphology and physiology of the individual bacterium. Temperatures above or below the optimum may lead to considerable changes in metabolism, cell morphology and reproduction. The synthesis of enzymes and, in consequence, the ability to break down certain substances may be either promoted or inhibited (Rheinheimer, 1976).

Temperature measurements indicated that the water temperature ranged from 26° to 36°C for all the sampling sites (Table 2a - 2p; 10a 10d). Temperature of surface waters is influenced by latitude, altitude, season, time of day, air circulation, cloud cover and the flow and depth of the water body. It means, therefore, that the data

obtained provided a general guide and determinations of the water temperature at other times of the day and other days of each month may provide different values. It was noteworthy that, the Pearson product moment correlation did not show any positive and significant correlation between the air and water temperatures of the three open systems (Tables 2n, 2o and 2p) whereas there was significant positive correlation in nine, Aduabenba, Boateng, Agyeman, Asare, Frimpong, K.K., Pacific, Sagoe and Akuse farms (Tables 2a, 2b, 2c, 2e, 2f, 2h, 2i, 2l and 10a, 10b, and 10d) out of the 13 cultured systems. Probably, factors such as air circulation and flow and depth of the water body had a significant effect on the temperature of the large water bodies. Temperature affects physical, chemical and biological processes in water bodies. But with temperatures recorded, which were quite close, the differences obtained would not change drastically these processes. More so, no relevant information was gathered on these processes during the course of study. The temperature range recorded, anyway, will favour the activities of heterotrophic bacteria responsible for decomposition of organic matter in the water.

Temperatures recorded in this study are close to those obtained in similar water bodies in the tropics. The surface temperatures of Stanley reservoir formed by damming the River Cauvery at Mettur, South India measured from June 1946 to June 1948 ranged from 29.2 to 30.8°C (Ganapati, 1969). Biswas (1969) recorded a temperature range of 27.25 to 30.83°C of the surface water of the Volta Lake in Ghana from June 1964 to June 1966.

Comparatively turbidity was very low in the open system, ranging from 0.17 to 3.22 NTU in Kpong Head Pond (Table 2n), 1.00 to 3.77 NTU in Volta River (Table 2o) and 2.50 to 6.33 NTU in Weija Dam which also had the highest content of suspended solids among the three water bodies (Table 2p). High turbidity readings with corresponding heavy suspended solids were recorded for the cultured systems. This could, naturally, be the result of the addition of both organic manures and fish feed. The highest values were recorded in Agyeman farm, where the turbidity was between 68.30 and 96.00 NTU and suspended solids between 94.67 and 112.20 mg/l (Table 2c). The turbidity of the water, which determines the depth to which light penetrates, affects more directly the algae and aquatic higher plants on which the fishes feed, as high turbidity reduces photosynthesis.

There were many parameters, which would affect the bacteria directly. The optimum pH for most bacteria is between pH 6.5 and 8.5 which corresponds to the pH range of most freshwater bodies (Rheinheimer, 1976) and growth and multiplication take place over pH 4 to pH 8 (Thimann, 1964). The pH of local water bodies either falls within this range, or closely outside this range. Entz (1969) recorded pH 6.99, 6.75 and 5.70 for the Volta Lake, Volta River and Dayi River, respectively. The pH values for all the sampling sites were all within the optimum range for bacterial growth. Hydrogen ion concentration influences many biological and chemical processes within a water body. At a given temperature, pH indicates the intensity of the acidic or basic character of a solution and is controlled by dissolved chemical compounds and biochemical processes in it. Acidity and alkalinity are the base - and acid-neutralising capacities (ANC) of water. When the water has no buffering capacity they are inter-related with pH. The acidity of water is produced by strong mineral acids, and weak acids such as carbonic, humic and fulvic and hydrolysing salts of metals (e.g. iron, aluminium). Acidity ranged from 5.0 mg/l¹ to 70.0 mg/l¹. It was generally high with pig manure-fertilized ponds ranging from 34.13 to 60.05 mg/l¹ (Tables 2g - 2i) as well as the first pond of the sewage-fed ponds (51.67 to 63.33 mg/l¹) (Table 10a). It was lower with the open waters (7.33 to 20.00 mg/l¹) (Tables 10a - 10c). Alkalinity of water is controlled by the sum of titratable bases and is mostly taken as an indication of the concentration of carbonate, bicarbonate and hydroxide but may include contributions from borate, phosphates, silicates and other basic compounds. The alkalinity markedly varied with the different sampling sites. Boahen Farms, for example, one of the lowest, between 42.73 and 52.67 mg/l¹ (Table 2j) and Pacific Farms one of the highest, between 203.33 and 280.00 mg/l¹ (Table 2i).

Nitrogen is essential for living organisms as an important constituent of proteins, including genetic materials. Plants and microorganisms convert inorganic nitrogen to organic forms. In the environment, inorganic nitrogen occurs in a range of oxidation states as nitrate (NO_3^-) and nitrite (NO_2^-), ammonium ion (NH_4^+) and molecular nitrogen (N_2). It undergoes biological and non-biological transformations in the environment as part of the nitrogen-cycle. The major non-biological processes involve phase transformations such as volatilisation, sorption and sedimentation.

The biological transformations consist of (a) assimilation of inorganic forms (ammonia and nitrate) by plants and micro-organisms to form organic nitrogen e.g. amino acids; (b) reduction of nitrogen gas to ammonia and organic nitrogen by micro-organisms; (c) complex heterotrophic conversions from one organism to another; (d) oxidation of ammonia to nitrate and nitrite (nitrification); (e) ammonification of organic nitrogen to produce ammonia during the decomposition of organic matter; and (f) bacterial reduction of nitrate to nitrous oxide (N_2O) and molecular nitrogen (N_2) under anoxic conditions (denitrification).

The concentration of ammonia was generally low at most of the sampling sites, agreeing with reports from elsewhere (e.g. Entz, 1969). Total ammonia concentration measured in surface waters are typically less than 0.2 mg l^{-1} but may reach $2.0 - 3.0 \text{ mg l}^{-1}$. Ammonia occurs naturally in water bodies arising from the breakdown of nitrogenous organic and inorganic matter, from excretion of biota, reduction of nitrogen gas by micro-organisms and from gas exchange with the atmosphere. Higher concentrations could be an indication of organic pollution such as from domestic sewage, industrial sewage and fertilizer run-off. Ammonia, therefore becomes a useful indicator of organic pollution. Natural seasonal fluctuations occur as a result of death and decay of aquatic organisms, particularly phytoplankton and bacteria in nutritionally rich waters.

The nitrate ion (NO_3^-) is the common form of combined nitrogen found in natural waters. It may be biochemically reduced to nitrite (NO_2^-) by denitrification processes, usually under anaerobic conditions. The nitrite ion is rapidly oxidised to nitrate. Natural levels seldom exceed 0.1 mg l^{-1} . Entz (1969) recorded 0.01 mg l^{-1} in the Volta Lake and a trace in Dayi River. Wastewater and inorganic fertilizers may, however, raise the nitrite levels. Indeed, the values recorded in this investigation were all very low, except in the ponds of Pacific Farms and Boahen Farms (Tables 2i and 2j) where the concentrations were about twice those of the farms. Natural sources of nitrate to surface waters include igneous rocks, land drainage and plant and animal debris. When influenced by human activities, surface waters normally contain nitrate in excess of 0.2 mg l^{-1} , but often less than 1.0 mg l^{-1} . Nitrate concentrations are usually very low, 0.001 mg l^{-1} and rarely higher than 1.0 mg l^{-1} . Nitrate values obtained for the ponds fell within this range.

Oxygen is essential to all forms of aquatic life, including those organisms responsible for the self-purification processes in natural waters. The oxygen content of natural waters varies with temperature, salinity, turbulence, the photosynthetic activity of algae and plants and atmospheric pressure. Concentrations of dissolved oxygen (DO) in unpolluted waters are usually close to but less than 10 mg l⁻¹. Values for cow manure-fertilized ponds ranged from 6.68 to 9.60 mg l⁻¹ (Tables 2a - 2b); poultry manure-fertilized ponds, 2.40 to 16.0 mg l⁻¹ (Tables 2c - 2f); pig manure-fertilized ponds, 4.40 to 18.40 mg l⁻¹ (Tables 2g - 2i); blood waste-fertilized ponds, 5.0 - 8.40 mg l⁻¹ (Table 2j); chemically fertilized ponds, 4.31 - 9.60 mg l⁻¹ (Tables 2k - 2l); ponds with no fertilization, 2.40 to 14.4 mg l⁻¹ (Table 2m); the open systems, 2.40 to 14.4 mg l⁻¹ (Tables 2n - 2p); and the sewage-fed ponds, 4.12 to 24.0 mg l⁻¹ (Tables 10a - 10d). Variations in DO can occur seasonally, or over a 24 hour period, in relation to temperature and biological activity (i.e. photosynthesis and respiration). Biological respiration, including that related to decomposition processes, reduces DO concentrations. Waste discharges high in organic matter and nutrients can lead to decreases in DO concentrations as a result of increased microbial respiration that accompanies increase in microbial population. DO values below 5.0 mg l⁻¹ may adversely affect the functioning and survival of biological communities, and below 2.0 mg l⁻¹ may lead to the death of most fishes. DO measurement is also used to measure biochemical oxygen demand (BOD). The BOD is an approximate measure of the amount of biochemically degradable organic matter present in a water sample. It is defined by the amount of oxygen required for the aerobic microorganisms present in the sample to oxidise the organic matter to a stable inorganic form. The presence of toxic substances in a sample may affect microbial activity leading to a reduction in the measured BOD. Unpolluted waters typically have BOD values of 2 mg l⁻¹ or less, whereas those receiving wastewaters may have up to 10 mg l⁻¹ or more (EIFAC, 1973). Sampling sites which had values close to and above 10 mg l⁻¹ were sewage ponds I and II which recorded values of 10.04 - 17.40 mg l⁻¹ and 8.10 - 12.46 mg l⁻¹, respectively (Table 10a - 10b).

Major ions determined in this study included calcium, magnesium, chloride and sulphate. Calcium is present in water as Ca²⁺ and is readily dissolved from rocks rich in calcium minerals, particularly as carbonates and sulphates, especially limestone and gypsum. Calcium is essential element for all organisms and is

incorporated into shells of many aquatic invertebrates as well as the bones of vertebrates. Calcium concentrations in natural waters are typically less than 15 mg l⁻¹. Entz (1969) recorded calcium levels of 7.82, 6.67 and 4.4 mg l⁻¹ for the Volta Lake, Volta River and Dayi River, respectively. Calcium levels for the sampling sites for most of the sampling periods were below 15 mg l⁻¹. Highest range was recorded for Weija dam (open system) which had values between 13.73 - 19.00 mg l⁻¹ (Table 2p).

Magnesium exists as Mg²⁺ and arises from the weathering of rocks containing ferromagnesium minerals and from some carbonate rocks. Magnesium in freshwater may differ from one body to the other. Studies on the cultured systems, open systems and the sewage fed ponds showed values ranging from 0 - 15.0 mg l⁻¹. Most of the values were significantly higher than the values of 2.06, 2.90, 1.30, obtained in Ghana by Entz (1969) for the Volta Lake, Volta River and Dayi River, respectively.

The hardness of water depends mainly on the presence of dissolved calcium and magnesium salts. Hardness vary over a wide range. The minimum value for hardness was recorded for the Kpong Headpond (20.33 mg l⁻¹ in May) (Table 2o) and the highest value of 98.00 mg l⁻¹ was recorded for Weija dam (also an open system) in March (Table 2n). Seasonal variations of hardness often occur reaching highest values during low flow conditions and lowest values during floods.

Chlorine occurs as chloride (Cl⁻) in solution. It enters water with atmospheric deposition of oceanic aerosols, with weathering of some sedimentary rocks, and from industrial and sewage effluents. In pristine freshwaters chloride concentrations are usually lower than 10 mg l⁻¹ and sometimes less than 2 mg l⁻¹. Higher concentrations can occur near sewage and other waste outlets. Cow manure-fertilized ponds recorded values ranging from 18.8 to 88.8 mg l⁻¹ (Tables 2a - 2b); poultry manure-fertilized ponds, 11.4 to 132 mg l⁻¹ (Tables 2c - 2f); pig manure-fertilized ponds, 12.2 to 180.0 mg l⁻¹ (Table 2g - 2i); blood waste-fertilized ponds, 14.7 to 19.2 mg l⁻¹ (Table 2j); chemically fertilized ponds, 16.8 to 26.0 mg l⁻¹ (Tables 2k - 2l); ponds with no fertilization, 8.9 to 27.5 mg l⁻¹ (Table 2m); the open systems, 8.0 to 57.0 mg l⁻¹ (Table 2n - 2p); and sewage-fed ponds, 14.0 to 35.0 mg l⁻¹ (see Tables 10a - 10d). These reflect the nature of amendments added to the various ponds

Sulphate is naturally present as SO_4^{2-} . It arises from the atmospheric deposition of oceanic aerosols and the leaching of sulphur compounds. Sulphate can be used as an oxygen source by bacteria which convert it to hydrogen sulphide (H_2S , HS^-) under anaerobic conditions. Sulphate concentrations in natural waters are usually between 2.0 and 80.0 mg l^{-1} . Surprisingly very low levels were recorded for all the sampling sites. The lowest being 0 mg l^{-1} and the highest 16.40 mg l^{-1} . Entz (1969) also recorded 12.7 mg l^{-1} sulphate for the Volta River.

Tolerance limits of water quality depend very much on the fish species cultivated, especially in respect to temperature and salinity. It is therefore important to consider only the water quality requirements that have significance in assessing environmental impact. These are mainly dissolved oxygen, pH, carbon dioxide, ammonia, nitrites, nitrates, hydrogen sulphide, pesticides and turbidity.

The optimum levels of many of these physico-chemical parameters are not accurately known for many species, but based on long-term sub-lethal toxicity tests and experience in experimental and production farms, "safety levels" have been indicated (Tiews, 1981).

In salmonid and warm water crustacean culture, DO levels are not allowed to go below 5.0 mg l^{-1} for more than a few hours. Eel, carp and tilapia in farms can tolerate lower concentrations ranging from 3.0 to 4.0 mg l^{-1} . The optimum levels may be higher than this. According to Swingle (1969) and Boyd (1981), warm water fish survive at DO levels as low as 1.0 mg l^{-1} , but growth is slowed down by prolonged exposure. The desirable range being above 5.0 mg l^{-1} .

Slow growth results from pH levels below 6 to 6.5, and the acid death point is reported to be pH 4. The alkaline death occurs at pH 11. The desirable range for fish production is 6.5 to 9.0 at daybreak (Boyd, *op. cit.*).

In water used for intensive fish culture, free carbon dioxide levels fluctuate typically from 0 mg l^{-1} in the afternoon to 5.0 to 10.0 mg l^{-1} at daybreak with no obvious ill-effects on fish (Parks *et al.*, 1975). Higher concentrations of free carbon dioxide,

even up to 60 mg l⁻¹ may be tolerated provided that DO concentrations are high. Un-ionized ammonia (NH₃) is toxic to fish, but the ammonium ion (NH₄⁺) is not toxic (Downing and Merkens, 1955; Boyd, 1981). According to EIFAC (1973), toxic levels of ammonia for short-term exposure usually lie between 0.6 and 2.0 mg l⁻¹. Others consider the maximum tolerable concentration to be 0.1 mg l⁻¹ (Tiews, 1981) the preferred level being below this. Un-ionized ammonia becomes more toxic in low concentrations of DO, but this is of little importance in pond farms as the toxicity decreases with increasing carbon dioxide concentration which is usually the case when the DO is high.

Available information on safety levels of nitrites (NO₂) is very limited, although studies indicate that nitrite may be significant factor in channel catfish ponds. The suggested maximum level for prolonged exposure in hard freshwater is 0.1 mg l⁻¹. Nitrate (NO₃) levels suggested are below 100 mg l⁻¹.

Un-ionized hydrogen sulphide (H₂S) is extremely toxic to fish at concentrations that may occur in natural waters as well as in aquaculture farms. It has been demonstrated that high concentrations of hydrogen sulphide could result in poor growth of channel catfish (Bonn and Follis, 1967). Bioassays of several species of fish suggest that any detectable concentration of hydrogen sulphide should be considered detrimental to fish production (Boyd, 1981).

Many pesticides, particularly insecticides, are extremely toxic to fish. Acute toxicity values for several commonly used insecticides range from 5.0 to 100 mg l⁻¹ (Cope, 1964), and on longer exposure even lower concentrations may be toxic. Even when they do not cause mortality of the species under culture, they may affect the growth of food organisms and this reduces their growth and productivity.

Turbidity is also an important water quality which a fish farmer has to control. Turbidity caused by suspended soil particles has usually no direct effect on fish and shellfish, but it restricts light penetration and limits photosynthesis. Also, sedimentation of soil particles can destroy benthic communities and smother fish eggs. Turbidity caused by plankton is not harmful to fish, but clay turbidity

exceeding 20000 mg^l⁻¹ causes behavioural reactions in many species of fish. Appreciable mortality occurs at turbidities above 175000 mg^l⁻¹ (Boyd, 1981).

Generally concentrations of ammonium, nitrate, nitrite, phosphate, silicon dioxide and sulphate were found to be correlated in the various pond types. Similarly air and water temperatures were found to correlate in all the sampling sites.

The significance of the role of bacteria in water bodies has been difficult to ascertain. There are many different physiological types of bacteria ranging from strict chemoautotrophs to phototrophs and to heterotrophs. The present study considered the population of heterotrophic and coliform bacteria in the study area. To study the bacterial flora of the cultured systems, open systems and the sewage fed ponds; cultured plates were incubated at 37°C to obtain thermophiles which include many pathogenic species.

Actinobacillus sp., *Aeromonas* sp., *Bacillus* sp., *Bacteroides* sp., *Campylobacter* sp., *Citrobacter* sp., *Clostridium* sp., *Corynebacterium* sp., *Edwardsiella* sp., *Enterobacter* sp., *Escherichia* sp., *Flavobacterium* sp., *Hafnia* sp., *Klebsiella* sp., *Micrococcus* sp., *Pasteurella* sp., *Proteus* sp., *Pseudomonas* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Staphylococcus* sp., *Streptococcus* sp., *Vibrio* sp. and *Yersinia* sp were identified during this investigation. Most of these are predominantly psychrophilic species found in most water sources. Frazier (1958) stated that species of *Clostridium*, *Flavobacterium*, *Micrococcus*, *Proteus* and *Pseudomonas* are the major spoilage bacteria at near freezing temperatures. Raj and Liston (1961) found that some pathogenic and potentially pathogenic microorganisms including *E. coli*, *Staphylococcus* and some anaerobes survived when uncooked and pre-cooked fish foods were stored at freezing temperatures. Studies by Roberts (1978) showed that bacteria belonging mostly to the genera *Aeromonas*, *Corynebacterium*, *Pseudomonas* and *Vibrio* cause infectious diseases in fish. The presence of these twenty five genera in the fish culture systems is, therefore, a threat to the fish industry as fish which do not succumb to the attack may still be subjected to spoilage. The presence of the coliform group of bacteria, mainly *Citrobacter*, *Enterobacter*, *Escherichia* and *Klebsiella* in fish and fish products presents a health hazard (Fapohunda *et al*, 1994). Fish caught in polluted water have been found to

cause infections in human (Caldreich and Clarke, 1996; van Duijn, 1973). Allen and Hopher (1969) have stated that most of the epidemics attributed to wastewater sources are from raw sewage gaining access to food eaten directly by man, or from contamination of water supply systems by untreated sewage. Olayemi *et al* (1991) have reported that the presence of faecal coliform in fish intended for human consumption may constitute a potential danger not only in causing disease, but also because of the possible transfer of antibiotic resistance from aquatic bacteria to human infecting bacteria from non-aquatic sources. Some human pathogens such as *Aeromonas*, *Escherichia*, *Klebsiella*, *Pseudomonas*, *Salmonella* and *Vibrio* have been found to survive and multiply in the gut, mucus and tissues of fish and thus render fish a potential vector of human disease over long periods (Allen *et al*, 1979).

The coliform group of bacteria comprises mainly species of the genera *Citrobacter*, *Enterobacter*, *Escherichia* and *Klebsiella*, and include faecal coliforms, of which *Escherichia coli* is the predominant species. Several of the coliforms are able to grow outside of the intestine, especially in hot climate, hence their enumeration is unsuitable as a parameter for monitoring wastewater re-use systems. The faecal coliform test may also include some non-faecal organisms which can grow at 44°C so the *E. coli* count is the most satisfactory indicator parameter for wastewater.

Faecal streptococci organisms include species mainly associated with animals (*Streptococcus bovis* and *S. equinus*), other species with a wider distribution (e.g. *S. faecalis* and *S. faecium* which occur both in man and in other animals) as well as two biotypes (*S. faecalis* var. *liquifacicus* and a typical *S. faecalis* that hydrolyses starch) appear to be ubiquitous, occurring in both polluted and non-polluted environments. The enumeration of faecal streptococci in effluents is a simple routine procedure but has some limitations. These include (a) the possible presence of non-faecal biotypes as part of the natural microflora which may detract from their utility in assessing bacterial quality, (b) poorer survival of faecal streptococci at higher temperatures.

Values for total and faecal coliforms and the total heterotrophic bacteria (THB) were generally high in the sewage fed ponds as compared to the rest of the systems. The heavy faecal load might have provided abundant nutrients to stimulate greater bacterial growth. The population of coliform bacteria and faecal streptococci

differed from one sampling site to another (even for those receiving the same type of fertilizer) and from one period of sampling to another. Variations being highest with the open systems which were not subjected to consistent faecal contamination. THB values of the open systems were higher in 1996 than in the subsequent years of sampling.

The population of bacteria and the identity of the species associated with the fish in the cultured and open systems were studied. It was anticipated that not only will large numbers of the bacteria be present in view of the favourable and uniform physico-chemical parameters of the environment but also that the flora of bacteria in the systems would include some pathogenic forms. *Pseudomonas* sp. occurred most frequently in most of the ponds. Pig manure fertilized-ponds however recorded very high levels of *Clostridium* sp and *Streptococcus* sp. (Tables 4g - 4i). Poultry manure fertilized-ponds also had *Salmonella* sp. occurring in higher percentage along with the *Pseudomonas* sp. (Tables 4c - 4f).

During this study another important aspect of bacteriology considered was the diversity of bacteria based on the evaluation of the kinetics of biochemical reactions. All isolates within an investigation were compared to each other pairwise, and the similarity between each pair was calculated as the momentum correlation coefficient (r) which varies between +1 and -1. A value close to +1 for the compared isolates meant similar biochemical fingerprints (Kuhn and Mollby, 1993). The identity level was determined by the reproducibility of the assay, and it was defined as the mean correlation coefficient (n) between multiple assays of same isolates minus two standard deviations (SD). This yielded a 95% confidence level, thus the probability that two isolates which were indeed identical had less than 5% to be reported as non-identical. The correlation matrix was clustered, and dendrograms printed out (Figs. 2a - 8o; 10a - 10t) Isolates which showed correlation coefficients to each other higher than the ID level were regarded as identical and assigned to the same biochemical phenotype (or PhP type). PhP-types containing several isolates were named as such, whereas other PhP-types which were found only seldom were named as single PhP-types (Appendices 1a - 8t). The cophenetic correlation coefficient was calculated together with the dendrogram. It described how well the outcome of the clustering procedure corresponded to the data from which the dendrogram was

derived. All the typed populations from the study were from high cophenetic correlations. The diversities of bacterial populations were calculated as Simpson's diversity index (Di) (Kuhn *et al*, 1991). A high Di (maximum value is +1) meant that the assayed isolates were evenly distributed into different types, whereas low Di (minimum value is 0) meant that one or a few types of bacteria dominated the studied population. High Di values were obtained in this study (Tables 5a - 5g; Table 12). The mean diversity of the bacterial flora in the cow manure-fertilized ponds was 0.977 with PhP types ranging from 17 to 59. The mean diversity in the poultry manure fertilized-ponds was 0.972 with PhP types ranging from 31 to 64. Mean diversity in the pig manure-fertilized ponds was 0.981 with PhP types between 27 to 56 and mean diversity in the blood waste-fertilized ponds being 0.989 and the PhP types ranged from 46 to 63. The mean diversity of the chemically fertilized ponds was 0.972 with PhP types ranging from 34 to 64. Ponds with no fertilization had mean diversity of 0.989 and their PhP types ranged from 55 to 66. The open systems had mean diversity of 0.950 and the PhP types ranged from 29 to 41. The population similarity (Sp) coefficient measured the proportion of isolates that were identical in two or more compared sampling sites (Tables 6 and 13). Comparison between the different fertilisation types, i.e. the cow manure, poultry manure, pig manure, blood waste, chemical fertiliser, ponds with no fertilisation as well as the open systems had Sp values mostly below 0.50, an indication of related populations with high diversities; Similarly comparison between farms with same fertilization type, thus where two or more farms were studied for the same fertilization type showed Sp values below 0.50. There was, however, more fluctuations in the populations of bacteria and their diversity in the pig manure-fertilized ponds. This was observed from the high Sp value when different sampling periods were compared. This may be due to the daily input of the pig manure into the ponds unlike the other types where the manure was added less frequently.

The similar pattern of variation in the water and fish tissues of the population of bacterial flora is a possible indication that bacterial biomass forms an important part of the diet in *Oreochromis niloticus* and that gut microflora, whether it be autochthonous or allochthonous or both, could possibly play an important role in the nutrition of the fish. A higher bacterial load in the gut of fish has been observed than in the surrounding waters (Henebry *et al*, 1988; Mary, 1977; Shiranee *et al*,

1993). This may suggest that fish selectively feed on detrital particles with high numbers of bacterial biomass per unit weight (Odum, 1968; Moriarty, 1976), thus concentrating bacteria in their foreguts at levels higher than those in the surrounding environment. Henebry, *et al.* (*op cit.*) observed increased bacterial population in the midgut of silver carp and suggested that bacterial populations may increase in the midgut before being ultimately digested, thereby providing high quality protein for the fish. Sera and Ishida (1972) observed increased total heterotrophic bacteria count from 10^4 to 10^8 cells per gram in the intestine of red sea bream snapper (*Pargus major*) 16 hours after ingestion of food. However, since in the present study separate counts for the flora in the foregut, midgut and hindgut were not done, it is difficult to determine whether bacteria serve directly as source of protein for *O. niloticus* or indirectly by synthesizing vitamins required by the fish. Most probably they perform both functions, and their relatively high density in the gut of fish is of important survival value.

It is well established that many human and animal feeds carry high bacterial load (Thatcher and Clark, 1968). Because food and feeds have served to distribute bacteria inimical to human and animals, limits have been established for the numbers of pertinent categories of microorganisms tolerable in various foods (Powers *et al.*, 1970; Statutory Orders and Regulations, 1955; Thatcher, 1963). Feed itself may be a source of nutrients required for bacterial growth and contains significant bacterial inoculum. The water in the pond may also become ideal bacterial culture medium. When eleven different fish feeds and four different organic manures commonly used to fertilise ponds were examined during this investigation, all the feeds were found to contain resident bacteria identified simply as THB and coliforms (Table 8). Since bacterial action and bacterial growth are nearly directly proportional to a temperature rise from 21 to 30°C (Axelrod and Schultz, 1969), the size of bacterial inoculum in any feed type should be of great concern. The detection of the species of the Enterobacteriaceae in these feeds does indicate a potential for contamination of such feedstuffs with enteric pathogens. It is most probable that handling of the feeds *per se* could cause infection by direct ingestion or by indirect transfer of the organism to the mouth or respiratory passage via the hands. The fact that detrital bacteria in the water may play a role in the nutrition of the *O. niloticus* suggests the possibility of culturing the fish on a combination of artificial feeds and cheap agricultural wastes,

as bacteria are able to convert the low quality fertilizers to high quality food, or this may be an active process in the gut of the fish itself.

Most species of fish which breed in fast flowing rivers normally swim against the currents when feeding, and this is very true of plankton feeders. When such fish are kept in an almost stationary body of water, their feeding capacity is adversely affected especially if the water is not very productive. That is why useful fertilizers in the form of inorganic and organic manures may be applied, while the necessary precautions are taken.

Selected bacterial species able to cause disease in human and fishes were also found to survive and grow using the organic manures being used to fertilise the ponds as sole source of nutrients. In the natural situation such bacteria could be introduced into the ponds with the fish during fertilization, through tending the pond, or with the feed. Because of the potential ability of bacteria to multiply in the pond, *Vibrio parahaemolyticus* which did not survive long in the feeds (Table 9h) is still important, as it will thrive in the pond once the causative factors become diluted or suitable nutrients become available in the pond. Because fish feeds have been shown to be vectors of bacterial diseases of humans (Janssen, 1970) attempts must be made to reduce as much as possible in diets of fish being raised for human consumption by appropriate treatments, and also, by storing the feeds under conditions that discourage rapid growth of the bacteria. Many species of bacteria which are normally considered saprophytic, including species of *Bacillus*, *Micrococcus* and *Proteus* have been isolated from infections of tropical fish (Almeda *et al.*, 1968). Species of Enterobacteriaceae and strains of Enterococci similar to *Streptococcus faecalis* have also been implicated in fish infections and mortalities (Bullock *et al.*, 1971). The digestive tract and intraperitoneal fluid of fish may contain high concentrations of pathogens, such as *Salmonella*, even at lower concentrations in pond water. Handling and cleaning of such contaminated fish can result in contamination of the hands of farm workers and through them their family members and others. If the fish is eventually infected, its effect on humans could still be lessened by avoiding certain organs in food preparations. It was shown that the skin, gills and gut had significantly heavy populations of certain species, such as *Bacillus*, *Bacteroides*, *Citrobacter*, *Clostridium*, *Corynebacterium*, *Escherichia*,

Flavobacterium, *Micrococcus*, *Pseudomonas*, *Salmonella*, and *Streptococcus* (Tables 7a — 7f; Table 14) and could be discarded. But, in the final analysis, the rule is, 'consumption of raw fish must not be encouraged'.

Fish can be cultured in sewage treatment plants, which naturally contain high numbers of bacteria. This may demand additional attention to the proper maintenance and management of the sewage treatment plants. In such cases it will be proper to use the secondary plant for the fish culture. In the current study not much difference was observed between values obtained from the sewage fed ponds of Akuse as compared to the other cultured ponds which used the cow manure, poultry manure, pig manure or the blood waste. Similarly there was not much difference between the Akuse values and those from the chemically fertilised and non-fertilised ponds as well as the open systems.

There was no pattern in the distribution of pathogens in the farmers or their families as those working on ponds with no input and consuming fish from those ponds also harboured many pathogens. It means that neither the location of the ponds geographically or treatment given the ponds could determine the exact bacterial flora to be encountered.

Intensive forms of flow-through aquaculture systems use comparatively large quantities of water. In well-managed ponds the mean water supply range between 8 and 25 l per ton of annual production (Pillay, 1992). Production farms generally depend on surface and spring water, most of which flow back to the wasteways as residual waste water. In stagnant water pond farms, water used is generally limited to the initial filling to the required depth and subsequent topping up to make up for loss due to evaporation and seepage (Pillay, *op cit*). For a fish pond with an average depth of 1.5m, the amount of water required to fill it initially is about 15,000 m³ha⁻¹ (Pillay, 1990). User conflicts therefore arise with downstream users cut short of their water supply, or when streams or rivers are contaminated by effluents discharged from farms, especially when farms are infected by pathogenic organisms. Where animal wastes are to be used, the number of animals can be regulated to ensure that the wastes discharged into the ponds do not exceed the quantities that the biological processes can handle to ensure safety for subsequent users.

Pathogens are always present in the aquatic environment. The main concern therefore is introduction of new disease or causing environmental deterioration that can result in increased populations and virulence of indigenous pathogens, and disease outbreaks in the environment as a result of waste discharges into the water.

The incidence of disease in farms can be explained by the higher density of cultured animals than in the natural habitats, and differences in water quality conditions (Pillay, 1992). Dumping of carcasses of infected fish into natural waterways is another practice that contributes to increased populations of pathogens in the environment.

Animals that die from infectious diseases are a major source of pathogens, as clinical illness is associated with significant increases in the pathogenic populations. It is therefore important to remove sick and dead individuals among the stock to minimize the presence of pathogens in the environment. Collection and destruction of dead fish in such a way as to prevent dissemination of pathogens is therefore a legal requirement in fish culture (Pillay, *op cit*). Similarly when a farm is infected with viral diseases for which there are no control measures, farmers are required to destroy the stock to prevent the spread of the disease to other farms and to the external environment.

The safety of products for consumption is prime concern from the point of view of managing of the fish culture systems, as well as ensuring public health. Official regulatory bodies in many countries specify maximum permissible concentrations of toxic substances or the number of harmful bacteria that a product may contain, in order to ensure that unfit or unwholesome food does not reach the consumer. Even though not usually covered by regulations, unattractive appearance and tainting of products affect their marketability. Water quality and culture practices play important roles in determining product quality. Both in open and culture systems, fish can be exposed to contaminants, some of which can be persistent and have the capacity for bioaccumulation. In Ghana most of the fish consumed is bought directly from the fishermen and does not pass through any health-safety checks. The health of consumers would be protected by instituting this safe-guard.

It is well known that wastewater stabilisation ponds in common use perform by virtue of the symbiotic alga-bacterium system, which always result in a high concentration of algae in effluents, thus causing secondary pollution to the receiving waters. It is therefore necessary that this type of ponds is followed by alga removal facilities, such as microstraining, flocculation/coagulation/setting, air floatation, rock or sand filtration units despite the expense involved in their construction, operation and maintenance.

Ponds and lagoons being used for the treatment and utilisation of wastewater can be made free of such troubles through multi-purpose utilisation of the treated wastewater. This can include growing aquatic plants, fish farming and duck/geese raising, which together with microorganisms, planktons and benthos constitute various food chains which further form a whole food web, a complete, more complicated and stable ecological system than the symbiotic algae/bacterial system thus established. This ecological system established thus has, not only bacteria and fungi as decomposers, and algae and other aquatic plants as producers as in conventional ponds, but also zooplankton, shrimp, clams, snails, fish, duck, and geese, etc. as consumers at different trophic levels, which along with the environment, the ponds proper where the food web exists constitute the eco-pond system. Effluents from these eco-pond systems can be applied on farmlands through irrigation. The selection of aquatic plants should be done with great care as some species may cause immense inconvenience. In lakes and ponds the dense growth of certain water species such as water hyacinth (*Eichhornia speciosa*), sometimes cause inconvenience to fishery activities especially in the operation of the nets. The wild growth of submerged and emergent plants leads to over-population with stunted fish and the natural reduction in the fish crop. Excessive production of organic matter which eventually decays sometimes results in the fouling of the water and the death of fish.

A multi-cell pond system can therefore be adopted in applying wastewater for fish farming; the wastewater can include human and animal manure and sewage. The multi-cell pond system can consist of pre-positioned treatment pond and post-positioned fish farming ponds. The treatment pond system in front of the fish pond

generally comprises of anaerobic, facultative and aerobic ponds in series. For example the Yorhu Pond System in the suburb of Wuhan City (Wang, 1985, 1987) consisted of five ponds in series: anaerobic pond - facultative pond I - facultative pond II aerobic pond fish pond. The effluent contained a wide variety of organic compounds including refractory ones such as parathion, malathion, roger, nitrophenol and HCCH, and were degraded through diversified anaerobic, facultative and aerobic microbes into inorganic products such as carbon dioxide, ammonia, nitrite, nitrate and phosphate. These inorganic products are taken up by algae and other aquatic plants as nutrients for their growth, while oxygen is released, which is used by for aerobic bacteria to further decompose organic pollutants. The fish then feed on the algae, aquatic plants and zooplankton. Fish production rate for the Yorhu Pond System was an average of 2000 kg/ha²/an.

The use of wastewater and animal waste in fish farms has not reported public health risk so far, albeit the controversial hypothesis of influenza pandemic from pig-duck-fish-zoonosis in China integrated farming (Schotissek and Naylor, 1988), the possibility of hazards continue to be raised, mainly because of successful experimental infections. Ponds fertilized with untreated sewage or other wastes can contain human pathogenic organisms. Laboratory experiments with tilapia, common carp and silver carp have shown that when bacteria are present in high concentrations in experimental ponds for long periods, the bacteria could be recovered from all organs and muscles of fish, although normally they are found only in the digestive tract and not in the muscle tissue. Some pathogens were recovered from the muscle of the tilapia tissue in this study. Guidelines issued by the World Health Organisation for use of wastewater (WHO, 1989) suggested that there is little accumulation of enteric organisms and pathogens on, or penetrating into, edible fish tissue when faecal coliform concentration in fish pond waters is below 10^3 per 100 ml. When the concentration is greater than 10^4 and 10^5 per 100 ml, the potential for invasion of fish muscle by bacteria increases with the duration of exposure of the fish to the contaminated water.

Results from the Akuse sewage fed ponds have shown that by appropriate treatment and management including adequate retention time in oxidation ponds or lagoons, bacterial concentrations in wastewater can be reduced and maintained at the required

levels to prevent transmission of pathogens to consumers. Such a practice should be more widely adopted in the country.

For the biologist there are many fields of research on ponds leading to the production of fish. This includes the chemical and solar input to lakes in so far as these factors affect the primary productivity of algae and macrophytes; the zooplankton and invertebrate organisms which feed on plants and detritus are of importance in that they provide food for fish, and all aspects of the biology of commercially important fish species require close examination. Further, at each of these levels, decomposition processes start and complex biological materials are broken down to relatively simple chemicals. This also requires study if any understanding is to be gained of the processes involved in re-circulation of nutritive materials. Water chemistry, algology, invertebrate zoobenthos and decomposition processes have deliberately been rated as equally important in fishery exploitation if we are to understand and utilize properly the resources of culture ponds. Those aspects which could not be covered in the present investigation should be for future investigation. Studies of other ponds that may be carried out in the country should also adopt these important aspects while organizing the research programme.

SUMMARY

1. Thirteen fish farms and three river bodies representing fish culture systems in Ghana were studied for their bacterial populations and bacterial species diversities with special reference to species pathogenic to fish and human.
2. The farms were Aduabenba, Agyeman, Aheto, Akuse, ARDEC Station, Asare, Boadi, Boahen, Boateng, Frimpong, KK, Pacific and Sagoe, and the rivers were the Kpong Head Pond, Volta River and the Weija Dam.
3. Species of bacteria belonging to 25 genera were identified as associated with the fish culture systems in this study. The identified species included a **Spiral and curved bacterium** (*Campylobacter* sp.), a **Gram-negative aerobic rod** (*Pseudomonas* sp.), **16 Gram-negative facultative anaerobic rods** (*Actinobacillus* sp., *Aeromonas* sp., *Citrobacter* sp., *Edwardsiella* sp., *Enterobacter* sp., *Escherichia* sp., *Flavobacterium* sp., *Hafnia* sp., *Klebsiella* sp., *Pasteurella* sp., *Proteus* sp., *Salmonella* sp., *Serratia* sp., *Shigella* sp., *Vibrio* sp. and *Yersinia* sp.), a **Gram-negative anaerobic bacterium** (*Bacteroides* sp.), three **Gram-positive cocci** (*Micrococcus* sp., *Staphylococcus* sp. and *Streptococcus* sp.), two **endospore-forming rods** (*Bacillus* sp. and *Clostridium* sp.) and an **Actinomycetes related organism** (*Corynebacterium* sp.)
4. Some of the physico-chemical parameter of the ponds showed a positive correlation with the bacterial population while others showed a negative correlation.
5. At the Aduabenba Farms, there was negative correlation between acidity of the pond and faecal coliform counts, pH and faecal coliform, and, between turbidity and total heterotrophic bacteria count, while air temperature and total coliform count showed negative correlation.
6. At Agyeman Farms, there was positive correlation between air temperature and faecal coliform count, water temperature and faecal streptococci count, and, nitrite and faecal streptococci count.

7. At Aheto Farms, there was positive correlation between alkalinity of the water and total heterotrophic bacteria, suspended solids and faecal coliform count, and, total dissolved solids and faecal coliform count. Negative correlation was detected between nitrate ion and faecal coliform count, and, phosphate ion and total heterotrophic bacteria.

8. At Akuse Pond I, there was positive correlation between calcium ion and total coliform count, chloride ion and total heterotrophic bacteria, and, water temperature and total heterotrophic bacteria. There was negative correlation between acidity and total heterotrophic bacteria, nitrate ion and total coliform, and, total dissolved solids and total coliform. Akuse Pond II showed positive correlation between acidity and faecal streptococci, air temperature and faecal streptococci, turbidity and faecal streptococci, water temperature and faecal coliform, and, between phosphate ion and total heterotrophic bacteria. Total hardness and faecal coliform, and, suspended solids and faecal coliform, on the other hand, showed negative correlation. Akuse Pond III showed positive correlation between calcium ion and faecal coliform, and, between calcium ion and total coliform, whereas ammonium ion and total coliform, chloride ion and total coliform, chloride and total heterotrophic bacteria, dissolved oxygen and total coliform, and magnesium ion and faecal coliform showed negative correlation. Akuse Pond IV showed positive correlation between biochemical oxygen demand and total heterotrophic bacteria, and, nitrite ion and faecal streptococci count. Negative correlation was found between air temperature and faecal streptococci, ammonium ion and faecal coliform, biochemical oxygen demand and total coliform, magnesium ion and faecal streptococci, and, between water temperature and faecal streptococci.

9. ARDEC 3 showed positive correlation between calcium ion and total heterotrophic bacteria and, total hardness and total heterotrophic bacteria. At ARDEC 20, there was positive correlation between sulphate ion and faecal coliform, and, between sulphate ion and total heterotrophic bacteria.

10. Calcium ion and total coliform, nitrate ion and faecal coliform, silicon and faecal coliform, nitrate and total heterotrophic bacteria, and, silicon and total heterotrophic bacteria showed negative correlation at Asare Farms.
11. At Boadi Farms, there was positive correlation between ammonium ion and total coliform, phosphate ion and faecal coliform, and, suspended solids and total heterotrophic bacteria.
12. Boahen Farms showed positive correlation between alkalinity and faecal coliform, magnesium ion and faecal coliform, pH and faecal streptococci count, and, between total dissolved solids and faecal streptococci count. Negative correlation was detected between acidity and total coliform, and air temperature and faecal coliform count.
13. At Boateng Farms, there was negative correlation between alkalinity and faecal coliform, calcium ion and faecal coliform, calcium ion and faecal streptococci, and, between turbidity and faecal coliform.
14. At Frimpong Farms, there was positive correlation between chloride ion and faecal coliform, and, pH and faecal streptococci count.
15. KK Farms showed positive correlation between total hardness and faecal coliform count, phosphate ion and faecal streptococci, and, between silicon and total heterotrophic bacteria.
16. At Pacific Farms there was positive correlation between air temperature and total heterotrophic bacteria, ammonium ion and faecal coliform, and negative correlation between nitrite ion and faecal coliform, ammonium ion and faecal coliform, and, between total dissolved solids and total coliform count.
17. Sagoe Farms showed positive correlation between air temperature and total coliform, alkalinity and total coliform, and, between biochemical oxygen demand and total heterotrophic bacteria; and negative correlation between phosphate ion and faecal streptococci count.

18. Kpong Head Pond showed positive correlation between ammonium ion and faecal streptococci, conductivity and faecal streptococci, total dissolved solids and faecal streptococci, and, between total hardness and total coliform. There was negative correlation between conductivity and total heterotrophic bacteria, phosphate ion and faecal coliform, and, between total dissolved solids and total heterotrophic bacteria.
19. The Volta river showed positive correlation between chloride ion and faecal coliform, chloride ion and faecal streptococci, and, water temperature and total heterotrophic bacteria.
20. Weija dam showed positive correlation between chloride ion and total coliform, silicon and faecal coliform, silicon and total coliform, silicon and total heterotrophic bacteria, and, between sulphate ion and total heterotrophic bacteria. Alkalinity and total heterotrophic bacteria, and, chloride ion and faecal coliform count showed negative correlation.
21. The diversity of bacteria in each of the ponds was generally high (more than 0.90) indicating that the bacterial populations in the fish culture systems consisted of many different types of bacteria.
22. Determination of the diversities was done with the Phene Plate (PhP) procedure. The PhP types of bacteria for the Aduabenba farm, cow manure-fertilized pond, ranged from 17 to 34 different strains of bacteria, and for Boateng farm, also fertilized with cow manure, 50 to 59. For the poultry manure-fertilized ponds the PhP types were 31 to 64, 43 to 53, 56 to 63, and, 41 to 58 for Agyeman, ARDEC 20, Asare and Frimpong farms, respectively. PhP types for the pig manure-fertilized ponds were 43 to 56, 42 to 51 and, 27 to 41, for Boadi, KK and Pacific farms, respectively. Blood waste-fertilized ponds showed 46 to 63 different strains, and chemically fertilized ponds 59 to 64 and 34 to 43 for Aheto and Sagoe farms, respectively while 55 to 56 PhP types were recorded for non-fertilized ponds. The open systems showed PhP types of 35 to 41, 30 to 39 and 29 to 41 for the Kpong Head Pond, Volta River and Weija Dam, respectively.

23. The percent occurrence of the different bacterial strains varied from pond to pond, and from one fertilisation type to another. *Pseudomonas* sp. was the predominant species in cow manure-fertilized ponds, blood waste-fertilized ponds, sewage-fed ponds, ponds with no fertilisation and in the open systems. *Salmonella* sp. was the predominant species in the poultry manure-fertilized ponds while the predominant species in the pig manure-fertilized ponds was *Streptococcus* sp.
24. Fish caught from the various culture systems were found to harbour bacteria belonging to the 25 genera of bacteria isolated from the different culture systems. Certain species of bacteria associated more with certain tissues of fish than with others.
25. Eleven feed types usually used in feeding the fish and the four organic manures used to fertilise the ponds all had resident bacteria. Bacterial groups detected in the feed included the heterotrophic bacteria, total coliform, faecal coliform and faecal streptococci.
26. Low heterotrophic bacterial count of the 11 feed types, banana waste, biscuit waste, bread waste, brewery spent grain, cassava waste, fufu waste, groundnut husk, rice bran, termites and wheat bran ranged from 2.85 log₁₀ CFU g⁻¹ to 4.28 log₁₀ CFU g⁻¹, while a much higher count of 6.17 - 6.86 log₁₀ CFU g⁻¹ was obtained for the four organic manures of blood waste, cow manure, pig manure and poultry manure. The values for the Most Probable Number (MPN) for Total Coliform and Faecal Streptococci were also high for the organic manures and very low for the feed types.
27. Eight pathogenic bacteria showed different longevities in five organic manures, blood waste, cow manure, pig manure, poultry manure and sewage. *Enterobacter* sp. KI-MTC-003K, *Klebsiella* sp. KI-MTC-004K, *Proteus* sp. KI-MTC-006K and *Pseudomonas* sp. KI-MTC-001K grew very well in the organic manures. *Citrobacter* sp. KI-MTC-005K, *Salmonella* sp. KI-MTC-007K and *Shigella* p. KI-MTC-002K showed moderate growth while *Vibrio parahaemolyticus* KI-MTC-008K grew very poorly.

28. In all a total of 20 different bacterial species were isolated from the fishermen and members of communities associated with the ponds. The number of species involved differed with the ponds.
29. Fifteen, 14, 13, 12 and 10 species were identified in communities of cow manure- (e.g. Aduabenba farm) and pig manure- (e.g. Boadi farm) fertilized ponds, chemically fertilized ponds (e.g. Sagoe farm), poultry manure-fertilized ponds (e.g. Frimpong farm), blood waste-fertilized ponds (e.g. Boahen farm), and sewage-fertilized ponds (e.g. Akuse farm), respectively. Nine species were recorded in communities of non-fertilized ponds (e.g. ARDEC 3) and 17 species in the open system communities (e.g. Weija dam).
30. i. Fishermen and families from cow manure-fertilized ponds recorded the highest number of individuals harbouring four of the isolates, namely, *Citrobacter diversus*, *Klebsiella oxytoca*, *Enterobacter cloacae* and *Pseudomonas* sp.
- ii. Poultry manure fertilized ponds communities recorded the highest number of individuals associated with *Klebsiella rhinoscleromatis*, *Salmonella* sp. and *Staphylococcus* sp.
- iii. Strains which were isolated from the highest number of individuals of communities of pig manure-fertilized pond farms were *Alcalescens dispar* and *Klebsiella ozanae*.
- iv. A higher number of individuals among fishermen and families working in and consuming fish from, blood waste-fertilized pond had *Micrococcus* sp. than any other species.
- v. Chemically-fertilized pond fishermen and their families recorded higher number of individuals harbouring *Alcalescens dispar* than any other species.
- vi. Fishermen and families working in and consuming fish from ponds which were not fertilized recorded the highest number of individuals with *Klebsiella oxytoca* and *Streptococcus faecalis*.
- vii. The greatest number of individuals with either, *Escherichia coli*, *Klebsiella pneumoniae*, *Proteus mirabilis*, *Proteus vulgaris*, *Pseudomonas* sp., *Shigella* sp. or *Streptococcus faecalis* was found in sewage-fed pond communities.

PHENOTYPES In adubenbt/ Identity (oval - 0.975
 *CALCULATED DIVERSITY INDEX * 0.922 TRUE DIVERSITY INDEX - 0.922

No	Name	PhP- typα	sim mln	sim mean	sim max	lo	PhP typκ
1.	BACILLUS	1	0.993	0.996 *	0.903 *	32	(14)
6.	6	1	0.989	0.996 *	0.897 *	32	(14)
59.	59	1	0.993	0.996 *	0.903 *	32	(14)
19.	19	1	0.992	0.995 *	0.906 *	32	(14)
9.	9	1	0.990	0.994 *	0.883 *	32	(14)
14.	14	1	0.991	0.995 *	0.888 *	32	(1<
42.	42	1	0.991	0.994 *	0.876 *	32	(14)
25.	25	1	0.991	0.994 *	0.904 *	32	(14)
69.	69	1	0.992	0.994 *	0.905 *	32	(14)
52.	52	1	0.989	0.992 *	0.888 *	32	(14)
73.	73	1	0.989	0.993 *	0.894 ■	32	(14)
32.	CONTROL	14	1.000	1.000 *	0.906 *	19	(D
80.	CONTROL	14	1.000	1.000 *	0.906 ■	19	(1)
30.	30	12	0.997	0.999 *	0.857 *	52	(1)
55.	55	12	0.997	0.999 *	0.857 *	52	(1)
76.	76	12	0.997	0.999 *	0.857 *	52	(1)
34.	34	12	0.995	0.996 *	0.856 *	52	(1)
48.	48	12	0.995	0.997 ■	0.862 *	52	(1)
4.	MICROCOCOCCUS LUT	3	0.999	0.999 *	0.847 *	32	(14)
23.	23	3	0.998	0.998 *	0.860 *	32	(14)
37.	37	3	0.998	0.998 *	0.852 *	32	(14)
51.	51	3	0.998	0.998 *	0.850 *	32	(14)
67.	67	3	0.998	0.998 *	0.861 *	32	(14)
74.	74	3	0.998	0.998 *	0.841 *	32	(14)
7.	PSEUDO AEROG	5	0.994	0.997 *	0.768 *	48	(12)
18.	18	5	0.996	0.998 *	0.777 *	48	(12)
40.	40	5	0.994	0.997 *	0.768 *	48	(12)
47.	47	5	0.994	0.997 *	0.771 *	48	(12)
50.	50	5	0.995	0.997 *	0.784 *	48	(12)
12.	12	5	0.992	0.995 *	0.789 *	48	(12)
75.	75	5	0.994	0.997 *	0.768 *	48	(12)
29.	29	5	0.993	0.996 *	0.796 *	48	(12)
57.	57	5	0.992	0.995 *	0.790 *	48	(12)
68.	68	5	0.992	0.996 *	0.788 ■	48	(12)
8.	PSEUDO AERO	6	1.000	1.000 *	0.850 *	60	(7)
28.	28	6	1.000	1.000 *	0.850 ■	60	(7)
10.	PSEUDO FLOURE	7	0.998	0.999 *	0.834 ■	8	(6)
45.	45	7	0.998	0.999 *	0.834 *	8	(6)
79.	79	7	0.998	0.999 *	0.834 *	8	(6)
26.	26	7	0.995	0.997 *	0.828 *	8	(6)
60.	60	7	0.995	0.997 *	0.850 *	8	(6)
2.	[CORYNEBACTERIUM DIPH	Si			0.000 *	32	(14)
3.	FLAVOBAC AQUA	2	0.996	0.997 *	0.918 *	27	(Si)
11.	11	2	0.995	0.997 *	0.920 *	27	(Si)
53.	53	2	0.993	0.996 *	0.919 *	27	(Si)
21.	21	2	0.992	0.996 *	0.923 *	27	(SO)
63.	63	2	0.995	0.997 *	0.921 *	27	(Si)
71.	71	2	0.991	0.996 *	0.923 *	27	(Si)
78.	78	2	0.993	0.995 *	0.921 *	27	(SO)
44.	44	2	0.991	0.994 *	0.908 *	27	(Si)
35.	35	2	0.991	0.994 *	0.911 *	27	(Si)
65.	65	2	0.991	0.994 *	0.909 *	27	(Si)
27.	27	Si			0.923 *	21	(2)
5.	PROTEUS MIRA	4	0.999	0.999 *	0.722 *	37	(3)
36.	36	4	0.999	0.999 *	0.722 *	37	(3)
38.	38	4	0.999	0.999 *	0.722 *	37	(3)
46.	46	4	0.999	0.999 *	0.721 *	37	(3)
58.	58	4	0.999	0.999 *	0.721 *	37	(3)
13.	SALMONELLA TYPH	8	1.000	1.000 *	0.816 *	66	(9)
77.	77	8	1.000	1.000 *	0.816 ■	66	(9)
15.	STPPLYLOCOCCUS AU	9	0.995	0.999 *	0.807 *	13	(8)
22.	22	9	0.996	0.999 *	0.807 *	13	(8)
33.	33	9	0.996	0.999 *	0.807 *	13	(8)
49.	49	9	0.996	0.999 *	0.807 *	13	(8)
70.	70	9	0.996	0.999 *	0.807 *	13	(8)
20.	20	9	0.992	0.997 *	0.814 *	13	(8)
66.	66	9	0.990	0.996 *	0.816 *	13	(8)
41.	41	9	0.990	0.995 *	0.786 *	13	(8)
62.	62	Si			0.754 *	15	(9)
16.	STREPTOCOCCUS FAE	10	0.998	0.999 *	0.732 *	62	(Si)
43.	43	10	0.998	0.999 *	0.732 *	62	(Si)
72.	72	10	0.998	0.999 *	0.732 *	62	(Si)
24.	24	10	0.995	0.997 *	0.749 *	62	(Si)
33.	33	10	0.995	0.997 *	0.749 *	62	(Si)
54.	54	10	0.995	0.997 *	0.724 *	62	(Si)
56.	56	10	0.995	0.997 *	0.724 *	62	(SO)
17.	ENTEROBACTER AERO	11	0.998	0.998 *	0.687 *	42	(1)
61.	61	11	0.998	0.998 *	0.694 *	42	(1)
31.	E COLI	13	0.990	0.999 *	0.696 *	35	(2)
64.	64	13	0.999	0.999 *	0.695 *	35	(2)

PHENOTYPES In »duiten2/		Identity Index		IT-		.CALCULATED DIVERSITY INDEX - 0.W8		TRUE DIVERSITY INDEX		0.908	
No	Na«	PhP- typ*	sim mln	aim moan	tun max	(0 nr	PhP typ«				
13.	13	1	0.999	0.999 *	0.708 *	59	(4)				
22.	22	1	0.999	0.999 *	0.711 *	59	(4)				
25.	25	1	0.999	0.999 *	0.708 *	59	(4)				
27.	27	1	0.999	0.999 *	0.701 *	59	(4)				
31.	31	1	0.999	0.999 *	0.718 *	59	(4)				
70.	70	1	0.999	0.999 *	0.711 *	59	(4)				
73.	73	1	0.999	0.999 *	0.708 *	59	(4)				
78.	75	1	0.999	0.999 *	0.701 *	59	(4)				
79.	79	1	0.999	0.999 *	0.718 *	59	(4)				
2.	ECOU	2	0.999	1.000 *	0.676 *	53	(5)				
7.	7	2	0.999	0.999 *	0.685 *	53	(5)				
24.	24	2	0.999	1.000 *	0.676 *	53	(5)				
72.	72	2	0.999	1.000 *	0.676 *	53	(5)				
3.	MICROCOCCLUS	3	0.999	1.000 *	0.945 *	19	(7)				
41.	41	3	0.999	1.000 *	0.945 *	19	(7)				
48.	46	3	0.999	1.000 *	0.945 *	19	(7)				
58.	58	3	0.999	1.000 *	0.945 *	19	(7)				
61.	61	3	0.999	0.999 *	0.944 *	19	(7)				
8.	8	7	0.999	1.000 *	0.927 *	3	(3)				
18.	16	7	0.999	1.000 *	0.927 *	3	(3)				
18.	18	7	0.999	1.000 *	0.927 *	3	(3)				
19.	19	7	0.998	0.999 *	0.945 *	3	(3)				
28.	28	7	0.999	1.000 *	0.927 *	3	(3)				
39.	39	7	0.998	0.999 *	0.928 *	33	(9)				
66.	66	7	0.999	1.000 *	0.927 *	3	(3)				
67.	67	7	0.998	0.999 *	0.945 *	3	(3)				
76.	76	7	0.999	1.000 *	0.927 *	3	(3)				
6.	PROTEUS MIRA	6	0.999	1.000 *	0.917 *	38	(SO)				
15.	15	6	0.999	0.999 *	0.917 *	38	(SO)				
21.	21	6	0.999	1.000 *	0.917 *	38	(SO)				
36.	36	6	0.999	1.000 *	0.917 *	38	(SO)				
62.	62	6	0.999	1.000 *	0.917 *	38	(SO)				
69.	69	6	0.999	1.000 *	0.917 *	33	(SO)				
38.	38	SI			0.917 *	6	(6)				
11.	11	SI			0.910 *	38	(SO)				
55.	55	SI			0.824 *	33	(SO)				
4.	14	4	0.992	0.997 *	0.909 *	64	(9)				
14.	114	4	0.992	0.996 *	0.899 *	64	(9)				
40.	140	4	0.992	0.996 *	0.899 *	64	(9)				
49.	49	4	0.993	0.996 *	0.894 *	64	(9)				
20.	120	4	0.992	0.997 *	0.903 *	64	(9)				
42.	142	4	0.994	0.996 *	0.897 *	64	(9)				
68.	168	4	0.992	0.997 *	0.903 *	64	(9)				
26.	126	4	0.993	0.996 *	0.910 *	64	(9)				
74.	174	4	0.993	0.996 *	0.910 *	64	(9)				
35.	135	4	0.993	0.997 *	0.909 *	64	(9)				
47.	147	4	0.990	0.995 *	0.897 *	64	(9)				
51.	151	4	0.990	0.996 *	0.894 *	64	(9)				
59.	159	4	0.987	0.993 *	0.908 *	64	(9)				
32.	132	4	0.987	0.992 *	0.905 *	64	(9)				
60.	160	4	0.987	0.992 *	0.905 *	64	(9)				
33.	CONTROL	9	0.998	0.998 *	0.928 *	39	(7)				
64.	CONTROL	9	0.998	0.998 *	0.925 *	39	(7)				
17.	17	8	0.996	0.997 *	0.848 *	47	(4)				
65.	65	8	0.996	0.997 *	0.848 *	47	(4)				
29.	29	8	0.996	0.998 *	0.851 *	47	(4)				
44.	44	8	0.996	0.998 *	0.855 *	47	(4)				
57.	57	8	0.996	0.998 *	0.853 *	47	(4)				
63.	63	8	0.996	0.998 *	0.851 *	47	(4)				
77.	77	8	0.996	0.998 *	0.851 *	47	(4)				
56.	56	SI			0.854 *	49	(4)				
50.	50	11	1.000	1.000 *	0.808 *	56	(SO)				
52.	52	11	1.000	1.000 *	0.808 *	56	(SI)				
54.	54	11	1.000	1.000 *	0.808 *	56	(SO)				
5.	5	5	0.999	0.999 *	0.928 *	46	(SO)				
9.	9	5	0.999	0.999 *	0.927 *	46	(SO)				
10.	10	5	0.999	0.999 *	0.928 *	46	(SI)				
23.	23	5	0.999	0.999 *	0.927 *	46	(SO)				
30.	30	5	0.999	0.999 *	0.927 *	46	(SO)				
34.	34	5	0.999	0.999 *	0.928 *	46	(SO)				
37.	37	5	0.999	0.999 *	0.928 *	46	(SO)				
53.	53	5	0.999	0.999 *	0.916 *	46	(SO)				
71.	71	5	0.999	0.999 *	0.927 *	46	(SO)				
78.	78	5	0.999	0.999 *	0.927 *	46	(SO)				
46.	46	SI			0.028 *	5	(5)				
60.	60	SI			0.874 *	9	(5)				
12.	PROTEUS MIRA	SI			0.457 *	43	(10)				
43.	43	10	1.000	1.000 *	0.500 *	11	(SO)				
45.	45	10	1.000	1.000 *	0.500 *	11	(SO)				

Appendix 1c

PHENOTYPES In aduabong/ CALCULATED DIVERSITY INDEX □ 0.944		Identity level * 0.975 TRUE DIVERSITY INDEX - 0.944				
No Nama	PhP- sim type min	aim mean	aim max	to nr	PhP type	
1.	STREPTOCOCCUS FAE	1	1.000	1.000	0.793 *	21 (9)
3.	STREPTOFOE	1	1.000	1.000	0.793 *	21 (9)
7.	5	1	1.000	1.000	0.793 *	21 (9)
24.	22	1	1.000	1.000	0.793 *	21 (9)
40.	36	1	1.000	1.000	0.793 *	21 (9)
21.	CITROBACTER	9	1.000	1.000	0.793 *	1 (1)
29.	27	9	1.000	1.000	0.793 *	1 (1)
37.	CITROBACTER	9	1.000	1.000	0.793 *	1 (1)
45.	43	9	1.000	1.000	0.793 *	1 (1)
60.	58	9	1.000	1.000	0.793 *	1 (1)
79.	77	9	1.000	1.000	0.793 *	1 (1)
2.	2	2	1.000	1.000	0.771 *	28 (11)
4.	PSEUDO FLUORE	2	1.000	1.000	0.771 *	28 (11)
18.	16	2	1.000	1.000	0.771 *	28 (11)
28.	26	11	0.991	0.998 *	0.771 *	2 (2)
44.	42	11	0.991	0.998 *	0.771 *	2 (2)
51.	49	11	0.991	0.998 *	0.771 *	2 (2)
54.	52	11	0.991	0.998 *	0.771 *	2 (2)
68.	66	11	0.991	0.998 *	0.771 *	2 (2)
70.	68	11	0.991	0.998 *	0.771 *	2 (2)
61.	59	11	0.991	0.991 *	0.750 *	55 (15)
5.	PROTEUS VULG	Si			0.882 *	67 (Si)
67.	AEROMONAS HYDRO	Si			0.882 *	5 (Si)
36.	34	Si			0.841 *	67 (Si)
12.	10	6	0.999	1.000	0.836 *	67 (Si)
15.	13	6	0.999	1.000	0.836 *	67 (Si)
20.	18	6	0.999	1.000	0.836 *	67 (Si)
31.	29	6	0.999	1.000	0.836 *	67 (SO)
47.	45	6	0.999	1.000	0.836 *	67 (Si)
75.	73	6	0.999	1.000	0.836 *	67 (Si)
55.	53	15	1.000	1.000	0.786 *	67 (Si)
58.	56	15	1.000	1.000	0.786 *	67 (Si)
66.	64	15	1.000	1.000	0.786 *	67 (Si)
72.	70	15	1.000	1.000	0.786 *	67 (Si)
77.	75	15	1.000	1.000	0.786 *	67 (Si)
6.	ECOLI	3	1.000	1.000	0.655 *	55 (15)
13.	11	3	1.000	1.000	0.655 *	55 (15)
8.	PROTEUS MIRA	4	0.997	0.999 *	0.724 *	52 (13)
11.	9	4	0.996	0.998 *	0.723 *	52 (13)
27.	25	4	0.997	0.999 *	0.724 *	52 (13)
30.	28	4	0.997	0.999 *	0.724 *	52 (13)
43.	41	4	0.997	0.999 *	0.724 *	52 (13)
46f	44	4	0.997	0.999 *	0.724 *	52 (13)
39.	37	4	0.996	0.997 *	0.724 *	52 (13)
9.	PSEUDO AERO	5	0.998	1.000	0.806 *	48 (8)
10.	PROTEUS MIRA	5	0.998	1.000	0.806 *	48 (S)
17.	15	5	0.998	1.000	0.806 *	48 (8)
22.	20	5	0.998	1.000	0.806 *	48 (8)
33.	31	5	0.998	1.000	0.806 *	48 (8)
36.	36	5	0.998	1.000	0.806 *	48 (8)
49.	47	5	0.998	0.998 *	0.805 *	25 (10)
25.	23	10	1.000	1.000	0.805 *	49 (5)
41.	39	10	1.000	1.000	0.805 *	49 (5)
62.	60	10	1.000	1.000	0.805 *	49 (5)
19.	17	8	0.992	0.999 *	0.842 *	34 (12)
26.	24	8	0.992	0.999 *	0.842 *	34 (12)
32.	30	8	0.992	0.999 *	0.842 *	34 (12)
35.	33	8	0.992	0.999 *	0.842 *	34 (12)
42.	40	8	0.992	0.999 *	0.842 *	34 (12)
57.	55	8	0.992	0.999 *	0.842 *	34 (12)
65.	63	8	0.992	0.999 *	0.842 *	34 (12)
71.	69	8	0.992	0.999 *	0.842 *	34 (12)
80.	78	8	0.992	0.999 *	0.842 *	34 (12)
48.	46	8	0.992	0.992 *	0.850 *	34 (12)
34.	CONTROL	12	1.000	1.000	0.922 *	53 (14)
50.	CONTROL	12	1.000	1.000	0.922 *	53 (14)
81.	CONTROL	12	1.000	1.000	0.922 *	53 (14)
69.	167	18	1.000	1.000	0.903 *	34 (12)
76.	174	16	1.000	1.000	0.903 *	34 (12)
52.	50	13	0.992	0.992 *	0.922 *	53 (14)
56.	54	13	0.992	0.998 *	0.927 *	53 (14)
59.	57	13	0.992	0.998 *	0.927 *	53 (14)
64.	62	13	0.992	0.998 *	0.927 *	53 (14)
78.	76	13	0.992	0.998 *	0.927 *	53 (14)
53.	51	14	1.000	1.000	0.927 *	53 (13)
63.	61	14	1.000	1.000	0.927 *	58 (13)
14.	ENTEROBACTER AERO	7	1.000	1.000	0.677 *	69 (16)
16.	14	7	1.000	1.000	0.677 *	69 (16)
23.	21	Si			0.744 *	53 (14)
73.	71	Si			0.879 *	55 (15)
74.	72	Si			0.405 *	14 (7)

Appendix							
PHENOTYPES in ad u a boo?		Identity level - 0.975					
CALCULATED DIVERSITY INDEX - 0.962		TRUE DIVERSITY INDEX + 0.962					
No	Name	PhP- type	aim mkl	aim moan	aim mu	to nr	PhP type
1.	STREP FAEC	1	0.983	0.997 *	0.578 *	14	OD
10.	10	1	0.993	0.997 *	0.578 *	14	(11)
36.	35	1	0.992	0.995 *	0.589 *	14	(11)
19.	19	1	0.992	0.993 *	0.593 *	14	(11)
2.	STAP AUR	2	0.979	0.989 *	0.838 *	14	(11)
44.	43	2	0.983	0.991 *	0.647 *	14	(11)
22.	22	2	0.983	0.990 *	0.825 *	14	(11)
15.	15	2	0.963	0.987 *	0.846 *	14	(11)
26.	25	2	0.979	0.985 *	0.829 *	14	(11)
14.	14	11	1.000	1.000 *	0.847 *	44	(2)
21.	21	11	1.000	1.000 *	0.647 *	44	(2)
7.	PROTEUS-OUL	7	0.996	0.998 *	0.809 *	14	(11)
17.	17	7	0.998	0.998 *	0.811 *	14	(11)
6.	PROTEUS MIRA	8	0.997	0.997 *	0.969 *	40	(17)
33.	33	3	0.997	0.997 *	0.965 *	40	(17)
38.	37	17	0.997	0.997 *	0.965 *	8	(8)
40.	39	17	0.997	0.997 *	0.969 *	8	(8)
9.	MICRO SP	9	0.991	0.995 *	0.951 *	54	(Si)
62.	61	9	0.991	0.995 *	0.951 *	54	(Si)
49.	46	9	0.987	0.992 *	0.933 *	27	(13)
42.	41	9	0.987	0.990 *	0.944 *	54	(Si)
54.	53	Si			0.951 *	9	(9)
27.	26	13	1.000	1.000 *	0.933 *	49	(9)
34.	33	13	1.000	1.000 *	0.933 *	49	(9)
64.	CONTROL	Si			0.922 *	27	(13)
30.	29	14	0.999	0.999 *	0.969 *	63	(Si)
56.	55	14	0.999	0.999 *	0.969 *	63	(Si)
59.	58	14	0.999	0.999 *	0.970 *	63	(Si)
63.	62	Si			0.970 *	59	(14)
32.	31	15	1.000	1.000 *	0.903 *	64	(Si)
51.	50	15	1.000	1.000 *	0.903 *	64	(Si)
3.	STAPEVID	3	0.987	0.994 *	0.782 *	48	(Si)
31.	30	3	0.986	0.994 *	0.773 *	48	(SO)
60.	59	3	0.986	0.994 *	0.773 *	48	(SO)
58.	57	3	0.985	0.993 *	0.776 *	5	(5)
52.	51	3	0.976	0.988 *	0.609 *	5	(5)
12.	12	3	0.976	0.984 *	0.779 *	48	(Si)
5.	PSEUDO FLUORE	5	1.000	1.000 *	0.809 *	52	(3)
20.	20	5	1.000	1.000 *	0.809 *	52	(3)
4.	SERMER	4	1.000	1.000 *	0.771 *	14	(11)
13.	13	4	1.000	1.000 *	0.771 *	14	(11)
16.	16	4	1.000	1.000 *	0.771 *	14	(11)
6.	PSEUDO AUR	6	0.987	0.994 *	0.776 *	23	(12)
24.	24	6	0.987	0.994 *	0.776 *	23	(12)
50.	49	6	0.987	0.994 *	0.776 *	23	(12)
47.	46	6	0.973	0.985 *	0.788 *	23	(12)
41.	40	6	0.973	0.983 *	0.813 *	59	(14)
23.	23	12	0.994	0.998 *	0.788 *	47	(6)
29.	26	12	0.994	0.998 *	0.788 *	47	(6)
48.	45	12	0.994	0.998 *	0.788 *	47	(6)
57.	58	12	0.994	0.998 *	0.788 *	47	(6)
55.	54	12	0.994	0.994 *	0.766 *	47	(6)
25.	25	Si			0.969 *	37	(16)
28.	27	Si			0.962 *	35	(16)
35.	34	16	0.983	0.992 *	0.962 *	28	(SO)
45.	44	16	0.983	0.992 *	0.962 *	28	(SO)
37.	36	16	0.983	0.983 *	0.969 *	25	(SO)
48.	47	Si			0.956 *	35	(16)
53.	52	19	1.000	1.000 *	0.619 *	28	(SO)
61.	60	19	1.000	1.000 *	0.819 *	28	(SO)
11.	ENTEROBACTER COLI	10	1.000	1.000 *	0.492 *	63	(SO)
16.	18	10	1.000	1.000 *	0.694 *	28	(SO)
39.	36	16	1.000	1.000 *	0.677 *	32	(15)
43.	42	16	1.000	1.000 *	0.677 *	32	(15)

Appendix 1 Q

PHENOTYPES in aduabens/
IDENTITY level = 0.975
*CALCULATED DIVERSITY INDEX * 0.962 TRUE DIVERSITY INDEX * 0.962

No	Name	PhP- type	sim min	sim mean	sim max	lo nr	PhP type
1	STAPHYLOCOCCUS	i	0.986	0.997 *	0.983 ?	21	(14)
34	34	i	0.986	0.997 *	0.983 ?	21	(14)
37	37	i	0.986	0.997 *	0.983 ?	21	(14)
43	43	i	0.986	0.997 *	0.983 ?	21	(14)
31	31	i	0.981	0.994 *	0.982 ?	21	(14)
39	39	i	0.991	0.996 *	0.984 ?	21	(14)
17	17	i	0.981	0.986 *	0.974 *	24	(S)
24	24	Si			0.974 *	17	d)
21	21	14	0.975	0.984 *	0.984 ?	39	(1)
26	26	14	0.984	0.989 *	0.978 ?	1	(1)
28	28	14	0.975	0.979 *	0.965 *	1	(1)
3	PSEUDO FLOURE	3	0.991	0.991 ■	0.956 *	33	(S)
41	41	3	0.991	0.996 *	0.964 *	33	(S)
60	60	3	0.991	0.996 *	0.964 *	33	(S)
33	33	Si			0.964 *	41	(3)
46	46	Si			0.965 *	48	(S)
48	48	Si			0.965 *	46	(S)
7	MICROCOCCLUS LOT	7	0.983	0.983 *	0.983 ?	45	(18)
40	40	7	0.983	0.994 *	0.960 *	35	(SO)
54	54	7	0.983	0.994 *	0.960 *	35	(S)
54	54	7	0.983	0.994 *	0.960 *	35	(S)
42	42	16	0.984	0.984 *	0.964 *	7	(7)
45	45	16	0.984	0.984 *	0.983 ?	7	(7)
67	67	Si			0.957 *	7	(7)
20	20	13	0.998	0.998 *	0.972 *	35	(S)
22	22	13	0.996	0.997 *	0.974 *	35	(S)
75	75	13	0.996	0.997 *	0.969 *	35	(S)
35	35	Si			0.974 *	22	(13)
32	CONTROL	15	1.000	1.000 *	0.922 *	7	(7)
64	CONTROL	15	1.000	1.000 *	0.922 *	7	(7)
80	CONTROL	15	1.000	1.000 ■	0.922 *	7	(7)
66	66	Si			0.930 *	7	(7)
10	CORYNEBACTERIUM DIPH	10	1.000	1.000 ■	0.894 *	65	(S)
56	56	10	1.000	1.000 *	0.854 *	65	(S)
11	BACILLUS	11	0.989	0.995 *	0.957 *	65	(S)
14	14	11	0.989	0.995 *	0.957 *	65	(S)
63	63	11 ■	0.988	0.994 *	0.970 *	65	(SO)
59	59	11	0.975	0.987 *	0.948 ■	65	(SO)
69	69	11	0.981	0.988 *	0.972 *	77	(S)
74	74	11	0.985	0.992 *	0.972 *	77	(S)
72	72	11	0.986	0.992 *	0.950 *	65	(SO)
78	78	11	0.975	0.986 *	0.947 *	77	(S)
65	65	Si			0.970 *	63	(11)
77	77	Si			0.972 *	69	(11)
68	68	Si			0.957 *	11	(11)
4	PSEUDO AERO	4	0.975	0.975 *	0.966 *	12	(SO)
25	25	4	0.975	0.975 *	0.935 *	19	(12)
12	12	Si			0.966 *	4	<-)
19	19	12	0.986	0.986 *	0.966 *	4	(4)
58	58	12	0.986	0.993 *	0.942 *	4	<-)
62	62	12	0.988	0.993 *	0.942 *	4	(4)
5	PROTEUS MIRA	5	1.000	1.000 *	0.966 *	50	(17)
13	13	5	1.000	1.000 *	0.966 *	50	(17)
50	50	17	0.997	0.997 *	0.966 *	5	(5)
55	55	17	0.997	0.997 *	0.963 *	5	(5)
6	PROTEUS VULG	6	0.958	0.970 *	0.774 *	38	(8)
47	47	6	0.907	0.979 *	0.701 *	38	(8)
44	44	6	0.969	0.979 ■	0.836 *	5	(5)
53	53	6	0.967	0.978 *	0.849 *	5	(5)
8	FLAVOBAC AQUA	8	0.972	0.984 *	0.972 *	71	(SO)
36	36	8	0.972	0.984 *	0.972 *	71	(S)
38	38	8	0.979	0.979 *	0.953 *	71	(SO)
70	70	8	0.972	0.974 ?	0.972 *	71	(SO)
71	71	Si			0.972 *	8	(8)
73	73	Si			0.971 *	79	(SO)
79	79	Si			0.971 *	73	(S)
2	STRETOCOCCUS FAE	2	0.971	0.988 *	0.557 *	73	(S)
18	18	2	0.973	0.983 *	0.528 *	73	(SO)
29	29	2	0.961	0.984 *	0.581 *	73	(S)
52	52	2	0.977	0.988 *	0.532 *	73	(S)
49	49	2	0.955	0.983 *	0.597 *	73	(SO)
57	57	2	0.952	0.978 *	0.570 *	73	(S)
23	23	2	0.973	0.981 *	0.525 *	68	(SO)
16	16	2	0.952	0.967 ?	0.523 *	68	(SO)
9	E COU	9	1.000	1.000 *	0.725 *	71	(S)
27	27	9	1.000	1.000 *	0.725 *	71	(so)
30	30	9	1.000	1.000 *	0.725 *	71	(S)
15	1 15	Si			0.940 *	61	(so)
61	161	Si			0.940 *	15	(S)
76	76	Si			0.110 *	12	(S)

Appendix If

No	Nam*	PhP- typ*	µm min	µm maan	µm max	to nr	PhP type
1	BACILLUS	1	1.000	1.000	0.913 *	32	(12)
47.	47	1	1.000	1.000	0.913 *	32	(12)
87.	67	1	1.000	1.000	0.913 *	32	(12)
72.	72	i	1.000	1.000	0.913 *	32	(12)
32.	CONTROL	12	0.691	0.991	0.913 *	1	(1)
80.	CONTROL	12	0.991	0.991	0.922 *	62	(SO)
01.	61	SI			0.858 *	1	(1)
5.	MICROCO SP	SI			0.926 *	62	(SI)
02.	62	SI			0.926 *	5	(SO)
54.	54	SI			0.902 *	62	(SI)
49.	49	SI			0.887 *	62	(SI)
76.	76	SI			0.902 *	62	(SI)
75.	75	SI			0.858 *	1	(1)
4.	FLAVOBAC SP	4	1.000	1.000	0.925 *	13	(SI)
03.	63	4	1.000	1.000	0.925 *	13	(SO)
13.	13	SI			0.925 *	4	(4)
25.	25	SI			0.919 *	4	(4)
38.	38	SI			0.913 *	25	(SO)
59.	59	SI			0.902 *	38	(SO)
50.	50	SI			0.849 *	4	(4)
58.	58	SI			0.815 *	38	(so)
2.	CORYNEBAC	2	1.000	1.000 ¹	0.910 *	41	(so)
77.	77	2	1.000	1.000 ¹	0.910 *	41	(so)
79.	79	2	1.000	1.000 ¹	0.910 *	41	(so)
41.	41	SI			0.910 *	2	(2)
7.	PSEUDO AEROG	6	1.000	1.000 ¹	0.941 *	22	(SO)
11.	11	6	1.000	1.000 ¹	0.941 *	22	(SI)
22.	22	SI			0.951 *	35	(so)
35.	35	SI			0.951 *	22	(SO)
14.	14	9	1.000	1.000 ¹	0.916 *	7	(0)
53.	53	9	1.000	1.000	0.910 *	7	(6)
19.	19	SI			0.896 *	7	(6)
52.	52	SI			0.868 *	7	(6)
00.	00	SI			0.826 *	7	(6)
6.	PROTEUS MIRA	5	1.000	1.000	0.932 *	15	(SO)
57.	57	5	1.000	1.000	0.932 *	15	(so)
88.	08	5	1.000	1.000	0.932 *	15	(so)
15.	15	SI			0.932 *	6	(5)
09.	69	SI			0.875 *	54	(SO)
04.	64	SI			0.870 *	6	(5)
17.	17	SI			0.880 *	6	(5)
27.	27	SI			0.863 *	17	(SO)
9.	9	8	1.000	1.000	0.834 *	31	(SO)
42.	42	8	1.000	1.000	0.834 *	31	(SO)
31.	31	SI			0.834 *	9	(8)
20.	20	SI			0.775 *	13	(SO)
21.	21	SI			0.755 *	9	(8)
20.	26	SI			0.755 *	9	(8)
30.	30	11	1.000	1.000 ¹	0.896 *	73	(SO)
30.	36	11	1.000	1.000	0.896 *	73	(SO)
73.	73	SI			0.896 *	30	(ii)
40.	40	SI			0.865 *	30	(ii)
51.	51	SI			0.753 *	30	(11)
78.	78	SI			0.880 *	5	(SO)
3.	ECOLI	3	1.000	1.000	0.939 *	55	(so)
33.	33	3	1.000	1.000	0.939 *	55	(SO)
45.	45	3	1.000	1.000	0.939 *	55	(SI)
74.	74	3	1.000	1.000	0.939 *	55	(SO)
55.	55	SI			0.939 *	3	(3)
10.	10	SI			0.886 *	3	(3)
29.	29	SI			0.886 *	3	(3)
8.	STREPTOCO FAE	7	1.000	1.000	0.959 *	44	(SO)
18.	18	7	1.000	1.000	0.959 *	44	(SO)
39.	39	7	1.000	1.000	0.959 *	44	(SO)
56.	56	7	1.000	1.000	0.959 *	44	(SO)
44.	44	SI			0.959 *	8	(7)
12.	12	SI			0.957 *	8	(7)
20.	26	SI			0.955 *	8	(7)
10.	16	SI			0.923 *	8	(7)
23.	23	SI			0.926 *	8	(7)
24.	24	10	1.000	1.000	0.513 *	54	(SO)
65.	OS	10	1.000	1.000	0.513 *	54	(SO)
34.	34	13	1.000	1.000	0.735 *	17	(SO)
48.	48	13	1.000	1.000	0.735 *	17	(SO)
37.	37	SI			0.630 *	27	(SO)
43.	43	SI			0.751 *	35	(SO)
48.	46	SI			0.569 *	34	(13)
66.	1166	14	1.000	1.000	0.000 *	54	(SO)
70.	11 70	14	1.000	1.000	0.000 *	54	(SI)
71.	71	SI			0.645 *	29	(SI)

PHENOTYPES in boaleng2/		Idonilly/lava/ 0.978 *		TRUE DIVERSITY INDEX - 0.973		
*CALCULATED DIVERSITY INDEX = 0.978						
No	Name	PhP- sim	sim	to	PhP	
		typo min mean	max	nr	typ*	
1.	BACILLUS	1	1.000	1.000	0.908	40 (SI)
9.	9	1	1.000	1.000	0.908	40 (SI)
40.	CONTROL	Si			0.908	1 (1)
2.	CORYNEBAC	Si			0.866	40 (SI)
13.	13	Si			0.851	2 (SI)
5.	MICROCO SP	Si			0.823	40 (SI)
4.	FLAVOBAC	Si			0.929	20 (SI)
20.	20	Si			0.929	4 (SI)
12.	12	Si			0.915	75 (SO)
75.	75	Si			0.915	12 (SI)
7.	PSEUDO AERO	Si			0.893	3B (SI)
36.	36	Si			0.893	7 (SI)
24.	24	Si			0.919	50 (SI)
50.	50	Si			0.919	24 (SI)
60.	60	Si			0.786	24 (SI)
73.	! 73	Si			0.775	24 (SO)
3.	E COLI	2	0.982	0.982	0.938	10 (SI)
23.	23	2	0.982	0.982	0.944	30 (SO)
44.	44	2	0.982	0.982	0.944	30 (SI)
30.	30	Si			0.944	23 (2)
10.	10	Si			0.938	3 (2)
67.	67	Si			0.856	10 (SO)
35.	35	Si			0.924	23 (2)
39.	39	Si			0.924	23 (2)
6.	PROTEUS MIRA	Si			0.904	32 (SO)
32.	32	Si			0.904	6 (SI)
25.	25	Si			0.874	6 (so)
16.	16	Si			0.835	6 (so)
8.	STREPTOCO FAE	3	0.990	0.990	0.942	19 (SO)
26.	26	3	0.990	0.990	0.953	19 (SO)
53.	53	3	0.990	0.990	0.953	19 (SO)
19.	19	Si			0.953	26 (3)
14.	14	Si			0.942	19 (SO)
31.	31	Si			0.914	26 (3)
48.	48	Si			0.886	14 (SI)
36.	36	Si			0.918	26 (3)
11.	11	4	0.977	0.977	0.748	22 (so)
33.	33	4	0.977	0.977	0.816	22 (SO)
22.	22	Si			0.816	33 (e)
15.	! 15	Si			0.562	73 (SI)
17.	17	5	1.000	1.000	0.690	71 (SI)
63.	63	5	1.000	1.000	0.690	71 (SI)
18.	18	6	1.000	1.000	0.838	27 (8)
61.	61	6	1.000	1.000	0.838	27 (8)
27.	! 27	8	1.000	1.000	0.838	18 (6)
54.	! 54	8	1.000	1.000	0.838	18 (6)
21.	21	7	1.000	1.000	0.551	78 (SO)
34.	34	7	1.000	1.000	0.551	76 (SO)
28.	28	Si			0.704	50 (SO)
29.	29	Si			0.733	40 (SI)
37.	37	Si			0.590	27 (8)
41.	41	Si			0.786	46 (SO)
46.	46	Si			0.786	41 (SI)
42.	42	9	1.000	1.000	0.699	71 (so)
52.	52	9	1.000	1.000	0.699	71 (so)
43.	! 43	10	1.000	1.000	0.000	71 (SO)
45.	! 45	10	1.000	1.000	0.000	30 (SI)
55.	! 55	10	1.000	1.000	0.000	18 (0)
56.	! 56	10	1.000	1.000	0.000	18 (6)
58.	! 58	10	1.000	1.000	0.000	18 (6)
64.	! 64	10	1.000	1.000	0.000	71 (SO)
68.	! 68	10	1.000	1.000	0.000	10 (SO)
70.	! 70	10	1.000	1.000	0.000	74 (SI)
77.	! 77	10	1.000	1.000	0.000	73 (SO)
78.	H 78	10	1.000	1.000	0.000	73 (SI)
80.	! 80	10	1.000	1.000	0.000	65 (SI)
47.	47	Si			0.949	49 (SO)
49.	49	Si			0.949	47 (SO)
51.	! 51	Si			0.585	4 (SI)
57.	57	Si			0.504	18 (6)
59.	59	Si			0.724	47 (SI)
62.	162	Si			0.772	72 (SI)
72.	72	Si			0.772	62 (SI)
65.	65	Si			0.612	79 (SI)
66.	166	Si			0.476	10 (SI)
69.	69	Si			0.618	74 (SI)
71.	71	Si			0.699	42 (9)
74.	74	Si			0.656	32 (SO)
76.	76	Si			0.664	73 (SO)
79.	179	Si			0.612	65 (so)

Appendix 1 b
 PHENOTYPES in boalong3/ Idnility Usvd - 0.075
 ..CALCULATED DIVERSITY INDEX - 0.987 TRUE DIVERSITY INDEX - 0.867

No	Nama	PhP- typ*	»lm mln	aim moan	aim max	to nr	PhP type
1.	STREPTOCO FAE	1	1.000	1.000 *	0.953 *	29	(SI)
12.	12	1	1.000	1.000 *	0.953 *	29	(SI)
19.	19	1	1.000	1.000 *	0.953 *	29	(SI)
29.	28	SI			0.953 *	1	(1)
46.	45	SI			0.914 *	1	(1)
38.	35	SI			0.918 *	1	(1)
2.	IICORYNEBAC	2	1.000	1.000 *	0.000 *	29	(SI)
5.	IIMICROCO SP	2	1.000	1.000 *	0.000 *	28	(SO)
8.	IIBACILLUS	2	1.000	1.000 *	0.000 *	39	(SO)
35.	1134	2	1.000	1.000 *	0.000 *	7	(SO)
63.	II 62	2	1.000	1.000 *	0.000 *	25	(SO)
74.	II 73	2	1.000	1.000 *	0.000 *	42	(12)
81.	IICONTROL	2	1.000	1.000 *	0.000 *	73	(SI)
3.	ECOU	3	0.982	0.994 *	0.922 *	37	(SO)
11.	11	3	0.982	0.994 *	0.922 *	37	(SO)
22.	22	3	0.982	0.994 *	0.922 *	37	(SO)
54.	53	3	0.982	0.982 *	0.909 *	37	(SO)
37.	38	SI			0.922 *	3	(3)
59.	58	SI			0.901 *	37	(SO)
45.	44	SI			0.857 *	3	(3)
31.	30	SI			0.860 ■	3	(3)
4.	IIFLAVOBAC	4	1.000	1.000 *	0.829 *	28	(SO)
9.	19	4	1.000	1.000 *	0.829 *	28	(SO)
20.	120	4	1.000	1.000 *	0.829 *	28	(SO)
28.	27	SI			0.829 *	4	(4)
32.	131	SI			0.796 *	4	(4)
8.	PROTEUS MIRA	SI			0.794 *	80	(SO)
80.	79	SI			0.838 *	73	(SO)
18.	18	9	1.000	1.000 *	0.926 *	42	(12)
52.	51	9	1.000	1.000 ■	0.926 *	42	(12)
42.	41	12	1.000	1.000 *	0.926 *	18	(9)
58.	57	12	1.000	1.000 *	0.926 *	18	(9)
73.	72	SI			0.902 *	42	(12)
66.	65	SI			0.875 *	41	(1)
41.	CONTROL	11	0.977	0.977 *	0.924 *	56	(SI)
70.	69	11	0.977	0.977 *	0.900 *	78	(SO)
56.	55	SI			0.924 *	41	(11)
78.	77	SI			0.900 *	70	(11)
43.	42	SI			0.887 *	42	(12)
28.	26	SI			0.932 *	71	(SO)
71.	70	SI			0.932 *	26	(SO)
40.	39	SI			0.898 *	26	(SI)
7.	PSEUDO AERO	SI			0.883 *	39	(SO)
34.	33	SI			0.786 *	7	(SO)
14.	14	SI			0.830 *	64	(SO)
25.	25	SI			0.918 *	39	(SO)
39.	38	SI			0.918 *	25	(SI)
49.	48	SI			0.916 *	25	(SO)
64.	63	SI			0.884 *	25	(SO)
77.	76	SI			0.903 *	25	(SO)
10.	16	6	1.000	1.000 ■	0.830 *	55	(SO)
21.	21	8	1.000	1.000 *	0.830 *	55	(SO)
55.	54	SI			0.830 *	16	(8)
27.	27	10	0.997	0.997 *	0.923 *	68	(SO)
53.	52	10	0.997	0.997 *	0.925 *	68	(SO)
61.	60	SI			0.929 *	68	(SO)
68.	87	SI			0.929 *	61	(SI)
44.	43	SI			0.903 *	45	(SO)
48.	47	SI			0.903 *	44	(SO)
72.	71	SI			0.855 *	44	(SO)
50.	49	SI			0.854 *	70	(11)
89.	88	SI			0.885 *	44	(SO)
57.	56	SI			0.880 *	18	(9)
85.	64	SI			0.837 *	75	(SO)
75.	74	SI			0.837 *	65	(SO)
67.	66	SI			0.763 *	70	(11)
79.	78	SI			0.858 *	56	(SO)
10.	10	5	1.000	1.000 *	0.690 *	24	(SO)
17.	17	5	1.000	1.000 *	0.690 *	24	(SO)
13.	13	8	1.000	1.000 *	0.690 *	29	(SI)
23.	23	8	1.000	1.000 *	0.690 *	29	(SO)
15.	15	7	1.000	1.000 ■	0.624 *	28	(SO)
33.	32	7	1.000	1.000 *	0.624 *	28	(SI)
24.	24	SI			0.690 **	10	(5)
30.	29	SI			0.686 *	14	(SO)
30.	37	SI			0.563 *	45	(SI)
47.	46	SI			0.578 *	50	(SO)
51.	50	SI			0.282 *	30	(SO)
60.	59	SI			0.749 *	75	(SO)
02.	61	SI			0.698 *	25	(SO)
78.	75	SI			0.604 *	30	(SI)

PHENOTYPES m boateng4/
 CALCULATED DIVERSITY INDEX * 0.978 TRUE DIVERSITY INDEX □ 0.976

Appendix 1j

Identity level □ 0.975

No	Name	PhP- lypκ	slm mln	sun mean	max	to nr	PhP typκ
1.	BACILLUS	1	1.000	1.000 *	0.000 *	6	(S)
17.	1117	1	1.000	1.000 *	0.000 *	4	(3)
30.	1130	1	1.000	1.000 *	0.000 *	6	(Si)
40.	IICONTROL	1	1.000	1.000 *	0.000 *	73	(Si)
41.	1141	1	1.000	1.000 *	0.000 *	73	(Si)
43.	1143	1	1.000	1.000 *	0.000 *	64	(*)
47.	1147	1	1.000	1.000 *	0.000 *	78	(Si)
49.	1149	1	1.000	1.000 *	0.000 *	73	(Si)
65.	1165	1	1.000	1.000 *	0.000 *	60	(Si)
68.	1168	1	1.000	1.000 *	0.000 *	72	(Si)
76.	1176	1	1.000	1.000 *	0.000 *	34	(Si)
2.	CORYNEBAC	SI			0.861 *	80	(Si)
80.	CONTROL	SI			0.861 *	2	(Si)
29.	29	SI			0.825 *	2	(Si)
6.	FLAVOBAC	SI			0.929 *	24	(SO)
24.	24	SI			0.929 *	6	(Si)
22.	22	SI			0.941 *	33	(SO)
33.	33	SI			0.941 *	22	(Si)
7.	MICROCOCO SP	5	1.000	1.000 *	0.893 *	14	(so)
23.	23	5	1.000	1.000 *	0.893 *	14	(SO)
14.	14	SI			0.898 *	20	(Si)
20.	20	SI			0.898 *	14	(Si)
56.	56	SI			0.839 *	69	(Si)
69.	69	SI			0.839 *	56	(Si)
3.	PSEUDO AEROG	2	1.000	1.000 *	0.896 *	10	(SO)
26.	26	2	1.000	1.000 *	0.896 *	10	(SO)
10.	10	SI			0.896 *	3	(2)
44.	44	SI			0.881 *	3	(2)
8.	PROTEUS MIRA	6	0.987	0.987 *	0.835 *	72	(SO)
67.	67	6	0.987	0.987 *	0.839 *	72	(SO)
72.	72	SI			0.839 *	67	(6)
21.	21	SI			0.791 *	80	(Si)
70.	70	SI			0.761 *	56	(Si)
4.	ECOLI	3	0.982	0.981 *	0.939 *	16	(SO)
19.	19	3	0.982	0.981 *	0.939 *	16	(SO)
55.	55	3	0.982	0.982 *	0.924 *	32	(SO)
16.	16	SI			0.939 *	4	(3)
59.	59	SI			0.925 *	4	(3)
28.	28	SI			0.923 *	55	(3)
32.	32	SI			0.924 *	55	(3)
50.	50	SI			0.921 *	32	(Si)
13.	13	SI			0.938 *	4	(3)
36.	36	SI			0.901 *	13	(Si)
5.	STREPTOCO FAE	4	0.990	0.990 *	0.957 *	18	(SO)
64.	64	4	0.990	0.995 *	0.955 *	60	(SO)
71.	71	4	0.990	0.995 *	0.955 *	60	(SO)
18.	18	SI			0.957 *	5	(<)
60.	60	SI			0.955 *	64	(4)
42.	42	SI			0.953 *	64	(<)
51.	51	SI			0.953 *	64	(*)
12.	12	6	0.986	0.986 *	0.926 *	5	(*)
77.	77	8	0.986	0.986 *	0.918 *	64	(*)
38.	38	SI			0.914 *	64	(*)
57.	57	SI			0.868 *	38	(Si)
9.	9	7	1.000	1.000 *	0.659 *	36	(SO)
15.	15	7	1.000	1.000 *	0.659 *	36	(Si)
11.	11	SI			0.727 *	69	(Si)
25.	125	SI			0.673 *	53	(SO)
27.	27	9	1.000	1.000 *	0.536 *	73	(Si)
48.	48	9	1.000	1.000 *	0.536 *	73	(SO)
31.	31	SI			0.862 *	37	(SO)
37.	137	SI			0.862 *	31	(Si)
58.	58	SI			0.762 *	37	(Si)
34.	34	SI			0.789 *	75	(Si)
75.	75	SI			0.789 *	34	(so)
35.	35	SI			0.636 *	62	(Si)
39.	139	SI			0.706 *	73	(Si)
45.	45	SI			0.432 *	61	(Si)
46.	146	10	1.000	1.000 *	0.796 *	78	(Si)
74.	174	10	1.000	1.000 *	0.796 *	78	(SO)
78.	178	SI			0.796 *	46	(to)
52.	52	SI			0.591 *	10	(Si)
53.	53	SI			0.673 *	25	(Si)
54.	54	SI			0.674 *	80	(so)
61.	61	SI			0.541 *	37	(SO)
62.	62	SI			0.672 *	31	(Si)
63.	63	SI			0.655 *	28	(Si)
66.	66	11	1.000	1.000 *	0.642 *	14	(SO)
79.	79	11	1.000	1.000 *	0.642 *	14	(Si)
73.	73	SI			0.706 *	39	(Si)

Appendix 5. II.
 PHENOTYPES in boateng5/
 Identity level = 0.975
 ..CALCULATED DIVERSITY INDEX = 0.987 TRUE DIVERSITY INDEX = 0.987

No	Name	PhP- type	sim mln	sim mean	sim	lo nr	PhP type
1.	PROTEUS MIRA	1	0.987	0.993 *	0.923 *	31	(SI)
5.	MICROCO SP	1	0.987	0.993 *	0.923 *	31	(SI)
42.	41	1	0.987	0.987 *	0.934 *	31	(SI)
31.	30	SI			0.934 *	42	(1)
14.	14	SI			0.917 *	1	(1)
13.	13	6	0.983	0.983 *	0.870 *	42	(1)
52.	51	6	0.983	0.983 *	0.859 *	1	(1)
55.	54	13	1.000	1.000 *	0.858 *	81	(SI)
75.	74	13	1.000	1.000 *	0.858 ■	61	(SI)
73.	72	SI			0.858 *	41	(SI)
68.	87	SI			0.825 *	39	(9)
85.	64	SI			0.840 *	55	(13)
81.	60	SI			0.810 *	55	(13)
28.	25	SI			0.929 *	39	(9)
39.	38	9	1.000	1.000 *	0.929 *	26	(SI)
51.	50	9	1.000	1.000 *	0.929 *	26	(SI)
29.	28	SI			0.929 *	39	(9)
71.	70	SI			0.859 *	39	(9)
41.	CONTROL	SI			0.955 *	81	(SI)
81.	CONTROL	SI			0.955 *	41	(SI)
43.	42	10	1.000	1.000 *	0.868 *	41	(SI)
53.	52	10	1.000	1.000 *	0.868 *	41	(SI)
47.	46	11	0.992	0.996 *	0.912 *	41	(SO)
78.	75	11	0.992	0.996 *	0.912 *	41	(SI)
68.	65	11	0.992	0.992 *	0.912 *	41	(SO)
64.	63	SI			0.834 *	47	(11)
79.	78	SI			0.858 *	43	(10)
72.	71	SI			0.808 *	41	(SO)
49.	48	SI			0.902 *	59	(SO)
59.	58	SI			0.902 *	49	(SO)
63.	62	SI			0.815 *	49	(SO)
3.	PSEUDO AEROG	SI			0.883 *	58	(SO)
23.	22	SI			0.848 *	30	(SO)
30.	29	SI			0.889 *	80	(SO)
80.	79	SI			0.889 *	30	(SO)
50.	49	SI			0.918 *	58	(SO)
58.	57	SI			0.918 *	50	(SO)
70.	69	SI			0.896 *	50	(SO)
40.	39	SI			0.826 *	50	(SO)
77.	76	SI			0.792 *	23	(SO)
74.	* 73	SI			0.791 *	43	(10)
2.	ICORYNEBAC	2	1.000	1.000 *	0.000 ■	31	(SO)
8.	IIBACILLUS	2	1.000	1.000 *	0.000 *	12	(so)
10.	1110	2	1.000	1.000 *	0.000 *	63	(SO)
35.	11 34	2	1.000	1.000 *	0.000 ■	32	(SO)
58.	11 55	2	1.000	1.000 *	0.000 ■	81	(SO)
69.	11 68	2	1.000	1.000 *	0.000 *	39	(9)
4.	ECOU	3	0.982	0.982 *	0.868 *	60	(so)
28.	27	3	0.982	0.991 *	0.888 *	60	(SO)
46.	45	3	0.982	0.991 *	0.888 *	60	(SO)
60.	59	SI			0.900 *	21	(SO)
11.	11	SI			0.914 *	21	(SO)
21.	20	SI			0.914 *	11	(SO)
32.	31	SI			0.886 *	28	(3)
18.	18	SI			0.866 *	4	(3)
57.	56	SI			0.843 *	28	(3)
6.	IFLAVOBAC	4	1.000	1.000 *	0.608 *	26	(S.)
45.	144	4	1.000	1.000 *	0.608 *	26	(SI)
7.	STREPTOCO FAE	5	0.986	0.991 *	0.885 *	12	(SO)
18.	16	5	0.993	0.996 *	0.882 *	12	(SI)
27.	26	5	0.990	0.995 *	0.872 *	12	(SO)
33.	32	5	0.986	0.992 *	0.852 *	12	(SO)
12.	12	SI			0.885 *	7	(5)
36.	35	SI			0.831 *	12	(SI)
9.	9	SI			0.645 *	63	(so)
15.	15	7	1.000	1.000 *	0.645 *	32	(so)
34.	33	7	1.000	1.000 *	0.645 *	32	(SO)
38.	37	7	1.000	1.000 *	0.645 *	32	(SO)
17.	17	SI			0.442 *	78	(SI)
19.	19	8	0.995	0.998 *	0.634 *	29	(SO)
20.	19	8	0.995	0.998 *	0.634 *	29	(SO)
37.	36	8	0.995	0.995 *	0.683 *	29	(SO)
22.	121	SI			0.460 *	6	(4)
24.	23	SI			0.690 *	12	(SO)
25.	24	SI			0.750 *	52	(6)
44.	43	SI			0.834 *	48	(12)
48.	47	12	1.000	1.000 *	0.834 ■	44	(SO)
67.	66	12	1.000	1.000 *	0.834 *	44	(SO)
54.	53	SI			0.591 *	62	(SO)
62.	61	SI			0.672 ■	48	(12)
78.	77	SI			0.650 *	3	(SO)

1Igg£aaatlaaaag£aaa£S !§EE==gggaa£££££22a22agggg~Ig22Ia\$gggagggIggIgg
26««->s~sss>"-«sssssKESs2=ss;!s5SssteSiftS"\$sss;::;"5:>BSsas;ss">»sss;i3;s2SS!jKc3S'f:R

iiis

iii! ii ii ii iii iii! ii 11iiii11 ii iiiiiii iiiii ii iii
nil ii ii i§ in mi ii mini ii iiiiiii mi ii in

SS"»SSa-^ = :55SSi5iS""i5""""""»"a»i5i5i5a3II^~SM22»»i5SScio«S55i»SS25

ii
i

5 J 8 J 5 „ I 2 > 2
11 s i! I ■ fl | || 1 i | | | | I |
[";|sS3sisSs|8S8P:S§lssa2S|5ISSr,RSSSSslis5£SSSR?SSSS:55:SSKSSSE5?SS5SSg;cisS!?!s|s3||5
S~::~ss sta»=sftsi2ssas«"sssffsss"\$ssss»assis:f.3ts'sgssp!s'<i5s5ftsa'-';asssss^s:s?ss!;

IlgalgIa2£££?aaIIIII£lSaIl£22£agIllgl2£l222alaaaSaaa22£2£222S£aaSSlgg£g=E=IEgIEl
2s~<.<~ss""»"RKSsKSSSssaasss»*-ssss--s?e5s;sssssssasss=r= = : =5sssssssss55sstsss!5

if «!!!! SHHHHSSSBHS ii iiiiii IIII!5?!?!?8!!?!H!!! §«!!« !!
si SSISIiII ssiIIIIHhHHh **n mii** !!i!!i!!!!!!II!11!«!!!I i11111S II
Ils'i5as2-;;;SBS!2SS~~~~2S o?"® 22 s-i'ss<>>a><>«.«."25i

fihi S 4 J I ihii 1!... i!
mu SS^IKSSsisgKiaKksllssSdSSgsllsHss^^EsiSSSSKSSsfK
S^~S2^ris2Kf:fsS12SC!VS'KSSg~KSRSS2S^S»®SS5'52R-aSKSS5;-?;SS,S!?!S'5 2SSS3iR?SS;5tSSiSS

Appendix 7r

PHENOTYPES in a9eyman3/ Identity level »0.975
 *CALCULATED DIVERSITY INDEX * 0.986 TRUE DIVERSITY INDEX - 0.906

No	Name	PHP- typo	sim min	aim mean	sim max	10 nr	PHP typo
1.	STRETOCO FAE	1	1.000	1.000 *	0.957 *	14	(SI)
67.	66	1	1.000	1.000 ■	0.957 *	14	(SI)
14.	14	SI			0.957 *	1	(1>
80.	79	SI			0.926 *	1	(1>
8.	CITROBAC AMA	8	1.000	1.000 *	0.793 *	1	(1>
17.	17	8	1.000	1.000 *	0.793 *	1	(1>
47.	46	8	1.000	1.000 *	0.793 *	1	(1)
2.	PSEUDO AEROG	2	1.000	1.000 *	0.899 *	30	(SI)
19.	19	2	1.000	1.000 *	0.899 *	30	(SI)
23.	23	2	1.000	1.000 ■	0.899 *	30	(SI)
30.	29	SI			0.915 *	45	(SI)
44.	44	SI			0.915 *	30	(SI)
45.	44	SI			0.915 *	30	(SI)
80.	59	SI			0.893 *	45	(SI)
11.	11	SI			0.838 *	45	(SI)
21.	21	SI			0.858 *	9	(9)
9.	AEROMON HYDRO	9	1.000	1.000 *	0.920 *	65	(SI)
62.	61	9	1.000	1.000 *	0.920 *	65	(SI)
65.	64	SI			0.920 *	9	(9)
32.	31	10	1.000	1.000 *	0.868 *	65	(SI)
73.	72	10	1.000	1.000 *	0.868 *	65	(SI)
10.	10	SI			0.934 *	74	(SI)
74.	73	SI			0.934 *	10	(SI)
18.	18	SI			0.888 *	74	(SI)
4.	MICROCO SP	4	0.998	0.999 *	0.900 *	49	(17)
33.	32	4	0.998	0.999 *	0.900 *	49	(17)
40.	39	4	0.998	0.999 *	0.900 *	49	(17)
50.	49	4	0.998	0.998 *	0.887 *	49	(17)
24.	24	SI			0.893 *	4	(4)
34.	33	11	1.000	1.000 *	0.958 *	75	(SI)
53.	52	11	1.000	1.000 *	0.958 *	75	(SI)
75.	74	SI			0.958 *	34	(11)
49.	CONTROL	17	0.997	0.997 *	0.933 *	34	(11)
81.	CONTROL	17	0.997	0.997 *	0.920 *	34	(11)
42.	41	SI			0.938 ■	49	(17)
6.	CORYNEBAC DIPH	6	1.000	1.000 ■	0.842 *	49	(17)
20.	20	6	1.000	1.000 ■	0.842 *	49	(17)
31.	30	6	1.000	1.000 *	0.842 *	49	(17)
69.	68	6	1.000	1.000 *	0.842 *	49	(17)
35.	34	12	1.000	1.000 *	0.790 *	50	(4)
70.	69	12	1.000	1.000 *	0.790 *	50	(4)
3.	PROTEUS MIRA	3	1.000	1.000 *	0.932 *	28	(SI)
13.	13	3	1.000	1.000 *	0.932 *	28	(SI)
26.	25	3	1.000	1.000 *	0.932 ■	28	(SI)
54.	53	3	1.000	1.000 *	0.932 *	28	(SI)
28.	27	SI			0.932 *	3	(3)
6.	ECOLI	5	1.000	1.000 *	0.939 *	37	(SI)
22.	22	5	1.000	1.000 *	0.939 *	37	(SI)
48.	47	5	1.000	1.000 *	0.939 *	37	(so
77.	76	5	1.000	1.000 *	0.939 *	37	(SI)
37.	36	SI			0.939 *	5	(5)
52.	51	SI			0.942 *	56	(SI)
56.	55	SI			0.942 *	52	(SI)
57.	56	SI			0.911 *	5	(5)
29.	26	SI			0.934 ■	63	(SI)
63.	62	SI			0.938 ■	5	(5)
12.	12	SI			0.904 ■	56	(SI)
55.	54	SI			0.912 *	70	(SI)
78.	77	SI			0.912 *	55	(SI)
38.	37	SI			0.787 *	63	(SI)
27.	26	SI			0.891 *	39	(SI)
39.	38	SI			0.891 *	27	(SI)
36.	35	13	0.981	0.981 ■	0.970 *	66	(19)
71.	70	13	0.981	0.981 *	0.957 *	79	(19)
66.	65	19	0.982	0.982 *	0.970 *	36	(13)
79.	78	19	0.982	0.982 *	0.967 *	71	(13)
51.	50	SI			0.902 *	79	(19)
76.	75	SI			0.903 *	71	(13)
41.	40	14	1.000	1.000 *	0.779 *	49	(17)
58.	57	14	1.000	1.000 *	0.779 *	49	(17)
43.	42	15	1.000	1.000 *	0.788 *	30	(SI)
61.	60	15	1.000	1.000 *	0.788 *	30	(SI)
64.	63	18	0.998	0.998 *	0.772 *	11	(SI)
72.	71	18	0.998	0.998 *	0.765 *	11	(SI)
7.	7	7	1.000	1.000 ■	0.852 *	7	(SI)
16.	16	7	1.000	1.000 *	0.652 *	57	(SI)
15.	15	SI			0.695 *	8	(8)
25.	25	SI			0.609 *	18	(SI)
44.	43	16	1.000	1.000 *	0.750 *	10	(SI)
68.	67	16	1.000	1.000 *	0.750 *	10	(SI)
46.	45	SI			0.642 *	79	(19)
59.	58	SI			0.521 *	25	(SI)

Appendix 2.c

PHENOTYPES In α yeiTian4/ Identity level -0.976
[CALCULATED DIVERSITY INDEX - 0.893 TRUE DIVERSITY INDEX - 0.993

No	Nams	PhP type	sim min	sim mean	sim man	to nr	PhP type
1.	STREPTOCO FAE	Si			0.937 *	65	(Si)
64.	64	Si			0.950 *	65	(Si)
65.	65	Si			0.950 *	64	(Si)
53.	53	Si			0.933 *	65	(Si)
11.	11	Si			0.906 *	1	(Si)
15.	15	Si			0.949 *	25	(Si)
25.	25	Si			0.949 *	15	(Si)
41.	41	Si			0.819 *	13	(6)
57.	57	Si			0.879 *	53	(Si)
77.	77	Si			0.820 *	32	(8)
3.	PSEUDO FLUORE	Si			0.804 *	17	(Si)
17.	17	Si			0.845 *	62	(Si)
62.	62	Si			0.927 *	68	(Si)
69.	68	Si			0.927 *	62	(Si)
73.	73	Si			0.926 *	68	(Si)
4.	PROTEUS MIRA	1	1.000	1.000 *	0.570 *	9	(SO)
42.	42	1	1.000	1.000 *	0.870 *	9	(SO)
0.	9	Si			0.870 *	4	(1)
21.	21	Si			0.831 *	4	(1)
50.	50	Si			0.828 *	21	(SO)
5.	MICROCOCCLUS LUT	2	1.000	1.000 *	0.922 *	32	(8)
72.	72	2	1.000	1.000 *	0.922 *	32	(8)
32.	CONTROL	8	1.000	1.000 *	0.922 *	5	(2)
55.	CONTROL	8	1.000	1.000 *	0.922 *	5	(2)
80.	CONTROL	8	1.000	1.000 *	0.922 *	5	(2)
33.	33	Si			0.908 *	3	(2)
23.	23	Si			0.867 *	35	(7)
58.	58	Si			0.868 *	23	(so)
27.	27	7	0.983	0.985 *	0.910 *	38	(so)
35.	35	7	0.966	0.976 *	0.931 *	38	(SO)
48.	48	7	0.966	0.974 *	0.901 *	38	(SO)
38.	38	Si			0.931 *	35	(7)
10.	AEROMON HYDRO	5	1.000	1.000 *	0.920 *	45	(so)
20.	20	5	1.000	1.000 *	0.920 *	45	(Si)
45.	45	Si			0.920 *	10	(5)
66.	66	11	0.981	0.981 *	0.868 *	45	(SO)
76.	76	11	0.981	0.981 *	0.850 *	45	(so)
26.	26	Si			0.892 *	52	(SO)
52.	52	Si			0.892 *	26	(SO)
43.	43	Si			0.799 *	26	(SO)
2.	SERRA MARC	Si			0.862 *	30	(Si)
30.	30	Si			0.862 *	2	(SO)
39.	39	Si			0.860 *	2	(SO)
6.	ECOU	3	1.000	1.000 *	0.938 *	44	(9)
22.	22	3	1.000	1.000 *	0.938 *	44	(9)
37.	37	3	1.000	1.000 *	0.938 *	44	(9)
67.	67	3	1.000	1.000 *	0.938 *	44	(9)
44.	44	9	1.000	1.000 *	0.938 *	6	(3)
61.	61	9	1.000	1.000 *	0.938 *	6	(3)
51.	51	Si			0.938 *	6	(3)
12.	12	Si			0.910 *	71	(SO)
71.	71	Si			0.938 *	6	(3)
3.	CITROBAC DIV	4	1.000	1.000 *	0.800 *	46	(SO)
19.	19	4	1.000	1.000 *	0.800 *	46	(SO)
59.	59	4	1.000	1.000 *	0.800 *	46	(Si)
46.	46	Si			0.800 *	8	(4)
13.	13	8	0.984	0.984 *	0.826 *	52	(Si)
24.	24	6	0.084	0.084 *	0.802 *	52	(Si)
14.	14	Si			0.790 *	24	(6)
16.	PSEUDO AEROG	Si			0.844 *	60	(Si)
60.	60	Si			0.844 *	16	(SO)
36.	36	Si			0.837 *	60	(Si)
56.	56	Si			0.833 *	70	(Si)
70.	70	Si			0.833 *	56	(SO)
75.	75	Si			0.830 *	70	(SO)
49.	49	Si			0.802 *	78	(Si)
78.	78	Si			0.806 *	56	(SO)
18.	18	Si			0.381 *	28	(SO)
28.	28	Si			0.831 *	18	(Si)
29.	29	Si			0.769 *	32	(8)
34.	34	Si			0.845 *	64	(Si)
7.	KLEBSIELLA PNEU	Si			0.845 *	47	(Si)
40.	40	Si			0.856 *	47	(SO)
47.	47	Si			0.872 *	54	(SO)
54.	54	Si			0.872 *	47	(Si)
63.	63	10	1.000	1.000 *	0.913 *	74	(Si)
69.	69	10	1.000	1.000 *	0.913 *	74	(Si)
74.	74	Si			0.913 *	63	(10)
79.	79	Si			0.842 *	32	(8)
31.	31	Si			0.698 *	7	(Si)

Appendix 9 P

PHENOTYPES IN agyoman5 Identity level - 0.975
CALCULATED DIVERSITY INDEX - 0.978 TRUE DIVERSITY INDEX - 0.978

No	Name	PhP- type	nm min	»im mean	sim max	lo nr	PhP typa
1.	STREPTOCO FAE	1	1.000	1.000 *	0.924 *	19	(SI)
34.	34	1	1.000	1.000 *	0.924 *	19	(SI)
19.	19	SI			0.924 *	1	(1)
24.	24	SI			0.917 *	19	(SI)
43.	43	17	1.000	1.000 *	0.878 *	24	(SI)
62.	62	17	1.000	1.000 *	0.878 *	24	(so)
8.	CITROBAC DIV	8	1.000	1.000 *	0.875 *	10	(SO)
54.	54	8	1.000	1.000 *	0.875 *	10	(SO)
10.	10	SI			0.875 *	8	(8)
39.	39	SI			0.800 *	8	(8)
2.	SERRETIA MARC	2	1.000	1.000 *	0.771 *	9	(9)
50.	50	2	1.000	1.000 *	0.771 *	9	(9)
67.	67	2	1.000	1.000 *	0.771 *	9	(9)
9.	AEROMON HYDRO	9	1.000	1.000 *	0.920 ■	47	(10)
35.	35	9	1.000	1.000 *	0.920 *	47	(18)
47.	47	18	1.000	1.000 ■	0.920 *	9	(9)
55.	55	18	1.000	1.000 *	0.920 *	9	(9)
61.	61	SI			0.858 *	47	(18)
4.	PROTEUS MIRA	4	1.000	1.000 *	0.818 *	51	(19)
41.	41	4	1.000	1.000 *	0.818 *	51	(19)
69.	69	4	1.000	1.000 *	0.818 *	51	(19)
5.	MICROCO SP	5	1.000	1.000 *	0.938 *	44	(SO)
15.	15	5	1.000	1.000 *	0.938 *	44	(SO)
31.	31	5	1.000	1.000 ■	0.938 ■	44	(SO)
65.	65	5	1.000	1.000 *	0.938 *	44	(SO)
44.	44	SI			0.938 *	5	(5)
17.	17	12	1.000	1.000 *	0.940 *	38	(so)
25.	25	12	1.000	1.000 *	0.940 *	38	(SI)
38.	38	SI			0.940 *	17	(12)
16.	CONTROL	11	0.983	0.992 *	0.922 *	21	(14)
72.	CONTROL	11	0.983	0.992 *	0.922 *	21	(14)
48.	CONTROL	11	0.983	0.983 *	0.923 *	21	(14)
21.	21	14	1.000	1.000 *	0.926 *	5	(5)
33.	33	14	1.000	1.000 *	0.926 *	5	(5)
36.	36	14	1.000	1.000 *	0.926 *	5	(5)
46.	46	14	1.000	1.000 *	0.926 *	5	(5)
51.	51	19	1.000	1.000 *	0.896 *	48	(11)
64.	64	19	1.000	1.000 *	0.898 *	48	(11)
14.	14	10	0.986	0.986 *	0.797 *	51	(19)
22.	22	10	0.986	0.993 *	0.832 *	59	(SI)
30.	30	10	0.986	0.993 *	0.832 ■	59	(SO)
59.	59	SI			0.832 *	22	(10)
23.	23	15	1.000	1.000 *	0.806 *	48	(11)
32.	32	15	1.000	1.000 *	0.806 *	48	(ID)
45.	45	SI			0.820 *	16	(01)
3.	PSEUDO AEROG	3	1.000	1.000 *	0.890 *	56	(so)
20.	20	3	1.000	1.000 ■	0.890 *	56	(so)
53.	53	SI			0.966 *	56	(SO)
56.	56	SI			0.966 *	53	(SO)
42.	42	SI			0.905 ■	58	(20)
56.	58	20	1.000	1.000 *	0.905 *	42	(so)
68.	68	20	1.000	1.000 *	0.905 *	42	(SO)
6.	KLEBSIELLA PNEU	6	1.000	1.000 ■	0.578 *	45	(SI)
13.	13	6	1.000	1.000 *	0.578 *	45	(SO)
29.	29	6	1.000	1.000 *	0.578 *	45	(SI)
40.	40	6	1.000	1.000 *	0.578 *	45	(SI)
71.	71	0	1.000	1.000 *	0.570 *	45	(SI)
7.	E COLI	7	1.000	1.000 *	0.940 *	20	(16)
37.	37	7	1.000	1.000 *	0.940 *	26	(16)
49.	49	7	1.000	1.000 *	0.940 *	26	(16)
66.	66	7	1.000	1.000 *	0.940 *	26	(16)
70.	70	7	1.000	1.000 *	0.940 *	26	(16)
26.	26	16	1.000	1.000 ■	0.940 *	7	(7)
57.	57	18	1.000	1.000 ■	0.940 *	7	(7)
18.	18	13	1.000	1.000 *	0.920 *	26	(18)
63.	63	13	1.000	1.000 *	0.920 *	26	(16)
11.	11	SI			0.694 *	23	(15)
12.	12	SI			0.927 *	28	(SI)
28.	28	SI			0.927 *	12	(SI)
27.	27	SI			0.689 *	4	(4)
52.	52	SI			0.684 *	16	(11)
60.	60	SI			0.544 *	7	(7)

Appendix 2f

PHENOTYPES in ardoc201/

Identity level - 0.975

*CALCULATED DIVERSITY INDEX - 0.965 TRUE DIVERSITY INDEX - 0.965

No	Nam*	PhP- typ«	sim min	aim m«an	aim max	lo nr	PhP typ«
1.	MICROCO SP	i	1.000	1.000 *	0.893 *	33	(SI)
50.	50	1	1.000	1.000 *	0.893 *	33	(SI)
73.	73	i	1.000	1.000 *	0.893 *	33	(SI)
33.	33	SI			0.893 *	1	(1)
75.	75	SI			0.862 *	1	(1)
7.	CORYNEBAC DIPH	SI			0.910 *	20	(SO)
20.	20	SI			0.910 *	7	(SI)
27.	27	SI			0.905 *	7	(SO)
24.	24	SI			0.910 *	7	(SO)
78.	79	SI			0.890 *	1	(1)
32.	CONTROL	12	0.983	0.983 *	0.880 *	1	(1)
80.	CONTROL	12	0.983	0.983 *	0.881 *	1	(1)
35.	35	13	1.000	1.000 *	0.864 *	80	(12)
51.	51	13	1.000	1.000 *	0.854 *	80	(12)
2.	PROTEUS MIRA	2	1.000	1.000 *	0.932 *	37	(SO)
34.	34	2	1.000	1.000 *	0.932 *	37	(SO)
69.	69	2	1.000	1.000 *	0.932 *	37	(SO)
37.	37	SI			0.932 *	2	(2)
59.	59	SI			0.931 *	2	(2)
44.	44	SI			0.932 *	2	(2)
62.	62	SI			0.931 *	2	(2)
8.	8	SI			0.935 *	48	(SI)
48.	48	SI			0.935 *	8	(SO)
42.	42	SI			0.932 *	8	(SO)
5.	SALMONELLA PARA	5	0.986	0.995 *	0.942 *	31	(SO)
23.	23	5	0.986	0.995 *	0.942 *	31	(SO)
49.	49	5	0.988	0.995 *	0.942 *	31	(SO)
67.	67	5	0.986	0.995 *	0.942 *	31	(SO)
38.	38	5	0.987	0.989 *	0.952 *	14	(9)
74.	74	5	0.986	0.989 *	0.952 *	14	(9)
14.	14	9	1.000	1.000 *	0.952 *	38	(5)
47.	47	9	1.000	1.000 *	0.952 *	38	(5)
53.	53	SI			0.952 *	38	(5)
12.	12	7	0.985	0.983 *	0.940 *	5	(5)
60.	60	7	0.905	0.983 *	0.940 *	5	(5)
78.	78	7	0.985	0.985 *	0.933 *	74	(5)
25.	25	SI			0.940 *	5	(5)
31.	31	SI			0.942 *	5	(5)
64.	64	SI			0.942 *	5	(5)
3.	PSEUDO AEROG	3	1.000	1.000 *	0.903 *	71	(SO)
39.	39	3	1.000	1.000 *	0.903 *	71	(SO)
63.	63	3	1.000	1.000 *	0.903 *	71	(SO)
71.	71	SI			0.903 *	3	(3)
72.	72	SI			0.903 *	3	(3)
46.	46	14	1.000	1.000 *	0.896 *	3	(3)
68.	68	14	1.000	1.000 *	0.896 *	3	(3)
61.	61	15	1.000	1.000 *	0.896 *	3	(3)
68.	68	15	1.000	1.000 ■	0.896 *	3	(3)
43.	43	SI			0.902 *	58	(SO)
58.	58	SI			0.902 *	43	(so)
4.	ECOU	4	1.000	1.000 *	0.964 *	76	(SO)
18.	18	4	1.000	1.000 *	0.964 *	76	(SO)
38.	38	4	1.000	1.000 *	0.964 *	76	(SO)
65.	65	4	1.000	1.000 *	0.964 *	76	(SO)
76.	76	SI			0.964 *	4	(4)
10.	10	SI			0.930 *	4	(4)
55.	55	SI			0.939 *	4	(4)
26.	26	SI			0.939 *	4	(4)
29.	29	SI			0.945 *	4	(4)
13.	13	a	1.000	1.000 ■	0.938 *	4	(4)
41.	41	9	1.000	1.000 *	0.938 *	4	(4)
70.	70	8	1.000	1.000 *	0.938 *	4	(4)
22.	22	11	1.000	1.000 ■	0.938 *	4	(4)
45.	45	11	1.000	1.000 *	0.938 *	4	(4)
6.	STREPTOCO FAE	6	1.000	1.000 *	0.959 *	57	(SO)
15.	15	6	1.000	1.000 *	0.959 *	57	(SO)
17.	17	8	1.000	1.000 *	0.959 *	57	(SI)
57.	57	SI			0.959 *	6	(6)
19.	19	SI			0.957 *	6	(6)
52.	52	SI			0.957 *	6	(6)
28.	28	SI			0.957 *	6	(6)
56.	56	SI			0.957 *	6	(6)
30.	30	SI			0.958 ■	6	(6)
54.	54	SI			0.958 *	6	(6)
9.	9	SI			0.723 *	28	(SO)
11.	11	SI			0.646 *	26	(SO)
16.	16	10	1.000	1.000 *	0.863 *	40	(SO)
21.	21	10	1.000	1.000 *	0.863 *	40	(SQ)
40.	40	SI			0.863 *	16	(10)
77.	77	SI			0.694 *	32	(12)

Appendix 2g
 PHENOTYPES in ardec202/ Identity level 0.975*
 CALCULATED DIVERSITY INDEX - 0.979 TRUE DIVERSITY INDEX - 0.979

No	Name	Ph- lypa	aim min	aim mean	slm max	to nr	PhP type
1.	PSEUDO AEROG	1	1.000	1.000 *	0.915'	40	(SI)
14.	14	1	1.000	1.000 *	0.915'	40	(SI)
32.	32	1	1.000	1.000 *	0.915'	40	(SI)
74.	74	1	1.000	1.000 *	0.915'	40	(SI)
40.	40	SI			0.915'	1	(1)
29.	29	SI			0.901' ■	1	(1)
18.	18	13	1.000	1.000 *	0.896'	1	(1)
78.	78	13	1.000	1.000 *	0.896'	1	(1)
22.	22	SI			0.896'	1	(1)
7.	MICROCO SP	7	1.000	1.000 *	0.893'	52	(SI)
45.	45	7	1.000	1.000 *	0.893'	52	(SI)
57.	57	7	1.000	1.000 *	0.893'	52	(SI)
52.	52	SI			0.893'	7	(7)
71.	71	SI			0.893'	7	(7)
48.	40	18	1.000	1.000 *	0.890'	7	(7)
64.	64	18	1.000	1.000 *	0.890'	7	(7)
56.	CONTROL	SI			0.963'	80	(SO)
80.	CONTROL	SI			0.963'	56	(SO)
50.	60	19	1.000	1.000 *	0.882'	76	(SI)
69.	69	19	1.000	1.000 *	0.882'	76	(SI)
76.	76	SI			0.882'	60	(19)
2.	SALMONELLA TYPH	2	0.986	0.994 *	0.937' ■	12	(9)
9.	9	2	0.986	0.994'	0.937'	12	(9)
41.	41	2	0.986	0.994'	0.937'	12	(9)
37.	37	2	0.983	0.992 *	0.937'	12	(9)
53.	53	2	0.983	0.988 *	0.950'	25	(SO)
61.	61	2	0.984	0.989 *	0.954'	25	(SO)
25.	25	SI			0.954'	61	(2)
12.	12	9	1.000	1.000 *	0.937'	2	(2)
59.	59	9	1.000	1.000 *	0.937'	2	(2)
30.	30	16	1.000	1.000 *	0.937'	2	(2)
35.	35	16	1.000	1.000 *	0.937'	2	(2)
21.	21	SI			0.935'	37	(2)
44.	44	SI			0.935'	37	(2)
4.	ECOU	4	1.000	1.000 **	0.945'	73	(SI)
13.	13	4	1.000	1.000 *	0.945'	73	(SI)
38.	33	4	1.000	1.000 *	0.945'	73	(SI)
50.	50	4	1.000	1.000 *	0.945'	73	(SI)
62.	62	4	1.000	1.000 *	0.945'	73	(SI)
73.	73	SI			0.945'	4	(4)
16.	16	11	1.000	1.000 *	0.938'	4	(4)
34.	34	11	1.000	1.000 *	0.938'	4	(4)
23.	23	SI			0.939' ■	4	(4)
20.	20	14	1.000	1.000 *	0.938'	4	(4)
79.	79	14	1.000	1.000 ■	0.938'	4	(4)
28.	28	15	1.000	1.000 *	0.938'	4	(4)
67.	67	15	1.000	1.000 *	0.938'	4	(4)
10.	10	SI			0.805'	17	(12)
17.	17	12	1.000	1.000 *	0.805'	10	(SO)
24.	24	12	1.000	1.000 *	0.805'	10	(SO)
66.	66	12	1.000	1.000 *	0.805'	10	(SO)
72.	72	12	1.000	1.000 *	0.805'	10	(SO)
8.	PROTEUS MIRA	8	1.000	1.000 *	0.934'	36	(SO)
26.	26	8	1.000	1.000 *	0.934'	36	(SO)
47.	47	8	1.000	1.000 *	0.934'	36	(SO)
36.	30	SI			0.934'	0	(0)
31.	31	SI			0.932'	0	(0)
55.	55	SI			0.932'	8	(8)
58.	58	SI			0.932'	8	(8)
3.	ENTEROBACTER CLOA	3	0.977	0.977 *	0.719'	60	(19)
42.	42	3	0.977	0.988 ■	0.740'	60	(19)
65.	65	3	0.977	0.988'	0.740'	60	(19)
5.	CITROBAC FRE	5	1.000	1.000 ■	0.909'	54	(SI)
49.	49	5	1.000	1.000 *	0.909'	54	(SO)
54.	54	SI			0.909'	5	(5)
6.	STREPTOCO FAE	6	0.998	0.999 *	0.959'	39	(SI)
11.	11	6	0.998	0.999 *	0.959'	39	(SO)
19.	19	6	0.998	0.999 *	0.959'	39	(SI)
63.	63	6	0.998	0.998'	0.972'	15	(10)
39.	39	SI			0.959' ■	6	(6)
27.	27	SI			0.958'	6	(6)
33.	33	SI			0.957'	6	(6)
77.	77	SI			0.957'	6	(6)
46.	46	SI			0.957'	6	(6)
15.	15	10	0.994	0.994 *	0.972'	63	(6)
75.	75	10	0.994	0.994 *	0.949'	63	(6)
43.	43	17	1.000	1.000 *	0.857'	70	(20)
51.	51	17	1.000	1.000 *	0.857'	70	(20)
68.	68	20	0.997	0.997 *	0.857'	43	(17)
70.	70	20	0.997	0.997 *	0.857'	43	(07)

Appendix - 2b

PHENOTYPES ln ando:203/ kmUy level - 0.875
 CALCULATED DIVERSITY INDEX - 0.881 TRUE DIVERSITY INDEX - 0.881

No	Name	PhP- ilm tya	mln	aim maan	sim max	lo nr	PhP typ*
1.	BACILLUS	1	1.000	1.000	0.882 *	67	(so)
59.	59	1	1.000	1.000 *	0.882 *	67	(SI)
67.	67	SI			0.882 *	1	(1)
77.	77	SI			0.876 *	1	(1)
3.	CORYNEBAC	3	1.000	1.000 ■	0.910	65	(SO)
63.	63	3	1.000	1.000 *	0.910 *	65	(SI)
65.	65	SI			0.910 *	3	(3)
48.	CONTROL	SI			0.956 *	60	(Sj)
80.	CONTROL	SI			0.956 *	4a	(Sj)
6.	PSEUDO AEROG	6	1.000	1.000 *	0.903 ■	11	(SI)
20.	20	6	1.000	1.000 ■	0.903 ■	11	(SI)
44.	44	6	1.000	1.000 *	0.903 ■	11	(SO)
46.	46	6	1.000	1.000 *	0.903 *	11	(SO)
74.	74	6	1.000	1.000 *	0.903 *	11	(SO)
11.	11 *	SI			0.903 *	6	(6)
23.	23	SI			0.896 *	6	(6)
29.	29	17	1.000	1.000 *	0.896 *	6	(6)
55.	55	17	1.000	1.000 *	0.896 *	6	(6)
13.	13	11	1.000	1.000 *	0.926 *	73	(19)
21.	21	11	1.000	1.000 *	0.926 *	73	(19)
73.	73	19	1.000	1.000 *	0.926 *	13	(11)
78.	78	19	1.000	1.000 *	0.926	13	(11)
58.	58	SI			0.839 *	13	(11)
5.	PROTEUS MIRA	5	1.000	1.000 ■	0.934 *	62	(so)
17.	17	5	1.000	1.000 ■	0.934 ■	62	(so)
57.	57	5	1.000	1.000 *	0.934 *	62	(SO)
62.	62	SI			0.934 *	5	(5)
10.	10	9	1.000	1.000 ■	0.932 *	5	(5)
66.	66	9	1.000	1.000 *	0.932 *	5	(5)
15.	15	12	1.000	1.000 *	0.932 *	5	<5)
71.	71	12	1.000	1.000 *	0.932 *	5	(5)
7.	SALMONELLA PARA	7	0.986	0.994 *	0.942 *	38	(SI)
16.	16	7	0.956	0.994 *	0.942 *	38	(SO)
19.	19	7	0.956	0.994 *	0.942 *	38	(SO)
76.	76	7	0.986	0.994 *	0.942 *	38	(SO)
9.	9	7	0.986	0.989 *	0.952 *	24	(U)
33.	33	7	0.936	0.989 *	0.952 *	24	(14)
32.	32	SI			0.952 *	9	(7)
12.	12	10	0.987	0.987 *	0.937 *	7	(7)
64.	64	10	0.987	0.987 *	0.942 *	7	(7)
49.	49	SI			0.941 *	7	(7)
38.	38	SI			0.942 *	7	(7)
42.	42	SI			0.940 *	7	(7)
25.	25	15	0.985	0.985 *	0.940 *	7	(7)
40.	40	15	0.985	0.955 *	0.933 *	9	(7)
24.	24	14	0.985	0.985 *	0.952 *	9	(7)
47.	47	14	0.985	0.985 *	0.937 *	9	(7)
34.	34	SI			0.780 *	11	(SO)
2.	CITROBAC AMA	2	1.000	1.000 *	0.930 *	70	(SO)
52.	52	2	1.000	1.000 *	0.930 *	70	(SI)
70.	70	SI			0.930 ■	2	(2)
79.	79	SI			0.952 *	43	(SI)
8.	STREPTOCO FAE	B	1.000	1.000 ■	0.959 *	43	(SI)
14.	14	8	1.000	1.000 *	0.959 *	43	(SO)
22.	22	8	1.000	1.000 *	0.959 *	43	(SI)
28.	23	S	1.000	1.000 ■	0.959 *	43	(SO)
43.	43	SI			0.919 *	8	(8)
51.	51	SI			0.953 *	8	(8)
36.	36	SI			0.957 *	8	(8)
60.	60	SI			0.958 *	8	(6)
68.	68	SI			0.954 *	8	(8)
18.	18	13	1.000	1.000 *	0.957 *	8	(8)
64.	64	13	1.000	1.000 *	0.957 *	8	(8)
75.	75	SI			0.948 *	18	(13)
4.	ECOLI	4	0.995	0.999 *	0.939 *	53	(SO)
31.	31	4	0.995	0.999 *	0.939 *	53	(SO)
37.	37	4	0.995	0.999 *	0.939 *	53	(SO)
61.	61	4	0.995	0.999 *	0.939 *	53	(SI)
41.	41	4	0.995	0.995 *	0.940 *	45	(SI)
45.	45	SI			0.940 *	41	(4)
69.	69	SI			0.940 *	41	(4)
50.	50	SI			0.940 *	41	(4)
53.	53	SI			0.939 *	4	(4)
26.	26	SI			0.954 *	39	(18)
39.	39	18	1.000	1.000 *	0.954 *	26	(SO)
58.	56	18	1.000	1.000 *	0.954 *	26	(SO)
27.	27	16	1.000	1.000 *	0.741 *	58	(SO)
35.	35	16	1.000	1.000 *	0.741 *	58	(SO)
30.	30	SI			0.627 *	28	(SI)
72.	(72)	SI			0.315 *	34	(SO)

Appendix 2j

PHENOTYPES in ardec204/ CALCULATED DIVERSITY INDEX - 0.977		Identity level ■ 0.975 TRUE DIVERSITY INDEX - 0.977						
No	Name	PhP- typ	skn mln	>sim mean	aim	to	PhP type	
1.	MICROCO SP	1	1.000	1.000 *	0.926 *	66	(18)	
24.	24	1	1.000	1.000 *	0.926 *	66	(18)	
74.	73	1	1.000	1.000 *	0.926 ■	66	(18)	
66.	65	18	1.000	1.000 *	0.920 ■	1	(D)	
73.	72	18	1.000	1.000 *	0.926 ■	1	(1)	
32.	CONTROL	SI			0.910 *	81	(SI)	
81.	CONTROL	SI			0.910 ■	32	(SI)	
12.	12	SI			0.862 *	1	(1)	
79.	78	SI			0.893 *	1	(1)	
2.	PROTEUS MIRA	2	0.997	0.998 *	0.932 *	11	(10)	
27.	27	2	0.997	0.998 *	0.932 *	11	(10)	
33.	33	2	0.997	0.997 ■	0.925 *	11	(10)	
11.	11	10	1.000	1.000 *	0.932 *	2	(2)	
37.	37	10	1.000	1.000 *	0.932 *	2	(2)	
51.	50	16	1.000	1.000 *	0.817 *	81	(SI)	
61.	60	16	1.000	1.000 ■	0.817 *	81	(SI)	
3.	EDWARDSI	3	0.988	0.994 *	0.815 *	66	(18)	
48.	57	3	0.980	0.994 *	0.815 *	66	(16)	
65.	64	3	0.988	0.988 ■	0.764 *	66	(18)	
4.	ECCOU	4	0.992	0.998 *	0.940 *	68	(SI)	
43.	43	4	0.992	0.998 *	0.940 *	68	(SI)	
63.	62	4	0.992	0.998 *	0.940 *	68	(SI)	
72.	71	4	0.992	0.998 *	0.940 *	68	(SI)	
76.	75	4	0.992	0.992 *	0.959 *	53	(17)	
53.	52	17	1.000	1.000 *	0.959 *	76	(4)	
59.	58	17	1.000	1.000 *	0.959 *	76	(M)	
68.	67	SI			0.940 *	4	(4)	
42.	42	SI			0.938 *	4	(4)	
47.	47	SI			0.938 *	4	(4)	
57.	56	SI			0.939 *	4	(4)	
80.	79	SI			0.938 *	57	(SI)	
5.	SALMONELLA TYPH	5	0.986	0.990 *	0.959 *	62	(SI)	
30.	30	5	0.986	0.990 *	0.959 *	62	(SI)	
8.	SALMONELLA PARA	5	0.986	0.993 *	0.959 *	41	(15)	
15.	15	5	0.986	0.993 *	0.950 *	41	(15)	
26.	26	5	0.986	0.993 *	0.950 *	41	(15)	
62.	61	SI			0.959 *	5	(5)	
23.	23	SI			0.941 *	8	(5)	
17.	17	12	0.985	0.993 *	0.940 *	8	(5)	
49.	48	12	0.985	0.993 *	0.940 *	8	(5)	
36.	36	12	0.985	0.985 *	0.933 *	5	(5)	
10.	10	9	0.985	0.993 *	0.952 *	5	(5)	
38.	38	9	0.985	0.993 *	0.952 *	5	(5)	
44.	44	9	0.905	0.985 *	0.937 *	5	(5)	
41.	41	15	0.988	0.988 *	0.950 *	8	(5)	
50.	49	15	0.988	0.988 *	0.942 *	8	(5)	
54.	53	SI			0.941 *	50	(15)	
7.	PSEUDO AEROG	7	1.000	1.000 ■	0.896 *	14	(SI)	
18.	18	7	1.000	1.000 ■	0.898 *	14	(SI)	
77.	76	7	1.000	1.000 *	0.896 *	14	(SI)	
14.	14	SI			0.896 *	7	(7)	
35.	35	SI			0.891 *	39	(14)	
39.	39	14	1.000	1.000 *	0.958 ■	46	(SI)	
55.	54	14	1.000	1.000 ■	0.958 *	46	(SI)	
46.	46	SI			0.958 *	39	(14)	
29.	29	SI			0.074 *	30	(SI)	
10.	16	11	1.000	1.000 *	0.940 *	31	(SI)	
20.	20	11	1.000	1.000 *	0.940 *	31	(SI)	
25.	25	11	1.000	1.000 *	0.940 *	31	(SI)	
31.	31	SI			0.940 *	16	(11)	
6.	STREPTOCO FAE	6	0.996	0.999 *	0.959 *	19	(SI)	
13.	13	6	0.996	0.999 *	0.959 *	19	(SI)	
40.	40	6	0.996	0.999 *	0.959 ■	19	(SI)	
45.	45	6	0.996	0.999 *	0.959 *	19	(SI)	
64.	63	6	0.996	0.999 *	0.959 *	19	(SI)	
70.	69	6	0.996	0.999 *	0.959 *	19	(SI)	
56.	55	6	0.996	0.996 *	0.978 ?	52	(SI)	
52.	51	SI			0.978 ?	58	(6)	
9.	9	8	1.000	1.000 *	0.958 *	6	(6)	
34.	34	8	1.000	1.000 *	0.958 *	6	(6)	
19.	19	SI			0.059 *	8	(6)	
22.	22	SI			0.957 *	6	(0)	
60.	59	SI			0.957 *	0	(0)	
28.	28	SI			0.957 *	6	(6)	
75.	74	SI			0.880 *	19	(SI)	
21.	11 21	13	1.000	1.000 *	0.000 *	31	(SI)	
48.	11 47	13	1.000	1.000 *	0.000 *	4	(4)	
67.	66	19	1.000	1.000 *	0.740 *	51	(18)	
71.	70	19	1.000	1.000 *	0.740 *	51	(16)	
69.	68	20	1.000	1.000 *	0.693 *	52	(8)	
78.	77	20	1.000	1.000 *	0.693 *	52	(SI)	

Appendix 2/
PHENOTYPES In = fdoc205/
Wanility tovol - 0.075
 *CALCULATED DIVERSITY INDEX - 0.963 TRUE DIVERSITY INDEX - 0.962

No	Name	PhP- type	»lm mln	lm maan	tun max	lo nr	PhP type
1.	SALMONELLA TYPHI	1	0.979	0.988 *	0.952 *	25	(10)
13		1	0.979	0.988 *	0.952 *	25	(10)
75.		1	0.979	0.988 *	0.952 *	25	(10)
7.	SALMONELLA PARA	1	0.986	0.994 *	0.941 *	25	(10)
14.		1	0.986	0.994 *	0.941 *	25	(10)
38.		1	0.986	0.994 *	0.941 *	25	(10)
60.		1	0.986	0.994 *	0.941 *	25	(10)
9.		1	0.979	0.989 *	0.942 *	25	(10)
21.		1	0.979	0.989 *	0.942 *	25	(10)
48.		1	0.985	0.991 *	0.946 *	65	(SI)
53.		1	0.985	0.991 *	0.946 *	65	(SI)
24.		10	0.985	0.985 *	0.937 *	1	(1)
25.		10	0.985	0.993 *	0.952 *	1	(1)
70.		10	0.985	0.993 *	0.952 *	1	(1)
29.	■ 29 ■	11	0.985	0.985 *	0.933 *	1	(1)
30.		11	0.985	0.985 *	0.941 *	9	(1)
65.		SI			0.946 ■	48-	(1)
3.	ECOU	3	1.000	1.000 *	0.938 *	76	(SI)
18.		3	1.000	1.000 *	0.938 *	76	(SI)
34.		3	1.000	1.000 *	0.938 *	76	(SI)
45.		3	1.000	1.000 *	0.938 *	76	(SI)
58.		3	1.000	1.000 *	0.938 *	76	(SI)
64.		3	1.000	1.000 *	0.938 *	76	(SI)
74.		3	1.000	1.000 *	0.938 *	76	(SO)
76.		SI			0.938 *	3	(3)
17.		SI			0.911 *	78	(SO)
78.		SI			0.932 *	49	(so)
49.		SI			0.933 *	73	(SO)
73.		SI			0.933 *	49	(SO)
5.	PSEUDO AERO	5	1.000	1.000 *	0.919 *	61	(SO)
15.		5	1.000	1.000 *	0.919 *	61	(SO)
28.		5	1.000	1.000 *	0.919 *	61	(SO)
54.		5	1.000	1.000 *	0.919 *	61	(SO)
71.		5	1.000	1.000 *	0.919 *	61	(so)
61.		SI			0.919 *	5	(5)
25.		SI			0.912 *	5	(5)
19.		SI			0.915 *	5	(5)
36.		SI			0.912 *	5	(5)
11.		SI			0.896 *	5	(5)
39.		SI			0.912 *	5	(5)
67.		SI			0.903 *	5	(5)
33.		SI			0.840 *	40	(12)
40.	CONTROL	12	0.969	0.989 *	0.894 ■	66	(SO)
80.	CONTROL	12	0.989	0.989 *	0.908 *	66	(SO)
66.		SI			0.908 *	80	(12)
79.		SI			0.890 *	66	(SO)
55.		SI			0.862 *	66	(SO)
72.		SI			0.093 *	66	(SO)
β	PROTEUS MIRA	7	1.000	1.000 *	0.934 *	50	(SO)
22.		7	1.000	1.000 *	0.934 *	50	(SO)
41.		7	1.000	1.000 *	0.934 *	50	(SO)
69.		7	1.000	1.000 *	0.934 *	50	(SO)
50.		SI			0.934 *	8	(7)
57.		SI			0.932 ■	8	(n)
62.		SI			0.932 *	8	(7)
44.		SI			0.930 -	B	(7)
6.	PSEUDO FLOUHE	6	1.000	1.000 *	0.7M	33	(SI)
32.		8	1.000	1.000 ■	0.756 *	33	(SO)
37.		SI			0.762 *	80	(12)
2.	ENTEROBACTER AERO	2	1.000	1.000 *	0.919 *	59	(SO)
43.		2	1.000	1.000 *	0.919 *	59	(so)
59.		SI			0.919 *	2	(2)
47.		SI			0.913 *	2	(2)
4.	STREPTOCO FAE	4	0.994	0.997 *	0.959 *	46	(SO)
42.		4	0.994	0.997 *	0.959 *	46	(SO)
16.		4	0.992	0.995 *	0.959 *	46	(SI)
23.		4	0.988	0.992 *	0.952 *	51	(SO)
35.		4	0.988	0.994 *	0.980 7	46	(SO)
46.		SI			0.980 7	35	(4)
20.		9	1.000	1.000 *	0.957 *	4	(4)
63.		9	1.000	1.000 *	0.957 *	4	(4)
58.		SI			0.959 *	16	(4)
51.		SI			0.957 *	4	(4)
31.		SI			0.957 *	4	(4)
68.		SI			0.95 B *	4	(4)
10.		8	1.000	1.000 *	0.880 *	46	(SI)
27.		8	1.000	1.000 *	0.880 *	46	(SO)
52.		8	1.000	1.000 *	0.830 *	46	(so)
77.		8	1.000	1.000 *	0.880 *	46	(SO)
12.		SI			0.745 *	6	(6)

Appendix 2 k,

HENOTYPES in asarel/ Identity level = 0.975
 CALCULATED DIVERSITY INDEX = 0.990 TRUE DIVERSITY INDEX = 0.990

No	Name	PhP- typ	sim min	sim mean	sim max	to nr	PhP type
1.	ECOLI	1	1.000	1.000 *	0.945'	73	(Si)
14.	14	1	1.000	1.000 *	0.945 *	73	(SO)
70.	69	1	1.000	1.000 *	0.945 *	73	(Si)
73.	72	Si			0.945 *	1	(D)
28.	27	10	1.000	1.000 *	0.938 *	1	(1)
75.	74	10	1.000	1.000 *	0.938 *	1	(1)
77.	76	Si			0.939 *	1	(1)
30.	29	Si			0.938 *	1	(1)
2.	FLAVOBAC AQUA	2	1.000	1.000 *	0.929 *	45	(Si)
12.	12	2	1.000	1.000 *	0.929 *	45	(Si)
45.	44	Si			0.929 *	2	(2)
22.	21	Si			0.925 '	2	(2)
19.	19	Si			0.919 *	2	(2)
39.	38	Si			0.920 *	44	(Si)
44.	43	Si			0.920 *	39	(Si)
37.	36	Si			0.919 *	2	(2)
58.	57	Si			0.918 *	37	(Si)
47.	46	Si			0.863 ■	37	(Si)
6.	STAPHYLOCOCCUS AERO	6	0.995	0.998 *	0.959 *	15	(Si)
9.	9	6	0.995	0.998 *	0.959 *	15	(Si)
35.	34	6	0.995	0.995 '	0.955 *	15	(Si)
15.	15	Si			0.959 '	6	(6)
18.	18	Si			0.947 *	6	(6)
38.	37	Si			0.938 '	35	(6)
4.	PROTEUS MIRA	4	1.000	1.000 *	0.932 *	21	(9)
78.	77	4	1.000	1.000 *	0.932 *	21	(O)
21.	20	9	1.000'	1.000 *	0.932 *	4	(4)
41.	40	9	1.000	1.000 *	0.932 *	4	(4)
61.	60	Si			0.928'	21	(9)
40.	39	Si			0.908 *	8	(8)
8.	MICROCO SP	8	0.999	1.000 *	0.917 *	23	(Si)
10.	10	8	0.999	1.000 *	0.917 *	23	(Si)
16.	16	8	0.999	1.000 *	0.917 *	23	(Si)
36.	35	8	0.999	0.999 *	0.915 *	23	(SO)
23.	22	Si			0.917 ■	8	(8)
32.	31	Si			0.917 *	8	(8)
26.	25	Si			0.908 *	8	(8)
33.	CONTROL	Si			0.967 *	81	(Si)
81.	CONTROL	Si			0.967'	33	(Si)
60.	59	15	1.000	1.000 *	0.868 *	33	(Si)
63.	62	15	1.000	1.000 *	0.868 *	33	(Si)
51.	50	13	1.000	1.000 *	0.908 *	53	(Si)
67.	66	13	1.000	1.000 *	0.908 *	53	(Si)
53.	52	Si			0.908 *	51	(13)
55.	54	Si			0.903 *	51	(13)
7.	PSEUDO AEROG	7	1.000	1.000'	0.941 ■	50	(Si)
56.	55	7	1.000	1.000 *	0.941 ■	50	(Si)
66.	65	7	1.000	1.000 *	0.941 *	50	(Si)
50.	49	Si			0.941'	7	(7)
72.	71	Si			0.941'	7	(7)
76.	75	Si			0.915 *	7	(7)
42.	41	12	1.000	1.000 *	0.910'	65	(Si)
71.	70	12	1.000	1.000 *	0.910 ■	65	(Si)
79.	78	12	1.000	1.000 *	0.910'	65	(Si)
65.	64	Si			0.910 *	42	(12)
52.	51	Si			0.905'	42	(12)
3.	KLEBSIELLA PNEU	3	1.000	1.000 ■	0.918 *	24	(Si)
68.	67	3	1.000	1.000 ■	0.918 *	24	(Si)
24.	23	Si			0.918 *	3	(3)
80.	79	Si			0.854 *	3	(3)
13.	13	Si			0.846'	29	(Si)
29.	28	Si			0.846 *	13	(Si)
43.	42	Si			0.846 *	13	(SO)
49.	48	Si			0.846 *	13	(Si)
59.	58	Si			0.846 *	13	(Si)
64.	63	Si			0.848 *	13	(Si)
5.	STREPTOCO FAE	5	1.000	1.000 *	0.958 *	27	(Si)
11.	11	5	1.000	1.000 *	0.958 *	27	(Si)
46.	45	5	1.000	1.000 *	0.958'	27	(Si)
25.	24	Si			0.957 *	5	(5)
27.	26	Si			0.958'	5	(5)
54.	53	Si			0.957 *	5	(5)
31.	30	Si			0.958 *	5	(5)
57.	56	14	1.000	1.000 *	0.795 *	54	(Si)
62.	61	14	1.000	1.000 *	0.795 *	54	(Si)
17.	17	Si			0.519 *	3	(3)
20.	20	Si			0.748 *	21	(9)
34.	33	11	1.000	1.000 *	0.555 *	19	(Si)
48.	47	11	1.000	1.000 ■	0.555 *	19	(Si)
69.	68	Si			0.506 *	20	(Si)
74.	73	Si			0.690 *	7	(7)

Appendix 21

Identity level <= 0.975
TRUE DIVERSITY INDEX = 0.989

PHENOTYPES In asaro2/
CALCULATED DIVERSITY INDEX = 0.989

No	Name	PhP- type	slm min	slm mean	sim max	to nr	PhP type
1.	PSEUDO AEROG	1	1.000	1.000 *	0.941 *	25	(SO)
18.	18	1	1.000	1.000 ■	0.941 *	25	(SO)
25.	25	Si			0.941 *	1	(1)
23.	23	Si			0.896 *	1	(D)
3.	MICROCO LUT	3	1.000	1.000 *	0.926 *	41	(11)
45.	45	3	1.000	1.000 *	0.926 *	41	(01)
41.	41	11	1.000	1.000 *	0.926 *	3	(3)
49.	49	11	1.000	1.000 *	0.926 *	3	(3f)
79.	79	Si			0.897 *	3	(3)
38.	36	Si			0.874 *	3	(3)
40.	CONTROL	Si			0.973 *	80	(Si)
80.	CONTROL	Si			0.973 *	40	(Si)
73.	73	Si			0.882 *	8	(8)
77.	77	Si			0.876 *	8	(8)
63.	63	Si			0.928 *	72	(Si)
65.	65	Si			0.927 *	63	(Si)
72.	72	Si			0.928 *	63	(Si)
7.	CORYNEBACTERIUM DIPH	7	1.000	1.000 *	0.910 *	66	(16)
28.	28	7	1.000	1.000 *	0.910 *	66	(16)
44.	44	7	1.000	1.000 *	0.910 *	66	(16)
64.	64	16	0.997	0.997 *	0.908 *	7	(7)
66.	66	16	0.997	0.997 *	0.910 *	7	(7)
74.	74	Si			0.910 *	7	(7)
48.	48	Si			0.905 *	7	(7)
8.	BACILLUS	8	1.000	1.000 *	0.903 *	71	(SO)
50.	50	8	1.000	1.000 *	0.903 *	71	(Si)
57.	57	8	1.000	1.000 *	0.903 *	71	(SO)
71.	71	Si			0.903 *	8	(B)
61.	61	Si			0.890 *	8	(8)
54.	54	Si			0.905 *	7	(7)
68.	68	Si			0.882 *	8	(8)
6.	FLAVOBACAQUA	6	1.000	1.000 -	0.929 *	56	(Si)
12.	12	6	1.000	1.000 *	0.929 *	56	(SO)
16.	16	6	1.000	1.000 *	0.929 *	56	(SO)
52.	52	6	1.000	1.000 *	0.929 *	56	(SO)
56.	56	Si			0.929 *	6	(6)
21.	21	Si			0.919 *	6	(6)
5.	ECOLI	5	1.000	1.000 *	0.939 *	19	(SO)
15.	15	5	1.000	1.000 ■	0.939 *	19	(SO)
60.	60	5	1.000	1.000 *	0.939 *	19	(SO)
19.	19	Si			0.939 *	5	(5)
24.	24	Si			0.938 *	5	(5)
29.	29	Si			0.938 *	5	(5)
10.	10	Si			0.931 *	5	(5)
34.	34	Si			0.944 ■	38	(SO)
38.	38	Si			0.944 *	34	(SO)
9.	9	Si			0.932 *	14	(Si)
14.	14	Si			0.932 *	9	(SO)
17.	17	Si			0.932 *	9	(Si)
11.	11	9	1.000	1.000 *	0.965 *	51	(so)
22.	22	9	1.000	1.000 *	0.965 *	51	(Si)
55.	55	9	1.000	1.000 ■	0.965 *	51	(SO)
51.	51	Si			0.965 *	11	(9)
26.	26	Si			0.846 *	11	(9)
31.	31	Si			0.846 *	11	(9)
27.	27	10	1.000	1.000 *	0.935 *	37	(Si)
32.	32	10	1.000	1.000 *	0.935 *	37	(Si)
58.	58	10	1.000	1.000 *	0.935 *	37	(SO)
37.	37	Si			0.935 *	27	(10)
75.	75	Si			0.935 *	27	(10)
67.	67	Si			0.933 *	27	(10)
33.	33	Si			0.846 ■	11	(9)
2.	STAPHYLOCOCCUS AERO	2	1.000	1.000 *	0.956 *	20	(SO)
13.	13	2	1.000	1.000 *	0.956 *	20	(SO)
20.	20	Si			0.956 *	2	(2)
47.	47	Si			0.811 *	79	(SO)
4.	STREPTOCO FAE	4	1.000	1.000 *	0.958 *	35	(SO)
30.	30	4	1.000	1.000 *	0.958 *	35	(Si)
46.	46	4	1.000	1.000 *	0.958 ■	35	(SO)
35.	35	Si			0.958 *	4	(4)
39.	39	Si			0.957 *	4	(4)
43.	43	12	1.000	1.000 *	0.957 *	4	(4)
69.	69	12	1.000	1.000 *	0.957 *	4	(4)
62.	62	15	1.000	1.000 *	0.957 *	4	(4)
78.	78	15	1.000	1.000 *	0.957 *	4	(*)
53.	53	13	1.000	1.000 *	0.958 *	4	(4)
76.	76	13	1.000	1.000 *	0.958 *	4	(4)
42.	42	Si			0.866 *	39	(Si)
59.	59	14	1.000	1.000 *	0.474 *	48	(Si)
70.	70	14	1.000	1.000 ■	0.474 *	48	(SO)

li gg5\$S£ggg££ggg£££|g£gg£gg£gg£gg£££gggEggggg£ggggg£££££gg£5£l£££gg2gggggS£g£rggg
s s ES-S8-SK8<>s;"'"5s;sP!saf!Si5<">asi-sS"'"<">sKi:o5:p:Ks«sa-««sS'"'-'5 = ~^":^s2SSS2S!;fiK"'"^<"«sss

11 111111111!1!!11i1&11111!!11s!1S1181S111S5i1!!i1S1!!111?111131isalil1S?!!S3!S11i

i! II 11 ill!
N' ii ?| |i || si ii in §§ ii • ii ii im li
n
n



{3ES5f:ra2B2sSKCSSSggS8B;SSHISsS5B1SSSSSgEiK8£S£5<2S2S!SKS = aR2S:5SSg£es»5SSfeR5SSS
-aES3S = S2S"SSSKSSSS3aSg5S3S«SSSS?SIS5fSSSP:H^2«S;5-"s«i?SaS^t:2SR2S;iSSS!5S«<5SRSt:ISS!!!S

II ggggg£g"gg5£gggSg££ggS££gggg£S£tg£gg£££££gggggg££££££l=gggEE£E=gg££l££5S£S£ggg
SSSSS'5R"SS»»£S!3@K"-l:!,""2222»»SS-22--'-'-S!;!;??SS«<-><>«-«<'SS?S?SRStf!SSSSS^

II !T!Tl!TlIIIIi!T!TiiIIIIIIi!III!!ii!Tii!il!lll!l!ii!i!Tl!s!II!!!!T!!i!llli!!!!!!

ii in §1 ii mi ii ii iiim mu I? mmrn n
II m ii ii mi n ii Him mil ii §§§§§§§11 n
is "-▶->0>c5225j«"S»i55iS5i"'">"'"i55i»i5S«j"'" = = i5S»2Si5S««"SE!2222w«33

H I M S i i
2tsiS88SSgSSKSSSK8KSg2SSSt;|s8£2rt;ass§22sasSK2;S"o,2S?XSSSSSRSS5S!23Ks5SSSSK?KSSaS?S
gissaRsBS^gsssisS^e^wsRss^sss^sd^s^sris^ssciijo^dssiisRSSsRis^KSSRSs-sssssssscs

Appendix 10

Identity level = 0.875

PHENOTYPES In asareSS
CALCULATED DIVERSITY INDEX * 0.991

TRUE DIVERSITY INDEX - 0.891

No Name	PhP- sim typo min	sim moan	sim max	lo nr	PhP typo
1. BACILLUS	1	1.000	1.000 *	0.908 *	59 (SI)
+44. 44	1	1.000	1.000 *	0.908 *	59 (SI)
59. 59	SI			0.908 *	1 (1)
13. 13	SI			0.890 *	1 (1)
48. 48	SI			0.890 *	1 (1)
2. CORYNEBAC	2	0.996	0.998 *	0.910 *	23 (SI)
35. 35	2	0.996	0.998 *	0.910 *	23 (SI)
54. 64	2	0.996	0.996 *	0.939 *	31 (SI)
31. 31	SI			0.939 *	64 (2)
39. 39	11	0.992	0.992 *	0.908 *	2 (2)
57. 57	11	0.992	0.992 *	0.908 *	2 (2)
51. 51	SI			0.908 *	64 (2)
27. 27	SI			0.905 *	2 (2)
3Z CONTROL	SI			0.958 *	80 (SI)
80. CONTROL	SI			0.953 *	32 (SI)
70. 70	SI			0.884 *	80 (SI)
66. 66	SI			0.882 *	1 (1)
6. MICROCO SP	6	1.000	1.000 *	0.917 *	61 (SI)
53. 53	6	1.000	1.000 *	0.917 *	61 (SI)
61. 61	SI			0.917 *	6 (6)
65. 65	SI			0.917 *	6 (6)
69. 69	SI			0.893 *	5 (6)
79. 79	SI			0.904 *	57 (11)
74. 74	SI			0.893 *	6 (6)
76. 76	SI			0.862 *	6 (6)
3. FLAVOBAC	3	1.000	1.000 *	0.929 *	26 (SI)
17. 17	3	1.000	1.000 *	0.929 *	28 (SI)
28. 28	SI			0.929 *	3 (3)
24. 24	SI			0.919 *	3 (3)
12. 12	SI			0.958 *	33 (SI)
33. 33	SI			0.958 *	12 (SI)
37. 37	SI			0.925 *	12 (SI)
54. 54	SI			0.958 *	60 (SI)
60. 60	SI			0.958 *	54 (SI)
63. 63	SI			0.880 *	54 (SI)
5. PSEUDO FLUORE	5	1.000	1.000 *	0.846 *	25 (SI)
22. 22	5	1.000	1.000 *	0.846 *	25 (SI)
25. 25	SI			0.846 *	5 (5)
40. 40	SI			0.846 *	5 (5)
7. 7	7	0.998	0.999 *	0.934 *	30 (SI)
14. 14	7	0.998	0.999 *	0.934 *	30 (SI)
49. 49	7	0.998	0.998 *	0.931 *	30 (SI)
30. 30	SI			0.934 *	7 (7)
56. 56	SI			0.932 *	7 (7)
18. 18	10	1.000	1.000 *	0.930 *	7 (7)
42. 42	10	1.000	1.000 *	0.930 *	7 (7)
8. PSEUDO AEROG	8	1.000	1.000 *	0.942 *	46 (SI)
20. 20	8	1.000	1.000 *	0.942 *	46 (SI)
43. 43	8	1.000	1.000 *	0.942 *	46 (SI)
46. 46	SI			0.942 *	8 (SI)
26. 26	SI			0.941 *	8 (SI)
11. 11	SI			0.896 *	8 (SI)
23. 23	SI			0.910 *	2 (2)
50. 50	SI			0.396 *	8 (SI)
68. 68	13	0.999	0.999 *	0.854 *	75 (SI)
77. 77	13	0.999	0.999 *	0.854 *	75 (SI)
75. 75	SI			0.154 *	0 (0)
36. 36	SI			0.709 *	60 (SI)
41. 41	12	1.000	1.000 *	0.959 *	52 (SI)
45. 45	12	1.000	1.000 *	0.959 *	52 (SI)
52. 52	SI			0.959 *	41 (12)
47. 47	SI			0.939 *	41 (12)
4. E COLI	4	1.000	1.000 *	0.939 *	10 (SI)
16. 16	4	1.000	1.000 *	0.939 *	10 (SI)
73. 73	4	1.000	1.000 *	0.939 *	10 (SI)
10. 10	SI			0.939 *	4 (4)
29. 29	SI			0.938 *	4 (4)
78. 78	SI			0.938 *	4 (4)
21. 21	SI			0.938 *	4 (4)
9. STREPTOCO FAE	9	1.000	1.000 *	0.958 *	71 (SI)
34. 34	9	1.000	1.000 *	0.958 *	71 (SI)
38. 38	9	1.000	1.000 *	0.958 *	71 (SI)
55. 55	9	1.000	1.000 *	0.958 *	71 (SI)
58. 58	SI			0.957 *	9 (9)
67. 67	SI			0.957 *	9 (9)
71. 71	SI			0.958 *	9 (SI)
19. 19	SI			0.366 *	67 (SI)
15. 15	SI			0.474 *	27 (SI)
62. 62	SI			0.680 *	65 (SI)
72. 72	SI			0.683 *	12 (SI)

PHENOTYPES In Irmpsoni		Identity level = 0.976		V			
-CALCULATED DIVERSITY INDEX - 0.9B8		TRUE DIVERSITY INDEX -		0.036			
NO	Name	PhP- typ*	sum mln	sum mean	sum	to PhP nr type	
20	PSEUCMMOORE	1	1.000	1.000 *	0.910 *	42	SO
20		1	1.000	1.000 *	0.910 *	42	SO
28		1	1.000	1.000 *	0.910 *	42	Si)
42		SI			0.910 *	1	1)
53		SI			0.846 *	42	SO
2	CLOSTRIDIUM	2	1.000	1.000 *	0.876 *	66	Si
59		2	1.000	1.000 *	0.876 *	66	Si
63		2	1.000	1.000 *	0.876 *	66	Si)
66		SI			0.876 *	2	2)
39		SI		*	0.802 *	40	so
3	BACILLUS	3	1.000	1.000 *	0.899 *	40	SO
61		3	1.000	1.000 *	0.899 *	40	so
40	CONTROL	SI			0.965 *	80	so
80	CONTROL	SI			0.965 *	40	so
57		SI			0.836 *	80	SO
6	MICROCO SP	SI			0.926 *	17	10)
17		10	1.000	1.000 *	0.926 *	6	SO
37		10	1.000	1.000 *	0.926 *	6	so
71		SI			0.848 *	76	sp
76		SI			0.848 *	71	so
5	SALMONELLA PARA	5	1.000	1.000 *	0.936 *	10	so
29		5	1.000	1.000 *	0.936 *	10	so
43		5	1.000	1.000 *	0.936 *	10	so
58		5	1.000	1.000 *	0.936 *	10	so
69		5	1.000	1.000 *	0.936 *	10	SO
10		SI			0.936 *	5	5)
62		SI			0.935 *	10	so
26		SI			0.935 *	5	5)
34		SI			0.934 *	5	5)
38		SI			0.924 *	34	Si)
15		SI			0.935 *	18	Si)
18		SI			0.938 *	14	7)
47		SI			0.874 *	18	Si)
50		SI			0.934 *	5	5)
54		SI			0.895 *	50	sp
6	SHIGE OVS	7	0.989	0.994 *	0.950 *	30	so
23		7	0.989	0.994 *	0.950 *	30	so
14		7	0.989	0.989 *	0.950 *	18	so
30		SI			0.950 *	8	7)
21		11	1.000	1.000 *	0.879 *	10	so
33		11	1.000	1.000 *	0.879 *	10	so
22		SI			0.914 *	18	SO
77		SI			0.935 *	10	so
64		SI			0.876 *	62	so
7	STREPTOCO FAE	6	1.000	1.000 *	0.959 *	51	so
27		6	1.000	1.000 *	0.959 *	51	SO
45		6	1.000	1.000 *	0.959 *	51	so
51		SI			0.959 *	7	6)
13		SI			0.957 *	7	6)
19		SI			0.957 *	7	6)
56		SI			0.957 *	7	6)
32		SI			0.924 *	7	6)
35		SI			0.907 *	7	6)
9		8	1.000	1.000 *	0.760 *	26	so
31		8	1.000	1.000 *	0.760 *	26	SO
36		8	1.000	1.000 *	0.760 *	26	SO
11		SI			0.785 *	17	10)
41		SI			0.755 *	1	1)
52		SI			0.828 *	38	SO
65		SI			0.776 *	52	SO
67		SI			0.954 *	78	Si)
78		SI			0.954 *	67	so
72		SI			0.882 *	67	SO
70		SI			0.762 *	57	Si
4	ECOLI	4	1.000	1.000 *	0.039 *	00	SO
44		4	1.000	1.000 *	0.939 *	60	Si)
60		SI			0.939 *	4	4)
55		SI			0.938 *	4	4)
49		SI			0.886 *	4	4)
46		SI			0.845 *	4	-)
12		9	1.000	1.000 *	0.748 *	9	8)
24		9	1.000	1.000 *	0.748 *	9	8)
16		SI			0.650 *	46	SO
25		SI			0.662 *	76	so
48		SI			0.693 *	56	sn
68	1760	12	1.000	1.000 *	0.000 *	78	so
70	1170	12	1.000	1.000 *	0.000 *	10	Si)
73	1173	12	1.000	1.000 *	0.000 *	67	so
74	1174	12	1.000	1.000 *	0.000 *	67	Si)
75	75	SI			0.000 *	67	Si)

Appendix On

Identity level = 0.975
TRUE DIVERSITY INDEX - 0.990

PHENOTYPES in frimpon2/
CALCULATED DIVERSITY INDEX - 0.990

No	Name	PhP- type	Sim min	sim mean	sim max	Io PhP nr type
1	BACILLUS	1	1.000	1.000 *	0.869 *	41
46	45	SI	1.000	1.000 *	0.869 *	41
41	CONTROL	SI	1.000	1.000 *	0.939 *	32
82	CONTROL	SI			0.939 *	41
2	CLOSTRIDIUM	2	1.000	1.000 *	0.837 *	1
39	38	SI	1.000	1.000 *	0.837 *	1
60	58	SI			0.839 *	62
62	60	SI			0.839 *	60
34	33	SI			0.802 *	42
17	17	SI			0.844 *	42
42	41	SI			0.911 *	41
52	51	SI			0.910 *	42
7	PSEUDO FLUORE	7	1.000	1.000 *	0.826 *	32
25	25	SI	1.000	1.000 *	0.826 *	32
66	64	SI	1.000	1.000 *	0.826 *	32
32	31	SI			0.863 *	82
4	SHGEL DYS	4	0.989	0.994 ■	0.946 *	18
45	44	SI	0.989	0.994 ■	0.946 *	18
80	78	SI	0.989	0.989 ■	0.954 *	12
12	12	SI	1.000	1.000 *	0.954 *	60
68	66	SI	1.000	1.000 *	0.954 *	80
9	9	SI			0.940 *	63
18	18	SI			0.946 *	4
31	30	SI			0.926 *	4
8	SALMONELLA PARA	8	1.000	1.000 *	0.941 *	63
20	20	SI	1.000	1.000 *	0.941 *	63
27	27	SI	1.000	1.000 *	0.941 *	63
33	32	SI	1.000	1.000 *	0.941 *	63
44	43	SI	1.000	1.000 *	0.941 *	63
63	61	SI			0.941 *	8
38	37	SI			0.938 *	63
61	59	SI			0.890 *	8
15	15	SI			0.938 *	53
53	52	SI			0.938 *	15
36	35	SI			0.938 *	53
59	57	SI	1.000	1.000 *	0.870 *	81
72	70	SI	1.000	1.000 *	0.870 *	81
73	71	SI			0.894 *	8
81	79	SI			0.891 *	73
6	MICROCO SP	6	1.000	1.000 *	0.913 *	82
35	34	SI	1.000	1.000 *	0.913 *	82
48	47	SI	1.000	1.000 *	0.913 *	82
40	39	SI			0.880 *	6
56	55	SI			0.862 *	6
23	23	SI			0.810 *	6
14	14	SI	1.000	1.000 *	0.756 *	73
29	29	SI	1.000	1.000 *	0.756 *	73
16	16	SI			0.873 *	75
75	73	SI			0.873 *	16
26	26	SI			0.855 *	82
49	48	SI	1.000	1.000 *	0.841 *	16
50	49	SI	1.000	1.000 *	0.841 *	16
70	68	SI			0.819 *	26
19	19	SI			0.809 *	1
67	65	SI			0.851 *	74
74	72	SI			0.851 *	67
28	28	SI			0.837 *	78
78	76	SI			0.837 *	23
3	ECOU	3	1.000	1.000 *	0.938 *	53
24	24	SI	1.000	1.000 *	0.938 *	58
43	42	SI	1.000	1.000 *	0.938 *	58
58	56	SI			0.938 *	58
11	11	SI			0.886 *	5
5	STREPTOCO FAE	5	1.000	1.000 *	0.957 *	55
79	77	SI	1.000	1.000 *	0.957 *	55
55	54	SI	1.000	1.000 *	0.957 *	5
69	67	SI	1.000	1.000 *	0.957 *	5
76	74	SI			0.922 *	5
51	50	SI			0.922 *	5
71	69	SI			0.907 *	51
54	53	SI			0.900 *	65
65	63	SI			0.922 *	5
77	75	SI			0.926 *	5
10	10	SI			0.660 *	7
13	13	IQ	1.000	1.000 *	0.682 *	81
22	22	IQ	1.000	1.000 *	0.632 *	81
21	21	SI			0.376 *	10
30	30	SI			0.354 *	14
37	36	SI			0.662 *	19
57	56	SI			0.458 *	77
64	62	SI			0.690 *	71

Appendix 2
 Identity javal = 0.97 S
 TRUE DIVERSITY INDEX - 0.882

No	Nam*	PKP- type*	alm min	sim mean	sim max	to nr	PHP type
14	14	1	1.000	1.000	0.909 *	57	(S)
33	33	1	1.000	1.000 *	0.909 *	57	(S)
67	87	Si			0.909 *	1	M
62	82	Si			0.881 *	57	(SO)
2	MICROCO SP	2	1.000	1.000 *	0.926 *	42	
16	18	2	1.000	1.000 *	0.926 *	42	
42	42	14	1.000	1.000 *	0.926 *	2	(2)
49	49	14	1.000	1.000 *	0.926 *	2	(2)
5	BACILLUS	5	1.000	1.000 *	0.887 *	80	(SO)
67	67	5	1.000	1.000 *	0.887 *	80	(SO)
55	55	Si			0.866 *	5	(5)
35	35	Si			0.644 *	38	(SO)
6	CLOSTRIDIUM	6	1.000	1.000 *	0.909 *	80	(SO)
65	65	6	1.000	1.000 *	0.909 *	80	(so)
72	72	6	1.000	1.000 *	0.909 *	80	(so)
40	CONTROL	Si			0.965 *	80	(SO)
80	CONTROL	Si			0.965 *	40	(SO)
25	25	Si			0.890 *	40	(SO)
22	22	Si			0.828 *	6	(6)
18	18	11	1.000	1.000 *	0.916 *	38	(SO)
43	43	11	1.000	1.000 *	0.916 *	39	(SO)
39	39	Si			0.916 *	18	(11)
26	26	Si			0.897 *	37	(so)
37	37	Si			0.897 *	28	(SO)
53	53	Si			0.868 *	18	(S)
3	SHIGELLA DY	3	1.000	1.000 *	0.939 *	13	(5)
11	11	3	1.000	1.000 *	0.939 *	13	(9)
13	13	3	0.996	0.996 *	0.939 *	3	(3)
45	45	9	0.996	0.996 *	0.939 *	3	(3)
73	73	9	0.996	0.996 *	0.933 *	3	(3)
7	SALMONELLA PARA	7	0.996	0.996 *	0.940 *	9	(SO)
21	21	7	0.996	0.996 *	0.940 *	9	(SO)
27	27	7	0.996	0.996 *	0.940 *	9	(SO)
34	34	7	0.996	0.996 *	0.940 *	9	(SO)
58	58	7	0.996	0.996 *	0.940 *	9	(SO)
79	79	7	0.996	0.996 *	0.940 *	9	(SO)
54	54	7	0.996	0.997 *	0.935 *	9	(so)
70	70	9	0.996	0.997 *	0.935 *	9	(SO)
9	9	Si			0.940 *	7	(7)
64	64	Si			0.894 *	7	(7)
38	38	Si			0.893 *	7	(7)
29	29	13	0.996	0.996 *	0.936 *	66	(16)
61	61	13	0.996	0.996 *	0.934 *	66	(16)
66	66	16	1.000	1.000 *	0.936 *	29	(13)
75	75	16	1.000	1.000 *	0.936 *	29	(13)
50	50	Si			0.932 *	61	(13)
17	17	10	1.000	1.000 *	0.954 *	19	(12)
41	41	10	1.000	1.000 *	0.954 *	19	(12)
19	19	12	1.000	1.000 *	0.954 *	17	(10)
30	30	12	1.000	1.000 *	0.954 *	17	(10)
47	47	Si			0.909 *	19	(12)
38	38	Si			0.851 *	19	(12)
4	STREPTOCO FAE	4	0.990	0.997 *	0.959 *	71	(SO)
31	31	4	0.990	0.997 *	0.959 *	71	(S)
74	74	4	0.990	0.997 *	0.959 *	71	(SO)
52	52	4	0.990	0.990 *	0.953 *	76	(SO)
63	63	Si			0.957 *	4	(4)
71	71	Si			0.959 *	4	(4)
69	69	Si			0.957 *	4	(4)
76	76	Si			0.953 *	52	(4)
78	78	Si			0.926 *	4	(4)
60	60	Si			0.935 *	15	(SO)
IS	IS	B.			0.892 *	15	(SO)
10	10	8	1.000	1.000 *	0.874 *	48	(SO)
20	20	8	1.000	1.000 *	0.874 *	48	(SO)
32	32	8	1.000	1.000 *	0.874 *	48	(SO)
48	48	Si			0.874 *	10	(8)
59	59	Si			0.834 *	48	(S)
12	112	Si			0.406 *	53	(SO)
23	23	Si			0.882 *	3	(3)
24	1124	Si			0.000 *	3	(3)
28	128	Si			0.463 *	56	
44	44	15	1.000	1.000 *	0.728 *	5	(5)
51	51	15	1.000	1.000 *	0.728 *	5	(5)
46	46	Si			0.609 *	23	(SO)
56	58	Si			0.463 *	28	(SO)
68	68	Si			0.744 *	76	(S)
77	77	Si			0.712 *	61	(13)

Appendix 2 s
 Identity level = 0.926
 ■ 0.934 TRUE DIVERSITY INDEX » 0.934

No	Name	PhP-type	sim min	sim mean	sim max	to nr	PhP type
1	ECOLI	1	1.000	1.000 *	1.000 *	35	(SI)
9.	9	1	1.000	1.000 ■	0.856 ■	35	(SI)
*73.	73	1	1.000	1.000 *	0.856 ■	35	(SI)
31	31	SI			0.855 ■	1	!!!
35.	35	SI			0.856 *	1	!>
2	SHIG DYS	2	1.000	1.000 *	0.781 ■	14	?)
20.	20	2	1.000	1.000 *	0.781 ■	14	?)
3	SALMONELLA PARA	3	0.996	0.996 *	0.945 *	58	(SI)
10	10	3	0.996	0.999 *	0.936 *	43	(SI)
24.	24	3	0.996	0.999 *	0.936 *	43	(SI)
36.	36	3	0.996	0.999 *	0.936 *	43	(SI)
39.	39	3	0.996	0.999 *	0.936 *	43	(SO)
46.	46	3	0.996	0.999 *	0.936 *	43	(SO)
74.	74	3	0.996	0.998 *	0.936 *	43	(SI)
79.	79	3	0.996	0.999 *	0.936 ■	43	
58.	58	SI			0.945 *	3	f
43.	43	SI			0.937 *	26	(SO)
54.	54	SI			0.917 *	58	(SI)
14.	14	7	1.000	1.000 *	0.949 *	26	(SI)
22.	22	7	1.000	1.000 *	0.949 *	26	(SI)
26.	26	SI			0.949 *	14	(7)
66.	66	SI			0.933 *	19	(SI)
19.	19	SI			0.934 *	10	(3)
61.	61	SI			0.934 *	19	(SI)
72.	72	SI			0.930 *	61	ism
13.	13	6	1.000	1.000 *	0.933 *	69	(SI)
30.	30	6	1.000	1.000 *	0.933 *	69	(SI)
50.	50	6	1.000	1.000 *	0.932 *	13	(6)
69.	69	SI			0.933 *	13	(6)
77.	77	SI			0.846 *	69	(SO)
48.	48	11	1.000	1.000 *	0.917 *	65	(SI)
53.	53	11	1.000	1.000 *	0.917 *	65	(6)
65.	65	SI			0.917 *	48	(ID)
68.	68	SI			0.839 *	48	(in)
4.	*BACILLUS	4	1.000	1.000 *	0.000 *	58	(SI)
7.	!!CLOSTRIDIUM	4	1.000	1.000 *	0.000 *	29	(9)
8.	HMICROCO SP	4	1.000	1.000 *	0.000 *	29	(9)
11.	!! 11	4	1.000	1.000 *	0.000 *	43	(SI)
16.	!! 16	4	1.000	1.000 *	0.000 *	29	(9)
21.	! 21	4	1.000	1.000 *	0.000 *	14	
25.	!! 25	4	1.000	1.000 *	0.000 *	43	
33.	!! 33	4	1.000	1.000 *	0.000 *	48	!f,
40.	*CONTROL	4	1.000	1.000 *	0.000 *	43	(SI)
41.	!!41	4	1.000	1.000 *	0.000 *	43	(SI)
44.	!! 44	4	1.000	1.000 *	0.000 *	26	
49.	!! 49	4	1.000	1.000 *	0.000 *	65	(SI)
52.	!! 52	4	1.000	1.000 *	0.000 *	59	(SO)
55.	!! 55	4	1.000	1.000 *	0.000 *	58	so
60.	!! 60	4	1.000	1.000 *	0.000 *	5	5)
64.	!! 64	4	1.000	1.000 *	0.000 *	31	(SI)
71.	*171	4	1.000	1.000 *	0.000 *	6	
80.	UCONTROL	4	1.000	1.000 *	0.000 *	43	(SI)
5.	STREPTOCO FAE	5	0.990	0.998 *	0.955 *	59	(SO)
27.	27	5	0.990	0.998 *	0.955 *	59	(SI)
34.	34	5	0.990	0.998 *	0.955 *	59	(SI)
51.	51	5	0.990	0.998 *	0.955 *	59	(SI)
67.	67	5	0.990	0.998 *	0.955 *	59	(SI)
42.	42	5	0.990	0.990 *	0.951 *	59	(SI)
59.	59	SI			0.955 *	5	(5)
12.	12	SI			0.932 *	47	(SI)
23.	23	SI			0.938 ■	47	(SO)
47.	47	SI			0.938 *	23	1
18.	18	SI			0.833 *	5	
56.	56	12	1.000	1.000 *	0.755 *	23	(SI)
76.	76	12	1.000	1.000 *	0.755 *	23	(SO)
6.	PSEUDO FLUORE	SI			0.704 *	29	(9)
15.	15	SI			0.676 *	29	(9)
17.	17	SI			0.724 *	62	(SO)
28.	28	8	0.999	0.999 *	0.721 *	35	(SI)
45.	45	8	0.999	0.999 *	0.722 *	35	(SI)
29.	29	9	1.000	1.000 *	0.704 *	6	(SO)
70.	70	9	1.000	1.000 *	0.704 *	a	so
32.	3,32	SI			0.408 *	48	ID
37.	37	10	0.998	0.998 *	0.670 *	15	(SI)
75.	75	10	0.998	0.998 *	0.659 *	15	(SI)
38.	38	SI			0.494 *	35	(SI)
57.	57	SI			0.487 *	43	(SI)
62.	62	SI			0.724 □	17	18
63.	63	SI			0.554 *	31	
78.	78	SI			0.362 □	50	(SI)

oft

Appendix -21
 Identity level 0.975
 TRUE DIVERSITY INDEX >= 0.974

No	Name	PhP type	sim min	sim mean	sim max	lo nr	type
2	PSSUBCTIUOE	Si			0.704 *	47	(10)
2	IICLOSTRIDIUM	1	1.000	1.000 *	0.000 *	47	(10)
32	IICONTROL	1	1.000	1.000 *	0.000 *	71	(S)
34	I142	1	1.000	1.000 *	0.000 *	22	(7)
49	I157	1	1.000	1.000 *	0.000 *	30	(Si)
54	I162	1	1.000	1.000 *	0.000 *	38	(3)
60	I168	1	1.000	1.000 *	0.000 *	42	(S)
65	I173	1	1.000	1.000 *	0.000 *	29	(Si)
66	I173	1	1.000	1.000 *	0.000 *	29	(Si)
73	IICONTROL	1	1.000	1.000 *	0.000 *	20	(S)
3	ECOU	2	0.982	0.991 *	0.862 *	23	(S)
12	20	2	0.982	0.991 *	0.862 *	23	(S)
19	27	2	0.982	0.982 *	0.886 *	23	(S)
23	31	2			0.886 *	19	(2)
46	54	Si			0.856 *	3	(2)
4	MICROCO SP	Si			0.926 *	15	(S)
15	23	Si			0.926 *	4	(S)
5	BACILLUS	Si			0.940 *	10	(S)
6	STREPTOCO FAE	3	0.990	0.990 *	0.952 *	53	(SB)
36	46	3	0.990	0.997 *	0.955 *	29	(S)
64	72	3	0.990	0.997 *	0.955 *	29	(S)
67	74	3	0.990	0.997 *	0.955 *	29	(so)
29	37	Si			0.955 *	38	(3)
53	61	4			0.953 *	38	(3)
7	SHIG DYS	4	0.985	0.987 *	0.933 *	27	(S)
9	17	4	0.988	0.983 *	0.940 *	27	(S)
18	26	4	0.985	0.992 *	0.949 *	27	(S)
27	35	Si			0.949 *	18	(4)
37	45	Si			0.859 *	7	(4)
62	70	Si			0.852 *	9	(4)
28	36	Si			0.903 *	52	(SO)
52	60	Si			0.903 *	28	(S)
8	SALMONELLA PARA	5	0.993	0.997 *	0.934 *	42	(S)
35	43	5	0.993	0.997 *	0.934 *	42	(S)
59	67	5	0.993	0.997 *	0.934 *	42	(S)
70	77	5	0.990	0.993 *	0.920 *	42	(sg)
68	75	5	0.990	0.992 *	0.925 *	42	(so)
42	50	Si			0.934 *	8	(5)
44	52	Si			0.934 *	8	(5)
50	58	Si			0.915 *	68	(5)
14	22	Si			0.899 *	68	(5)
11	19	Si			0.881 *	8	(5)
17	25	7	0.987	0.987 *	0.917 *	33	(S)
22	30	7	0.987	0.987 *	0.932 *	33	(S)
33	41	Si			0.932 *	22	(7)
24	32	Si			0.839 *	17	(7)
26	34	Si			0.770 *	33	(S)
30	38	Si			0.822 *	48	(S)
48	56	Si			0.822 *	30	(S)
55	63	Si			0.769 *	48	1
10	18	6	0.985	0.985 *	0.758 *	69	1
16	24	6	0.985	0.993 *	0.792 *	69	1
39	47	6	0.985	0.993 *	0.792 *	69	1
69	76	Si			0.792 *	16	1
13	21	Si			0.645 *	23	(S)
20	28	Si			0.834 *	72	(S)
72	79	Si			0.834 *	20	(S)
21	29	Si			0.728 *	5	(S)
25	33	Si			0.745 *	37	(S)
31	39	8	1.000	1.000 *	0.683 *	71	(S)
41	49	8	1.000	1.000 *	0.683 *	71	(S)
36	44	Si			0.826 *	58	(S)
58	66	11	1.000	1.000 *	0.826 *	36	(S)
63	71	11	1.000	1.000 *	0.826 *	36	(S)
40	48	Si			0.784 *	45	(9)
45	53	9	1.000	1.000 *	0.784 *	40	(S)
56	64	9	1.000	1.000 *	0.784 *	40	(S)
43	I5-1	Si			0.486 *	5	(S)
47	55	10	1.000	1.000 *	0.749 *	40	(S)
57	65	10	1.000	1.000 *	0.749 *	40	(S)
51	0	Si			0.683 *	58	(11)
61	69	Si			0.719 *	47	(10)
71	178	Si			0.683 *	31	(8)

Appendix 3a

PHENOTYPES <i>in</i> boacM/		Identity level * 0.975		CALCULATED DIVERSITY INDEX - 0.974		TRUE DIVERSITY INDEX - 0.974			
No	Name	PhP-type	sim mln	sim mean	sim max	to nr	PhP type		
1.	CLOSTRIDIUM	1	1.000	1.000 *	0.899 *	59	(SI)		
30.	30	1	1.000	1.000 *	0.899 *	59	(SI)		
69.	69	1	1.000	1.000 *	0.899 *	59	(SI)		
59.	59	SI			0.899 *	1	(1)		
71.	71	SI			0.899 *	1	(1)		
74.	74	SI			0.888 ■	1	(1)		
55.	55	SI			0.891 *	63	(SI)		
63.	63	SI			0.891 *	55	(SI)		
77.	77	SI			0.870 *	80	(SI)		
2.	MICROCO LUT	2	1.000	1.000 *	0.926 *	53	(SI)		
14.	14	2	1.000	1.000 *	0.926 *	53	(SI)		
72.	72	2	1.000	1.000 *	0.926 *	53	(SI)		
53.	53	SI			0.926 *	2	(2)		
40.	CONTROL	SI			0.963 *	80	(SI)		
SO.	CONTROL	SI			0.963 *	40	(SI)		
33.	33	SI			0.874 *	2	(2)		
22.	22	SI			0.862 ■	53	(SO)		
39.	39	SI			0.874 *	2	(2)		
8.	BACILLUS SP	SI			0.895 *	56	(11)		
56.	56	11	1.000	1.000 *	0.895 *	8	(SO)		
79.	79	11	1.000	1.000 *	0.895 *	8	(SO)		
46.	46	SI			0.870 *	2	(2)		
57.	57	SI			0.818 *	46	(SI)		
4.	PROTEUS MIRA	4	1.000	1.000 *	0.956 *	76	(so)		
49.	49	4	1.000	1.000 *	0.956 *	76	(SO)		
66.	66	4	1.000	1.000 *	0.958 *	76	(so)		
76.	76	SI			0.956 *	4	(4)		
52.	52	SI			0.932 *	4	(4)		
47.	47	SI			0.903 *	52	(SI)		
66.	66	SI			0.875 ■	1	(1)		
3.	ECOU	3	1.000	1.000 *	0.945 *	15	(SO)		
19.	19	3	1.000	1.000 *	0.945 *	15	(SO)		
15.	15	SI			0.945 *	3	(3)		
64.	64	SI			0.939 *	3	(3)		
51.	51	SI			0.939 *	3	(3)		
26.	26	SI			0.939 *	3	(3)		
60.	60	SI			0.939 *	3	(3)		
24.	24	SI			0.938 *	3	(3)		
10.	10	SI			0.938 *	3	(3)		
5.	PSEUDO AEROG	5	1.000	1.000 *	0.941 *	35	(SI)		
45.	45	5	1.000	1.000 *	0.941 *	35	(SI)		
35.	35	SI			0.941 *	5	(5)		
29.	29	SI			0.915 *	5	(5)		
6.	STREPTOCO FAE	6	0.996	1.000 *	0.959 *	18	(8)		
12.	12	6	0.996	1.000 *	0.959 *	18	(3)		
13.	13	6	0.996	1.000 *	0.959 *	18	(8)		
25.	25	6	0.996	1.000 *	0.959 *	18	(8)		
34.	34	6	0.998	1.000 *	0.959 *	18	(8)		
42.	42	6	0.996	1.000 *	0.959 *	18	(8)		
54.	54	6	0.996	1.000 *	0.959 ■	18	(S)		
65.	65	6	0.996	1.000 *	0.959 *	18	(6)		
70.	70	6	0.996	1.000 *	0.959 *	18	(8)		
75.	75	6	0.996	1.000 *	0.959 ■	18	(4)		
73.	78	6	0.996	1.000 *	0.959 *	18	(8)		
62.	62	6	0.996	0.998 *	0.973 *	16	(SI)		
16.	16	SI			0.973 *	62	(6)		
18.	18	8	1.000	1.000 *	0.959 *	6	(6)		
28.	28	8	1.000	1.000 *	0.959 *	6	(6)		
36.	36	10	1.000	1.000 *	0.958 *	6	(6)		
73.	73	10	1.000	1.000 *	0.958 ■	6	(6)		
23.	23	SI			0.957 *	6	(6)		
21.	21	9	1.000	1.000 *	0.957 *	6	(6)		
48.	48	9	1.000	1.000 *	0.957 *	6	(6)		
41.	41	SI			0.957 *	6	(6)		
50.	50	SI			0.957 *	6	(6)		
32.	32	SI			0.957 *	6	(6)		
53.	58	SI			0.953 *	32	(SI)		
9.	9	SI			0.958 *	6	(6)		
67.	67	SI			0.953 *	16	(SI)		
17.	17	SI			0.880 *	18	(8)		
7.	PSEUDO FLUORE	7	1.000	1.000 *	0.846 ■	20	(SI)		
43.	43	7	1.000	1.000 *	0.848 *	20	(SO)		
20.	20	SI			0.879 *	55	(SI)		
27.	27	SI			0.846 *	7	(7)		
37.	37	SI			0.846 *	7	(7)		
11.	11	SI			0.785 *	2	(2)		
44.	44	SI			0.790 *	4	(4)		
31.	31	SI			0.677 *	8	(SI)		
38.	38	SI			0.628 *	77	(so)		
61.	61	SI			0.723 *	32	(SO)		

264

Appendix. 3t> _

PHENOTYPES Inboard3 Identity level= 0.975
 CALCULATED DIVERSITY INDEX - 0.905 TRUE DIVERSITY INDEX 0.984

No	Name	PhP-type	IMT1 mln	sim mean	sim max	to nr	PhP type
1.	CLOSTRIDIUM	1	1.000	1.000 [†]	0.899 [*]	28	(11)
22		1	1.000	1.000 [■]	0.899 [*]	28	(11)
50, 60		1	1.000	1.000 [*]	0.899 [*]	28	(11)
56, 56		1	1.000	1.000 [*]	0.699 [*]	23	(11)
78, 78		1	1.000	1.000 [*]	0.899 [*]	28	(11)
20, 28		11	0.997	0.997 [*]	0.899 [*]	1	(1)
70, 70		11	0.997	0.997 [*]	0.897 [*]	1	(1)
37, 37		12	1.000	1.000 [†]	0.899 [*]	1	(1)
42, 42		12	1.000	1.000 [*]	0.899 [*]	1	(1)
66, 66		12	1.000	1.000 [*]	0.899 [*]	1	(1)
53, 53		SI			0.883 [*]	1	(1)
34, 34		SI			0.878 [*]	1	(1)
61, 61		SI			0.878 [*]	1	(1)
6.	PROTEUS MIRA	6	1.000	1.000 [■]	0.932 [*]	63	(SI)
54, 54 [*]		6	1.000	1.000 [*]	0.932 [■]	63	(SI)
63, 63		SI			0.932 [*]	6	(6)
71, 71		SI			0.930 [*]	6	(6)
14, 14		SI			0.873 [*]	20	(10)
20, 20		10	1.000	1.000 [*]	0.903 [*]	63	(SI)
43, 43		10	1.000	1.000 [*]	0.903 [*]	63	(SI)
3.	MICROCO SP	3	1.000	1.000 [*]	0.926 [*]	75	(SI)
10, 10		3	1.000	1.000 [*]	0.926 [*]	75	(SI)
52, 52		3	1.000	1.000 [*]	0.926 [*]	75	(SO)
73, 73		3	1.000	1.000 [*]	0.926 [*]	75	(SI)
75, 75		SI			0.926 [*]	3	(3)
77, 77		SI			0.897 [*]	3	(3)
48, 48	CONTROL [†]	SI			0.972 [*]	80	(SI)
80, 80	CONTROL	SI			0.972 [*]	48	(SI)
58, 58		SI			0.874 [*]	3	(3)
64, 64		SI			0.870 [■]	3	(3)
7.	PSEUDO CAV	7	1.000	1.000 [*]	0.862 [*]	75	(SI)
59, 59		7	1.000	1.000 [*]	0.862 [*]	75	(SI)
31, 31		SI			0.878 [*]	44	(SI)
44, 44		SI			0.878 [*]	31	(SI)
74, 74		SI			0.817 [*]	31	(SO)
2.	ECOLI	2	1.000	1.000 [*]	0.939 [*]	24	(SO)
9, 9		2	1.000	1.000 [*]	0.939 [*]	24	(SO)
18, 18		2	1.000	1.000 [*]	0.939 [*]	24	(SO)
24, 24		SI			0.939 [*]	2	(2)
27, 27		SI			0.938 [■]	2	(2)
8, 8		8	1.000	1.000 [*]	0.938 [*]	2	(2)
39, 39		a	1.000	1.000 [*]	0.938 [*]	2	(2)
45, 45		SI			0.933 [*]	8	(8)
36, 36		SI			0.938 [*]	2	(2)
36, 36		SI			0.774 [*]	2	(2)
4.	STREPTOCO FAE	4	0.994	0.998 [*]	0.969 [*]	33	(SO)
15, 15		4	0.994	0.998 [*]	0.969 [*]	33	(SO)
19, 19		4	0.994	0.998 [*]	0.969 [*]	33	(SO)
25, 25		4	0.994	0.998 [*]	0.969 [*]	33	(SO)
11, 11		4	0.994	0.994 [*]	0.984 [?]	49	(SO)
49, 49		SI			0.984 [?]	11	(4)
33, 33		SI			0.969 [*]	4	(4)
13, 13		9	0.992	0.996 [*]	0.956 [*]	4	(4)
21, 21		9	0.993	0.997 [*]	0.957 [*]	4	(4)
40, 40		9	0.991	0.995 [*]	0.972 [*]	57	(SO)
32, 32		9	0.991	0.992 [*]	0.982 [?]	47	(SO)
47, 47		SI			0.982 [?]	32	(9)
23, 23		SI			0.958 [*]	4	(4)
41, 41		SI			0.951 [*]	23	(SI)
55, 55		SI			0.950 [*]	23	(SI)
60, 60		SI			0.956 [*]	65	(SO)
65, 65		SI			0.956 [*]	60	(SO)
69, 69		SI			0.852 [*]	21	(9)
57, 57		SI			0.972 [*]	40	(9)
30, 30		SI			0.973 [*]	67	(SI)
67, 67		SI			0.973 [*]	30	(SO)
72, 72		SI			0.952 [*]	49	(SO)
5.	PSEUDO FLUORE	5	1.000	1.000 [*]	0.755 [*]	29	(SO)
12, 12		5	1.000	1.000 [*]	0.755 [*]	29	(SO)
17, 17		5	1.000	1.000 [*]	0.755 [*]	29	(SO)
29, 29		SI			0.755 [*]	5	(5)
16, 16		SI			0.799 [*]	6	(6)
26, 26		SI			0.792 [*]	73	(SO)
73, 73		SI			0.801 [*]	48	(SO)
62, 62		SI			0.776 [*]	26	(SO)
46, 46		SI			0.811 [*]	77	(SO)
76, 76		SI			0.803 [*]	46	(SO)
51, 51		SI			0.781 [*]	47	(SO)
35, 35		SI			0.737 [*]	57	(SO)
68, 68		SI			0.714 [*]	76	(SO)

Appendix 3 c

PHENOTYPES in board/		Identity level = 0.975		TRUE DIVERSITY INDEX -		0.971	
CALCULATED DIVERSITY INDEX - 0.975							
No	Name	PhP- type	min	mean	sim	lo	PhP type
1.	MICROCO LUT	1	1.000	1.000 *	0.874 ■	9	(S)
17.	17	1	1.000	1.000 ■	0.874 *	9	(S)
9.	9	Si			0.874 *	1	(1)
22.	22	Si			0.874 *	1	(1)
30.	30	Si			0.874 *	1	(1)
25.	25	Si			0.870 *	1	(1)
3.	CLOSTRIDIUM	3	0.979	0.995 *	0.918 *	81	(S)
15.	15	3	0.979	0.995 *	0.918 *	81	(S)
27.	27	3	0.979	0.995 ■	0.918 *	81	(S)
42.	42	3	0.979	0.995 *	0.918 *	81	(S)
21.	21	3	0.979	0.979 *	0.938 *	81	(S)
32.	CONTROL	Si			0.972 *	81	(S)
81.	CONTROL	Si			0.972 *	32	(S)
71.	70	12	1.000	1.000 *	0.883 *	32	(S)
76.	75	12	1.000	1.000 *	0.883 *	32	(S)
46.	46	Si			0.891 *	3	(3)
31.	31	S	0.999	0.999 *	0.896 *	3	(3)
63.	62	9	0.999	0.999 *	0.899 *	3	(3)
10.	10	Si			0.899 *	3	(-3)
24.	24	Si			0.896 *	49	(Si)
34.	34	Si			0.942 *	49	(S)
49.	49	Si			0.942 *	34	(S)
37.	37	Si			0.861 '	71	(12)
39.	39	10	0.982	0.982 *	0.873 *	3	(3)
56.	55	10	0.982	0.982 ■	0.878 *	3	(3)
68.	67	Si			0.869 *	3	(3)
11.	11	Si			0.771 *	18	(8)
4.	PROTEUS MIRA	Si			0.932 *	13	(S)
13.	13	Si			0.932 *	4	(S)
26.	26	Si			0.931 *	4	(S)
23.	23	Si			0.932 *	4	(S)
29.	29	Si			0.925 *	4	(S)
18.	18	8	1.000	1.000 *	0.878 '	3	(3)
52.	52	8	1.000	1.000 *	0.878 *	3	(3)
6.	STREPTOCO FAE	5	0.989	0.997 *	0.984 ?	79	(S)
14.	14	5	0.989	0.997 *	0.984 ?	79	(S)
35.	35	5	0.989	0.997 *	0.984 ?	79	(S)
43.	43	5	0.989	0.997 *	0.984 ?	79	(S)
70.	69	5	0.989	0.997 *	0.984 ?	79	(S)
74.	73	5	0.989	0.997 *	0.984 ?	79	(S)
67.	66	5	0.989	0.996 *	0.984 ?	79	(S)
54.	53	5	0.977	0.992 *	0.990 ?	79	(S)
55.	54	5	0.988	0.993 *	0.986 ?	79	(S)
75.	74	5	0.983	0.992 *	0.977 ?	79	(S)
78.	77	5	0.977	0.987 *	0.973 *	36	(S)
64.	63	Si			0.973 *	78	(5)
48.	48	11	1.000	1.000 *	0.971 *	75	(5)
72.	71	11	1.000	1.000 *	0.971 *	75	(5)
38.	38	Si			0.973 *	79	(S)
79.	78	Si			0.990 ?	54	(5)
62.	61	Si			0.957 *	6	(5)
36.	36	Si			0.973 *	78	(5)
51.	51	Si			0.953 *	40	(S)
40.	40	Si			0.957 *	6	(5)
2.	PSEUDO AEROG	2	1.000	1.000 *	0.941 *	50	(S)
41.	41	2	1.000	1.000 *	0.941 *	50	(S)
57.	56	2	1.000	1.000 *	0.941 '	50	(S)
50.	50	Si			0.941 *	2	(2)
47.	47	Si			0.896 *	2	(2)
20.	20	Si			0.817 '	47	(S)
7.	PSEUDO FLUORE	6	1.000	1.000 *	0.846 *	58	(S)
45.	45	6	1.000	1.000 *	0.846 *	58	(S)
80.	79	6	1.000	1.000 *	0.846 *	58	(S)
65.	64	Si			0.879 *	33	(S)
66.	65	Si			0.846 *	7	(6)
33.	33	Si			0.891 *	59	(S)
59.	58	Si			0.891 *	33	(S)
44.	44	Si			0.803 *	61	(S)
61.	60	Si			0.834 *	7	(6)
58.	57	Si			0.875 *	73	(S)
73.	72	Si			0.875 *	58	(S)
5.	ECOU	4	1.000	1.000 *	0.944 *	77	(S)
16.	16	4	1.000	1.000 *	0.944 ■	77	(S)
60.	59	4	1.000	1.000 *	0.944 *	77	(S)
77.	76	Si			0.944 *	5	(4)
12.	12	Si			0.938 *	5	(4)
19.	19	Si			0.938 '	5	(4)
69.	68	Si			0.938 *	5	(4)
8.	KLE BSI ELIA 02AN	7	1.000	1.000 *	0.698 *	2	(2)
28.	28	7	1.000	1.000 *	0.698 *	2	(2)
53.	53	Si			0.575 *	64	(S)

Appendix 3d

PHENOTYPES Inboard Identity level 0.975
 *CALCULATED DIVERSITY INDEX * 0.971 TRUE DIVERSITY INDEX ■ 0.968

No	Nome	PhP- sim typ# mln	sim mean	sim max	TO nr	PhP type
t	PSEUDO FLUORE	1	1.000	1.000 ■	0.846 *	71 (SI)
17.	17	1	1.000	1.000 *	0.848 *	71 (SI)
74.	74	SI			0.846 *	1 (1)
77.	77	SI			0.846 *	1 (1)
67.	67	SI			0.956 *	71 (SI)
71.	71	SI			0.956 *	67 (SI)
2.	PROTEUS MIRA	2	0.979	0.979 *	0.924 *	72 (SI)
10.	19	2	0.979	0.989 *	0.932 *	72 (SI)
66.	66	2	0.979	0.989 *	0.932 *	72 (SI)
72.	72	SI			0.932 *	19 (2)
73.	73	SI			0.932 *	19 (2)
50.	50	SI			0.878 *	4 (4)
4.	CLOSTRIDIUM	4	1.000	1.000 *	0.899 *	20 (14)
15.	15	4	1.000	1.000 *	0.899 *	20 (14)
25.	25	4	1.000	1.000 *	0.899 *	20 (14)
64.	64	4	1.000	1.000 *	0.899 *	20 (14)
68.	68	4	1.000	1.000 *	0.899 *	20 (*)
20.	20	14	1.000	1.000 *	0.901 *	32 (SO)
54.	54	14	1.000	1.000 *	0.901 *	32 (SI)
30.	30	SI			0.899 *	4 (4)
58.	58	SI			0.899 *	4 (4)
61.	61	SI			0.899 *	4 (4)
44.	44	16	1.000	1.000 *	0.883 *	4 (4)
76.	76	16	1.000	1.000 *	0.883 *	4 (4)
24.	24	15	1.000	1.000 *	0.894 *	32 (SI)
56.	56	15	1.000	1.000 *	0.894 *	32 (SI)
79.	79	15	1.000	1.000 *	0.894 *	32 (SI)
32.	32	SI			0.901 *	20 (14)
8.	MICROCO SP	8	1.000	1.000 *	0.926 *	33 (SI)
22.	22	8	1.000	1.000 *	0.926 *	33 (SI)
65.	65	8	1.000	1.000 *	0.926 *	33 (SI)
33.	33	SI			0.926 *	8 (8)
40.	CONTROL	SI			0.952 *	80 (SI)
80.	CONTROL	SI			0.952 *	40 (SI)
78.	78	SI			0.874 *	8 (8)
69.	69	SI			0.874 *	8 (8)
10.	10	10	1.000	1.000 *	0.895 *	18 (SI)
34.	34	10	1.000	1.000 *	0.895 *	18 (SI)
18.	18	SI			0.895 *	10 (10)
38.	38	SI			0.863 *	18 (SI)
27.	27	SI			0.858 *	38 (SI)
16.	16	13	1.000	1.000 *	0.910 *	31 (SI)
75.	75	13	1.000	1.000 *	0.910 *	31 (SI)
31.	31	SI			0.910 *	16 (16)
48.	48	SI			0.879 *	31 (SI)
3.	PSEUDO AERO	3	1.000	1.000 *	0.941 *	55 (SO)
51.	51	3	1.000	1.000 *	0.941 *	55 (SO)
55.	55	SI			0.941 ■	3 (3)
36.	36	SI			0.780 *	40 (SO)
5.	STREPTOCO FAE	5	0.990	0.998 *	0.980 7	49 (17)
28.	28	5	0.991	0.998 *	0.980 7	49 (17)
41.	41	5	0.990	0.998 *	0.980 7	49 (17)
42.	42	5	0.990	0.998 *	0.980 7	49 (17)
53.	53	5	0.990	0.998 *	0.980 7	49 (17)
62.	62	5	0.990	0.998 *	0.980 7	49 (17)
70.	70	5	0.990	0.998 *	0.980 7	49 (17)
23.	23	5	0.988	0.996 *	0.989 7	49 (17)
26.	26	5	0.989	0.997 *	0.978 7	49 (17)
37.	37	5	0.988	0.995 *	0.978 7	49 (17)
63.	63	5	0.986	0.989 *	0.972 *	9 (9)
9.	9	9	1.000	1.000 *	0.972 *	63 (5)
59.	59	9	1.000	1.000 *	0.972 *	63 (5)
11.	11	SI			0.972 *	63 (5)
49.	49	17	0.985	0.985 *	0.989 7	23 (5)
57.	57	17	0.985	0.985 *	0.958 *	23 (5)
13.	13	11	0.996	0.996 *	0.958 *	28 (5)
35.	35	11	0.996	0.996 *	0.957 *	37 (5)
47.	47	SI			0.958 *	28 (5)
45.	45	SI			0.899 *	35 (11)
6.	ECOU	6	1.000	1.000 ■	0.945 *	60 (SI)
21.	21	6	1.000	1.000 *	0.945 *	60 (SO)
52.	52	6	1.000	1.000 ■	0.945 *	60 (SO)
60.	60	SI			0.945 *	6 (6)
12.	12	SI			0.938 *	6 (6)
29.	29	SI			0.938 *	6 (6)
14.	14	12	0.980	0.980 *	0.917 *	6 (6)
43.	43	12	0.980	0.980 *	0.939 *	6 (6)
7.	ENTEROBACTER CLOA	7	1.000	1.000 *	0.740 *	18 (SI)
39.	39	7	1.000	1.000 *	0.740 *	18 (SO)
46.	46	7	1.000	1.000 *	0.740 *	18 (SI)

Appendix						
PHENOTYPES in boad5/ _CALCULATED DIVERSITY INDEX » 0.982		Identity level - 0.975 TRUE DIVERSITY INOEX - 0.982				
No	Name	PhP- typo	sim mlh	sim mean	to nt	PhP typo
1	STREPTOCO FAE	1	1.000	1.000 *	0.959 ■	26 (10)
18	18	1	1.000	1.000 *	0.959 *	26 (10)
30	30	1	1.000	1.000 *	0.959 *	26 (10)
35	35	1	1.000	1.000 *	0.959 *	26 (10)
39	39	1	1.000	1.000 *	0.959 *	26 (10)
42	42	1	1.000	1.000 *	0.959 *	26 (10)
52	51	1	1.000	1.000 *	0.959 *	26 (10)
66	65	1	1.000	1.000 *	0.959 *	26 (10)
26	26	10	1.000	1.000 *	0.959 *	1 (1)
50	49	10	1.000	1.000 ■	0.959 *	1 (1)
10	10	7	1.000	1.000 *	0.957 *	1 (1)
45	45	7	1.000	1.000 *	0.957 *	1 (1)
46	45	7	1.000	1.000 *	0.957 *	1 (1)
33	33	Si			0.957 *	1 (1)
49	48	15	1.000	1.000 *	0.957 *	1 (1)
55	54	15	1.000	1.000 *	0.957 *	1 (1)
15	15	Si			0.957 *	1 (1)
62	61	Si			0.958 *	1 (1)
21	21	Si			0.957 *	1 (1)
59	58	Si			0.958 *	1 (1)
71	70	Si			0.957 *	1 (1)
51	50	16	1.000	1.000 *	0.880 *	26 (10)
58	57	16	1.000	1.000 *	0.880 *	26 (10)
3	CLOSTRIDIUM	3	1.000	1.000 *	0.968 *	29 (SI)
9	9	3	1.000	1.000 *	0.968 *	29 (SO)
43	43	3	1.000	1.000 *	0.966 *	29 (SI)
75	74	3	1.000	1.000 ■	0.968 *	29 (SI)
29	29	Si			0.973 *	53 (SI)
53	52	Si			0.973 *	29 (SI)
76	75	Si			0.908 *	44 (SI)
44	44	Si			0.917 *	48 (SI)
48	47	Si			0.917 *	44 (SI)
16	16	Si			0.921 *	61 (SI)
61	60	Si			0.921 *	16 (SO)
47	46	14	1.000	1.000 ■	0.917 *	48 (SI)
79	78	14	1.000	1.000 *	0.917 *	48 (so)
37	37	13	1.000	1.000 *	0.883 *	61 (SO)
56	55	13	1.000	1.000 *	0.883 *	61 (SI)
54	53	Si			0.878 *	3 (SI)
23	23	Si			0.879 *	34 (12)
34	34	12	1.000	1.000 *	0.923 *	64 (SI)
80	79	12	1.000	1.000 *	0.923 *	64 (SO)
64	63	Si			0.923 *	34 (12)
67	66	17	1.000	1.000 *	0.895 *	70 (SI)
73	72	17	1.000	1.000 *	0.895 *	70 (SI)
70	69	Si			0.895 *	67 (17)
31	31	11	1.000	1.000 *	0.869 *	3 (3)
72	71	11	1.000	1.000 *	0.869 *	3 (3)
77	76	11	1.000	1.000 *	0.869 *	3 (3)
5	MICROCO SP	5	0.995	0.995 *	0.926 *	41 (SI)
8	MICROCO Litt	5	0.995	0.995 *	0.922 *	41 (SI)
41	41	Si			0.926 *	5 (5)
81	CONTROL	Sf			0.913 *	8 (5)
32	32	Si			0.900 ■	8 (5)
57	56	Si			0.874 *	41 (SO)
38	38	Si			0.917 ■	5 (5)
05	04	Si			0.002 *	5 (5)
6	PROTEUS MIRA	6	1.000	1.000 *	0.932 *	25 (SI)
17	17	6	1.000	1.000 *	0.932 *	25 (SO)
25	25	Si			0.932 *	6 (6)
7	PSEUDO AEROG	Si			0.896 *	13 (SI)
13	13	Si			0.896 *	7 (SI)
26	28	Si			0.896 *	7 (SI)
74	73	Si			0.785 *	41 (SI)
2	PSEUDO FLUORE	2	1.000	1.000 ■	0.846 *	12 (SI)
78	77	2	1.000	1.000 *	0.846 *	12 (SI)
12	12	Si			0.846 *	2 (2)
68	67	Si			0.846 *	2 (2)
4	E COLI	4	1.000	1.000 *	0.939 *	63 (SO)
27	27	4	1.000	1.000 *	0.939 *	63 (SI)
36	36	4	1.000	1.000 *	0.939 *	63 (SI)
60	59	4	1.000	1.000 *	0.939 *	63 (SI)
65	62	Si			0.939 ■	4 (4)
11	'11	Si			0.938 *	4 (4)
22	22	9	1.000	1.000 *	0.938 *	4 (4)
69	68	9	1.000	1.000 ■	0.938 *	4 (4)
19	19	Si			0.938 *	4 (4)
14	14	8	1.000	1.000 *	0.796 *	11 (SI)
24	24	8	1.000	1.000 *	0.796 *	11 (SI)
20	20	Si			0.658 *	64 (SI)
40	HCONTROL	Si			0.000 ■	20 (10)

266

Appendix • 3F

PHENOTYPES In km/		Identity level * 0.975		TRUE DIVERSITY INDEX -		0.959	
*CALCULATED DIVERSITY INDEX - 0.958							
No	Nama	PhP- aim type min	sim mean	swm max	to nr	PhP type	
1.	PSEUDO FLUORE	1	1.000	1.000 *	0.690 *	24	(SI)
10.	10	1	1.000	1.000 *	0.690 *	24	(SI)
2.	PROTEUS MIRA	2	1.000	1.000 *	0.852 *	43	(SO)
17.	17	2	1.000	1.000 *	0.852 *	43	(SI)
32	32	2	1.000	1.000 *	0.852 *	43	(SO)
43.	43	SI			0.852 *	2	(2)
11.	11	SI			0.847 *	2	(2)
3.	1IMICROCO SP	3	1.000	1.000 *	0.000 *	43	(so)
5.	JIBACILLUS	3	1.000	1.000 *	0.000 *	51	(11)
0.	ICLOSTRIDIUM	3	1.000	1.000 *	0.000 *	51	(11)
12	I112	3	1.000	1.000 *	0.000 *	2	(2)
19.	11 19	3	1.000	1.000 *	0.000 *	51	(11)
25.	It 25	3	1.000	1.000 *	0.000 *	1	(1)
26.	M 26	3	1.000	1.000 *	0.000 *	1	(1)
40.	I1CONTROL	3	1.000	1.000 *	0.000 *	76	(SO)
42.	II 42	3	1.000	1.000 *	0.000 *	23	(SO)
50.	II 50	3	1.000	1.000 *	0.000 *	4	(4)
54.	II 54	3	1.000	1.000 *	0.000 *	8	(6)
57.	II 57	3	1.000	1.000 *	0.000 *	21	(SO)
65.	II 65	3	1.000	1.000 *	0.000 *	4	(#)
78.	II 78	3	1.000	1.000 *	0.000 *	4	(4)
80.	I1CONTROL	3	1.000	1.000 *	0.000 *	51	(11)
4.	STREPTOCO FAE	4	1.000	1.000 *	0.955 *	51	(11)
18.	18	4	1.000	1.000 *	0.955 *	51	(11)
59.	59	4	1.000	1.000 *	0.955 *	51	(11)
72.	72	4	1.000	1.000 *	0.955 *	51	(11)
79.	79	4	1.000	1.000 *	0.955 *	51	(11)
51.	51	11	1.000	1.000 *	0.955 *	4	(4)
70.	70	11	1.000	1.000 *	0.955 *	4	(4)
45.	45	SI			0.948 *	64	(SI)
64.	64	SI			0.953 *	4	(<)
67.	67	SI			0.949 *	4	(4)
76.	76	SI			0.946 *	67	(SO)
77.	77	SI			0.914 *	4	(*)
39.	39	SI			0.881 *	76	(SO)
49.	49	10	1.000	1.000 *	0.918 *	4	(4)
73.	73	10	1.000	1.000 *	0.918 *	4	(4)
69.	69	SI			0.881 *	4	(<)
9.	9	SI			0.868 *	74	(SO)
62.	62	SI			0.942 *	74	(SO)
74.	74	SI			0.942 *	62	(SO)
66.	66	SI			0.807 *	74	(SO)
30.	30	SI			0.807 *	39	(so)
37.	37	SI			0.826 *	44	(SO)
44.	44	SI			0.826 *	37	(SO)
55.	55	SI			0.813 *	44	(SI)
60.	60	SI			0.769 *	55	(SO)
58.	58	SI			0.760 *	37	(SO)
7.	ECOLI	5	1.000	1.000 *	0.862 *	29	(SO)
13.	13	5	1.000	1.000 *	0.862 *	29	(SO)
38.	38	5	1.000	1.000 *	0.862 *	29	(SI)
29.	29	SI			0.862 *	7	(5)
23.	23	SI			0.855 *	7	(5)
8.	PSEUDO AERO	6	1.000	1.000 *	0.531 *	53	(so)
28.	28	6	1.000	1.000 *	0.531 *	53	(SI)
14.	14	7	1.000	1.000 *	0.417 *	53	(SI)
22	22	7	1.000	1.000 *	0.417 *	53	(SI)
15.	15	8	i.poo	1.000 *	0.771 *	36	(9)
20.	20	8	1.000	1.000 *	0.771 *	36	(9)
36.	36	9	1.000	1.000 *	0.771 *	15	(8)
47.	47	9	1.000	1.000 *	0.771 *	15	(8)
16.	16	SI			0.793 *	35	(SO)
35.	35	SI			0.793 *	16	(SI)
21.	121	SI			0.604 *	56	(SO)
24.	24	SI			0.690 *	1	(1)
27.	27	SI			0.704 *	15	(8)
31.	31	SI			0.689 *	29	(SI)
33.	33	SI			0.642 *	f	<D
34.	34	SI			0.492 *	63	(SI)
41.	41	SI			0.554 *	23	(SO)
48.	48	SI			0.848 *	71	(SO)
71.	71	SI			0.848 *	46	(SO)
48.	48	SI			0.605 *	61	(SI)
52.	152	SI			0.725 *	46	(SO)
53.	53	SI			0.531 *	8	(6)
56.	156	SI			0.604 *	21	(SI)
61.	181	SI			0.605 *	48	(SO)
63.	63	SI			0.700 *	52	(SI)
88.	1 68	SI			0.699 *	15	(8)
75.	175	SI			0.610 *	30	(SI)

Appendix							
PHENOTYPES In kkk/ CALCULATED DIVERSITY INDEX * 0.924		Identity level * 0.975 TRUE DIVERSITY INDEX - 0.924					
No	Name	PhP- type	sim min	sim mean	sim max	lo nr	PhP typ ^o
1.	IBACILLUS	1	1.000	1.000 *	0.000 *	(S	
5.	II CLOSTRIDIUM	1	1.000	1.000 *	0.000 *	71	(SI)
7.	IMICROCO SP	1	1.000	1.000 *	0.000 *	11	(6)
13.	II 13	1	1.000	1.000 *	0.000 *	45	(SI)
14.	II 14	1	1.000	1.000 *	0.000 *	45	(SI)
22.	II 22	1	1.000	1.000 *	0.000 *	29	(SI)
23.	II 23	1	1.000	1.000 *	0.000 *	29	(SI)
24.	II CONTROL	1	1.000	1.000 *	0.000 *	29	(SI)
25.	II 25	1	1.000	1.000 *	0.000 *	29	(SI)
28.	II 28	1	1.000	1.000 *	0.000 *	49	(SI)
30.	H 30	1	1.000	1.000 *	0.000 *	38	(SI)
33.	II 33	1	1.000	1.000 *	0.000 *	20	(SI)
40.	II 40	1	1.000	1.000 *	0.000 *	16	(SI)
43.	II 43	1	1.000	1.000 *	0.000 *	8	(5)
47.	II 47	1	1.000	1.000 *	0.000 *	75	(SO)
54.	II 54	1	1.000	1.000 *	0.000 *	8	(5)
63.	1163	1	1.000	1.000 *	0.000 *	27	(SO)
66.	1166	1	1.000	1.000 *	0.000 *	52	(SO)
69.	II 69	1	1.000	1.000 *	0.000 *	19	(0)
78.	II 78	1	1.000	1.000 *	0.000 *	36	(SO)
80.	II CONTROL	1	1.000	1.000 *	0.000 *	52	(SI)
2.	PSEUDO AEROG	2	1.000	1.000 *	0.485 *	45	(SO)
12.	12	2	1.000	1.000 *	0.485 *	45	(SO)
3.	ECOU	3	1.000	1.000 *	0.934 *	16	(SI)
26.	26	3	1.000	1.000 *	0.934 *	16	(SO)
39.	39	3	1.000	1.000 *	0.934 *	16	(SI)
16.	16	Si			0.934 *	3	(3)
9.	9	Si			0.924 *	3	(3)
44.	44	Si			0.924 *	3	(3)
34.	34	Si			0.923 *	3	(3)
4.	PROTEUS MIRA	4	1.000	1.000 *	0.914 *	71	(6)
41.	41	4	1.000	1.000 *	0.914 *	71	(SI)
67.	67	4	1.000	1.000 *	0.914 *	71	(SO)
71.	71	Si			0.914 *	4	(4)
73.	73	Si			0.847 *	4	(4)
8.	STREPTOCO FAE	5	1.000	1.000 *	0.955 *	52	(SO)
15.	15	5	1.000	1.000 *	0.955 *	52	(SI)
57.	57	5	1.000	1.000 *	0.955 *	52	(SO)
61.	61	5	1.000	1.000 *	0.955 *	52	(SO)
65.	65	5	1.000	1.000 *	0.955 *	52	(SI)
79.	79	5	1.000	1.000 *	0.955 *	52	(SO)
52.	52	Si			0.955 *	8	(5)
53.	53	Si			0.955 *	8	(5)
60.	60	Si			0.953 *	8	(5)
70.	70	Si			0.937 *	8	(5)
19.	19	8	1.000	1.000 *	0.953 *	8	(5)
42.	42	8	1.000	1.000 *	0.953 *	8	(5)
55.	55	8	1.000	1.000 *	0.953 *	8	(5)
64.	64	Si			0.954 *	52	(SO)
76.	76	Si			0.948 *	19	(3)
56.	56	Si			0.953 *	B	(5)
68.	68	Si			0.947 *	19	(0)
27.	27	Si			0.946 *	49	(SO)
49.	49	Si			0.935 *	8	(5)
62.	62	Si			0.932 *	27	(SI)
75.	75	Si			0.945 *	49	(SI)
48.	48	Si			0.854 *	56	(SI)
B.	PSEUDO FLUORE	Si			0.704 *	11	(6)
10.	110	Si			0.501 *	31	(SI)
11.	11	6	1.000	1.000 *	0.719 *	29	(SO)
17.	17	6	1.000	1.000 *	0.719 *	29	(SO)
21.	21	6	1.000	1.000 *	0.719 *	29	(SI)
18.	18	7	1.000	1.000 *	0.587 *	37	(SI)
35.	35	7	1.000	1.000 *	0.587 *	37	(SI)
20.	120	Si			0.638 *	36	(SI)
29.	29	Si			0.787 *	38	(SO)
38.	38	Si			0.787 *	29	(SI)
31.	31	Si			0.718 *	60	(SI)
32.	32	Si			0.552 *	20	(SI)
36.	136	Si			0.636 *	20	(SI)
37.	37	Si			0.67G *	74	(SI)
45.	145	Si			0.485 *	2	(2)
46.	46	Si			0.641 *	75	(SI)
50.	150	Si			0.553 *	16	(SI)
51.	51	Si			0.545 *	29	(SI)
58.	58	Si			0.573 *	31	(SI)
59.	59	Si			0.680 *	53	(SI)
72.	72	Si			0.873 *	74	(SO)
74.	74	Si			0.873 *	72	(SI)
77.	177	Si			0.635 *	36	(SI)

268

Appendix 33

PHENOTYPES in kks/ klenMy level- 0.975
 ^CALCULATED DIVERSITY INDEX - 0.915 TRUE DIVERSITY INDEX - 0.915

No	Nama	PhP- typo	kn min	sim mean	max	to nr	PhP typ«
1.	ECOU	1	1.000	1.000 *	0.924 *	69	(SO)
44.	43	1	1.000	1.000 *	0.824 *	69	(Si)
50.	49	1	1.000	1.000 *	0.924 *	69	(Si)
80.	88	SI			0.924 *	1	(1)
62.	81	SI			0.922 *	1	d)
2.	IIBACILLUS	2	1.000	1.000 *	0.000 *	69	(Si)
3.	IICLOSTRIDIUM	2	1.000	1.000 *	0.000 *	69	(SO)
7.	NMICROCO SP	2	1.000	1.000 *	0.000 *	75	(SO)
11.	Mil	2	1.000	1.000 *	0.000 *	75	(SO)
14.	I114	2	1.000	1.000 *	0.000 *	52	(4)
21.	I120	2	1.000	1.000 *	0.000 *	49	(Si)
24.	I123	2	1.000	1.000 *	0.000 *	6	(<)
26.	I125	2	1.000	1.000 *	0.000 *	29	(SO)
33.	I132	2	1.000	1.000 *	0.000 *	59	(so)
35.	I134	2	1.000	1.000 *	0.000 *	15	(7)
38.	I137	2	1.000	1.000 *	0.000 *	67	(SO)
41.	IICONTROL	2	1.000	1.000 *	0.000 *	34	(SO)
43.	I142	2	1.000	1.000 *	0.000 *	75	(SO)
45.	I144	2	1.000	1.000 *	0.000 *	69	(SO)
46.	I145	2	1.000	1.000 *	0.000 *	69	(SO)
51.	I150	2	1.000	1.000 *	0.000 *	69	(SO)
53.	I152	2	1.000	1.000 *	0.000 *	13	(so)
57.	I158	2	1.000	1.000 *	0.000 *	48	(10)
63.	I162	2	1.000	1.000 *	0.000 *	1	(1)
71.	I170	2	1.000	1.000 *	0.000 *	56	(4)
76.	I175	2	1.000	1.000 *	0.000 *	6	(4)
81.	IICONTROL	2	1.000	1.000 *	0.000 *	75	(SO)
4.	PROTEUS MIRA	3	1.000	1.000 *	0.917 *	12	(SO)
64.	63	3	1.000	1.000 *	0.917 *	12	(SO)
12.	12	SI			0.917 *	4	(3)
73.	72	SI			0.917 *	4	(3)
5.	PSEUDO AEROG	SI			0.451 *	67	(Si)
6.	STREPTOCO FAE	4	0.993	0.998 *	0.955 *	75	(Si)
10.	10	4	0.993	0.998 *	0.955 *	75	(SO)
42.	41	4	0.993	0.998 *	0.955 *	75	(Si)
65.	64	4	0.993	0.998 *	0.955 *	75	(SO)
80.	79	4	0.993	0.998 *	0.955 *	75	(SO)
62.	51	4	0.989	0.996 *	0.969 *	13	(SO)
56.	55	4	0.989	0.992 *	0.955 *	48	(10)
77.	76	4	0.990	0.992 *	0.982 ?	48	(10)
48.	47	10	1.000	1.000 *	0.982 ?	77	(4)
68.	67	10	1.000	1.000 *	0.982 ?	77	(4)
75.	74	SI			0.955 *	6	(4)
13.	13	SI			0.969 *	52	(4)
23.	22	9	1.000	1.000 *	0.953 *	6	(4)
28.	27	9	1.000	1.000 *	0.953 *	6	(4)
72.	71	SI			0.921 *	56	(4)
70.	69	SI			0.928 *	56	(4)
8.	PSEUDO FLUORE	5	1.000	1.000 *	0.704 *	15	(7)
39.	38	5	1.000	1.000 *	0.704 *	15	(7)
9.	9	6	1.000	1.000 *	0.430 *	49	(SO)
20.	19	6	1.000	1.000 *	0.430 *	49	(SO)
15.	15	7	1.000	1.000 *	0.726 *	34	(SO)
40.	39	7	1.000	1.000 *	0.726 *	34	(SO)
79.	78	7	1.000	1.000 *	0.726 *	34	(SO)
16.	16	SI			0.833 *	19	(SO)
19.	18	SI			0.833 *	16	(SO)
17.	17	8	1.000	1.000 *	0.564 *	67	(SO)
18.	17	S	1.000	1.000 *	0.564 *	67	(Si)
37.	36	8	1.000	1.000 *	0.564 *	67	(SO)
22.	21	SI			0.646 *	49	(SO)
25.	24	SI			0.787 *	29	(Si)
29.	28	SI			0.787 *	25	(SO)
27.	26	SI			0.618 *	70	(SO)
30.	29	SI			0.558 *	70	(Si)
31.	130	SI			0.836 *	74	(SO)
47.	46	SI			0.949 *	74	(SO)
74.	73	SI			0.949 *	47	(Si)
32.	31	SI			0.910 *	59	(Si)
59.	58	SI			0.910 *	32	(SO)
34.	33	SI			0.726 *	15	(7)
36.	35	SI			0.484 *	73	(SO)
49.	148	SI			0.646 *	22	(SO)
54.	153	SI			0.542 *	61	(Si)
55.	154	SI			0.698 *	74	(SO)
58.	57	SI			0.652 *	55	(Si)
60.	59	SI			0.706 *	31	(SO)
61.	60	SI			0.542 *	54	(Si)
60.	65	SI			0.729 *	69	(SO)
67.	166	SI			0.564 *	17	(8)
78.	177	SI			0.665 *	66	(Si)

PHENOTYPES M p3c1w Identity (oval *0.875)
 CALCULATED DIVERSITY INDEX = 0.899 TRUE DIVERSITY INDEX = 0.898

Appendix >. Tlf

No	Name	PJP- type	sfm min	sim mean	sim	to	PhP type
1	ECOU	1	0.999	1.000 *	0.923 *	53	(SI)
24	24	1	0.999	1.000 *	0.923 *	53	(SI)
36	35	1	0.999	1.000 *	0.923 ■	53	(SI)
46	46	1	0.999	0.999 *	0.920 *	53	(SI)
53	53	SI			0.923 *	1	(1)
62	62	SI			0.870 *	46	(1)
2	IBACILLUS	2	1.000	1.000 *	0.000 *	53	(SI)
S	IMICROCO LUT	2	1.000	1.000 *	0.000 *	61	(SI)
7	CLOSTRIDIUM	2	1.000	1.000 *	0.000 *	71	(SI)
11	!! 11	2	1.000	1.000 *	0.000 *	69	(SI)
15	*1 15	2	1.000	1.000 *	0.000 *	22	(10)
21	!! 21	2	1.000	1.000 *	0.000 ■	71	(SI)
29	!! 29	2	1.000	1.000 *	0.000 ■	76	(SI)
33	■1 33	2	1.000	1.000 *	0.000 *	22	(10)
40	ICONTROL	2	1.000	1.000 *	0.000 *	69	(so)
44	!! 44	2	1.000	1.000 *	0.000 *	17	(SI)
45	!! 45	2	1.000	1.000 *	0.000 ■	17	(SO)
51	!! 51	2	1.000	1.000 *	0.000 *	57	(SI)
52	!! 52	2	1.000	1.000 *	0.000 *	57	(so)
56	!! 56	2	1.000	1.000 *	0.000 ■	57	(SO)
59	!! 59	2	1.000	1.000 *	0.000 *	61	(SO)
60	!! 60	2	1.000	1.000 *	0.000 *	61	(SO)
65	1165	2	1.000	1.000 *	0.000 ■	4	(4)
66	!! 66	2	1.000	1.000 *	a ooo *	4	(4)
66	1168	2	1.000	1.000 *	0.000 *	71	(SO)
74	1174	2	1.000	1.000 *	0.000 *	61	(so)
75	!! 75	2	1.000	1.000 *	0.000 ■	61	(SO)
78	!! 78	2	1.000	1.000 *	0.000 *	76	(SO)
80	ICONTROL	2	1.000	1.000 *	0.000 *	61	(SO)
3	PROTEUS MIRA	3	1.000	1.000 *	0.614 *	8	(6)
19	19	3	1.000	1.000 *	0.614 *	8	(6)
4	STREPTOCO FAE	4	0.990	0.997 *	0.963 ■	61	(SO)
47	47	4	0.987	0.997 ■	0.961 *	23	(SO)
9	9	4	0.984	0.995 *	0.969 *	23	(SO)
54	54	4	0.984	0.995 *	0.969 *	23	(SO)
58	58	4	0.990	0.997 *	0.963 *	61	(SI)
63	63	4	0.990	0.997 *	0.963 *	61	(SO)
73	73	4	0.990	0.997 *	0.963 *	61	(SO)
18	18	4	0.982	0.995 *	0.964 ■	61	(SO)
30	30	4	0.976	0.987 *	0.940 ■	64	(SO)
79	79	4	0.976	0.990 *	0.986 ?	61	(SO)
61	61	SI			0.986 ?	79	(4)
64	64	SI			0.953 ■	4	(4)
13	13	SI			0.953 *	4	(4)
23	23	SI			0.969 *	9	(4)
38	38	SI			0.949 *	23	(SI)
6	PSEUDO FLUORE	5	1.000	1.000 *	0.690 *	71	(SI)
20	20	5	1.000	1.000 *	0.690 ■	71	(SO)
67	67	5	1.000	1.000 *	0.690 *	71	(SI)
8	SERMAR	6	1.000	1.000 *	0.614 *	3	(3)
34	34	6	1.000	1.000 *	0.614 *	3	(3)
10	10	SI			0.336 ■	69	(SO)
12	! 12	7	1.000	1.000 *	0.959 *	69	(SI)
39	! 39	7	1.000	1.000 *	0.959 *	69	(SI)
69	69	SI			0.959 *	12	(7)
48	! 48	SI			0.868 *	12	(7)
72	72	SI			0.814 *	69	(SI)
14	1<J	8	1.000	1.000 *	0.949 *	22	(10)
32	32	8	1.000	1.000 ■	0.949 ■	22	(10)
22	22	10	1.000	1.000 *	0.949 *	14	(8)
42	42	10	1.000	1.000 *	0.949 *	14	(8)
16	16	9	0.991	0.991 *	0.554 *	55	(SI)
26	26	9	0.991	0.991 *	0.558 *	55	(SI)
17	17	SI			0.450 *	55	(SI)
25	25	11	1.000	1.000 *	0.908 *	49	(SO)
31	31	11	1.000	1.000 *	0.908 *	49	(SI)
49	49	SI			0.908 *	25	(11)
41	41	SI			0.905 *	25	(11)
37	37	14	1.000	1.000 *	0.917 *	57	(SI)
50	50	14	1.000	1.000 *	0.917 *	57	(SI)
57	57	SI			0.917 *	37	(14)
55	55	SI			0.786 *	57	(SO)
27	27	12	1.000	1.000 *	0.139 ■	17	(SI)
43	43	12	1.000	1.000 *	0.139 *	17	(SI)
28	28	13	1.000	1.000 *	0.639 ■	76	(SO)
70	70	13	1.000	1.000 ■	0.639 *	76	(SI)
77	77	13	1.000	1.000 *	0.639 *	76	(SO)
35	35	SI			0.694 *	62	(SI)
71	71	SI			0.702 *	76	(SI)
76	76	SI			0.702 *	71	(SI)

_PHENOTYPES In pad2/ CALCULATED DIVERSITY INDEX - O.BrO		Identity level - 0.975 TRUE DIVERSITY INDEX - 0.908				
NO	Name	PhP- type	sun	sim mean	to	PhP type
1.	ICLOSTRIDIUM	1	1.000	1.000 *	0.000 *	(S)
2.	IBACILLUS	1	1.000	1.000 *	0.000 *	(S)
7.	IMICROCO LUT	1	1.000	1.000 *	0.000 *	46 (Si)
11.	II 11	1	1.000	1.000 *	0.000 *	20 (10)
22.	1122	1	1.000	1.000 *	0.000 *	53 (Si)
29.	1129	1	1.000	1.000 *	0.000 *	10 (7)
34.	1134	1	1.000	1.000 *	0.000 *	23 (Si)
40.	ICONTROL	1	1.000	1.000 *	0.000 *	23 (SO)
42.	1142	1	1.000	1.000 *	0.000 *	46 (Si)
44.	1144	1	1.000	1.000 *	0.000 *	76 (5)
45.	1145	1	1.000	1.000 *	0.000 *	76 (5)
47.	1147	1	1.000	1.000 *	0.000 *	6 (5)
50.	II 50	1	1.000	1.000 *	0.000 *	59 (Si)
52.	II 52	1	1.000	1.000 *	0.000 *	30 (Si)
57.	II 57	1	1.000	1.000 *	0.000 *	55 (Si)
58.	1158	1	1.000	1.000 *	0.000 *	55 (Si)
68.	II 68	1	1.000	1.000 *	0.000 *	8 (6)
72.	II 72	1	1.000	1.000 *	0.000 *	6 (5)
74.	1174	1	1.000	1.000 *	0.000 *	6 (5)
77.	1177	1	1.000	1.000 *	0.000 *	46 (Si)
80.	ICONTROL	1	1.000	1.000 *	0.000 *	46 (Si)
3.	PROTEUS MIRA	2	0.993	0.996 *	0.614 *	8 (6)
67.	67	2	0.993	0.996 *	0.614 *	8 (6)
75.	75	2	0.993	0.996 *	0.614 *	8 (6)
14.	14	2	0.983	0.991 *	0.580 *	8 (6)
31.	31	2	0.983	0.991 *	0.657 *	8 (6)
4.	ECOU	3	0.993	0.998 *	0.923 *	53 (SO)
26.	26	3	0.993	0.998 *	0.923 *	53 (SO)
32.	32	3	0.993	0.998 *	0.923 *	53 (SO)
62.	62	3	0.993	0.998 *	0.923 *	53 (SO)
12.	12	3	0.989	0.994 *	0.915 *	53 (SO)
21.	21	3	0.989	0.995 *	0.926 *	53 (SO)
38.	38	3	0.989	0.992 *	0.909 *	53 (SO)
53.	53	SI			0.926 *	21 (3)
5.	PSEUDO FLUORE	4	1.000	1.000 *	0.690 *	78 (SO)
16.	16	4	1.000	1.000 *	0.690 *	78 (SO)
65.	65	4	1.000	1.000 *	0.690 *	78 (SO)
6.	STREPTOCO FAE	5	0.991	0.998 *	0.978 ?	46 (Si)
9.	9	5	0.991	0.998 *	0.978 ?	46 (SO)
13.	13	5	0.991	0.998 *	0.978 ?	46 (SO)
37.	37	5	0.991	0.998 *	0.978 ?	46 (SO)
41.	41	5	0.991	0.998 *	0.978 ?	46 (SO)
15.	15	5	0.990	0.996 *	0.976 ?	46 (Si)
76.	76	5	0.984	0.994 *	0.972 *	46 (SO)
79.	79	5	0.984	0.990 *	0.967 *	46 (SO)
46.	46	SI			0.978 ?	6 (5)
43.	43	11	0.991	0.994 *	0.971 *	76 (5)
48.	48	11	0.994	0.994 *	0.954 *	76 (5)
18.	18	8	1.000	1.000 *	0.940 *	79 (5)
64.	64	8	1.000	1.000 *	0.940 *	79 (5)
71.	71	13	0.993	0.993 *	0.953 *	6 (5)
73.	73	13	0.993	0.993 *	0.942 *	6 (5)
55.	55	SI			0.956 *	76 (5)
69.	69	SI			0.951 *	55 (SO)
30.	30	SI			0.966 *	76 (5)
51.	51	SI			0.948 *	30 (SO)
8.	SER MAR	6	1.000	1.000 *	0.657 *	31 (2)
36.	36	6	1.000	1.000 *	0.657 *	31 (2)
10.	10	7	1.000	1.000 *	0.704 *	20 (10)
27.	27	7	1.000	1.000 *	0.704 *	20 (10)
17.	17	SI			0.502 *	24 (SO)
19.	19	9	0.994	0.997 *	0.531 *	23 (SO)
33.	33	9	0.994	0.997 *	0.531 *	23 (SO)
39.	39	9	0.994	0.994 *	0.511 *	23 (SO)
20.	20	10	1.000	1.000 *	0.704 *	10 (7)
28.	28	10	1.000	1.000 *	0.704 *	10 (7)
23.	23	SI			0.531 *	19 (9)
24.	24	SI			0.787 *	78 (Si)
78.	78	SI			0.787 *	24 (Si)
25.	25	SI			0.948 *	35 (Si)
35.	35	SI			0.948 *	25 (Si)
49.	49	SI			0.893 *	59 (SO)
59.	59	SI			0.893 *	49 (SO)
54.	154	SI			0.636 *	63 (SO)
56.	56	12	1.000	1.000 *	0.549 *	55 (SO)
70.	70	12	1.000	1.000 *	0.549 *	55 (SO)
60.	60	SI			0.430 *	61 (SO)
61.	161	SI			0.636 *	63 (SO)
63.	163	SI			0.636 *	54 (SO)
66.	66	SI			0.566 *	73 (13)

PHENOTYPES		Jdonlly level - 0.875		TRUE DIVERSITY INDEX = 0.862		in partt/	
CALCULATED DIVERSITY INOEX - 0.862							
No	Name	PhP- sim typo mm	sim mean	sim max	lo nr	PhP typa	
1.	ECOU	1	1.000	1.000 *	0.924 *	55	(SI)
13.	13	1	1.000	1.000 *	0.924 *	55	(SI)
44.	44	1	1.000	1.000 *	0.924 *	55	(SI)
74.	74	1	1.000	1.000 *	0.924 *	55	(SI)
55.	55	SI			0.924 *	1	(1)
63.	63	SI			0.923 *	1	(1)
2.	SERMAR	SI			0.614 *	3	(2)
3.	PROTEUS MIRA	2	1.000	1.000 *	0.614 *	2	(SO)
28.	28	2	1.000	1.000 *	0.614 *	2	(SI)
40.	40	2	1.000	1.000 *	0.614 *	2	(SI)
4.	STREPTOCO FAE	3	0.990	0.997 *	0.953 *	23	(SI)
15.	15	3	0.990	0.997 *	0.953 *	23	(SO)
27.	27	3	0.990	0.997 *	0.953 *	23	(SI)
33.	33	3	0.990	0.997 *	0.953 *	23	(so)
41.	41	3	0.990	0.997 *	0.953 *	23	(so)
-50.	50	3	0.990	0.997 *	0.953 *	23	(SO)
66.	66	3	0.990	0.997 *	0.953 *	23	(SI)
77.	77	3	0.990	0.997 *	0.953 *	23	(SO)
56.	56	3	0.979	0.994 *	0.964 *	23	(SO)
60.	60	3	0.984	0.996 *	0.969 *	46	(so)
52.	52	3	0.974	0.991 *	0.982 *	7	(SO)
35.	35	3	0.989	0.995 *	0.971 *	71	(SO)
37.	37	3	0.981	0.992 *	0.967 *	71	(SO)
58.	58	3	0.974	0.983 *	0.969 *	71	(SI)
71.	71	SI			0.971 *	35	(3)
75.	75	SI			0.969 *	58	(3)
46.	46	SI			0.982 *	7	(3)
23.	23	4			0.964 *	56	(3)
5.	PSEUDO FLUORE	4	1.000	1.000 *	0.630 *	17	(8)
36.	36	4	1.000	1.000 *	0.630 *	17	(8)
57.	57	4	1.000	1.000 *	0.630 *	17	(8)
6.	ICLOSTRIDIUM	5	1.000	1.000 *	0.000 *	17	(8)
7.	HEACILLUS	5	1.000	1.000 *	0.000 *	17	(8)
8.	HMICROCO LUT	5	1.000	1.000 *	0.000 *	17	(8)
9.	119	5	1.000	1.000 *	0.000 *	17	(8)
12.	112	5	1.000	1.000 *	0.000 *	10	(SI)
19.	1119	5	1.000	1.000 *	0.000 *	65	(so)
21.	1121	5	1.000	1.000 *	0.000 *	47	(SI)
24.	1124	5	1.000	1.000 *	0.000 *	56	(3)
25.	1125	5	1.000	1.000 *	0.000 *	56	(3)
29.	1129	5	1.000	1.000 *	0.000 *	2	(SO)
32.	ICONTROL	5	1.000	1.000 *	0.000 *	23	(SI)
34.	1134	5	1.000	1.000 *	0.000 *	23	(SI)
33.	1138	5	1.000	1.000 *	0.000 *	71	(SO)
39.	1139	5	1.000	1.000 *	0.000 *	71	(SO)
42.	1142	5	1.000	1.000 *	0.000 *	23	(SO)
43.	1143	5	1.000	1.000 *	0.000 *	23	(SO)
45.	1145	5	1.000	1.000 *	0.000 *	55	(SI)
51.	1151	5	1.000	1.000 *	0.000 *	23	(SI)
53.	1153	5	1.000	1.000 *	0.000 *	46	(SO)
64.	1164	5	1.000	1.000 *	0.000 *	1	(1)
69.	1169	5	1.000	1.000 *	0.000 *	65	(SO)
70.	1170	5	1.000	1.000 *	0.000 *	65	(SO)
72.	1172	5	1.000	1.000 *	0.000 *	35	(3)
76.	1176	5	1.000	1.000 *	0.000 *	58	(3)
79.	1179	5	1.000	1.000 *	0.000 *	3	(2)
80.	ICONTROL	5	1.000	1.000 *	0.000 *	3	(2)
10.	110	SI			0.520 *	11	(8)
11.	111	e	1.000	1.000 *	0.520 *	10	(SI)
48.	48	6	1.000	1.000 *	0.526 *	10	(SI)
14.	114	SI			0.536 *	46	(SI)
16.	116	7	0.986	0.993 *	0.892 *	61	(SI)
22.	22	7	0.986	0.993 *	0.892 *	81	(SI)
49.	49	7	0.986	0.986 *	0.929 *	61	(SI)
61.	61	SI			0.929 *	49	(7)
17.	117	8	1.000	1.000 *	0.948 *	65	(SI)
26.	26	8	1.000	1.000 *	0.948 *	65	(SO)
65.	65	SI			0.948 *	17	(8)
18.	118	9	1.000	1.000 *	0.483 *	65	(SI)
68.	68	9	1.000	1.000 *	0.483 *	65	(SI)
20.	20	10	1.000	1.000 *	0.721 *	47	(SO)
30.	30	10	1.000	1.000 *	0.721 *	47	(SI)
31.	1131	SI			0.716 *	23	(SI)
47.	47	SI			0.721 *	20	(10)
54.	54	SI			0.653 *	71	(SI)
59.	59	SI			0.366 *	14	(SI)
62.	62	SI			0.521 *	54	(SI)
67.	167	SI			0.629 *	23	(SI)
73.	73	SI			0.690 *	46	(SI)
70.	178	SI			0.501 *	3	(2)

Appendix X

Identity level - **0.975**

PHENOTYPES in pacm/ CALCULATED DIVERSITY INDEX - 0.930 TRUE DIVERSITY INDEX - 0.928

No	Name	PhP-type	xim min	bn mean	max	lo nr	PhP type
1.	STREPTOCO FAE	1	0.993	0.990 *	0.955 *	29	(SI)
18.		1	0.992	0.997 *	0.961 *	55	(SI)
22.	22	1	0.993	0.998 *	0.955 *	29	(SO)
43.	43	1	0.993	0.998 *	0.955 *	29	(SI)
63.	62	1	0.993	0.998 *	0.955 *	29	(SI)
67.	66	1	0.993	0.998 *	0.955 *	29	(SI)
76.	75	1	0.993	0.998 *	0.955 *	29	(SI)
35.	35	1	0.987	0.994 *	0.976 7	55	(SI)
37.	37	1	0.992	0.996 *	0.956 *	29	(SI)
10.	10	1	0.982	0.992 *	0.982 ?	20	(SO)
14.	14	1	0.990	0.996 *	0.974 *	20	(SI)
26.	28	1	0.980	0.003 *	0.978 ?	20	(SI)
72.	71	1	0.980	0.990 ■	0.982 ?	31	(SI)
31.	31	B	1.000	1.000 *	0.982 7	72	(1)
52.	51	9	1.000	1.000 *	0.982 7	72	(1)
29.	29	SI			0.956 *	37	(1)
20.	20	SI			0.982 ?	10	(1)
46.	45	SI			0.956 *	37	(1)
49.	48	SI			0.956 *	37	(1)
55.	54	SI			0.976 7	35	(1)
59.	58	SI			0.946 *	1	(1)
21.	21	SI			0.866 *	29	(so)
74.	I 73	SI			0.802 *	49	(SO)
2.	PROTEUS MIRA	2	1.000	1.000 *	0.614 *	8	(so)
39.	39	2	1.000	1.000 *	0.614 *	8	(so)
3.	IIBACILLUS	3	1.000	1.000 *	0.000 *	8	(SO)
4.	IICLOSTRIDIUM	3	1.000	1.000 *	0.000 *	8	(SO)
7.	IIMICROCO LUT	3	1.000	1.000 *	0.000 *	73	(so)
13.	I113	3	1.000	1.000 *	0.000 *	44	(SO)
15.	I115	3	1.000	1.000 *	0.000 *	20	(SO)
17.	I117	3	1.000	1.000 ■	0.000 *	55	(SO)
18.	I118	3	1.000	1.000 ■	0.000 *	55	(SO)
34.	I134	3	1.000	1.000 *	0.000 *	77	(SO)
40.	IICONTROL	3	1.000	1.000 *	0.000 *	8	(SO)
48.	I147	3	1.000	1.000 *	0.000 *	2	(2)
51.	II 50	3	1.000	1.000 *	0.000 *	73	(SO)
53.	II 52	3	1.000	1.000 *	0.000 *	72	(1)
57.	II 56	3	1.000	1.000 *	0.000 ■	2	(2)
61.	II 60	3	1.000	1.000 *	0.900 *	49	(SO)
65.	II 64	3	1.000	1.000 *	0.000 *	12	(SO)
70.	II 69	3	1.000	1.000 *	0.000 *	41	(11)
82.	IICONTROL	3	1.000	1.000 *	0.000 *	80	(so)
5.	ECOU	4	1.000	1.000 *	0.924 *	78	(so)
25.	25	4	1.000	1.000 *	0.924 *	78	(SO)
66.	65	4	1.000	1.000 *	0.924 *	78	(so)
78.	77	SI			0.924 *	5	(4)
42.	42	SI			0.922 *	5	(4)
6.	PSEUDO FLUORE	5	1.000	1.000 *	0.773 *	73	(SO)
11.	11	5	1.000	1.000 *	0.773 *	73	(SO)
68.	67	5	1.000	1.000 *	0.773 *	73	(SO)
50.	49	SI			0.835 *	73	(SO)
73.	72	SI			0.835 *	50	(SO)
8.	SERMAR	SI			0.614 *	2	(2)
9.	9	6	1.000	1.000 *	0.430 *	38	(SO)
24.	24	6	1.000	1.000 *	0.430 *	38	(SO)
12.	12	SI			0.814 *	44	(SO)
44.	44	SI			0.814 *	12	(SO)
10.	10	7	1.000	1.000 *	0.037 *	80	(SI)
32.	32	7	1.000	1.000 *	0.037 *	80	(SI)
75.	74	7	1.000	1.000 *	0.637 *	80	(SO)
81.	79	7	1.000	1.000 *	0.637 *	80	(SO)
23.	23	SI			0.893 *	28	(SI)
28.	28	SI			0.893 *	23	(SO)
27.	I 27	8	1.000	1.000 *	0.762 *	79	(SO)
71.	I 70	8	1.000	1.000 *	0.762 *	79	(SO)
79.	78	SI			0.762 *	27	(8)
30.	30	SI			0.690 *	55	(SO)
33.	33	10	0.992	0.992 *	0.798 *	77	(SO)
36.	36	10	0.992	0.992 *	0.814 *	77	(SO)
41.	141	11	1.000	1.000 *	0.811 *	77	(so)
62.	I 61	11	1.000	1.000 *	0.811 *	77	(SO)
77.	76	SI			0.814 *	36	(10)
38.	38	SI			0.430 *	9	(6)
45.	45	SI			0.426 *	8	(SO)
47.	46	SI			0.514 *	2	(2)
54.	153	SI			0.388 *	44	(SO)
56.	155	SI			0.501 *	2	(2)
58.	57	SI			0.521 *	36	(10)
60.	59	SI			0.718 *	49	(so)
64.	163	SI			0.603 *	12	(SO)
69.	68	SI			0.430 *	41	(11)
80.	79	SI			0.654 *	36	(10)

Appendix 30

No	Name	PhP-type	sim min	mean	max	10 nr	PhP typo
1.	STREP FAEC	1	0.993	0.997 *	0.578 *	14	(ii)
ia	10	1	0.993	0.997 *	0.578 *	14	(11)
36.	35	1	0.992	0.995 "	0.589 *	14	(11)
19.	19	1	0.992	0.993 *	0.593 *	14	(11)
2.	STAP AUR	2	0.979	0.989 *	0.836 *	14	(11)
44.	43	2	0.983	0.991 *	0.847 *	14	di)
22.	22	2	0.983	0.990 *	0.825 *	14	(11)
15.	15	2	0.983	0.987 *	0.846 *	14	(11)
26.	25	2	0.979	0.985 *	0.629 *	14	(11)
14.	14	11	1.000	1.000 *	0.847 *	44	(2)
21.	21	11	1.000	1.000 *	0.847 *	44	(2)
7.	PROTEUS OUL	7	0.998	0.998 *	0.809 *	14	(11)
17.	17	7	0.998	0.998 *	0.811 *	14	(11)
B.	PROTEUS MIRA	8	0.997	0.997 *	0.969 *	40	(17)
33.	33	8	0.997	0.997 *	0.965 *	40	(17)
38.	37	17	0.997	0.997 *	0.963 *	8	(8)
40.	39	17	0.997	0.997 *	0.969 *	8	(8)
9.	MICRO SP	9	0.991	0.995 *	0.951 *	54	(S)
52.	61	9	0.991	0.995 *	0.951 *	54	(S)
49.	4B	9	0.987	0.992 *	0.933 *	27	(13)
42.	41	9	0.987	0.990 *	0.944 *	54	(S)
54.	53	Si			0.951 *	9	(9)
27.	26	13	1.000	1.000 *	0.933 *	49	(9)
34.	33	13	1.000	1.000 *	0.933 *	49	(9)
54.	CONTROL	Si			0.922 *	27	(13)
30.	29	14	0.999	0.999 *	0.969 *	63	(S)
56.	55	14	0.999	0.999 *	0.969 *	63	(S)
59.	58	14	0.999	0.999 *	0.970 *	63	(S)
53.	62	Si			0.970 *	59	(14)
32.	31	15	1.000	1.000 *	0.903 *	64	(S)
51.	50	15	1.000	1.000 *	0.903 *	64	(S)
3.	STAP EVID	3	0.987	0.994 *	0.782 *	48	(S)
31.	30	3	0.986	0.994 *	0.773 *	48	(S)
60.	59	3	0.986	0.994 *	0.773 *	48	(S)
58.	57	3	0.985	0.993 *	0.776 *	5	(5)
52.	51	3	0.976	0.988 *	0.809 *	5	(5)
12.	12	3	0.976	0.984 *	0.779 *	48	(S)
5.	PSEUDO FLUORE	5	1.000	1.000 *	0.809 *	52	(3)
20.	20	5	1.000	1.000 *	0.809 *	52	(3)
4.	SERMER	4	1.000	1.000 ■	0.771 *	14	(11)
13.	13	4	1.000	1.000 *	0.771 *	14	(11)
16.	16	4	1.000	1.000 *	0.771 *	14	(11)
6.	PSEUDO AUR	6	0.987	0.994 *	0.776 *	23	(12)
24.	24	6	0.987	0.994 *	0.776 *	23	(12)
50.	49	6	0.987	0.994 *	0.776 *	23	(12)
47.	46	6	0.973	0.985 *	0.788 *	23	(12)
41.	40	6	0.973	0.983 *	0.813 *	59	(14)
23.	23	12	0.994	0.998 *	0.788 *	47	(6)
29.	28	12	0.994	0.998 *	0.788 *	47	(6)
46.	45	12	0.994	0.998 *	0.788 *	47	(6)
57.	56	12	0.994	0.998 *	0.788 *	47	(6)
55.	54	12	0.994	0.994 *	0.766 *	47	(6)
25.	25	Si			0.969 *	37	(16)
28.	27	Si			0.962 *	35	(16)
35.	34	16	0.983	0.992 *	0.962 ■	28	(S)
45.	44	16	0.983	0.992 *	0.962 *	28	(S)
J7.	36	16	0.983	0.983 *	0.969 *	25	(S)
48.	47	Si			0.956 *	35	(16)
53.	52	19	1.000	1.000 ■	0.819 *	28	(S)
H.	60	19	1.000	1.000 ■	0.819 *	28	(S)
11.	ENTEROBACTER COLI	10	1.000	1.000 *	0.692 *	63	(S)
18.	18	10	1.000	1.000 *	0.694 *	28	(S)
19.	38	18	1.000	1.000 *	0.677 *	32	(15)
13.	42	18	1.000	1.000 *	0.677 *	32	(15)

Appendix E

PHENOTYPES In oditaben3/		Identity level - 0.975		TRUE DIVERSITY INDEX - 0.944		CALCULATED DIVERSITY INDEX - 0.944	
No	Name	PhP- sim type mln	sim mean	sim max	to nr	PhP type	
1.	STREPTOCOCCUS FAE	1	1.000	1.000	0.793 *	21	(9)
3.	STREPTOCOCCUS FAE	1	1.000	1.000	0.783 *	21	(9)
7.	5	1	1.000	1.000	0.783 *	21	(9)
24.	22	1	1.000	1.000	0.793 *	21	(9)
40.	38	1	1.000	1.000	0.793 *	21	(9)
21.	CITROBACTER	1	1.000	1.000	0.793 *	1	(1)
29.	27	9	1.000	1.000	0.793 *	1	(1)
37.	CITROBACTER	9	1.000	1.000	0.793 *	1	(1)
45.	43	9	1.000	1.000	0.793 *	1	(1)
60.	58	9	1.000	1.000	0.793 *	1	(1)
79.	77	9	1.000	1.000	0.793 *	1	(1)
2.	2	2	1.000	1.000	0.771 *	28	(11)
4.	PSEUDO FLUORE	2	1.000	1.000	0.771 *	28	(11)
16.	16	2	1.000	1.000	0.771 *	28	(11)
28.	26	11	0.991	0.998 *	0.771 *	2	(2)
44.	42	11	0.991	0.998 *	0.771 *	2	(2)
51.	49	11	0.991	0.998 *	0.771 *	2	(2)
47.	45	6	0.999	1.000 *	0.771 *	2	(2)
54.	52	11	0.991	0.998 *	0.771 *	2	(2)
68.	66	11	0.991	0.998 *	0.771 *	2	(2)
70.	68	11	0.991	0.998 *	0.771 *	2	(2)
61.	58	11	0.991	0.981 *	0.750 *	55	(15)
5.	PROTEUS VULG	SI			0.882 *	67	(S)
67.	AEROMONAS HYDRO	SI			0.882 *	5	(S)
36.	34	SI			0.841 *	67	(S)
12.	10	6	0.999	1.000 *	0.836 *	67	(S)
15.	13	6	0.999	1.000 *	0.836 *	67	(S)
20.	18	6	0.999	0.999 *	0.825 *	67	(S)
31.	29	6	0.999	1.000 *	0.836 *	67	(S)
47.	45	6	0.999	1.000 *	0.836 *	67	(S)
75.	73	6	0.999	1.000 *	0.836 *	67	(S)
55.	53	15	1.000	1.000 *	0.786 *	67	(S)
58.	56	15	1.000	1.000 *	0.766 *	67	(S)
66.	64	15	1.000	1.000 *	0.786 *	67	(S)
72.	70	15	1.000	1.000 *	0.786 *	67	(S)
77.	75	15	1.000	1.000 *	0.786 *	67	(S)
6.	ECOU	3	1.000	1.000 *	0.655 *	55	(15)
13.	11	3	1.000	1.000 *	0.655 *	55	(15)
8.	PROTEUS MIRA	4	0.997	0.999 *	0.724 *	52	(13)
11.	9	4	0.996	0.998 *	0.723 *	52	(13)
27.	25	4	0.997	0.999 *	0.724 *	52	(13)
30.	28	4	0.997	0.999 *	0.724 *	52	(13)
43.	41	4	0.997	0.999 *	0.724 *	52	(13)
46.	44	4	0.997	0.999 *	0.724 *	52	(13)
39.	37	4	0.996	0.997 *	0.728 *	52	(13)
9.	PSEUDO AERO	5	0.998	1.000 *	0.806 *	48	(8)
10.	PROTEUS MIRA	5	0.998	1.000 *	0.806 *	48	(8)
17.	15	5	0.998	1.000 *	0.806 *	48	(8)
22.	20	5	0.998	1.000 *	0.806 *	48	(8)
33.	31	5	0.998	1.000 *	0.806 *	48	(8)
38.	36	5	0.998	1.000 *	0.806 *	48	(8)
49.	47	5	0.998	0.998 *	0.805 *	25	(10)
25.	23	10	1.000	1.000 *	0.805 *	49	(5)
41.	39	10	1.000	1.000 *	0.805 *	49	(5)
62.	60	10	1.000	1.000 *	0.605 *	49	(5)
19.	17	8	0.992	0.999 *	0.842 *	34	(12)
26.	24	8	0.992	0.999 *	0.842 *	34	(12)
32.	30	8	0.992	0.999 *	0.842 *	34	(12)
35.	33	8	0.992	0.999 *	0.842 *	34	(12)
42.	40	8	0.992	0.999 *	0.842 *	34	(12)
57.	55	8	0.992	0.999 *	0.842 *	34	(12)
65.	63	8	0.992	0.999 *	0.842 *	34	(12)
71.	69	8	0.992	0.999 *	0.842 *	34	(12)
80.	78	8	0.992	0.999 *	0.842 *	34	(12)
48.	46	8	0.992	0.992 *	0.850 *	34	(12)
34.	CONTROL	12	1.000	1.000 *	0.922 *	53	(14)
50.	CONTROL	12	1.000	1.000 *	0.922 *	53	(14)
81.	CONTROL	12	1.000	1.000 *	0.922 *	53	(14)
69.	167	16	1.000	1.000 *	0.903 *	34	(12)
76.	174	16	1.000	1.000 *	0.903 *	34	(12)
52.	50	13	0.992	0.992 *	0.922 *	53	(14)
56.	54	13	0.992	0.998 *	0.927 *	53	(14)
59.	57	13	0.992	0.998 *	0.927 *	53	(14)
64.	62	13	0.992	0.998 *	0.927 *	53	(14)
78.	76	13	0.992	0.998 *	0.927 *	53	(14)
53.	51	14	1.000	1.000 *	0.927 *	56	(13)
63.	61	14	1.000	1.000 *	0.927 *	56	(13)
14.	ENTEROBACTER AERO	7	1.000	1.000 *	0.677 *	69	(16)
16.	14	7	1.000	1.000 *	0.677 *	69	(16)
23.	21	SI			0.744 *	53	(14)
73.	71	SI			0.679 *	55	(15)
74.	72	SI			0.405 *	14	(7)

Appendix 4b

PHENOTYPES in b05hen2/ Identity level -0.975
***CALCULATED DIVERSITY INOEX - 0.992 TRUE DIVERSITY INDEX 0.992**

No	Name	PhP-type	sim min	sim mean	=	lo	PhP typ
1	BACILLUS SP	Si			0.884 *	69	(SI)
40.	CONTROL	Si			0.971 *	69	(SSI)
69.	69	Si			0.971 *	40	(SI)
44.	44	8	1.000	1.000 *	0.891 ■	69	(SI)
54.	54	8	1.000	1.000 *	0.891 *	69	(SI)
20.	20	Si			0.823 *	65	(12)
65.	65	12	1.000	1.000 *	0.874 *	69	(SI)
75.	75	12	1.000	1.000 ■	0.874 *	69	(SI)
10.	10	6	1.000	1.000 *	0.865 *	31	(SI)
26.	26	6	1.000	1.000 *	0.865 *	31	(SI)
46.	48	6	1.000	1.000 *	0.865 *	31	(SI)
31.	31	Si			0.876 *	46	(9)
39.	39	Si			0.927 *	70	(SI)
70.	70	Si			0.927 *	39	(SI)
46.	46	9	1.000	1.000 *	0.926 *	70	(SI)
67.	67	9	1.000	1.000 *	0.926 *	70	(SI)
79.	79	Si			0.874 *	70	(SI)
18.	18	Si			0.903 *	27	(SO)
27.	27	Si			0.903 *	18	(SO)
33.	33	Si			0.797 *	56	(SO)
56.	56	Si			0.890 *	46	(9)
19.	19	Si			0.919 *	25	(SI)
25.	25	Si			0.919 *	19	(SI)
34.	34	Si			0.919 *	19	(SO)
3.	STAPHYLOCOCCUS AERO	2	1.000	1.000 *	0.939 *	35	(SO)
23.	23	2	1.000	1.000 *	0.939 *	35	(SO)
35.	35	Si			0.939 *	3	(2)
6.	PROTEUS VULG	Si			0.876 *	37	(SI)
11.	11	Si			0.895 *	37	(SO)
37.	37	Si			0.895 *	11	(SI)
5.	PSEUDO FLOURE	4	1.000	1.000 ■	0.940 *	30	(SI)
45.	45	4	1.000	1.000 *	0.940 *	30	(SO)
30.	30	Si			0.940 *	5	(4)
36.	36	Si			0.846 *	5	(4)
7.	FLAVOBAC SP	Si			0.920 *	15	(SO)
15.	15	Si			0.920 *	7	(SO)
28.	28	Si			0.896 *	7	(SI)
12.	12	Si			0.879 *	7	(SO)
8.	ECOU	5	1.000	1.000 *	0.945 *	62	(SO)
17.	17	5	1.000	1.000 *	0.945 *	62	(SO)
52.	52	5	1.000	1.000 *	0.945 ■	62	(SI)
62.	62	Si			0.945 *	8	(5)
13.	*13	Si			0.939 *	8	(5)
22.	22	Si			0.939 *	8	(5)
29.	29	Si			0.938 *	8	(5)
38.	38	Si			0.938 *	8	(5)
41.	41	7	1.000	1.000 *	0.932 *	58	(SI)
49.	49	7	1.000	1.000 *	0.932 *	58	(SI)
58.	58	Si			0.932 *	41	(7)
72.	72	Si			0.929 *	58	(SI)
55.	55	Si			0.930 *	41	(7)
64.	64	Si			0.932 *	41	(7)
42.	42	Si			0.895 *	59	(SO)
59.	56	Si			0.895 *	42	(SI)
2.	STREPTOCO FAE	1	1.000	1.000 *	0.957 *	47	(SI)
43.	43	1	1.000	1.000 *	0.957 *	47	(SO)
66.	66	1	1.000	1.000 *	0.957 *	47	(SI)
76.	76	1	1.000	1.000 *	0.957 *	47	(SI)
47.	47	Si			0.957 *	2	(1)
60.	60	Si			0.952 *	47	(SI)
78.	78	Si			0.897 *	60	(SI)
71.	71	Si			0.924 *	2	(D)
50.	50	Si			0.926 ■	2	(1)
53.	53	11	1.000	1.000 ■	0.922 *	2	(1)
61.	61	11	1.000	1.000 *	0.922 *	2	(1)
51.	51	10	1.000	1.000 *	0.947 *	74	(SI)
57.	57	10	1.000	1.000 ■	0.947 *	74	(SI)
74.	74	Si			0.947 *	51	(10)
68.	68	Si			0.779 *	11	(SI)
4.	HMBICROCO SP	3	1.000	1.000 *	0.000 *	35	(SI)
73.	11 73	3	1.000	1.000 *	0.000 *	58	(SI)
80.	HCONTROL	3	1.000	1.000 *	0.000 ■	70	(SI)
9.	9	Si			0.954 *	63	(SI)
63.	63	Si			0.954 *	9	(SO)
16.	16	Si			0.910 *	9	(SO)
14.	14	Si			0.698 *	18	(SI)
21.	21	Si			0.938 *	24	(SI)
24.	24	Si			0.938 *	21	(SI)
32.	32	Si			0.630 *	42	(SI)
77.	177	Si			0.415 *	14	(SI)

2/72

Appendix 4 C

PHENOTYPES in bioherit
-CALCULATED DIVERSITY INDEX - 0.890Identity level = 0.975
TRUE DIVERSITY INDEX = 0.990

No	Nama	PhP- type	aim min	aim maan	sun max	lo nr	PhP typo
1	E COLI	1	1.000	1.000 *	0.945 *	48	(Si)
20.	20	1	1.000	1.000 *	0.945 *	48	(Si)
48.	48	Si			0.945 *	1	(1)
28.	26	Si			0.938 *	1	(1)
39.	39	Si			0.935 *	1	(1)
62.	62	Si			0.935 *	66	(Si)
66.	66	Si			0.935 *	1	(1)
S.	EDWARD SP	5	1.000	1.000 *	0.935 *	72	(Si)
17.	17	5	1.000	1.000 ■	0.935 *	72	(Si)
72.	72	Si			0.935 *	5	(5)
4.	BACILLUS SP	4	1.000	1.000 *	0.896 *	80	(16)
58.	58	4	1.000	1.000 *	0.896 *	80	(16)
65.	65	4	1.000	1.000 *	0.896 *	80	(16)
67.	67	4	1.000	1.000 *	0.896 *	80	(16)
48.	CONTROL	16	0.987	0.987 *	0.888 *	74	(Si)
SO.	CONTROL	16	0.987	0.987 *	0.901 *	7	(7)
74.	74	Si			0.896 *	80	(16)
31.	31	13	1.000	1.000 *	0.885 *	48	(16)
38.	38	13	1.000	1.000 *	0.885 *	48	(16)
78.	78	Si			0.882 *	4	(4)
44.	44	Si			0.823 *	56	(18)
56.	56	18	1.000	1.000 *	0.866 *	48	(16)
63.	63	18	1.000	1.000 *	0.866 *	48	(16)
7.	MICROCO SP	7	1.000	1.000 *	0.926 *	18	(12)
10.	10	7	1.000	1.000 *	0.926 *	18	(12)
18.	18	12	1.000	1.000 *	0.926 *	7	(7)
24.	24	12	1.000	1.000 *	0.926 *	7	(7)
33.	33	Si			0.879 *	80	(16)
15.	15	11	1.000	1.000 *	0.862 *	7	(7)
30.	30	11	1.000	1.000 *	0.852 *	7	(7)
36.	36	Si			0.813 *	15	(11)
9.	9	Si			0.941 *	23	(Si)
23.	23	si			0.941 *	9	(Si)
21.	21	Si			0.898 *	29	(Si)
29.	29	Si			0.898 *	21	(SO)
51.	51	Si			0.890 *	7	(7)
64.	64	20	1.000	1.000 *	0.812 *	51	(SO)
76.	76	20	1.000	1.000 *	0.812 *	51	(SO)
2.	STAPOLYLOCOCCUS AERO	2	1.000	1.000 *	0.882 *	69	(SO)
59.	59	2	1.000	1.000 *	0.882 ■	69	(SO)
35.	35	Si			0.895 *	69	(SO)
69.	69	Si			0.895 *	35	(SO)
8.	PROTEUS VULG	8	1.000	1.000 *	0.933 *	27	(SO)
19.	19	8	1.000	1.000 *	0.933 *	27	(SO)
25.	25	8	1.000	1.000 *	0.933 *	27	(SO)
27.	27	Si			0.933 *	8	(6)
16.	16	Si			0.897 *	27	(SO)
14.	14	10	1.000	1.000 *	0.932 *	47	(SO)
42.	42	10	1.000	1.000 ■	0.932 *	47	(SO)
47.	47	Si			0.932 *	14	(10)
37.	37	Si			0.785 *	18	(12)
6.	PSEUDO FLUORE	6	1.000	1.000 *	0.846 *	11	(Si)
32.	32	6	1.000	1.000 *	0.846 *	11	(Si)
11.	11	Si			0.846 *	6	(6)
49.	49	Si			0.846 ■	6	(6)
40.	40	14	1.000	1.000 *	0.935 *	54	(SO)
43.	43	14	1.000	1.000 *	0.935 *	54	(SO)
54.	54	Si			0.935 *	<0	(14)
52.	52	Si			0.822 *	70	(SO)
70.	70	Si			0.822 *	52	(SO)
3.	STREPTOCO FAE	3	1.000	1.000 *	0.957 *	61	(SO)
13.	13	3	1.000	1.000 *	0.957 *	61	(SO)
73.	73	3	1.000	1.000 *	0.957 *	61	(SO)
61.	61	Si			0.957 *	3	(3)
55.	55	Si			0.924 *	3	(3)
71.	71	Si			0.922 *	3	(3)
68.	68	Si			0.923 *	3	(3)
75.	75	Si			0.926 *	3	(3)
79.	79	Si			0.924 *	3	(3)
12.	12	9	1.000	1.000 *	0.883 *	71	(SO)
28.	28	9	1.000	1.000 ■	0.683 *	71	(SO)
22.	22	Si			0.672 *	54	(SO)
34.	34	Si			0.732 *	5	(5)
41.	41	15	1.000	1.000 *	0.728 *	4	(4)
45.	45	15	1.000	1.000 *	0.728 *	4	(4)
50.	50	17	1.000	1.000 *	0.664 ■	44	(SO)
60.	60	17	1.000	1.000 *	0.664 *	44	(SO)
53.	53	Si			0.698 *	9	(SO)
57.	57	19	1.000	1.000 *	0.627 *	52	(S O)
77.	77	19	1.000	1.000 *	0.627 *	52	(Si)

45

PHENOTYPES in bootstraps / Identity level = 0.975
***CALCULATED DIVERSITY INDEX - 0.990 TRUE DIVERSITY INDEX = 0.990**

No	Name	PhP-type	sim min	sim mean	sim max	to	PhP type
1	EDWARD SP	1	1.000	1.000	0.855 *	52	(S)
27	27	1	1.000	1.000	0.855 *	52	(S)
70	68	1	1.000	1.000	0.855 *	52	(S)
61	59	Si			0.855 *	1	(D)
15	15	9	1.000	1.000	0.932 *	60	(S)
40	39	9	1.000	1.000	0.932 *	60	(S)
60	58	Si			0.932 *	15	(9)
52	51	Si			0.904 *	60	(S)
34	33	Si			0.930 *	15	(9)
50	49	Si			0.924 *	34	(S)
3	PROTEUS VULG	2	1.000	1.000	0.933 *	25	(S)
13	13	2	1.000	1.000	0.933 *	25	(S)
25	25	Si			0.933 *	3	(2)
47	46	Si			0.933 *	3	(2)
66	64	Si			0.874 *	15	(9)
4	ECOLI	3	0.995	0.995	0.940 *	14	(S)
19	19	3	0.995	0.998	0.939 *	48	(S)
63	61	3	0.995	0.998	0.939 *	48	(S)
14	14	Si			0.940 *	4	(3)
38	37	Si			0.934 *	14	(S)
23	23	Si			0.940 *	4	(3)
44	43	Si			0.935 *	48	(S)
48	47	Si			0.940 *	4	(3)
26	26	12	1.000	1.000	0.802 *	34	(S)
37	36	12	1.000	1.000	0.802 *	34	(S)
6	MICROCO SP	5	1.000	1.000	0.942 *	17	(S)
10	10	5	1.000	1.000	0.942 *	17	(S)
76	74	5	1.000	1.000	0.942 *	17	(S)
17	17	Si			0.942 *	6	(5)
16	16	10	1.000	1.000	0.927 *	17	(S)
58	57	10	1.000	1.000	0.927 *	17	(S)
75	73	10	1.000	1.000	0.927 *	17	(S)
81	79	Si			0.893 *	6	(5)
24	24	Si			0.915 *	65	(S)
65	63	Si			0.915 *	24	(S)
30	29	14	1.000	1.000	0.926 *	6	(5)
67	65	14	1.000	1.000	0.926 *	6	(5)
33	CONTROL	Si			0.942 *	82	(S)
82	CONTROL	Si			0.942 *	33	(S)
32	31	Si			0.904 *	24	(S)
56	55	Si			0.887 *	30	(14)
8	8	7	1.000	1.000	0.916 *	82	(SO)
55	54	7	1.000	1.000	0.916 *	82	(S)
57	56	Si			0.914 *	a	(7)
74	72	Si			0.858 *	8	(7)
72	70	Si			0.817 *	81	(6)
41	40	Si			0.941 *	42	(S)
42	41	Si			0.941 *	41	(S)
49	48	Si			0.896 *	41	(S)
64	62	Si			0.787 *	6	(7)
5	PSEUDO FLUORE	4	1.000	1.000	0.846 *	12	(S)
35	34	4	1.000	1.000	0.846 *	12	(S)
77	75	4	1.000	1.000	0.046 *	12	(S)
12	12	Si			0.873 *	43	(S)
43	42	Si			0.873 *	12	(S)
11	11	8	0.993	0.993	0.876 *	31	(SO)
21	21	8	0.993	0.993	0.851 *	31	(S)
31	30	Si			0.87G *	11	(8)
69	67	Si			0.811 *	8	(7)
54	53	Si			0.757 *	21	(8)
59	58	Si			0.786 *	60	(S)
2	STAPLYLOCOCUS AERO	Si			0.662 *	3	(2)
7	STREPTOCO FAE	6	1.000	1.000	0.959 *	80	(S)
9	9	6	1.000	1.000	0.959 *	80	(SO)
20	20	6	1.000	1.000	0.959 *	00	(S)
51	50	6	1.000	1.000	0.959 *	00	(S)
78	76	6	1.000	1.000	0.959 *	80	(S)
80	78	Si			0.959 *	7	(6)
28	28	13	0.995	0.995	0.955 *	7	(6)
29	28	13	0.995	0.995	0.957 *	7	(6)
46	45	Si			0.957 *	7	(6)
71	69	Si			0.956 *	(S)	
68	66	Si			0.956 *	71	(S)
62	60	Si			0.926 *	7	(6)
18	18	11	1.000	1.000	0.927 *	73	(S)
36	35	11	1.000	1.000	0.927 *	73	(S)
73	71	Si			0.927 *	10	(11)
79	77	Si			0.867 *	10	(11)
22	22	Si			0.478 *	43	(S)
39	38	Si			0.740 *	34	(S)
45	44	Si			0.646 *	(S)	
53	52	Si			0.516 *	33	(S)

PHENOTYPES in boahonS/ *CALCULATED DIVERSITY INDEX *» 0.984		Identity level = 0.975 TRUE DIVERSITY INDEX = 0.384				
No	Name	PhP- type	sim min	aim mean	sim max	to PhP type
1	BACHILLUS	1	1.000	1.000 *	0.911 *	80 (14)
43	43	1	1.000	1.000 *	0.911 *	80 (14)
73	73	1	1.000	1.000 *	0.911 *	80 (14)
40	CONTROL	14	0.983	0.983 *	0.922 *	42 (16)
80	CONTROL	14	0.983	0.983 *	0.914 *	42 (16)
51	51	Si			0.882 *	1 (1)
2	MICROCO SP	2	1.000	1.000 *	0.926 *	42 (16)
25	25	2	1.000	1.000 *	0.926 *	42 (16)
57	57	2	1.000	1.000 *	0.926 *	42 (16)
42	42	16	1.000	1.000 *	0.926 *	2 (2)
49	49	16	1.000	1.000 *	0.926 *	2 (2)
68	68	Si			0.902 *	42 (16)
64	64	Si			0.887 *	42 (16)
19	19	Si			0.893 *	2 (2)
38	38	Si			0.862 *	2 (2)
32	32	Si			0.893 *	2 (2)
10	10	8	1.000	1.000 *	0.932 *	16 (SO)
30	30	8	1.000	1.000 *	0.932 *	16 (SO)
16	16	Si			0.932 *	10 (8)
21	21	Si			0.932 *	10 (8)
6	ECOLI	5	1.000	1.000 *	0.945 *	27 (SO)
17	17	5	1.000	1.000 *	0.945 *	27 (SO)
44	44	5	1.000	1.000 *	0.945 *	27 (SO)
27	27	Si			0.945 *	6 (5)
23	23	Si			0.938 *	6 (5)
53	53	Si			0.936 *	62 (SO)
62	62	Si			0.939 *	6 (5)
37	37	Si			0.887 *	6 (5)
7	EOWARD SP	6	1.000	1.000 *	0.935 *	69 (SO)
63	63	6	1.000	1.000 *	0.935 *	69 (SO)
69	69	Si			0.935 *	7 (6)
3	STAPLYLOCOCCUS AERO	3	1.000	1.000 *	0.882 *	35 (SO)
76	76	3	1.000	1.000 *	0.882 *	35 (SO)
35	35	Si			0.882 *	3 (3)
5	PROTEUS VULG	Si			0.805 *	35 (SO)
13	13	11	0.986	0.986 *	0.821 *	65 (20)
20	20	11	0.986	0.995 *	0.807 *	3 (3)
24	24	11	0.986	0.995 *	0.807 *	3 (3)
36	36	11	0.986	0.995 *	0.807 *	3 (3)
65	65	20	1.000	1.000 *	0.821 *	13 (11)
71	71	20	1.000	1.000 *	0.821 *	13 (11)
8	PSEUDO FLUORE	7	1.000	1.000 *	0.846 *	31 (SO)
15	15	7	1.000	1.000 *	0.846 *	31 (SO)
39	39	7	1.000	1.000 *	0.846 *	31 (SO)
54	54	7	1.000	1.000 *	0.846 *	31 (SO)
31	31	Si			0.846 *	8 (7)
28	28	13	1.000	1.000 *	0.834 *	8 (7)
33	33	13	1.000	1.000 *	0.834 *	8 (7)
11	11	9	1.000	1.000 *	0.802 *	48 (SO)
18	18	9	1.000	1.000 *	0.802 *	48 (S)
26	26	9	1.000	1.000 *	0.802 *	48 (Si)
41	41	15	1.000	1.000 *	0.842 *	40 (14)
55	55	15	1.000	1.000 *	0.842 *	40 (14)
46	46	Si			0.842 *	41 (15)
48	48	Si			0.842 *	41 (15)
78	78	Si			0.858 *	1 (1)
50	50	18	1.000	1.000 *	0.837 *	66 (Si)
59	59	18	1.000	1.000 *	0.837 *	66 (Si)
66	66	Si			0.837 *	50 (18)
29	29	Si			0.753 *	53 (SO)
58	58	Si			0.858 *	1 (1)
75	75	Si			0.811 *	1 (1)
4	STREPTOCO FAE	4	1.000	1.000 *	0.958 *	74 (SO)
9	9	4	1.000	1.000 *	0.958 *	74 (Si)
34	34	4	1.000	1.000 *	0.958 *	74 (Si)
45	45	4	1.000	1.000 *	0.958 *	74 (S)
60	60	4	1.000	1.000 *	0.958 *	74 (Si)
74	74	Si			0.958 *	4 (4)
77	77	Si			0.951 *	74 (SO)
70	70	21	1.000	1.000 *	0.923 *	4 (4)
79	79	21	1.000	1.000 *	0.923 *	4 (4)
12	12	10	1.000	1.000 *	0.727 *	75 (SO)
22	22	10	1.000	1.000 *	0.727 *	75 (Si)
14	14	12	1.000	1.000 *	0.627 *	12 (10)
56	56	12	1.000	1.000 *	0.627 *	12 (10)
47	47	17	1.000	1.000 *	0.698 *	11 (9)
67	67	17	1.000	1.000 *	0.698 *	11 (9)
52	52	19	1.000	1.000 *	0.608 *	66 (SO)
61	61	19	1.000	1.000 *	0.608 *	66 (Si)
72	72	19	1.000	1.000 *	0.608 *	66 (SO)

Identity level $m = 0.975$
TRUE DIVERSITY INDEX => 0.993

No	Name	PhP-type	sim mm	sim mean	sim max	lo	PhP type
1.	1. CORYNERAC DIPH	Si			0.000 ■	<s	
2.	ECOU	1	1.000	1.000 *	0.939 *	25	(SI)
34.	34	1	1.000	1.000 ■	0.939 *	25	(SI)
37.	37	1	1.000	1.000 •	0.939 *	25	(SI)
73.	73	1	1.000	1.000 *	0.939 *	25	(SI)
25.	25	Si			0.939 *	2	(1)
41.	41	Si			0.944 *	62	(SI)
62.	62	Si			0.944 *	41	(SI)
42.	42	10	1.000	1.000 *	0.881 *	76	(SI)
58.	58	10	1.000	1.000 ■	0.881 *	76	(SI)
76.	76	Si			0.881 *	42	(10)
28.	28	Si			0.859 *	39	(SI)
39.	39	Si			0.859 *	28	(SI)
4.	MICROCOCCLUS LUT	2	1.000	1.000 *	0.922 *	48	(SI)
57.	57	2	1.000	1.000 *	0.922 *	48	(SI)
21.	21	Si			0.895 *	23	(SI)
23.	23	Si			0.895 *	21	(SI)
7.	PSEUDO AEROG	4	1.000	1.000 *	0.819 *	26	(S.)
15.	15	4	1.000	1.000 *	0.819 ■	26	(SI)
47.	47	4	1.000	1.000 *	0.819 *	26	(SI)
26.	26	Si			0.833 *	21	(SI)
18.	18	Si			0.860 ■	48	(SI)
53.	53	Si			0.843 *	33	(SI)
32.	32	Si			0.826 *	18	(SI)
50.	50	Si			0.804 *	70	(SI)
70.	70	Si			0.804 *	50	(SI)
12.	12	7	1.000	1.000 •	0.786 *	33	(SI)
61.	61	7	1.000	1.000 ■	0.786 *	33	(SI)
33.	33	Si			0.917 *	78	(SI)
45.	45	Si			0.857 *	33	(SI)
5.	PASTEU HAEM	Si			0.932 *	78	(SI)
78.	78	Si			0.932 *	5	(SI)
40.	40	Si			0.876 *	5	(SI)
10.	BACILLAS	Si			0.920 *	80	(SI)
48.	CONTROL	Si			0.955 *	80	(SI)
80.	CONTROL	Si			0.955 *	48	(SI)
59.	59	Si			0.906 *	66	(12)
64.	64	Si			0.910 *	66	(12)
66.	66	12	1.000	1.000 *	0.910 *	64	(SI)
74.	74	12	1.000	1.000 *	0.910 *	64	(SI)
14.	14	Si			0.868 *	17	(SI)
17.	17	Si			0.873 *	64	(SI)
27.	27	Si			0.828 *	63	(SI)
63.	63	Si			0.858 *	14	(SI)
8.	STREPTOCO FAE	5	1.000	1.000 •	0.957 *	46	(S.)
22.	22	5	1.000	1.000 •	0.957 *	46	(SI)
60.	60	5	1.000	1.000 •	0.957 *	46	(SI)
46.	46	Si			0.957 *	8	(5)
36.	36	Si			0.955 *	46	(S.)
24.	24	Si			0.925 *	8	(5)
19.	19	Si			0.875 ■	24	(SI)
13.	13	Si			0.922 *	8	(5)
29.	29	Si			0.874 *	43	(S.)
43.	43	Si			0.903 *	8	(5)
52.	52	Si			0.787 *	43	(SI)
9.	CITROBAC AMA	Si			0.926 *	38	(SI)
38.	38	Si			0.926 *	9	(SI)
54.	54	Si			0.911 *	38	(SI)
11.	SHIG SONNEI	6	0.989	0.989 *	0.838 *	31	(9)
67.	67	6	0.989	0.989 *	0.821 *	31	(9)
31.	31	9	0.986	0.986 *	0.838 *	11	(6)
75.	75	9	0.986	0.986 •	0.796 *	18	(SI)
20.	20	8	1.000	1.000 •	0.910 *	79	(SI)
77.	77	8	1.000	1.000 *	0.910 *	79	(SI)
79.	79	Si			0.910 *	20	(8)
69.	69	Si			0.876 *	79	(SI)
55.	55	Si			0.765 *	65	(SI)
65.	65	Si			0.793 *	64	(SI)
3.	CITROBAC FREU	Si			0.916 *	44	(SI)
35.	35	Si			0.919 *	44	(SI)
44.	44	Si			0.919 *	35	(SI)
16.	16	Si			0.859 *	30	(SI)
30.	30	Si			0.859 *	16	(SI)
6.	PROTEUS MIRA	3	1.000	1.000 *	0.754 *	16	(SI)
49.	49	3	1.000	1.000 *	0.754 *	16	(SI)
51.	51	11	1.000	1.000 •	0.730 *	6	(3)
56.	56	11	1.000	1.000 •	0.730 *	6	(3)
68.	68	Si			0.845 *	72	(SI)
72.	72	Si			0.845 *	68	(SI)
71.	71	Si			0.699 ■	13	(SI)

274

- AppelUI-X 5"b -

IDENTITY INDEX = 0.995 TRUE DIVERSITY INDEX = 0.995

No	Name	PhP-	sim	sim	sim	to	PhP
		type	min	mean	max		type
1.	MICROCOCCLUS LUT	1	1.000	1.000 *	0.922 *	16	(4)
45.	45	1	1.000	1.000 ■	0.922 *	16	(4)
14	14	SI			0.874 ■	1	(1)
25.	25	SI			0.918 *	30	(S)
30.	30	SI			0.918 *	25	(S)
36.	36	SI			0.831 *	57	(S)
11.	11	SI			0.837 *	17	(5)
16.	CONTROL	4	1.000	1.000 *	0.970 *	40	(S)
80.	CONTROL	4	1.000	1.000 *	0.970 *	40	(S)
40.	CONTROL	SI			0.970 *	16	(4)
17	17	5	1.000	1.000 *	0.903 *	16	(4)
75.	75	5	1.000	1.000 ■	0.903 *	16	(4)
57.	57	SI			0.876 *	17	(5)
2.	PSEUDO AEROG	SI			0.915 *	46	(11)
46	46	11	1.000	1.000 *	0.915 *	2	(S)
77.	77	11	1.000	1.000 ■	0.915 *	2	(S)
44.	44	SI			0.873 *	2	(S)
21.	21	7	1.000	1.000 *	0.910 *	61	(S)
50	50	7	1.000	1.000 *	0.910 *	61	(S)
61.	61	SI			0.910 *	21	(7)
27.	27	SI			0.896 *	2	(S)
55.	55	SI			0.896 *	21	(7)
6.	CORYNEBAC DIPH	3	1.000	1.000 *	0.910 ■	20	(6)
60.	60	3	1.000	1.000 *	0.910 *	20	(6)
20.	20	6	1.000	1.000 *	0.910 *	6	(3)
76.	76	6	1.000	1.000 *	0.910 *	6	(3)
51.	51	SI			0.874 ■	14	(S)
15.	15	SI			0.855 *	69	(S)
63.	63	SI			0.903 *	40	(S)
69.	69	SI			0.869 *	63	(S)
19.	19	SI			0.826 *	63	(S)
28.	28	SI			0.810 *	19	(S)
5.	ECOLI	2	1.000	1.000 *	0.939 *	59	(S)
24.	24	2	1.000	1.000 *	0.939 *	59	(S)
59.	59	SI			0.939 *	5	(2)
73.	73	SI			0.938 *	5	(2)
29.	29	10	1.000	1.000 ■	0.943 *	35	(S)
54.	54	10	1.000	1.000 *	0.943 *	35	(S)
64.	64	10	1.000	1.000 *	0.943 *	35	(S)
35.	35	SI			0.943 *	29	(10)
12.	12	SI			0.933 *	79	(S)
79.	79	SI			0.938 *	5	(2)
43.	43	SI			0.919 *	49	(S)
49.	49	SI			0.919 *	43	(S)
65.	65	SI			0.917 *	49	(S)
66.	66	SI			0.938 *	59	(S)
8.	SERRA MARC	SI			0.936 *	53	(S)
23.	23	9	1.000	1.000 *	0.935 ■	8	(S)
34.	34	9	1.000	1.000 *	0.935 *	8	(S)
53.	53	SI			0.936 *	a	(S)
38.	38	SI			0.882 *	53	(S)
9.	AEROMON HYDRO	SI			0.959 *	22	(8)
22.	22	8	1.000	1.000 *	0.959 *	9	(S)
32.	32	8	1.000	1.000 *	0.959 *	9	(S)
33.	33	SI			0.925 *	9	(S)
52.	52	SI			0.950 *	68	(S)
68.	68	SI			0.950 *	52	(S)
10.	ENTEROBACTER AERO	SI			0.917 *	48	(S)
48.	48	SI			0.917 *	10	(S)
41.	41	SI			0.915 *	10	(S)
56.	56	12	0.997	0.997 *	0.913 *	10	(S)
70.	70	12	0.997	0.997 *	0.917 *	10	(S)
42.	42	SI			0.764 *	16	(4)
47.	47	SI			0.806 *	2	(S)
78.	78	SI			0.817 *	27	(S)
3.	STREPTOCO FAE	SI			0.957 *	37	(S)
37.	37	SI			0.957 *	3	(S)
18.	18	SI			0.955 *	71	(S)
71.	71	SI			0.957 *	3	(S)
39.	39	SI			0.903 *	3	(S)
4.	CITROBAC DIV	SI			0.800 *	62	(S)
62.	62	SI			0.600 *	4	(S)
26.	26	SI			0.769 *	4	(S)
13.	13	SI			0.776 *	4	(S)
7.	KLEBSIELLA RHINO	SI			0.719 *	74	(S)
31.	31	SI			0.693 *	3	(S)
58.	58	SI			0.845 *	74	(S)
74.	74	SI			0.845 *	58	(S)
67.	67	SI			0.704 *	46	(11)
72.	72	SI			0.724 *	37	(S)

PHENOTYPES in ahdo3/ Identity level: 0.975
 CALCULATED DIVERSITY INDEX = 0.991 TRUE DIVERSITY INDEX = 0.991

No	Name	PhP- type	sim	mean	mox	n°r	PhP type
1	E COLI	1	1.000	1.000 ■	0.945 *	21	(Si)
47	47	1	1.000	1.000 *	0.945 *	21	(Si)
21	21	Si			0.945 *	1	(1)
52	52	Si			0.940 *	1	(1)
3a	38	Si			0.939 *	1	(1)
54	54	Si			0.939 *	1	(D)
43	43	Si			0.938 *	1	(1)
62	62	Si			0.938 *	1	(1)
18	18	Si			0.926 *	1	(1)
76	76	Si			0.817 *	62	(Si)
4	PROTEUS MIRA	4	1.000	1.000 *	0.931 *	51	(Si)
26	26	4	1.000	1.000 *	0.931 *	51	(Si)
48	48	4	1.000	1.000 *	0.931 *	51	(Si)
51	51	Si			0.931 *	4	<-)
5	MICROCO SP	5	0.991	0.991 °	0.926 *	7	(Si)
70	70	5	0.991	0.991 °	0.922 °	7	(Si)
7	MICROCOC LUT	Si			0.926 *	5	(5)
78	76	Si			0.908 *	5	(5)
15	15	11	0.989	0.934 *	0.869 *	73	(Si)
35	35	11	0.989	0.994 *	0.869 °	73	(Si)
24	24	11	0.989	0.989 °	0.850 °	73	(SO)
73	73	Si			0.908 *	5	(5)
58	58	Si			0.917 *	5	(5)
2	PSEUDO AEROG	2	1.000	1.000 *	0.925 ■	14	(Si)
25	25	2	1.000	1.000 *	0.925 *	14	(Si)
14	14	Si			0.931 °	57	(Si)
57	57	Si			0.931 *	14	(Si)
44	44	Si			0.901 *	2	(2)
64	64	Si			0.896 *	2	(2)
30	30	Si			0.833 *	19	(SO)
77	77	Si			0.849 *	44	(Si)
6	HAFNIA ALV	6	1.000	1.000 *	0.926 *	20	(Si)
12	12	6	1.000	1.000 *	0.926 *	20	(SO)
29	29	6	1.000	1.000 *	0.926 *	20	(Si)
20	20	Si			0.926 *	6	(6)
19	19	Si			0.910 *	6	(6)
39	39	Si			0.895 *	6	(6)
28	28	14	1.000	1.000 *	0.803 *	42	(SO)
31	31	14	1.000	1.000 *	0.803 *	42	(SO)
42	42	Si			0.834 *	19	(Si)
16	CONTROL	12	0.982	0.989 *	0.916 ■	20	(Si)
32	CONTROL	12	0.987	0.992 *	0.922 *	7	(SO)
80	CONTROL	12	0.902	0.984 *	0.927 *	66	(SO)
66	66	Si			0.927 *	00	(12)
75	75	Si			0.908 *	66	(Si)
33	33	Si			0.839 *	66	(Si)
74	74	Si			0.847 *	80	(12)
61	61	Si			0.905 *	69	(Si)
69	69	Si			0.905 *	61	(Si)
3	STREPTOCO FAE	3	1.000	1.000 *	0.957 *	22	(Si)
72	72	3	1.000	1.000 ■	0.957 *	22	(Si)
22	22	Si			0.957 °	3	(3)
37	37	Si			0.953 *	22	(SO)
60	60	Si			0.957 *	3	(3)
46	46	Si			0.922 *	3	(3)
65	65	Si			0.922 *	3	(3)
34	34	Si			0.926 *	3	(3)
59	59	Si			0.930 *	71	(Si)
71	71	Si			0.930 *	71	(Si)
9	SHIG SONNEI	8	0.989	0.994 °	0.838 *	49	(9)
13	13	8	0.989	0.994 *	0.838 °	49	(9)
17	17	8	0.989	0.909 *	0.821 *	49	(9)
10	10	9	0.986	0.986 °	0.772 *	9	(8)
-9	49	9	0.986	0.986 °	0.838 °	9	(8)
11	11	10	1.000	1.000 *	0.779 *	23	(13)
27	27	10	1.000	1.000 *	0.779 *	23	(13)
53	53	10	1.000	1.000 *	0.779 *	23	(13)
23	23	13	1.000	1.000 ■	0.895 °	50	(Si)
40	40	13	1.000	1.000 *	0.895 *	50	(Si)
50	50	Si			0.950 *	63	(Si)
63	63	Si			0.950 *	50	(Si)
56	56	15	1.000	1.000 *	0.876 °	50	(Si)
68	60	15	1.000	1.000 *	0.876 °	50	(Si)
79	79	Si			0.841 *	63	(Si)
55	55	Si			0.841 *	63	(Si)
8	KLEBSIELLA PNEU	7	1.000	1.000 *	0.854 *	45	(Si)
36	36	7	1.000	1.000 *	0.854 *	45	(Si)
45	45	Si			0.054 °	0	(7)
41	41	Si			0.045 *	0	(7)
67	67	Si			0.594 *	11	(10)

id

PHENOTYPES In abelt*/
CALCULATED DIVERSITY INDEX 0.003

Identity level - 0.975
TRUE DIVERSITY INDEX - 0.993

No	Name	PhP-type	sim min	sim mean	sim max	to nr	PhP type
1.	ECOU	1	1.000	1.000 *	0.939 *	24	(Si)
60.	68	1	1.000	1.000 *	0.939 *	24	(Si)
78.	78	1	1.000	1.000 *	0.939 *	24	(Si)
24.	24	Si			0.939 *	1	(8)
38.	38	Si			0.939 *	1	(8)
41.	41	Si			0.938 *	1	(8)
11.	11	Si			0.910 *	71	(Si)
71.	71	Si			0.910 *	11	(Si)
12.	12	Si			0.887 *	1	(1)
8.	PSEUDO AEROG	Si			0.912 *	58	(Si)
67.	67	Si			0.903 *	6	(Si)
15.	15	Si			0.908 *	77	(Si)
58.	58	Si			0.914 *	77	(Si)
77.	77	Si			0.914 *	58	(Si)
9.	9	4	1.000	1.000 *	0.817 *	55	(Si)
33.	33	4	1.000	1.000 *	0.817 *	55	(SO)
55.	55	Si			0.896 *	8	(SO)
14.	14	7	1.000	1.000 *	0.968 *	20	(SO)
47.	47	7	1.000	1.000 *	0.968 *	20	(8)
20.	20	Si			0.968 *	14	(7)
18.	18	9	1.000	1.000 *	0.926 *	14	(7)
57.	57	9	1.000	1.000 *	0.926 *	14	(7)
40.	40	Si			0.895 *	18	(8)
53.	53	Si			0.908 *	18	(8)
16.	16	8	1.000	1.000 *	0.922 *	14	(7)
48.	CONTROL	8	1.000	1.000 *	0.922 *	14	(8)
80.	CONTROL	8	1.000	1.000 *	0.922 *	14	(8)
54.	54	Si			0.900 *	16	(8)
23.	23	Si			0.874 *	14	(8)
3.	HAFNIA ALU	2	1.000	1.000 *	0.926 *	17	(SO)
30.	30	2	1.000	1.000 *	0.926 *	17	(SO)
49.	49	2	1.000	1.000 *	0.926 *	17	(8)
17.	17	Si			0.926 *	3	(8)
7.	PSEUDO FLUORE	Si			0.910 *	3	(2)
31.	31	Si			0.833 *	7	(SO)
19.	19	Si			0.833 *	7	(SO)
39.	39	Si			0.833 *	7	(SO)
5.	PASTEU HAEM	3	1.000	1.000 *	0.929 *	32	(SO)
75.	75	3	1.000	1.000 *	0.929 *	32	(8)
32.	32	Si			0.929 *	5	(3)
25.	25	Si			0.919 *	32	(SO)
5.	PROTEUS VULG	Si			0.903 *	35	(8)
35.	35	Si			0.932 *	10	(5)
21.	21	Si			0.895 *	36	(SO)
28.	28	11	0.997	0.997 *	0.941 *	36	(SO)
44.	44	11	0.997	0.997 *	0.950 *	36	(SO)
36.	36	Si			0.950 *	44	(11)
10.	PROTEUS MIRA	5	0.994	0.994 *	0.932 *	35	(Si)
61.	61	5	0.994	0.994 *	0.955 *	26	(8)
26.	26	Si			0.955 *	61	(8)
46.	46	Si			0.930 *	10	(8)
27.	27	10	0.986	0.993 *	0.922 *	63	(SO)
45.	45	10	0.986	0.993 *	0.922 *	63	(Si)
50.	50	10	0.986	0.986 *	0.940 *	63	(Si)
63.	63	Si			0.940 *	50	(10)
29.	29	12	0.969	0.989 *	0.838 *	50	(10)
42.	42	12	0.989	0.989 *	0.821 *	50	(10)
34.	34	13	1.000	1.000 *	0.779 *	21	(Si)
00.	00	13	1.000	1.000 *	0.779 *	21	(Si)
79.	79	Si			0.815 *	14	(7)
2.	CITROBAC DIV	Si			0.891 *	65	(SO)
65.	65	Si			0.891 *	2	(SO)
76.	76	Si			0.875 *	2	(Si)
64.	64	Si			0.870 *	2	(Si)
4.	KLEBSIELLA PNEU	Si			0.863 *	72	(SO)
72.	72	Si			0.863 *	4	(SO)
74.	74	Si			0.845 *	4	(SO)
51.	51	Si			0.874 *	56	(S.)
56.	56	Si			0.874 *	51	(Si)
62.	62	Si			0.872 *	56	(Si)
66.	66	Si			0.915 *	70	(SO)
70.	70	Si			0.915 *	66	(SO)
13.	13	6	1.000	1.000 *	0.959 *	22	(SO)
52.	52	6	1.000	1.000 *	0.959 *	22	(8)
22.	22	Si			0.959 *	13	(8)
37.	37	Si			0.957 *	13	(8)
43.	43	Si			0.953 *	37	(Si)
60.	60	Si			0.953 *	37	(SO)
59.	59	Si			0.736 *	25	(Si)
73.	173	Si			0.311 *	70	(Si)

011-
UCULÁTEQ DIVERSITY INDEX - 0.993 TRUE DIVERSITY INDEX ■ = 0.993

N _n	Name	PhP- -yp*	m TM	ma an	r*	nr	PhP ypa
1.	ECOLI	i	1.000	1.000 *	0.939 *	79	(-SI)
35.	35	1	1.000	1.000 *	0.939 *	79	(SI)
79.	79	SI			0.939 *	1	(1)
SB.	58	SI			0.938 *	1	(1)
74.	74	SI			0.937 *	79	(SI)
10.	10	7	1.000	1.000 *	0.938 *	1	(1)
66.	66	7	1.000	1.000 *	0.938 *	1	(1)
18.	18	SI			0.931 *	10	(7)
42.	42	SI			0.866 *	52	(SI)
52.	52	SI			0.938 *	1	(1)
27.	27	SI			0.877 *	18	(SO)
3.	CORYNEBAC DIPH	3	1.000	1.000 *	0.842 *	56	(fo)
44.	44	3	1.000	1.000 *	0.842 *	56	(14)
70.	70	3	1.000	1.000 *	0.842 *	56	(M)
51.	51	12	1.000	1.000 *	0.903 *	56	(14)
63.	63	12	1.000	1.000 *	0.903 *	56	(14)
7.	MICROCOCOCCUS LUT	5	1.000	1.000 *	0.922 *	56	(14)
54.	54	5	1.000	1.000 *	0.922 *	56	(14)
77.	77	5	1.000	1.000 *	0.922 *	56	(14)
56.	56	14	1.000	1.000 *	0.922 *	7	(5)
80.	CONTROL	14	1.000	1.000 *	0.922 *	7	(5)
40.	CONTROL	SI			0.911 *	56	(14)
64.	64	SI			0.874 *	7	(5)
31.	31	SI			0.947 *	45	(SO)
45.	45	SI			0.947 *	31	(SI)
8.	PSEUDO AEROG	SI			0.912 *	60	(SO)
60.	60	SI			0.912 *	8	(SI)
71.	71	SI			0.903 *	8	(SO)
67.	67	SI			0.912 *	8	(so)
14.	14	SI			0.901 *	8	(so)
9.	PSEUDO CAV	6	1.000	1.000 *	0.927 *	46	(SO)
73.	73	6	1.000	1.000 *	0.927 *	46	(SO)
46.	46	SI			0.927 *	9	(6)
53.	53	SI			0.927 *	9	(6)
24.	24	SI			0.901 *	8	(SI)
57.	57	SI			0.927 *	9	(6)
5.	PSEUDO FLUORE	SI			0.910 *	47	(SO)
47.	47	SI			0.910 *	5	(SI)
11.	11	SI			0.895 *	47	(SI)
49.	49	SI			0.879 *	47	(SI)
43.	43	SI			0.834 ■	5	(SI)
62.	62	SI			0.881 *	5	(SI)
30.	30	SI			0.833 *	5	(SI)
68.	68	SI			0.856 *	47	(SI)
36.	36	SI			0.833 *	5	(SO)
2.	KLEBSIELLA PNEU	2	1.000	1.000 ■	0.845 *	15	(SO)
33.	33	2	1.000	1.000 *	0.845 *	15	(SI)
61.	61	2	1.000	1.000 *	0.845 *	15	(SI)
15.	15	SI			0.845 *	2	(2)
21.	21	SI			0.845 *	2	(2)
29.	29	SI			0.845 *	2	(2)
6.	PROTEUS VULG	SI			0.935 *	48	(SO)
48.	48	SI			0.935 *	6	(SO)
69.	69	SI			0.933 *	6	(SO)
12.	12	8	1.000	1.000 *	0.895 *	20	(10)
39.	39	8	1.000	1.000 ■	0.895 *	20	(10)
20.	20	10	1.000	1.000 *	0.895 *	12	(B)
37.	37	10	1.000	1.000 *	0.895 *	12	(B)
17.	17	SI			0.947 *	32	(SI)
32.	32	SI			0.047 *	17	(SI)
19.	19	SI			0.833 *	5	(SO)
23.	23	SI			0.934 *	25	(SI)
25.	25	SI			0.934 *	23	(SI)
78.	78	SI			0.761 *	21	(SI)
4.	STREPTOCO FAE	4	1.000	1.000 *	0.959 *	65	(SO)
26.	26	4	1.000	1.000 *	0.959 *	65	(SI)
65.	65	SI			0.959 *	4	(4)
72.	72	SI			0.958 *	4	(4)
34.	34	SI			0.957 *	4	(4)
13.	13	SI			0.957 ■	4	(4)
22.	22	SI			0.952 *	13	(SI)
38.	38	SI			0.953 *	69	(SI)
59.	59	SI			0.957 *	4	(-)
76.	76	SI			0.880 *	65	(SI)
16.	16	9	0.989	0.989 *	0.838 *	41	(11)
28.	28	9	0.999	0.989 *	0.821 *	41	(11)
41.	41	11	1.000	1.000 *	0.838 *	16	(9)
50.	50	11	1.000	1.000 *	0.838 *	16	(9)
55.	55	13	0.992	0.992 *	0.671 *	60	(SI)
75.	75	13	0.992	0.992 *	0.641 *	60	(SI)

No	Name	PhP- type	aim mln	aim mean	aim	lo nr	PhP type
1.	11 BACILLUS	1	1.000	1.000 *	0.000 *	(S	
7.	IMICROCO SP	1	1.000	1.000 *	0.000 *	9	(7)
18.	II 16	1	1.000	1.000 *	0.000 *	36	(17)
26.	II 26	1	1.000	1.000 *	0.000 *	21	(15)
32.	ICONTROL	1	1.000	1.000 *	0.000 *	10	(8)
38.	h 38	1	1.000	1.000 ■	0.000 *	46	(SI)
41.	1141	1	1.000	1.000 *	0.000 *	36	(17)
45.	1145	1	1.000	1.000 *	0.000 *	10	(8)
57.	1157	1	1.000	1.000 *	0.000 *	21	(15)
68.	11 6B	1	1.000	1.000 ■	0.000 *	78	(SI)
73.	1173	1	1.000	1.000 *	0.000 *	78	(SI)
60.	ICONTROL	1	1.000	1.000 *	0.000 *	10	(8)
2.	E COLI	2	1.000	1.000 ■	0.653 *	46	(SI)
3.	PROTEUS MIRA	2	1.000	1.000 ■	0.614 *	8	(6)
11.	11	2	1.000	1.000 *	0.614 *	8	(6)
58.	58	2	1.000	1.000 ■	0.614 *	8	(6)
4.	STREPTOCO FAE	3	1.000	1.000 *	0.955 *	78	(SI)
67.	67	3	1.000	1.000 ■	0.955 *	78	(SI)
72.	72	3	1.000	1.000 *	0.955 *	78	(SI)
76.	76	3	1.000	1.000 *	0.955 *	78	(SI)
78.	78	SI			0.955 *	4	(3)
69.	69	20	1.000	1.000 *	0.953 *	4	(3)
74.	74	20	1.000	1.000 *	0.953 *	4	(3)
33.	33	16	1.000	1.000 *	0.866 ■	78	(SO)
77.	77	16	1.000	1.000 *	0.866 *	78	(so)
12.	12	9	1.000	1.000 *	0.888 *	51	(8)
39.	39	S	1.000	1.000 ■	0.888 *	51	(SO)
51.	51	SI			0.888 *	12	(9)
5.	ENTEROBACTER AERO	4	1.000	1.000 *	0.949 *	10	(8)
19.	19	4	1.000	1.000 *	0.949 *	10	(8)
31.	31	4	1.000	1.000 *	0.949 *	10	(8)
79.	79	4	1.000	1.000 *	0.949 *	10	(8)
10.	10	8	1.000	1.000 *	0.949 *	5	(4)
35.	35	6	1.000	1.000 *	0.949 *	5	(4)
61.	161	SI			0.836 *	5	(4)
44.	44	SI			0.814 *	10	(8)
6.	PSEUDO AERO	5	1.000	1.000 *	0.531 *	9	(7)
24.	24	5	1.000	1.000 *	0.531 *	9	(7)
8.	SERRA MARC	6	1.000	1.000 *	0.614 *	3	(2)
22.	22	6	1.000	1.000 *	0.614 *	3	(2)
50.	50	6	1.000	1.000 *	0.614 *	3	(2)
60.	60	6	1.000	1.000 *	0.614 *	3	(2)
9.	9	7	1.000	1.000 ■	0.551 *	30	(SO)
62.	62	7	1.000	1.000 *	0.551 *	30	(so)
13.	13	10	1.000	1.000 *	0.594 *	46	(SO)
17.	17	10	1.000	1.000 *	0.594 *	46	(SO)
37.	37	10	1.000	1.000 *	0.594 *	46	(SO)
64.	64	10	1.000	1.000 *	0.594 *	46	(SO)
14.	14	11	0.999	1.000 *	0.818 *	21	(15)
25.	25	11	0.999	1.000 *	0.818 *	21	(15)
28.	28	11	0.999	0.999 *	0.828 *	21	(15)
47.	47	11	0.999	1.000 ■	0.818 *	21	(15)
21.	21	15	1.000	1.000 *	0.917 *	29	(SO)
42.	42	15	1.000	1.000 *	0.917 *	29	(SO)
29.	29	SI			0.917 *	21	(15)
58.	56	SI			0.887 *	21	(15)
36.	36	17	1.000	1.000 *	0.853 *	21	(15)
53.	53	17	1.000	1.000 *	0.853 *	21	(15)
63.	63	17	1.000	1.000 *	0.853 *	21	(15)
15.	1 15	12	1.000	1.000 *	0.753 *	36	(17)
40.	140	12	1.000	1.000 *	0.753 *	36	(17)
55.	155	12	1.000	1.000 *	0.753 *	36	(17)
18.	18	13	1.000	1.000 *	0.514 *	3	(2)
27.	27	13	1.000	1.000 *	0.514 *	3	(2)
43.	43	13	1.000	1.000 *	0.514 *	3	(2)
20.	20	14	1.000	1.000 *	0.969 *	52	(SO)
34.	34	14	1.000	1.000 *	0.969 *	52	(SI)
52.	52	SI			0.969 *	20	(14)
23.	23	SI			0.463 *	36	(17)
30.	30	SI			0.551 *	9	(7)
46.	46	SI			0.653 ■	2	(SO)
48.	48	18	1.000	1.000 ■	0.434 *	30	(SO)
59.	59	18	1.000	1.000 *	0.434 *	30	(SO)
71.	71	18	1.000	1.000 *	0.434 *	30	(SO)
49.	49	SI			0.587 ■	44	(SO)
54.	54	SI			0.382 *	70	(SO)
65.	65	SI			0.576 *	8	(6)
66.	66	19	1.000	1.000 *	0.430 *	6	(5)
75.	75	19	1.000	1.000 *	0.430 *	6	(5)
70.	70	SI			0.423 *	15	(12)

PHENOTYPES IN 118990/ TAXONAL DIVERSITY INDEX - 0.344		Identity (eval) - 0.75 TRUE DIVERSITY INDEX - 0.944					
No	Nama	Phy- lipo	mln	mean	£	n°r	Phy type
1	ENTEROBACTER AERO	Si			0.949 *	16	<12)
16	16	12	1.000	1.000 ■	0.949 *	1	(Si)
64	64	12	1.000	1.000 *	0.949 ■	1	(Si)
34	34	Si			0.814 *	16	(12)
2	STREPTOCO FAE	1	1.000	1.000 ■	0.953 ■	12	(Si)
51	51	1	1.000	1.000 *	0.953 *	12	(Si)
71	71	1	1.000	1.000 *	0.953 ■	12	(Si)
12	12	Si			0.953 *	2	(1)
80	79	Si			0.953 *	2	<1>
77	77	Si			0.953 *	2	(1)
56	! 56	Si			0.854 ■	80	(SO)
38	38	Si			0.775 *	77	(SO)
3	PROTEUS MIRA	2	1.000	1.000 *	0.737 *	49	(SO)
27	27	2	1.000	1.000 *	0.737 *	49	(Si)
4	HBACILLUS	3	1.000	1.000 *	0.000 *	49	(Si)
8	HMICROCO SP	3	1.000	1.000 *	0.000 *	3	(2)
17	11 17	3	1.000	1.000 *	0.000 *	1	(Si)
18	11 18	3	1.000	1.000 *	0.000 *	1	(SO)
24	11 24	3	1.000	1.000 *	0.000 ■	46	07)
25	11 25	3	1.000	1.000 *	0.000 *	46	(17)
28	11 28	3	1.000	1.000 *	0.000 *	49	(SO)
31	1131	3	1.000	1.000 *	0.000 *	22	(Si)
32	hCONTROL	3	1.000	1.000 ■	0.000 ■	28	(SO)
37	11 37	3	1.000	1.000 *	0.000 *	22	(SO)
42	11 42	3	1.000	1.000 *	0.000 ■	68	(Si)
48	11 48	3	1.000	1.000 *	0.000 *	12	(SO)
50	11 50	3	1.000	1.000 ■	0.000 *	3	(2)
58	11 58	3	1.000	1.000 *	0.000 *	6	(5)
65	11 65	3	1.000	1.000 *	0.000 *	1	(Si)
72	11 72	3	1.000	1.000 *	0.000 ■	12	(SO)
74	11 74	3	1.000	1.000 *	0.000 *	49	(Si)
81	hCONTROL	3	1.000	1.000 *	0.000 *	2	(1)
5	PSEUDO AEROG	4	1.000	1.000 *	0.919 *	19	(SO)
9	9	4	1.000	1.000 *	0.919 *	19	(Si)
63	63	4	1.000	1.000 *	0.919 *	19	(SO)
19	19	Si			0.919 *	5	(4)
29	29	Si			0.786 *	5	(4)
6	E COLI	5	1.000	1.000 *	0.653 *	46	(17)
23	23	5	1.000	1.000 *	0.653 *	46	(17)
45	45	5	1.000	1.000 *	0.653 *	46	(17)
7	SERRA MARC	6	1.000	1.000 *	0.614 *	3	(2)
61	61	6	1.000	1.000 *	0.614 *	3	(2)
10	10	7	1.000	1.000 ■	0.693 *	35	-(Si)
39	39	7	1.000	1.000 *	0.693 *	35	(SO)
11	* 11	8	1.000	1.000 *	0.826 *	26	(Si)
72	72	8	1.000	1.000 *	0.826 *	26	(SO)
26	26	Si			0.826 *	11	(8)
13	13	9	1.000	1.000 *	0.594 *	46	07)
59	59	9	1.000	1.000 *	0.594 *	46	07)
14	14	10	1.000	1.000 *	0.690 *	12	(Si)
47	47	10	1.000	1.000 *	0.690 *	12	(Si)
67	67	10	1.000	1.000 *	0.690 *	12	(Si)
15	15	11	1.000	1.000 *	0.690 *	76	(so)
70	70	11	1.000	1.000 *	0.690 *	76	(Si)
20	20	13	1.000	1.000 *	0.892 *	40	(Si)
54	54	13	1.000	1.000 *	0.892 *	40	(Si)
40	40	Si			0.892 *	20	(13)
21	21	Si			0.544 *	15	01)
22	22	Si			0.925 *	36	(16)
36	36	18	0.995	0.995 *	0.925 *	22	(Si)
75	75	16	0.995	0.995 *	0.917 *	22	(Si)
30	30	14	1.000	1.000 *	0.853 *	22	(Si)
52	52	14	1.000	1.000 *	0.053 *	22	(SO)
69	69	14	1.000	1.000 *	0.853 ■	22	(Si)
33	33	15	1.000	1.000 *	0.912 *	53	(Si)
43	43	15	1.000	1.000 *	0.912 *	53	(Si)
53	53	Si			0.912 *	33	(15)
55	1 55	Si			0.755 *	30	(14)
35	35	Si			0.909 *	60	(SO)
60	68	Si			0.909 *	35	(Si)
41	41	Si			0.505 *	60	(SO)
44	44	Si			0.431 *	55	(Si)
48	48	17	1.000	1.000 *	0.653 *	6	(5)
57	57	17	1.000	1.000 *	0.653 *	6	(5)
49	1 49	Si			0.737 *	3	(2)
60	1 60	Si			0.529 *	40	(Si)
62	62	18	1.000	1.000 *	0.471 *	5	(-)
78	78	18	1.000	1.000 ■	0.471 *	5	(4)
66	65	19	1.000	1.000 *	0.575 *	49	(Si)
73	73	19	1.000	1.000 *	0.575 *	49	(SO)
76	76	Si			0.699 *	11	<B)

33

PHENOTYPES IN BIOGAS/IGORUV
CALCULATED DIVERSITY INDEX - 0.858 TRUE DIVERSITY INDEX - 0.959

IOVGR-O.B7S

No	Name	PhP-type	mim mean	max	lo nr	PhP type
1	SERRAIA MER	SI		0.614 ■	7	(S)
2	STREPTOCO FAE	SI	0.990	0.997 *	0.769 *	56 (SI)
23	23	1	0.990	0.997 *	0.769 *	56 (SI)
66	66	1	0.990	0.997 *	0.769 *	56 (SO)
78	78	1	0.990	0.990 *	0.724 *	56 (SO)
56	56	SI		0.769 *	2	(I)
3	I BACILLUS	2	1.000	1.000 *	0.000 ■	56 (so)
5	IMMICROCO SP	2	1.000	1.000 *	0.000 *	25 (SO)
14	1114	2	1.000	1.000 *	0.000 *	25 (so)
18	11 19	2	1.000	1.000 *	0.000 *	11 (SO)
24	1124	2	1.000	1.000 *	0.000 *	56 (SI)
33	I 33	2	1.000	1.000 *	0.000 *	22 (12)
40	ICONTROL	2	1.000	1.000 *	0.000 *	16 (0)
41	1141	2	1.000	1.000 *	0.000 *	16 (S)
46	II 46	2	1.000	1.000 *	0.000 *	57 (SO)
49	II 49	2	1.000	1.000 *	0.000 *	25 (SO)
52	II 52	2	1.000	1.000 *	0.000 *	21 (11)
58	II 55	2	1.000	1.000 *	0.000 *	43 (SO)
67	II 67	2	1.000	1.000 *	0.000 *	56 (SO)
80	ICONTROL	2	1.000	1.000 ■	0.000 *	1 (so)
4	E COU	3	1.000	1.000 *	0.924 *	25 (so)
13	13	3	1.000	1.000 *	0.924 *	25 (SO)
40	48	3	1.000	1.000 *	0.924 *	25 (SO)
25	25	SI		0.924 ■	4	(S)
73	73	SI		0.923 *	4	(S)
6	PSEUDO AEROG	4	1.000	1.000 *	0.786 *	50 (so)
15	15	4	1.000	1.000 *	0.786 *	50 (SO)
44	44	4	1.000	1.000 *	0.766 *	50 (so)
50	50	SI		0.786 *	6	(so)
7	PROTEUS MIRA	5	1.000	1.000 *	0.614 *	1 (so)
9	9	5	1.000	1.000 *	0.614 ■	1 (SO)
29	29	5	1.000	1.000 ■	0.614 *	1 (SO)
79	79	5	1.000	1.000 *	0.614 ■	1 (SO)
8	ENTEROBACTER AERO	SI		0.949 *	43	(SO)
43	43	SI		0.949 *	8	(SO)
62	62	SI		0.878 *	43	(SO)
54	54	SI		0.874 ■	43	(so)
10	10	6	1.000	1.000 *	0.604 ■	2 (1)
30	30	6	1.000	1.000 *	0.604 *	2 (1)
63	63	6	1.000	1.000 *	0.604 *	2 (1)
11	11	SI		0.917 *	28	(SO)
28	28	SI		0.917 *	11	(SO)
42	42	13	1.000	1.000 *	0.818 ■	11 (SO)
61	61	13	1.000	1.000 *	0.818 *	11 (SO)
68	68	13	1.000	1.000 ■	0.818 *	11 (SO)
18	18	SI		0.853 *	11	(SO)
57	1 57	SI		0.753 *	18	(SO)
12	12	7	1.000	1.000 *	0.551 *	21 (11)
38	38	7	1.000	1.000 ■	0.551 *	21 (11)
51	51	7	1.000	1.000 *	0.551 *	21 (11)
16	16	8	0.992	0.992 *	0.826 *	39 (SO)
26	26	8	0.992	0.992 ■	0.809 *	39 (SO)
39	39	SI		0.826 *	16	(S)
17	17	9	1.000	1.000 *	0.893 *	74 (SO)
27	27	9	1.000	1.000 *	0.893 *	74 (SO)
35	35	9	1.000	1.000 *	0.893 *	74 (SO)
74	74	SI		0.893 *	17	(9)
20	20	10	1.000	1.000 *	0.905 *	34 (SO)
65	65	10	1.000	1.000 ■	0.905 *	34 (SO)
34	34	SI		0.905 *	20	(10)
21	21	11	1.000	1.000 *	0.592 *	34 (Si)
31	31	11	1.000	1.000 *	0.592 *	34 (SO)
22	22	12	1.000	1.000 *	0.933 *	32 (SO)
60	60	12	1.000	1.000 *	0.933 *	32 (SO)
32	32	SI		0.933 *	22	(12)
37	37	SI		0.933 *	22	(12)
36	1 36	SI		0.612 *	50	(SO)
45	45	14	1.000	1.000 *	0.433 *	57 (SO)
71	71	14	1.000	1.000 *	0.433 *	57 (SO)
47	47	SI		0.945 *	53	(SO)
53	53	SI		0.959 *	70	(SO)
70	70	SI		0.959 *	53	(SO)
58	1 58	SI		0.508 *	21	(11)
59	59	15	1.000	1.000 *	0.658 *	75 (SO)
72	72	15	1.000	1.000 ■	0.658 *	75 (SI)
64	1 64	SI		0.529 *	21	(11)
69	69	SI		0.729 *	25	(SI)
75	75	SI		0.658 *	59	(15)
76	76	SI		0.711 *	54	(SI)
77	77	SI		0.682 *	22	(12)

PHENOTYPES in ardce31/ **Appendix 5. a**

*CALCULATED DIVERSITY INDEX - 0.992 Identily level + 0.978 TRUE DIVERSITY INDEX - 0.992

No	Na	PhP- sim	sim	to	PhP	
		typo min mean	max	nr	typo	
1.	ECOLI	1	1.000	1.000 *	0.938 *	23 (Si)
46.	46	1	1.000	1.000 *	0.938 *	23 (Si)
23.	23	SI			0.938 *	1 (1)
26.	26	14	1.000	1.000 *	0.938 *	1 (1)
31.	31	14	1.000	1.000 ■	0.936 *	1 (1)
11.	11	10	1.000	1.000 *	0.922 *	20 (SO)
32.	32	10	1.000	1.000 *	0.922 *	20 (Si)
20.	20	SI			0.922 *	11 (10)
10.	10	9	0.989	0.989 *	0.926 *	63 (15)
61.	61	9	0.989	0.989 *	0.900 *	56 (17)
12.	12	SI			0.893 *	10 (9)
28.	28	15	0.990	0.990 *	0.889 *	56 (17)
63.	63	15	0.990	0.990 *	0.926 *	10 (9)
58.	58	SI			0.897 *	63 (15)
69.	69	SI			0.817 *	58 (Si)
2.	PSEUDO CEP	2	1.000	1.000 *	0.834 *	6 (6)
77.	77	2	1.000	1.000 *	0.834 ■	6 (6)
52.	52	SI			0.816 *	2 (2)
6.	PSEUDO FLUORE	6	1.000	1.000 *	0.910 *	21 (SO)
45.	45	6	1.000	1.000 *	0.910 *	21 (Si)
15.	15	SI			0.954 *	21 (SO)
21.	21	SI			0.954 *	15 (SO)
43.	43	SI			0.846 *	21 (Si)
4.	PSEUDO AERO	4	1.000	1.000 *	0.903 *	74 (Si)
65.	65	4	1.000	1.000 *	0.903 *	74 (SO)
74.	74	SI			0.903 *	4 (4)
67.	67	SI			0.896 *	4 (4)
71.	71	SI			0.896 *	4 (4)
25.	25	13	1.000	1.000 *	0.910 *	73 (Si)
70.	70	13	1.000	1.000 *	0.910 *	73 (Si)
73.	73	SI			0.910 *	25 (13)
79.	79	SI			0.910 *	25 (13)
9.	BACILLUS	SI			0.888 *	22 (Si)
18.	18	SI			0.882 *	9 (SO)
24.	CONTROL	SI			0.956 *	80 (17)
56.	CONTROL	17	0.979	0.979 *	0.934 *	24 (SO)
80.	CONTROL	17	0.979	0.979 *	0.956 *	24 (Si)
59.	59	SI			0.912 *	24 (Si)
30.	30	SI			0.882 *	9 (SO)
22.	22	SI			0.904 *	44 (Si)
44.	44	SI			0.904 *	22 (Si)
49.	49	SI			0.834 *	44 (SO)
51.	51	16	1.000	1.000 ■	0.817 *	67 (Si)
64.	64	16	1.000	1.000 *	0.817 *	67 (SO)
3.	KLEBSIELLA	3	1.000	1.000 *	0.919 *	50 (SO)
47.	47	3	1.000	1.000 *	0.919 *	50 (Si)
50.	50	SI			0.919 *	3 (3)
54.	54	SI			0.917 *	3 (3)
8.	ENTEROBACTER CLOA	8	1.000	1.000 *	0.892 *	16 (Si)
35.	35	8	1.000	1.000 *	0.892 *	16 (SO)
16.	16	SI			0.892 *	8 (8)
39.	39	Sf			0.891 / *	8 (0)
17.	17	12	1.000	1.000 *	0.841 *	60 (Si)
55.	55	12	1.000	1.000 *	0.841 *	60 (SO)
27.	27	Sf			0.936 *	33 (Si)
33.	33	SI			0.936 *	27 (SO)
37.	37	SI			0.927 *	27 (SO)
75.	75	SI			0.911 *	37 (SO)
40.	40	SI			0.950 *	60 (Si)
60.	60	SI			0.950 *	40 (Si)
53.	53	SI			0.927 *	40 (Si)
48.	48	SI			0.927 *	40 (Si)
41.	41	SI			0.927 *	40 (Si)
42.	42	SI			0.888 *	37 (SO)
5.	STREPTOCO FAE	5	1.000	1.000 *	0.957 *	36 (Si)
29.	29	5	1.000	1.000 *	0.957 *	36 (SO)
36.	36	SI			0.957 *	5 (5)
62.	62	SI			0.957 *	5 (5)
13.	13	11	1.000	1.000 *	0.866 *	62 (Si)
68.	68	11	1.000	1.000 *	0.866 *	62 (Si)
7.	KLEBSIELLA PNEU	7	1.000	1.000 *	0.681 *	39 (Si)
19.	19	7	1.000	1.000 *	0.681 *	39 (SO)
34.	34	7	1.000	1.000 *	0.681 *	39 (Si)
38.	38	7	1.000	1.000 *	0.881 *	39 (Si)
14.	14	SI			0.732 *	40 (SO)
57.	57	SI			0.594 *	42 (SO)
66.	66	18	1.000	1.000 ■	0.664 *	43 (Si)
76.	76	18	1.000	1.000 ■	0.664 *	43 (Si)
72.	72	19	1.000	1.000 ■	0.672 *	59 (SO)
78.	78	19	1.000	1.000 *	0.672 ■	59 (Si)

Appendix 6b

PHENOTYPES In a'dec2/ CALCULATED DIVERSITY INDEX - 6.992		Identity level = 0.075 TRUE DIVERSITY INDEX - 0.992		sim	lo	PhP
No Name	PhP - sim type mln	sim mean	sim max	nr	nr	type
1	BACILLUS	1	1.000	1.000 *	0.903 *	70 (SI)
66. 66		1	1.000	1.000 *	0.903 *	70 (SI)
70. 70		SI			0.903 *	1 (1)
40. CONTROL		SI			0.965 *	80 (SI)
80. CONTROL		SI			0.965 *	40 (SI)
56. 56		SI			0.874 *	40 (SI)
66. 68		SI			0.882 *	1 (1)
46. 46		SI			0.810 *	50 (12)
50. 50		12	1.000	1.000 *	0.910 *	46 (SI)
55. 55		12	1.000	1.000 *	0.910 *	46 (SI)
60. 60		SI			0.910 *	46 (SI)
2. CAMPYLOBACTER		SI			0.905 *	35 (SO)
35. 35		SI			0.905 *	2 (SO)
20. 20		SI			0.902 *	2 (SO)
37. 37		SI			0.902 *	2 (SO)
6. PSEUDO AEROG		5	1.000	1.000 *	0.903 *	13 (10)
31. 31		5	1.000	1.000 *	0.903 *	13 (10)
13. 13		10	1.000	1.000 *	0.903 *	6 (5)
27. 27		10	1.000	1.000 *	0.903 *	6 (5)
7. PSEUDO CAV		6	1.000	1.000 *	0.928 *	9 (SO)
25. 25		6	1.000	1.000 *	0.928 *	9 (SO)
9. 9		SI			0.928 *	7 (6)
19. 19		SI			0.927 *	7 (6)
16. 16		SI			0.942 *	69 (13)
69. 69		13	1.000	1.000 *	0.942 *	16 (SO)
73. 73		13	1.000	1.000 *	0.942 *	16 (SO)
79. 79		SI			0.893 *	69 (13)
4. FLAVOBAC AQUA		3	1.000	1.000 *	0.919 *	51 (SO)
42. 42		3	1.000	1.000 *	0.919 *	51 (SO)
48. 48		3	1.000	1.000 *	0.919 *	51 (SO)
51. 51		SI			0.919 *	4 (3)
61. 61		SI			0.919 *	4 (3)
54. 54		SI			0.908 *	51 (SO)
5. PROTEUS VULG		4	1.000	1.000 *	0.932 *	65 (SO)
59. 59		4	1.000	1.000 *	0.932 *	65 (SO)
72. 72		4	1.000	1.000 *	0.932 *	65 (SO)
65. 65		SI			0.932 *	5 (4)
44. 44		SI			0.899 *	65 (SO)
58. 58		SI			0.845 *	62 (SO)
62. 62		SI			0.873 *	5 (4)
52. 52		SI			0.779 *	58 (SO)
3. ECOU		2	1.000	1.000 *	0.939 *	21 (SO)
64. 64		2	1.000	1.000 *	0.939 *	21 (SO)
21. 21		SI			0.939 *	3 (2)
39. 39		SI			0.939 *	3 (2)
12. 12		SI			0.938 *	3 (2)
18. 18		SI			0.938 *	3 (2)
14. 14		SI			0.938 *	3 (2)
23. 23		SI			0.792 *	39 (SO)
10. 10		6	1.000	1.000 *	0.845 *	30 (SO)
28. 28		8	1.000	1.000 *	0.845 *	30 (SO)
30. 30		SI			0.845 *	10 (8)
38. 38		SI			0.845 *	10 (8)
43. 43		11	1.000	1.000 *	0.954 *	71 (SO)
45. 45		11	1.000	1.000 *	0.954 *	71 (SO)
71. 71		SI			0.954 *	43 (11)
11. 11		9	0.986	0.986 *	0.821 *	41 (SO)
29. 29		9	0.986	0.993 *	0.765 *	47 (SO)
36. 36		9	0.986	0.993 *	0.765 *	47 (SO)
41. 41		SI			0.951 *	47 (SO)
47. 47		SI			0.951 *	41 (SO)
17. 17		SI			0.834 *	49 (SI)
49. 49		SI			0.834 *	17 (SI)
24. 24		SI			0.816 *	49 (SI)
34. 34		SI			0.785 *	56 (SO)
8. STREPTOCO FAE		7	1.000	1.000 *	0.959 *	63 (SI)
22. 22		7	1.000	1.000 *	0.959 *	63 (SO)
26. 26		7	1.000	1.000 *	0.959 *	63 (SI)
57. 57		7	1.000	1.000 *	0.959 *	63 (SO)
63. 63		SI			0.959 *	8 (7)
15. 15		SI			0.957 *	8 (7)
32. 32		SI			0.957 *	8 (7)
67. 67		SI			0.957 *	8 (7)
76. 76		SI			0.958 *	8 (7)
53. 53		SI			0.891 *	78 (SI)
78. 78		SI			0.891 *	53 (SI)
74. 74		SI			0.875 *	53 (SI)
33. 33		SI			0.751 *	38 (SO)
75. 75		14	0.998	0.998 *	0.664 *	34 (SO)
77. 77		14	0.998	0.998 *	0.662 *	56 (SO)

PHENOTYPES in α = deg33/ CALCULATED DIVERSITY INDEX \Rightarrow 0.909		kJOnly level α 0.975 TRUE DIVERSITY INDEX \blacksquare 0.989		\Rightarrow e			
No	Name	PhP- lyp α	im min	aim mean	sim	lo nr	PhP yp*
1.	BACILLUS	1	0.996	0.998 *	0.093 *	57	(SI)
17		1	0.996	0.998 *	0.893 *	57	(SI)
62.	62	1	0.996	0.996 *	0.095 *	57	(SI)
57	57	SI			0.895 *	62	(1)
51	51	SI			0.892 *	62	(1)
24.	24	SI			0.910 *	33	(SO)
33.	33	SI			0.910 *	24	(SI)
56.	56	SI			0.910 *	21	(SI)
4.	MICROCO SP	4	1.000	1.000 *	0.920 *	81	(SI)
23.	23	4	1.000	1.000 *	0.920 *	81	(SI)
16.	CONTROL	SI			0.959 *	81	(SI)
81.	CONTROL	SI			0.959 *	16	(SI)
25.	25	SI			0.944 *	28	(SI)
2a.	28	SI			0.944 *	25	(SI)
44.	44	SI			0.927 *	25	(SO)
10.	PSEUDO AEROG	9	1.000	1.000 *	0.903 *	55	(SO)
37.	37	9	1.000	1.000 *	0.903 *	55	(SO)
55.	55	SI			0.903 *	10	(9)
71.	71	SI			0.896 *	10	(9)
13.	13	11	1.000	1.000 *	0.905 *	77	(SI)
64.	64	11	1.000	1.000 *	0.905 *	77	(SI)
77.	77	SI			0.905 *	13	(11)
2.	ECOU	2	1.000	1.000 \square	0.945 \square	69	(SO)
20.	20	2	1.000	1.000 *	0.945 *	69	(SI)
69.	69	SI			0.945 *	2	(2)
12.	12	SI			0.938 *	2	(2)
74.	74	SI			0.938 *	2	(2)
53.	53	SI			-0.938 *	2	(2)
31.	31	SI			0.938 *	2	(2)
34.	34	14	1.000	1.000 *	0.938 *	2	(2)
59.	59	14	1.000	1.000 *	0.938 *	2	(2)
79.	79	SI			0.891 *	80	(SO)
80.	79	SI			0.891 *	79	(SO)
3.	FLAVOBACTER	3	0.992	0.996 \blacksquare	0.841 *	22	(12)
49.	49	3	0.992	0.996 *	0.841 *	22	(12)
14	14	3	0.992	0.992 *	0.822 *	40	(12)
5.	PROTEUS VULG	5	1.000	1.000 *	0.935 *	58	(SI)
46.	48	5	1.000	1.000 \square	0.935 *	58	(80)
21.	21	SI			0.968 *	58	(SO)
53.	58	SI			0.968 *	21	(SI)
11.	11	10	1.000	1.000 *	0.895 *	19	(13)
26.	26	10	1.000	1.000 *	0.895 *	19	(13)
- 15.	15	12	0.994	0.996 *	0.953 *	19	(13)
22.	22	12	0.997	0.997 *	0.950 *	19	(13)
40.	40	12	0.994	0.996 *	0.941 *	19	(13)
19.	19	13	0.990	0.995 *	0.953 *	15	(12)
36.	36	13	0.990	0.995 *	0.953 *	15	(12)
30.	30	13	0.990	0.990 *	0.945 *	15	(12)
9.	9	8	1.000	1.000 *	0.932 *	21	(SI)
18.	18	8	1.000	1.000 *	0.932 *	21	(80)
6.	SALMONELLA PARA	6	0.988	0.991 *	0.941 *	65	(SO)
54.	54	6	0.988	0.991 *	0.941 *	65	(SI)
8.	SALMONELLA TYPH	Q	0.988	0.991 *	0.952 *	65	(SO)
39.	39	6	0.986	0.991 *	0.952 *	65	(SI)
65.	65	SI			0.952 *	8	(6)
60.	60	SI			0.940 *	6	(8)
27.	27	SI			0.937 *	8	(6)
29.	29	SI			0.947 *	35	(SI)
35.	35	SI			0.947 *	29	(SO)
42.	42	SI			0.800 *	15	(12)
7.	STREPTOCO FAE	7	1.000	1.000 *	0.958 \blacksquare	63	(SO)
50.	50	7	1.000	1.000 *	0.958 *	63	(SO)
76.	76	7	1.000	1.000 *	0.958 *	63	(SO)
38.	38	SI			0.957 *	7	(7)
67.	67	SI			0.957 *	7	(7)
70.	70	SI			0.957 *	7	(7)
63.	63	SI			0.958 *	7	(7)
43.	43	16	1.000	1.000 *	0.866 *	67	(SI)
66.	66	16	1.000	1.000 *	0.868 *	67	(SI)
32.	32	SI			0.575 *	65	(SI)
41.	41	15	1.000	1.000 *	0.705 *	51	(SO)
47.	47	15	1.000	1.000 *	0.705 *	51	(SI)
45.	45	SI			0.899 *	75	(SI)
75.	75	SI			0.899 *	45	(SI)
72.	72	SI			0.896 *	45	(SI)
52.	52	18	1.000	1.000 *	0.834 *	81	(19)
68.	68	18	1.000	1.000 *	0.834 *	81	(10)
61.	61	19	1.000	1.000 *	0.834 *	52	(18)
78.	78	19	1.000	1.000 *	0.834 *	52	(18)
48.	48	17	1.000	1.000 *	0.723 *	38	(SO)
73.	73	17	1.000	1.000 *	0.723 *	38	(SI)

PHENOTYPES in arcs4/		Appetit-III				Identity level - 0.978	
CALCULATED DIVERSITY INDEX - 0.993 TRUE DIVERSITY INDEX - 0.993		PhP- jyp	sun	sim mean	max	to nr	PhP type
1	CORYNEBACTERIUM	1	0.938	0.993 *	0.910 *	18	(SI)
45	45	1	0.986	0.993 *	0.910 *	18	(SI)
40	40	i	0.986	0.986 *	0.905 *	18	(SI)
18	18	Si			0.910 *	1	(1)
24	24	SI			0.910 *	1	(1)
8	PSEUDO AEROG	5	1.000	1.000 *	0.903 *	52	(SI)
43	43	5	1.000	1.000 *	0.903 *	52	(SI)
52	52	Si			0.903 *	8	(5)
26	28	SI			0.896 *	8	(5)
3	FLAVOBACTERIUM	Si			0.925 *	38	(SI)
38	38	Si			0.925 *	3	(SI)
16	16	SI			0.919 *	3	(SI)
15	15	SI			0.896 *	8	(5)
65	65	17	1.000	1.000 *	0.905 *	59	(SI)
75	73	17	1.000	1.000 *	0.905 *	59	(SI)
59	59	Si			0.907 *	77	(SI)
77	75	Si			0.907 *	59	(SI)
11	11	6	1.000	1.000 *	0.812 *	62	(14)
35	35	6	1.000	1.000 *	0.812 *	62	(14)
32	CONTROL	10	0.982	0.982 *	0.938 *	51	(13)
82	CONTROL	10	0.982	0.982 *	0.898 *	51	(13)
51	51	13	1.000	1.000 *	0.938 *	32	(10)
57	57	13	1.000	1.000 *	0.938 *	32	(10)
80	78	13	1.000	1.000 *	0.938 *	32	(10)
64	64	16	1.000	1.000 *	0.888 *	32	(10)
74	72	16	1.000	1.000 *	0.888 *	32	(10)
42	42	SI			0.842 *	62	(14)
62	62	14	1.000	1.000 *	0.890 *	51	(13)
72	70	14	1.000	1.000 *	0.890 *	51	(13)
2	EDWARDSIEL	Si			0.935 *	30	(SI)
30	30	Si			0.935 *	2	(SO)
19	19	Si			0.920 *	2	(SO)
25	25	Si			0.920 *	2	(SO)
7	PROTEUS MIRA	SI			0.932 *	50	(SO)
50	50	SI			0.932 *	7	(SO)
67	65	Si			0.932 *	7	(SO)
6	MICROCO SP	4	1.000	1.000 *	0.894 *	55	(SO)
66	64	4	1.000	1.000 *	0.894 *	55	(SO)
81	79	4	1.000	1.000 *	0.894 *	55	(SO)
55	55	SI			0.894 *	6	(4)
49	49	SI			0.893 *	6	(4)
79	77	SI			0.862 *	6	(4)
4	ECOU	2	1.000	1.000 *	0.945 *	41	(SO)
61	61	2	1.000	1.000 *	0.945 *	41	(SO)
41	41	SI			0.945 *	4	(2)
12	12	SI			0.938 *	4	(2)
54	54	SI			0.939 *	4	(2)
71	69	SI			0.939 *	4	(2)
46	46	SI			0.938 *	4	(2)
37	37	SI			0.938 *	4	(2)
13	13	SI			0.821 *	70	(12)
44	44	12	0.986	0.986 *	0.927 *	47	(SI)
70	68	12	0.986	0.986 *	0.897 *	47	(SI)
47	47	SI			0.937 *	44	(12)
14	14	SI			0.950 *	21	(8)
21	21	8	1.000	1.000 *	0.950 *	14	(SO)
31	31	8	1.000	1.000 *	0.950 *	14	(SO)
17	17	7	0.997	0.997 *	0.895 *	14	(SI)
36	36	7	0.907	0.997 *	0.002 *	14	(SI)
58	58	Si			0.935 *	78	(SI)
78	76	SI			0.935 *	58	(SI)
63	63	15	1.000	1.000 *	0.932 *	58	(SO)
73	71	15	1.000	1.000 *	0.932 *	58	(SO)
39	39	11	0.993	0.993 *	0.791 *	21	(8)
53	53	11	0.993	0.993 *	0.789 *	62	(14)
23	23	SI			0.915 *	27	(SI)
27	27	SI			0.915 *	23	(SO)
5	KLEBSIELLA PNEU	3	1.000	1.000 *	0.719 *	56	(SO)
34	34	3	1.000	1.000 *	0.719 *	56	(SI)
9	STREPTOCO FAE	SI			0.958 *	20	(SO)
20	20	SI			0.958 *	9	(SO)
22	22	SI			0.957 *	9	(SO)
78	74	SI			0.793 *	9	(SI)
10	PSEUDO FLOURE	SI			0.834 *	29	(9)
29	29	9	1.000	1.000 *	0.834 *	10	(SO)
60	60	9	1.000	1.000 *	0.834 *	10	(SI)
68	66	SI			0.816 *	29	(9)
56	56	SI			0.803 *	29	(9)
28	28	SI			0.646 *	54	(SI)
33	33	SI			0.593 *	47	(SO)
48	48	SI			0.864 *	69	(SO)
69	67	SI			0.864 *	48	(SO)

Appendix 6

PHENOTYPES in ardee35/
"CALCULATED DIVERSITY INDEX = 0.894 Identity level = 0.975
TRUE DIVERSITY INDEX = 0.994

No	Name	PhP- type	sim min	sim mean	sim max	10	PhP type
1	**CORYNEBAC DIPH	SI			0.000 ■	(S)	
2	PSEUDO FLUORE	1	1.000	1.000 *	0.820 *	75	(S)
64	63	1	1.000	1.000 *	0.820 *	75	(S)
78	77	1	1.000	1.000 ■	0.820 *	75	(S)
75	74	SI			0.820 *	2	(D)
26	25	SI			0.776 *	45	(S)
67	66	SI			0.832 *	81	(S)
49	48	2	1.000	1.000 ■	0.920 *	14	(S)
3-	ECHWARDSIEL	2	1.000	1.000 ■	0.920 *	14	(S)
14	13	SI			0.920 *	3	(2)
55	54	SI			0.920 *	3	(2)
6	PROTEUS MIRA	5	1.000	1.000 *	0.934 *	74	(S)
51	50	5	1.000	1.000 *	0.934 *	74	(S)
74	73	SI			0.934 *	6	(S)
79	78	SI			0.931 *	6	(S)
56	55	SI			0.932 *	6	(S)
69	68	SI			0.932 ■	6	(S)
58	57	SI			0.888 *	62	(S)
43	42	SI			0.891 *	62	(S)
62	CONTROL	SI			0.943 ■	81	(S)
81	CONTROL	SI			0.943 *	62	(S)
80	79	SI			0.883 ■	43	(S)
48	47	SI			0.894 ■	81	(S)
72	71	SI			0.853 *	80	(S)
53	52	SI			0.842 *	80	(S)
59	58	SI			0.785 *	68	(S)
68	67	SI			0.842 *	77	(S)
77	76	SI			0.842 *	68	(S)
12	11	SI			0.954 *	28	(S)
28	27	SI			0.954 *	12	(S)
24	23	SI			0.910 *	12	(S)
7	SERRA MARC	SI			0.937 *	21	(S)
21	20	SI			0.937 ■	7	(S)
13	12	SI			0.935 *	7	(S)
IQ-	AEROMON HYDRO	7	1.000	1.000 *	0.895 *	18	(9)
30	29	7	1.000	1.000 *	0.895 *	18	(9)
18	17	9	1.000	1.000 *	0.950 *	36	(S)
25	24	9	1.000	1.000 ■	0.950 *	36	(S)
36	35	SI			0.950 *	18	(9)
44	43	SI			0.932 *	47	(S)
47	46	SI			0.932 *	44	(S)
4	ECOLI	3	1.000	1.000 *	0.938 *	32	(S)
27	26	3	1.000	1.000 *	0.938 *	32	(S)
54	53	3	1.000	1.000 *	0.938 ■	32	(S)
32	31	SI			0.938 *	4	(3)
41	40	12	1.000	1.000 *	0.938 *	4	(3)
61	60	12	1.000	1.000 *	0.938 *	4	(3)
71	70	SI			0.938 *	4	(3)
16	15	SI			0.791 *	36	(S)
20	19	SI			0.905 *	50	(S)
34	33	SI			0.910 *	50	(S)
50	49	SI			0.910 *	34	(S)
57	56	SI			0.910 *	50	(S)
45	44	SI			0.903 *	65	(S)
65	64	SI			0.903 *	45	(S)
52	51	SI			0.896 *	45	(S)
63	62	SI			0.915 *	65	(S)
hifi	65	SI			0.915 *	(VI)	(S)
73	72	SI			0.915 *	63	(S)
31	30	SI			0.811 *	62	(S)
37	36	SI			0.787 *	80	(S)
5	STREPTOCO FAE	4	1.000	1.000 ■	0.957 *	39	(11)
29	28	4	1.000	1.000 *	0.957 *	39	(11)
39	38	11	1.000	1.000 *	0.957 *	5	(4)
76	75	11	1.000	1.000 *	0.957 *	5	(4)
60	59	SI			0.957 *	5	(4)
70	69	SI			0.957 *	5	(4)
11	10	SI			0.930 *	33	(S)
33	32	SI			0.930 *	11	(S)
22	21	SI			0.948 *	39	(11)
8	KLEBSIELLA PNEU	6	1.000	1.000 *	0.666 *	66	(S)
15	14	6	1.000	1.000 *	0.666 *	66	(S)
23	22	6	1.000	1.000 *	0.666 *	66	(S)
9	AEROMON HYDRO	SI			0.638 *	21	(S)
17	16	8	1.000	1.000 *	0.723 *	60	(S)
38	37	8	1.000	1.000 *	0.723 *	60	(S)
19	18	10	1.000	1.000 *	0.654 *	67	(S)
35	34	10	1.000	1.000 *	0.654 *	67	(S)
40	39	SI			0.689 *	47	(S)
42	41	SI			0.672 *	13	(S)
46	45	SI			0.287 *	24	(S)

Appendix

	PhP- type	aim min	sim mean	sim max	to nr	type
11MICROCO SP	1	1.000	1.000	0.000 *	58	(S)
(ICORYNEBAC SP	1	1.000	1.000 ■	0.000 *	55	(7)
	1	1.000	1.000 †	0.000 *	6	(5)
	1	1.000	1.000 †	0.000 *	24	(Si)
	1	1.000	1.000 †	0.000 ■	5	(5)
11 23	1	1.000	1.000 ■	0.000 *	40	(S)
11 29	1	1.000	1.000 *	0.000 *	11	(S)
ICONTROL	1	1.000	1.000 *	0.000 *	38	(Si)
1134	1	1.000	1.000 *	0.000 *	55	(7)
1139	1	1.000	1.000 *	0.000 *	31	(13)
!! 42	1	1.000	1.000 *	0.000 *	62	(16)
!! 46	1	1.000	1.000 ■	0.000 *	11	(S)
!! 48	1	1.000	1.000 *	0.000 *	40	(S)
1154	1	1.000	1.000 *	0.000 *	66	(17)
11 56	1	1.000	1.000 ■	0.000 ■	6	(6)
!! 69	1	1.000	1.000 *	0.000 ■	75	(S)
1177	1	1.000	1.000 †	0.000 *	31	(13)
ICONTROL	1	1.000	1.000 *	0.000 *	78	(So)
ENTEROBACTER AERO	2	1.000	1.000 *	0.705 ■	78	(Si)
63	2	1.000	1.000 *	0.705 *	78	(SO)
79	2	1.000	1.000 *	0.705 ■	78	(SO)
PSEUDO FLUORE	3	1.000	1.000 *	0.704 *	66	(17)
	3	1.000	1.000 *	0.704 *	66	(17)
	3	1.000	1.000 *	0.704 *	66	(17)
KLEBSIELLA PNEU	4	1.000	1.000 *	0.551 *	11	(SO)
	4	1.000	1.000 *	0.551 *	11	(SO)
	4	1.000	1.000 *	0.551 *	11	(SO)
	5	1.000	1.000 *	0.924 *	43	(SO)
	5	1.000	1.000 *	0.924 *	43	(SO)
	5	1.000	1.000 *	0.924 *	43	(SO)
	Si			0.924 *	5	(5)
	Si			0.922 *	5	(5)
	Si			0.923 *	5	(5)
	Si			0.922 *	5	(5)
CITROBAC AMA	6	1.000	1.000 *	0.775 *	55	(7)
	6	1.000	1.000 *	0.775 *	55	(7)
	6	1.000	1.000 *	0.775 *	55	(7)
STREPTOCO FAE	7	0.998	0.999 *	0.769 *	6	(6)
	7	0.998	0.999 *	0.769 *	6	(6)
	7	0.998	0.999 *	0.769 *	6	(6)
	7	0.998	0.999 *	0.775 *	6	(6)
	Si			0.726 †	24	(SO)
	8	1.000	1.000 *	0.969 *	62	(16)
	8	1.000	1.000 *	0.969 *	62	(16)
	8	1.000	1.000 *	0.369 *	62	(IS)
	16	1.000	1.000 *	0.969 *	13	(8)
	16	1.000	1.000 *	0.969 *	13	(8)
	Si			0.907 *	62	(16)
	Si			0.850 †	13	(8)
	9	1.000	1.000 †	0.514 †	16	(so)
	9	1.000	1.000 ■	0.514 *	16	(SO)
	Si			0.514 †	14	(9)
	10	1.000	1.000 *	0.648 †	24	(SO)
	10	1.000	1.000 *	0.648 †	24	(Si)
	11	1.000	1.000 *	0.478 *	40	(SO)
	11	1.000	1.000 *	0.478 *	40	(SO)
	Si			0.726 †	11	(SO)
	12	1.000	1.000 *	0.523 *	6	(6)
	12	1.000	1.000 *	0.523 *	6	(6)
	Si			0.471 *	17	(10)
	Si			0.818 *	67	(Si)
	Si			0.853 †	73	(Si)
	Si			0.853 †	67	(SO)
	18	1.000	1.000 *	0.908 *	75	(SO)
	18	1.000	1.000 *	0.908 *	75	(SO)
	Si			0.908 *	68	(18)
75	Si			0.508 *	11	(Si)
128	Si			0.694 *	8	(7)
	13	1.000	1.000 *	0.837 *	38	(SO)
	13	1.000	1.000 *	0.837 *	38	(Si)
	Si			0.837 *	31	(13)
	Si			0.826 *	31	(13)
	14	1.000	1.000 *	0.604 *	8	(7)
	14	1.000	1.000 *	0.604 *	8	(7)
	Si			0.676 *	78	(SO)
	15	1.000	1.000 *	0.658 †	68	(18)
	15	1.000	1.000 *	0.658 †	68	(18)
	17	1.000	1.000 *	0.704 †	3	(3)
	17	1.000	1.000 *	0.704 †	3	(3)
	Si			0.683 *	31	(13)
	Si			0.705 *	2	(2)

PHENOTYPES in kponp2/ Idonlly lo^ol - 0.975
 *CALCULATED DIVERSITY INDEX - 0.955 TRUE DIVERSITY INDEX - 0.955

No	Name	PhP- type	* bn mln	mean	to	PhP type
1.	ECOLI	1	1.000	1.000 ■	0.923 *	17 (SI)
16.	16	1	1.000	1.000 ■	0.923 *	17 (SI)
2B.	28	1	1.000	1.000 *	0.923 *	17 (SI)
60.	60	1	1.000	1.000 *	0.923 *	17 (SI)
17.	17	SF			0.923 ■	1 (1)
37.	37	SI			0.923 ■	1 (1)
33.	33	SI			0.922 ■	1 (1)
2.	IMCROCOSP	2	1.000	1.000 *	0.000 ■	17 (SI)
6.	ICORYNEBAC	2	1.000	1.000 *	0.000 *	41 (12)
35	II35	2	1.000	1.000 ■	0.000 *	20 (SI)
39.	II39	2	1.000	1.000 *	0.000 *	77 (SI)
40.	ICONTROL	2	1.000	1.000 ■	0.000 *	77 (SI)
43.	1143	2	1.000	1.000 *	0.000 *	49 (SI)
46.	1146	2	1.000	1.000 ■	0.000 *	41 (12)
47.	1147	2	1.000	1.000 *	0.000 *	41 (12)
52.	1152	2	1.000	1.000 *	0.000 *	21 (SI)
54.	II54	2	1.000	1.000 *	0.000 *	66 (SI)
63.	I*63	2	1.000	1.000 *	0.000 *	48 (SI)
64.	1164	2	1.000	1.000 *	0.000 *	48 (SI)
76.	1174	2	1.000	1.000 *	0.000 *	53 (13)
73.	1176	2	1.000	1.000 *	0.000 ■	42 (SI)
82.	ICONTROL	2	1.000	1.000 *	0.000 *	48 (SI)
3.	STREPTOCO FAE	3	1.000	1.000 *	0.953 *	48 (SI)
14.	14	3	1.000	1.000 *	0.953 *	48 (SI)
62.	62	3	1.000	1.000 *	0.953 *	48 (SI)
81.	79	3	1.000	1.000 *	0.953 *	48 (SI)
48.	48	SI			0.953 *	3 (3)
50.	50	SI			0.953 *	3 (3)
30.	30	SI			0.918 *	3 (3)
8.	CITROBAC AMA	SI			0.851 *	50 (SI)
4.	KLEBSIELLA PNEU	4	1.000	1.000 *	0.784 *	56 (14)
22.	22	4	1.000	1.000 *	0.784 *	56 (14)
56.	56	14	1.000	1.000 ■	0.784 *	4 (-)
65-	65	14	1.000	1.000 *	0.784 ■	4 (4)
69.	69	14	1.000	1.000 *	0.784 *	4 (4)
71.	69	14	1.000	1.000 *	0.784 *	4 (4)
5.	PSEUDO FLUORE	5	1.000	1.000 ■	0.519 *	41 (12)
18.	18	5	1.000	1.000 *	0.519 ■	41 (12)
29.	29	5	1.000	1.000 *	0.519 *	41 (12)
36.	36	5	1.000	1.000 *	0.519 *	41 (12)
45.	45	5	1.000	1.000 ■	0.519 *	41 (12)
7.	ENTEROBACTER AERO	6	1.000	1.000 *	0.705 *	67 (SI)
10.	10	6	1.000	1.000 *	0.705 *	67 (SI)
32.	32	6	1.000	1.000 *	0.705 ■	67 (SI)
9.	9	7	1.000	1.000 *	0.698 ■	70 (17)
23.	23	7	1.000	1.000 *	0.698 *	70 (17)
11.	11	SI			0.487 *	77 (SI)
12.	12	8	1.000	1.000 *	0.905 *	24 (SI)
19.	19	8	1.000	1.000 *	0.905 *	24 (SI)
24.	24	SI			0.905 ■	12 (8)
13.	13	SI			0.818 *	42 (SI)
27.	27	11	1.000	1.000 *	0.832 *	77 (SO)
38.	38	11	1.000	1.000 *	0.832 *	77 (SI)
72.	70	SI			0.853 *	42 (SI)
42.	42	SI			0.917 *	49 (SO)
49.	49	SI			0.917 *	42 (SI)
77.	75	SI			0.904 *	42 (SI)
15.	115	SI			0.850 *	20 (SI)
20.	20	SI			0.909 *	26 (10)
26.	26	10	1.000	1.000 *	0.909 *	20 (SI)
34.	34	10	1.000	1.000 *	0.969 *	20 (SI)
21.	21	SI			0.653 *	1 (1)
25.	25	9	1.000	1.000 *	0.826 *	55 (SI)
31.	31	9	1.000	1.000 *	0.826 *	55 (SI)
44.	44	9	1.000	1.000 *	0.826 *	55 (SO)
55.	55	SI			0.826 *	25 (9)
41.	41	12	1.000	1.000 *	0.594 *	21 (SI)
51.	51	12	1.000	1.000 *	0.594 *	21 (SI)
53.	53	13	1.000	1.000 ■	0.868 *	66 (SI)
61.	61	13	1.000	1.000 *	0.868 *	66 (SI)
66.	66	SI			0.868 ■	53 (13)
73.	71	SI			0.864 *	53 (13)
75.	73	SI			0.864 ■	53 (13)
57.	57	15	1.000	1.000 *	0.931 *	88 (17)
79.	77	15	1.000	1.000 *	0.931 *	68 (17)
68.	68	17	0.980	0.980 *	0.931 *	57 (15)
70.	68	17	0.080	0.980 *	0.918 *	57 (15)
58.	58	SI			0.434 *	4 (4)
59.	59	16	1.000	1.000 *	0.587 *	67 (SO)
74.	72	16	1.000	1.000 *	0.587 *	87 (SI)
67.	67	SI			0.705 *	7 (6)
80.	178	SI			0.510 *	75 (SI)

PHENOTYPES Uvkpong3/
 CALCULATE DIVERSITY INDEX = 0.840 TRUE DIVERSITY INDEX - 0.040 Identity level = Q.Q75

No	Nam*	PhP- lyp*	bn	sim mean	max	lo	PhP typ*
1.	CITROBAC AMA	1	1.000	1.000 *	0.771 *	78	(SO)
41.	41	1	1.000	1.000 *	0.771 *	78	(SO)
4.	STREPTOCO FAE	4	0.996	0.999 ■	0.953 *	78	(SO)
g	g	4	0.696	0.999 *	0.953 *	78	(SO)
15.	15	4	0.996	0.999 *	0.953 *	78	(SO)
52.	52	4	0.996	0.999 *	0.953 *	78	(SO)
82.	82	4	0.996	0.999 *	0.953 *	78	(so)
74.	74	4	0.896	0.999 *	0.953 *	78	(SI)
63.	63	4	0.996	0.996 ■	0.938 *	78	(so)
78.	78	SI			0.953 *	4	(4)
70.	76	SI			0.924 *	63	(4)
2.	ECOU	2	1.000	1.000 ■	0.924 *	38	(SO)
12.	12	2	1.000	1.000 *	0.924 ■	38	(SO)
17.	17	2	1.000	1.000 *	0.924 *	38	(SO)
30.	30	2	1.000	1.000 ■	0.924 *	38	(so)
5B.	58	2	1.000	1.000 *	0.924 *	38	(so)
38.	38	SI			0.924 ■	2	(2)
34.	34	SI			0.923 *	2	(2)
19.	19	SI			0.922 *	2	(2)
45.	45	SI			0.858 *	2	(2)
3.	11MICROCO SP	3	1.000	1.000 *	0.000 *	38	(SO)
8.	MCCORYNEBAC	3	1.000	1.000 *	0.000 *	21	(10)
36.	1136	3	1.000	1.000 ■	0.000 *	22	(11)
40.	11CONTROL	3	1.000	1.000 *	0.000 *	45	(SO)
43.	1143	3	1.000	1.000 *	0.000 *	23	(SO)
53.	1153	3	1.000	1.000 *	0.000 *	78	(SO)
61.	1161	3	1.000	1.000 *	0.000 *	22	(11)
64.	1164	3	1.000	1.000 *	0.000 *	78	(SO)
65.	1165	3	1.000	1.000 *	0.000 *	78	(SO)
66.	1166	3	1.000	1.000 *	0.000 *	78	(SO)
69.	1169	3	1.000	1.000 *	0.000 *	11	(7)
70.	1170	3	1.000	1.000 *	0.000 *	11	(7)
71.	1171	3	1.000	1.000 ■	0.000 ■	11	(7)
72.	1172	3	1.000	1.000 *	0.000 ■	11	(7)
73.	1173	3	1.000	1.000 *	0.000 ■	11	(7)
77.	1177	3	1.000	1.000 *	0.000 ■	63	(4)
80.	11CONTROL	3	1.000	1.000 *	0.000 *	38	(SO)
5.	ENTEROBACTER AERO	5	1.000	1.000 ■	0.949 *	14	(SO)
48.	48	5	1.000	1.000 *	0.949 *	14	(SO)
55.	55	5	1.000	1.000 *	0.949 *	14	(so)
14.	14	SI			0.949 *	5	(5)
6.	PSEUDO FLUORE	6	1.000	1.000 ■	0.690 *	24	(SO)
10.	10	6	1.000	1.000 *	0.690 *	24	(so)
7.	KLEBSIELLA PNEU	SI			0.551 *	21	(10)
11.	11	7	1.000	1.000 *	0.694 *	45	(SO)
39.	39	7	1.000	1.000 *	0.694 *	45	(SO)
13.	13	8	1.000	1.000 *	0.256 ■	22	(11)
20.	20	8	1.000	1.000 *	0.256 *	22	(11)
35.	35	8	1.000	1.000 *	0.256 *	22	(11)
16.	16	9	1.000	1.000 *	0.905 *	29	(SO)
25.	25	9	1.000	1.000 *	0.905 *	29	(SO)
49.	49	9	1.000	1.000 *	0.905 *	29	(SO)
29.	29	SI			0.905 *	16	(9)
59.	59	16	1.000	1.000 *	0.852 *	29	(SO)
67.	67	16	1.000	1.000 ■	0.852 *	29	(SO)
44.	44	15	1.000	1.000 *	0.906 *	54	(SO)
47.	47	15	1.000	1.000 ■	0.806 *	54	(SO)
54.	54	SI			0.906 *	44	(15)
18.	18	SI			0.544 *	6	(6)
21.	21	10	1.000	1.000 *	0.634 *	46	(SI)
31.	31	10	1.000	1.000 ■	0.634 *	46	(SI)
22.	22	11	1.000	1.000 *	0.929 *	32	(13)
26.	26	11	1.000	1.000 *	0.929 *	32	(13)
32.	32	13	1.000	1.000 ■	0.929 *	22	(11)
60.	60	13	1.000	1.000 *	0.929 *	22	(11)
51.	51	SI			0.929 *	22	(SI)
23.	23	SI			0.969 *	42	(SI)
42.	42	SI			0.969 *	23	(SO)
24.	24	SI			0.690 *	6	(6)
27.	27	12	1.000	1.000 *	0.447 *	29	(SI)
57.	57	12	1.000	1.000 ■	0.447 *	29	(SO)
20.	28	SI			0.608 *	63	(4)
33.	33	14	1.000	1.000 *	0.699 *	37	(SO)
56.	56	14	1.000	1.000 *	0.699 *	37	(so)
37.	37	SI			0.699 *	33	(14)
46.	46	SI			0.634 *	21	(10)
50.	50	SI			0.434 *	7	(SO)
68.	68	17	1.000	1.000 *	0.594 *	11	(7)
75.	75	17	1.000	1.000 *	0.594 *	11	(7)
79.	79	SI			0.565 *	38	(SO)

PMENOTYPESinkpDngJ: Identity to vñl - 0.B75
 JCALCOLateb DIVERSITY INDEX - 0.961 TRUE DIVERSITY INDEX - 0.961

No	Name	PhP- type	aim mln	aim mean	lim	to n /	PhP type
1	rCORYNEBAC	1	1.000	1.000 ■	0.000 *	(S	
3	!!MICROCO SP	1	1.000	1.000 *	0.000 ■	43	(Si)
25	1125	1	1.000	1.000 ■	0.000 ■	13	(Si)
29	11 29	1	1.000	1.000 *	0.000 ■	20	(Si)
32	!CONTROL	1	1.000	1.000 *	0.000 *	14	(S)
53	11 58	1	1.000	1.000 *	0.000 ■	14	(S)
65	n 65	1	1.000	1.000 *	0.000 ■	56	(Si)
69	11 69	1	1.000	1.000 ■	0.000 *	20	(Si)
70	! 70	1	1.000	1.000 ■	0.000 *	20	(Si)
71	11 71	1	1.000	1.000 *	0.000 *	20	(Si)
78	11 78	1	1.000	1.000 *	0.000 *	57	(Si)
80	!CONTROL	1	1.000	1.000 *	0.000 ■	62	(17)
2	KLEBSIELLA PNEU	2	1.000	1.000 *	0.873 *	43	(Si)
10	10	2	1.000	1.000 *	0.873 *	43	(Si)
21	21	2	1.000	1.000 *	0.073 ' 2	43	(S)
43	43	Si			0.873 ' 2	(2)	
36	36	Si			0.862 ' 2	(2)	
4	CITROBAC AMA	Si'			0.769 *	8	(6)
8	STREPTOCO FAE	6	0.998	0.999 ■	0.953 ■	20	(Si)
51	51	6	0.998	0.999 *	0.953 *	20	(Si)
68	68	6	0.998	0.999 *	0.953 ' 20	(S)	
28	28	6	0.993	0.997 *	0.947 *	20	(SO)
44	44	6	0.996	0.997 *	0.956 *	20	(Si)
38	38	6	0.993	0.997 ' 20	0.956 *	(SO)	
20	20	Si			0.956 *	38	(6)
5	E COLI	3	1.000	1.000 *	0.934 *	34	(SO)
22	22	3	1.000	1.000 ■	0.934 ■	34	(SO)
40	40	3	1.000	1.000 *	0.934 *	34	(Si)
61	61	3	1.000	1.000 *	0.934 *	34	(SO)
34	34	Si			0.934 *	5	(3)
13	13	Si			0.922 *	5	(3)
53	53	Si			0.060 *	5	(3)
6	ENTEROBACTER AERO	4	1.000	1.000 *	0.588 ■	74	(Si)
11	11	4	1.000	1.000 ■	0.538 ' 74	(Si)	
47	47	4	1.000	1.000 *	0.508 ' 74	(SO)	
7	PSEUDO FLUORE	5	1.000	1.000 *	0.528 *	31	(SO)
9	9	5	1.000	1.000 *	0.528 ' 31	(SO)	
59	59	5	1.000	1.000 *	0.528 *	31	(SO)
12	12	7	1.000	1.000 *	0.460 ' 52	(Si)	
30	30	7	1.000	1.000 *	0.460 *	52	(Si)
14	14	8	1.000	1.000 *	0.919 *	57	(Si)
27	27	8	1.000	1.000 ■	0.919 ■	57	(SO)
77	77	8	1.000	1.000 *	0.919 ' 57	(SO)	
57	57	Si			0.919 ' 14	(S)	
31	31	Si			0.914 *	14	(S)
15	15	9	1.000	1.000 *	0.599 ' 13	(Si)	
24	24	9	1.000	1.000 ■	0.599 *	13	(Si)
16	16	10	1.000	1.000 ■	0.588 *	53	(Si)
37	37	10	1.000	1.000 *	0.588 *	53	(SO)
54	54	10	1.000	1.000 *	0.588 *	53	(Si)
17	17	11	1.000	1.000 ■	0.951 *	56	(Si)
48	49	11	1.000	1.000 *	0.951 *	56	(Si)
64	64	11	1.000	1.000 *	0.951 *	56	(Si)
56	56	Si			0.951 *	17	(11)
42	42	15	1.000	1.000 *	0.893 *	56	(Si)
49	49	15	1.000	1.000 *	0.093 ' 56	(Si)	
18	18	Si			0.600 *	60	(Si)
19	19	12	1.000	1.000 *	0.815 *	52	(SO)
39	39	12	1.000	1.000 ■	0.815 ' 52	(S)	
52	52	Si			0.815 ' 19	(12)	
23	23	13	0.997	0.999 ■	0.935 *	62	(17)
35	35	13	0.997	0.999 *	0.935 *	62	(17)
50	50	13	0.997	0.999 *	0.935 *	62	(17)
66	66	13	0.997	0.999 *	0.935 *	62	(17)
79	79	13	0.997	0.997 *	0.928 ■	62	(17)
62	62	17	1.000	1.000 *	0.935 *	23	(13)
72	72	17	1.000	1.000 *	0.935 ' 23	(13)	
73	73	Si			0.924 *	76	(Si)
76	76	Si			0.932 *	23	(13)
55	55	Si			0.876 *	23	(13)
26	26	Si			0.646 *	20	(Si)
33	33	Si			0.434 ' 2	(2)	
41	41	14	1.000	1.000 *	0.514 *	16	(10)
46	46	14	1.000	1.000 ■	0.514 *	16	(10)
45	45	16	1.000	1.000 *	0.653 *	5	(3)
63	63	16	1.000	1.000 ■	0.653 *	5	(3)
60	60	Si			0.600 ■	18	(Si)
67	67	18	1.000	1.000 *	0.682 ■	70	(SO)
75	75	18	1.000	1.000 *	0.682 ' 76	(SO)	
74	74	Si			0.508 ' 0	(4)	

PHENOTYPES In EptongS/ "CALCULATED DIVERSITY INDEX - 0.944		Identity (avol - 0.975 TRUE DIVERSITY INDEX - 0.943					
NO	Nama	PhP- type	"mi r/min	"mi mean	smi max	to nr	PhP type
1	STREPTOCO FAE	1	0.990	0.997 *	0.953 ■	23	(Si)
11.	11	1	0.990	0.997 ■	0.953 ■	23	(Si)
38.	38	1	0.990	0.997 *	0.953 *	23	(Si)
50.	50	1	0.990	0.997 *	0.953 *	23	(Si)
76.	76	1	0.975	0.969 *	0.982 ?	23	(Si)
79.	79	1	0.975	0.987 *	0.924 *	23	(Si)
23.	23	SI			0.982 7	76	(1)
6.	CITROBAC AMA	SI			0.769 ■	1	(1)
2.	MICROCOSP	2	1.000	1.000 *	0.000 *	23	(Si)
7.	ICORYNEBACTERIUM	2	1.000	1.000 ■	0.000 ■	1	(1)
15.	II 15	2	1.000	1.000 *	0.000 ■	8	(Si)
20.	II 20	2	1.000	1.000 *	0.000 *	4	(3)
22.	II 22	2	1.000	1.000 *	0.000 *	29	(Si)
27.	II 27	2	1.000	1.000 *	0.000 ■	57	(SO)
30.	II 30	2	1.000	1.000 *	0.000 *	5	(4)
31.	II 31	2	1.000	1.000 *	0.000 *	5	(4)
34.	II 34	2	1.000	1.000 *	0.000 *	26	(10)
37.	II 37	2	1.000	1.000 *	0.000 *	28	(11)
41.	II 41	2	1.000	1.000 *	0.000 *	74	(16)
45.	II 45	2	1.000	1.000 *	0.000 ■	49	(14)
46.	II 46	2	1.000	1.000 *	0.000 *	49	(14)
48.	II CONTROL	2	1.000	1.000 ■	0.000 *	17	(8)
53.	II 53	2	1.000	1.000 ■	0.000 *	4	(3)
80.	II CONTROL	2	1.000	1.000 *	0.000 *	23	(SO)
3.	ENTEROBACTER AERO	SI			0.415 ■	77	(SO)
4.	E COLI	3	1.000	1.000 *	0.923 ■	19	(SO)
13.	13	3	1.000	1.000 *	0.923 *	19	(SO)
43.	43	3	1.000	1.000 *	0.923 *	19	(SO)
66.	66	3	1.000	1.000 *	0.923 *	19	(SO)
19.	19	SI			0.923 *	4	(3)
28.	28	11	1.000	1.000 *	0.922 *	4	(3)
52.	52	11	1.000	1.000 *	0.922 *	4	(3)
36.	36	SI			0.911 *	28	(11)
12.	12	6	1.000	1.000 *	0.927 *	77	(SO)
56.	56	6	1.000	1.000 *	0.927 *	77	(SO)
77.	77	SI			0.927 *	12	(8)
71.	71	SI			0.923 *	12	(6)
73.	73	SI			0.923 *	12	(6)
5.	PSEUDO FLUORE	4	1.000	1.000 *	0.594 ■	29	(SO)
16.	16	4	1.000	1.000 *	0.594 *	29	(SO)
21.	21	4	1.000	1.000 *	0.594 ■	29	(SO)
8.	KLEBSIELLA PNEU	SI			0.586 ■	39	(7)
9.	9	SI			0.541 *	19	(SO)
10.	10	5	1.000	1.000 *	0.753 ■	57	(SO)
24.	24	5	1.000	1.000 ■	0.753 *	57	(SO)
40.	40	12	1.000	1.000 *	0.940 *	74	(16)
59.	59	12	1.000	1.000 *	0.940 *	74	(16)
61.	61	12	1.000	1.000 *	0.940 *	74	(16)
63.	63	12	1.000	1.000 *	0.940 *	74	(16)
68.	68	12	1.000	1.000 ■	0.940 *	74	(16)
74.	74	16	0.996	0.996 *	0.940 *	40	(12)
78.	78	16	0.996	0.996 *	0.908 *	40	(12)
44.	44	13	1.000	1.000 ■	0.917 *	49	(14)
62.	62	13	1.000	1.000 *	0.917 ■	49	(14)
49.	49	14	1.000	1.000 *	0.917 *	44	(13)
75.	75	14	1.000	1.000 *	0.917 *	44	(13)
57.	57	SI			0.853 *	44	(13)
14.	14	7	0.997	0.998 *	0.551 *	8	(Si)
69.	69	7	0.997	0.998 ■	0.551 *	8	(Si)
39.	39	7	0.997	0.997 *	0.586 *	8	(Si)
17.	17	8	1.000	1.000 *	0.826 *	47	(SO)
32.	32	8	1.000	1.000 *	0.826 *	47	(SO)
42.	42	8	1.000	1.000 *	0.826 *	47	(SO)
55.	55	8	1.000	1.000 *	0.826 *	47	(SO)
65.	65	B	1.000	1.000 *	0.826 ■	47	(Si)
47.	47	SI			0.826 *	17	(8)
18.	18	SI			0.575 *	44	(13)
25.	25	9	1.000	1.000 *	0.722 *	36	(SO)
60.	60	9	1.000	1.000 ■	0.722 ■	36	(SO)
26.	26	10	1.000	1.000 *	0.571 *	57	(SO)
35.	35	10	1.000	1.000 *	0.571 *	57	(SO)
29.	29	SI			0.594 *	5	(4)
33.	33	SI			0.512 *	26	(10)
51.	51	SI			0.690 ■	23	(SO)
54.	54	SI			0.367 *	33	(Si)
58.	58	SI			0.822 *	64	(SO)
64.	64	SI			0.822 *	58	(SO)
67.	67	15	1.000	1.000 *	0.449 *	70	(SO)
72.	72	15	1.000	1.000 *	0.449 *	70	(SO)
70.	70	SI			0.583 *	25	(9)

UNRELATED DIVERSITY INDEX - 0.954		TRUE DIVERSITY		UNRELATED DIVERSITY INDEX - 0.954		TRUE DIVERSITY	
No	Name	PhP- type	sim PhP	sim mean	sim max	to nr	PhP type
1.	BACILLUS	1	1.000	1.000	0.000	43	(S)
6.	CORYNEBAC	1	1.000	1.000	0.000	63	(S)
11.	!!11	1	1.000	1.000	0.000	75	(S)
25.	!!25	1	1.000	1.000	0.000	30	(16)
26.	!!28	1	1.000	1.000	0.000	15	(S)
31.	!!31	1	1.000	1.000	0.000	63	(S)
33.	!!33	1	1.000	1.000	0.000	63	(S)
40.	!!CONTROL	1	1.000	1.000	0.000	15	(S)
47.	!!47	1	1.000	1.000	0.000	38	(15)
51.	!!51	1	1.000	1.000	0.000	68	(19)
55.	!!55	1	1.000	1.000	0.000	7	(6)
52.	!!62	1	1.000	1.000	0.000	30	(16)
55.	!!65	1	1.000	1.000	0.000	5	(5)
30.	!!CONTROL	1	1.000	1.000	0.949	48	(S)
2.	ENTEROBACTER AERO	2	1.000	1.000	0.949	48	(S)
52.	52	2	1.000	1.000	0.949	2	(2)
18.	48	3	1.000	1.000	0.924	42	(S)
3.	ECOLI	3	1.000	1.000	0.924	42	(S)
12.	12	3	1.000	1.000	0.924	42	(S)
SO.	60	3	1.000	1.000	0.924	42	(SO)
56.	66	3	1.000	1.000	0.924	42	(SO)
4.	34	3	1.000	1.000	0.924	42	(SO)
'6.	76	3	1.000	1.000	0.924	3	(3)
12.	42	SI			0.922	3	(3)
9.	19	SI			0.969	21	OD
3.	9	8	1.000	1.000	0.969	21	OD
7.	67	8	1.000	1.000	0.969	9	(8)
1.	21	11	1.000	1.000	0.969	9	(8)
4.	34	11	1.000	1.000	0.969	9	(8)
8.	78	SI			0.908	9	(8)
1.	CAMPY JEJE	4	1.000	1.000	0.837	18	(S)
1.	41	4	1.000	1.000	0.837	18	(S)
8.	58	4	1.000	1.000	0.837	18	(SO)
B.	18	SI			0.837	4	(M)
3.	123	13	1.000	1.000	0.861	53	(S)
S.	136	13	1.000	1.000	0.861	53	(SO)
3.	53	SI			0.861	23	(13)
3.	13	9	1.000	1.000	0.818	14	(SO)
5.	45	9	1.000	1.000	0.818	14	(SO)
r.	14	SI			0.917	68	(19)
4.	54	SI			0.926	68	(19)
3.	68	19	1.000	1.000	0.926	54	(S)
7.	77	19	1.000	1.000	0.926	54	(S)
5.	26	15	0.996	0.996	0.901	50	(S)
3.	38	15	0.996	0.996	0.903	50	(SO)
3.	50	SI			0.903	38	(15)
	PROTEUS MIRA	5	1.000	1.000	0.514	43	(18)
7.	17	5	1.000	1.000	0.514	43	(0)
	STREPTOCO FAE	6	0.993	0.999	0.955	63	(S)
3.	10	6	0.993	0.999	0.955	63	(SO)
7.	37	6	0.993	0.999	0.955	63	(S)
3.	39	6	0.993	0.999	0.955	63	(SO)
7.	57	6	0.993	0.999	0.955	63	(S)
4.	74	6	0.993	0.999	0.955	63	(S)
2.	72	6	0.993	0.993	0.947	61	(SO)
	61	SI			0.953	7	(6)
3.	63	SI			0.955	7	(6)
2.	32	17	1.000	1.000	0.866	63	(SO)
9.	49	17	1.000	1.000	0.866	63	(SO)
1	PSEUDO AEROG	7	1.000	1.000	0.531	30	(0)
7.	27	7	1.000	1.000	0.531	30	(16)
4.	64	7	1.000	1.000	0.531	30	(16)
5.	15	SI			0.784	73	(SO)
3.	73	SI			0.784	15	(S)
6.	16	10	1.000	1.000	0.604	7	(6)
0.	20	10	1.000	1.000	0.604	7	(6)
2.	22	12	1.000	1.000	0.933	44	(S)
5.	35	12	1.000	1.000	0.933	44	(S)
4.	44	SI			0.933	22	(12)
9.	59	-SI			0.933	22	(02)
4.	24	14	1.000	1.000	0.924	75	(SO)
0.	70	14	1.000	1.000	0.924	75	(S)
5.	75	SI			0.924	24	(0-)
9.	29	SI			0.897	24	(04)
0.	30	16	1.000	1.000	0.551	15	(SO)
6.	46	16	1.000	1.000	0.551	15	(S)
13.	43	18	1.000	1.000	0.514	5	(5)
19.	69	18	1.000	1.000	0.514	5	(5)
9.	79	18	1.000	1.000	0.514	5	(5)
6.	156	SI			0.398	30	(16)
1.	71	SI			0.433	23	(13)

No	Namo	PHP- lypκ	•iii mln	sim moan	*im	10 nr	PHP type
1	CAMPYLOB	1	1.000	1.000 *	0.549 *	80	(23)
22	22	1	1.000	1.000 *	0.549 *	80	(23)
75.	74	1	1.000	1.000 *	0.549 *	80	(23)
83.	74	1	1.000	1.000 *	0.549 *	80	(23)
2.	PSEUDO AERO	SI			0.786 *	21	(S1)
21.	21	SI			0.786 *	2	(SO)
3.	II BACILLUS	2	1.000	1.000 ■	0.000 *	21	(SO)
4.	ICORYNEBAC	2	1.000	1.000 *	0.000 *	21	(SO)
11.	H 11	2	1.000	1.000 *	0.000 *	74	(20)
14.	1114	2	1.000	1.000 *	0.000 *	35	(12)
27.	II 26	2	1.000	1.000 *	0.000 *	47	(15)
28.	II 27	2	1.000	1.000 *	0.000 *	47	(15)
31.	II 30	2	1.000	1.000 *	0.000 *	5	(3)
33.	II 32	2	1.000	1.000 *	0.000 ■	74	(20)
34.	II 33	2	1.000	1.000 *	0.000 *	74	(20)
41.	ICONTROL	2	1.000	1.000 *	0.000 *	47	(15)
43.	11 42	2	1.000	1.000 *	0.000 ■	7	(5)
50.	11 49	2	1.000	1.000 *	0.000 ■	18	(11)
52.	1151	2	1.000	1.000 *	0.000 *	74	(20)
57.	II 56	2	1.000	1.000 *	0.000 *	7	(5)
63.	II 62	2	1.000	1.000 *	0.000 *	18	(11)
66.	II 65	2	1.000	1.000 *	0.000 *	74	(20)
79.	II 75	2	1.000	1.000 *	0.000 *	18	(11)
87.	II 78	2	1.000	1.000 ■	0.000 *	18	(11)
80.	ICONTROL	2	1.000	1.000 *	0.000 *	15	(9)
5.	E COLI	3	0.989	0.997 *	0.934 ■	76	(22)
17.	17	3	0.989	0.997 *	0.934 *	76	(22)
45.	44	3	0.989	0.997 *	0.934 *	76	(22)
53.	52	3	0.939	0.997 *	0.934 *	76	(22)
68.	67	3	0.989	0.939 *	0.918 *	76	(22)
76.	72	22	1.000	1.000 *	0.934 *	5	(3)
84.	75	22	1.000	1.000 *	0.934 *	5	(3)
30.	29	SI			0.923 *	5	(3)
38.	37	SI			0.924 *	5	(3)
6.	PROTEUS MIRA	4	1.000	1.000 *	0.621 *	74	(20)
10.	10	4	1.000	1.000 *	0.621 *	74	(20)
32.	31	4	1.000	1.000 *	0.621 *	74	(20)
51.	50	4	1.000	1.000 *	0.621 *	74	(20)
65.	64	4	1.000	1.000 *	0.621 *	74	(20)
7.	STREPTOCO FAE	5	1.000	1.000 *	0.769 *	35	(12)
13.	13	5	1.000	1.000 *	0.769 *	35	(12)
69.	68	5	1.000	1.000 *	0.769 *	35	(12)
77.	73	5	1.000	1.000 ■	0.769 *	35	(12)
85.	76	5	1.000	1.000 *	0.769 *	35	(12)
24.	24	12	0.990	0.995 *	0.757 *	7	(5)
25.	24	12	0.990	0.995 *	0.757 *	7	(5)
35.	34	12	0.990	0.990 *	0.769 *	7	(5)
8.	ENTEROBACTER AER	6	1.000	1.000 *	0.340 *	47	(15)
26.	25	6	1.000	1.000 *	0.340 *	47	(15)
39.	38	6	1.000	1.000 *	0.340 *	47	(15)
9.	9	7	1.000	1.000 *	0.969 *	47	(15)
40.	39	7	1.000	1.000 *	0.969 *	47	(15)
47.	46	15	1.000	1.000 *	0.969 *	9	(7)
55.	54	15	1.000	1.000 *	0.969 *	9	(7)
12.	12	8	1.000	1.000 *	0.551 *	16	(10)
23.	23	8	1.000	1.000 *	0.551 *	16	(10)
36.	35	8	1.000	1.000 *	0.551 *	16	(10)
15.	15	9	1.000	1.000 *	0.654 *	80	(23)
19.	19	9	1.000	1.000 *	0.654 *	80	(23)
46.	45	9	1.000	1.000 *	0.654 *	80	(23)
16.	16	10	0.997	0.998 *	0.551 *	12	(8)
58.	57	10	0.997	0.998 *	0.551 *	12	(8)
73.	72	10	0.997	0.988 *	0.557 *	21	(SO)
81.	72	10	0.997	0.998 *	0.557 *	21	(SO)
18.	18	11	1.000	1.000 *	0.774 *	44	(14)
37.	36	11	1.000	1.000 *	0.774 *	44	(14)
44.	43	14	1.000	1.000 *	0.885 *	70	(SO)
60.	59	14	1.000	1.000 *	0.885 *	70	(SO)
70.	69	SI			0.885 *	44	(K)
54.	53	18	1.000	1.000 *	0.816 *	44	(14)
71.	70	18	1.000	1.000 *	0.816 *	44	(14)
49.	148	17	1.000	1.000 *	0.753 *	13	(11)
62.	161	17	1.000	1.000 *	0.753 *	18	(11)
20.	20	SI			0.729 *	38	(SO)
29.	28	SI			0.434 *	12	(8)
42.	41	13	1.000	1.000 *	0.604 *	7	(5)
56.	55	13	1.000	1.000 *	0.604 *	7	(5)
48.	47	16	1.000	1.000 *	0.433 *	49	(17)
67.	68	16	1.000	1.000 ■	0.433 *	49	(17)
59.	58	19	1.000	1.000 *	0.527 *	61	(20)
64.	83	19	1.000	1.000 *	0.527 *	61	(20)
81.	60	20	0.998	0.993 *	0.614 *	6	(4)

Z53

7 1

PHENOTYPES		IDONUTY		TRUE DIVERSITY INDEX		CALCULATED DIVERSITY INDEX	
- 0.942		- 0.875		- 0.842		- 0.942	
No	Name	PhP- typ	f	mean	lo	PhP type	
1.	IQACILLUS	1	1.000	1.000 *	0.000 *	<8	
2.	MCORYNEBAC	1	1.000	1.000 ■	0.000 *	(S)	
15.	II 15	1	1.000	1.000 *	0.000 *	73 (SI)	
20.	II 20	1	1.000	1.000 *	0.000 *	65 (SI)	
22.	II 22	1	1.000	1.000 *	0.000 *	11 (O)	
31.	1131	1	1.000	1.000 *	0.000 *	53 (SO)	
32.	HCNTROL	1	1.000	1.000 *	0.000 *	53 (SO)	
33.	II 33	1	1.000	1.000 *	0.000 *	53 (SO)	
38.	1138	1	1.000	1.000 *	0.000 ■	24 (12)	
39.	11 39	1	1.000	1.000 *	0.000 *	24 (12)	
40.	II 40	1	1.000	1.000 *	0.000 *	24 (12)	
45.	1145	1	1.000	1.000 *	0.000 *	65 (so)	
55.	1154	1	1.000	1.000 *	0.000 *	64 (SO)	
60.	1159	1	1.000	1.000 *	0.000 *	41 (14)	
68.	1167	1	1.000	1.000 ■	0.000 *	73 (SO)	
71.	11 69	1	1.000	1.000 *	0.000 *	23 (SO)	
82.	HCNTROL	1	1.000	1.000 *	0.000 ■	65 (so)	
3.	ENTEROBACTER AERO	SI			0.949 *	25 (SO)	
25.	25	SI			0.949 ■	3 (so)	
4.	STREPTOCO FAE	2	1.000	1.000 □	0.953 *	23 (SO)	
13.	13	2	1.000	1.000 *	0.953 *	23 (so)	
17.	17	2	1.000	1.000 *	0.953 *	23 (so)	
70.	68	2	1.000	1.000 ■	0.953 *	23 (SO)	
23.	23	SI			0.953 *	4 (2)	
92.	62	SI			0.953 *	4 (2)	
77.	75	SI			0.953 *	4 (2)	
14.	14	10	1.000	1.000 *	0.915 *	73 (SO)	
46.	46	10	1.000	1.000 *	0.915 *	73 (SO)	
67.	66	10	1.000	1.000 *	0.915 *	73 (SO)	
28.	28	SI			0.953 *	4 (2)	
73.	71	SI			0.944 *	28 (SO)	
52.	52	SI			0.861 *	28 (so)	
18.	10	11	1.000	1.000 ■	0.888 *	53 (SO)	
30.	30	11	1.000	1.000 *	0.888 *	53 (SO)	
35.	35	11	1.000	1.000 *	0.888 ■	53 (SO)	
80.	78	11	1.000	1.000 *	0.888 *	53 (SO)	
53.	52	SI			0.888 *	18 (11)	
5.	ECOLI	3	1.000	1.000 *	0.653 *	41 (14)	
10.	10	3	1.000	1.000 *	0.653 ■	41 (14)	
57.	56	3	1.000	1.000 *	0.653 *	41 (14)	
59.	58	3	1.000	1.000 ■	0.653 *	41 (14)	
76.	74	3	1.000	1.000 *	0.653 *	41 (14)	
6 *	PSEUDO AEROG	4	1.000	1.000 ■	0.430 *	7 (5)	
36.	36	4	1.000	1.000 *	0.430 *	7 (5)	
7.	CAMPYLO JE	5	1.000	1.000 *	0.502 ■	65 (SI)	
50.	50	5	1.000	1.000 *	0.502 *	65 (SO)	
8.	PROTEUS MIRA	6	1.000	1.000 *	0.614 *	11 (8)	
21.	21	6	1.000	1.000 *	0.614 *	11 (8)	
49.	49	6	1.000	1.000 ■	0.614 *	11 (8)	
50.	57	6	1.000	1.000 *	0.614 *	11 (8)	
9.	9	7	1.000	1.000 *	0.642 *	65 (SO)	
19.	19	7	1.000	1.000 *	0.642 *	65 (SI)	
81.	79	7	1.000	1.000 *	0.642 *	65 (so)	
11.	11	8	1.000	1.000 ■	0.614 *	8 (6)	
16.	16	8	1.000	1.000 *	0.614 *	8 (6)	
61.	60	8	1.000	1.000 *	0.614 *	8 (6)	
12.	12	9	1.000	1.000 *	0.784 *	64 (SO)	
34.	34	9	1.000	1.000 *	0.784 *	64 (SO)	
54.	53	9	1.000	1.000 *	0.784 *	64 (SI)	
04.	63	SI			0.704 *	12 (O)	
24.	24	12	1.000	1.000 *	0.910 *	37 (SO)	
29.	29	12	1.000	1.000 *	0.910 *	37 (SI)	
37.	37	SI			0.910 *	24 (12)	
26.	26	SI			0.508 *	37 (SI)	
27.	27	13	1.000	1.000 *	0.347 *	72 (SI)	
42.	42	13	1.000	1.000 *	0.347 *	72 (SO)	
62.	61	13	1.000	1.000 *	0.347 *	72 (SO)	
78.	76	13	1.000	1.000 *	0.347 *	72 (SO)	
41.	41	14	1.000	1.000 ■	0.653 *	5 (3)	
66.	65	14	1.000	1.000 *	0.653 *	5 (3)	
43.	143	SI			0.408 *	8 (6)	
44.	44	15	1.000	1.000 *	0.435 *	65 (SO)	
51.	51	15	1.000	1.000 *	0.435 *	65 (SI)	
47.	47	16	1.000	1.000 □	0.641 *	5 (3)	
48.	48	16	1.000	1.000 *	0.641 *	5 (3)	
56.	55	16	1.000	1.000 *	0.641 *	5 (3)	
65.	64	SI			0.642 *	9 (7)	
69.	68	SI			0.426 *	11 (8)	
72.	70	SI			0.634 *	64 (SO)	
74.	72	17	1.000	1.000 ■	0.501 *	11 (8)	
79.	77	17	1.000	1.000 *	0.501 *	11 (8)	
75.	73	SI			0.633 *	41 (14)	

IdonUfy lavel*- 0.873
 • 0.950 TRUE DIVERSITY INDEX 0.950

1.	ENTEROBACTER CLOA	1	1.000	1.000 *	0.707 *	70	(SI)
24.	24	1	1.000	1.000 *	0.707 ■	70	(SI)
2.	IBACILLUS	2	1.000	1.000 *	0.000 *	70	(SI)
6.	IMICROCO LUT	2	1.000	1.000 *	0.000 *	33	(14)
11.	11 11	2	1.000	1.000 *	0.000 *	73	(SI)
13.	11 13	2	1.000	1.000 *	0.000 *	54	(20)
15.	11 15	2	1.000	1.000 *	0.000 *	53	(SI)
21.	>121	2	1.000	1.000 *	0.000 *	12	(9)
25.	11 25	2	1.000	1.000 *	0.000 *	55	(21)
27.	11 27	2	1.000	1.000 *	0.000 *	55	(21)
39.	1139	2	1.000	1.000 *	0.000 *	B	(7)
40.	IICONTROL	2	1.000	1.000 *	0.000 *	8	(7)
45.	1145	2	1.000	1.000 *	0.000 *	12	(9)
47.	11 47	2	1.000	1.000 *	0.000 *	86	(SI)
56.	1156	2	1.000	1.000 *	0.000 *	25	(13)
77.	*177	2	1.000	1.000 *	0.000 *	43	(17)
SO.	IICONTROL	2	1.000	1.000 ■	0.000 ■	55	(21)
3.	PROTEUS VULG	3	1.000	1.000 *	0.818 *	12	(9)
18.	18	3	1.000	1.000 ■	0.818 *	12	(9)
<4.	44	3	1.000	1.000 *	0.818 ■	12	(9)
12.	12	9	1.000	1.000 *	0.917 *	54	(20)
30.	30	9	1.000	1.000 *	0.917 *	54	(20)
37.	37	9	1.000	1.000 *	0.917 *	54	(20)
54.	54	20	1.000	1.000 *	0.917 *	12	(9)
53.	63	20	1.000	1.000 *	0.917 *	12	(9)
20.	20	SI			0.897 ■	12	(9)
43.	43	17	1.000	1.000 ■	0.897 *	76	(SI)
57.	67	17	1.000	1.000 *	0.897 *	76	(SI)
76.	76	SI			0.897 *	43	(17)
4.	1 FLAVOBAC AQUA	4	1.000	1.000 *	0.884 *	53	(SI)
14.	114	4	1.000	1.000 *	0.884 *	53	(SI)
35.	135	4	1.000	1.000 ■	0.884 *	53	(SI)
52.	152	4	1.000	1.000 *	0.884 *	53	(SO)
59.	159	4	1.000	1.000 *	0.884 *	53	(SI)
53.	53	SI			0.884 *	4	(4)
74.	174	SI			0.819 *	53	(SI)
5.	ECOU	5	0.997	0.999 *	0.653 *	33	(14)
16.	16	5	0.997	0.999 *	0.653 *	33	(14)
65.	65	5	0.997	0.999 *	0.653 *	33	(14)
29.	29	5	0.997	0.997 *	0.623 *	33	(14)
7.	STREPTOCO FAE	6	1.000	1.000 ■	0.869 ■	73	(SO)
9.	9	6	1.000	1.000 *	0.869 *	73	(SO)
36.	36	6	1.000	1.000 *	0.869 *	73	(SO)
57.	57	6	1.000	1.000 *	0.869 *	73	(SO)
10.	10	8	1.000	1.000 ■	0.915 *	73	(SO)
32.	32	8	1.000	1.000 *	0.915 *	73	(SO)
48.	48	8	1.000	1.000 *	0.915 ■	73	(SI)
73.	73	SI			0.915 *	10	(8)
8.	CAMPY JE	7	1.000	1.000 ■	0.476 *	64	(SO)
17.	17	7	1.000	1.000 *	0.476 *	64	(SO)
72.	72	7	1.000	1.000 *	0.476 *	64	(SI)
19.	19	10	1.000	1.000 *	0.784 *	42	(16)
31.	31	10	1.000	1.000 *	0.784 *	42	(16)
71.	71	10	1.000	1.000 *	0.784 *	42	(16)
42.	42	16	1.000	1.000 *	0.784 *	19	(10)
68.	68	16	1.000	1.000 *	0.784 *	19	(10)
22.	22	11	1.000	1.000 *	0.600 *	53	(SO)
34.	34	11	1.000	1.000 *	0.600 *	53	(SO)
58.	58	11	1.000	1.000 ■	0.000 *	53	(SI)
23.	23	12	1.000	1.000 *	0.430 *	8	(7)
33.	38	12	1.000	1.000 ■	0.430 *	8	(7)
25.	25	13	1.000	1.000 *	0.614 ■	55	(21)
79.	79	13	1.000	1.000 ■	0.614 *	55	(21)
28.	28	SI			0.666 *	73	(SO)
33.	33	14	1.000	1.000 *	0.653 *	5	(5)
50.	50	14	1.000	1.000 *	0.653 *	5	(5)
41.	41	15	1.000	1.000 *	0.663 *	73	(SI)
78.	78	15	1.000	1.000 *	0.663 *	73	(SI)
46.	46	SI			0.704 *	66	(SI)
49.	49	18	1.000	1.000 *	0.514 *	25	(13)
60.	60	18	1.000	1.000 *	0.514 *	25	(13)
51.	51	19	1.000	1.000 ■	0.434 *	42	(16)
61.	61	19	1.000	1.000 *	0.434 *	42	(16)
55.	55	21	1.000	1.000 *	0.614 *	25	(13)
62.	62	21	1.000	1.000 *	0.614 *	25	(13)
64.	64	SI			0.771 *	69	(SO)
69.	69	SI			0.771 *	64	(SO)
66.	66	SI			0.749 *	19	(10)
70	170	SI			0.707 *	1	(D)
75.	175	SI			0.386 *	23	(12)

PHENOTYPES in wo-log/ *CALCULATED DIVERSITY INDEX - 0.987		Identity level - 0.987 TRUE DIVERSITY INDEX - 0.967		€ 7m			
No	Name	Ph.P. type	sim	□Iml mean	sim max	to nr	Ph.P. type
1	II BACILLUS	I	1.000	1.000*	0.000*	(5)	
6	IMICROCO LUT	I	1.000	1.000*	0.000*	44	(Si)
11	II 11	I	1.000	1.000*	0.000*	4	(3)
12	II 12	I	1.000	1.000*	0.000□	4	(3)
15	II 15	I	1.000	1.000*	0.000*	29	(16)
21	1121	I	1.000	1.000*	0.000*	29	(16)
34	1134	I	1.000	1.000□	0.000■	51	(SO)
35	II 35	I	1.000	1.000*	0.000*	51	(SO)
40	ICONTROL	I	1.000	1.000■	0.000*	10	(6)
64	1164	I	1.000	1.000*	0.000*	56	(SO)
75	II 75	I	1.000	1.000*	0.000*	28	(15)
66	ICONTROL	I	1.000	1.000*	0.000*	50	(18)
2	CAMPYLOB	SI			0.502*	60	(SO)
3	IFLAVORAC AQUA	2	1.000	1.000□	0.884*	30	(SO)
16	116	2	1.000	1.000*	0.864*	30	(SO)
30	30	SI			0.884*	3	(2)
8	PROTEUS VULG	5	1.000	1.000*	0.816*	29	(16)
14	14	5	1.000	1.000*	0.816*	29	(16)
41	41	5	1.000	1.000*	0.816*	29	(16)
62	62	5	1.000	1.000*	0.816*	29	(16)
29	29	16	1.000	1.000*	0.876*	69	(SO)
38	38	16	1.000	1.000*	0.876*	69	(SO)
69	69	SI			0.876*	29	(16)
54	54	SI			0.868*	29	(16)
20	20	10	1.000	1.000*	0.774*	29	(16)
59	59	10	1.000	1.000*	0.774*	29	(16)
4	STREPTOCO FAE	3	1.000	1.000*	0.769*	10	(6)
9	9	3	1.000	1.000□	0.769*	10	(6)
39	39	3	1.000	1.000*	0.769*	10	(6)
77	77	3	1.000	1.000*	0.769*	10	(6)
10	10	6	1.000	1.000*	0.769*	4	(3)
42	42	6	1.000	1.000*	0.769*	4	(3)
72	72	6	1.000	1.000*	0.769*	4	(3)
5	ECOLI	4	1.000	1.000*	0.924*	44	(SO)
13	13	4	1.000	1.000*	0.924*	44	(SO)
32	32	4	1.000	1.000*	0.924*	44	(SO)
44	44	SI			0.924*	5	(4)
56	56	SI			0.924*	5	(4)
57	57	SI			0.923*	5	(4)
78	78	SI			0.922*	5	(4)
7	ENTEROBACTER CLOA	SI			0.949□	17	(7)
17	17	7	1.000	1.000*	0.949*	7	(SO)
36	36	7	1.000	1.000*	0.949*	7	(Si)
49	49	7	1.000	1.000*	0.949*	7	(SO)
18	18	8	1.000	1.000*	0.573*	50	(18)
37	37	8	1.000	1.000*	0.573*	50	(18)
53	53	8	1.000	1.000*	0.573*	50	(18)
19	19	9	1.000	1.000*	0.434*	51	(Si)
33	33	9	1.000	1.000*	0.434*	51	(Si)
22	22	SI			0.604*	4	(3)
23	23	11	1.000	1.000□	0.921*	71	(Si)
31	31	11	1.000	1.000*	0.921*	71	(SO)
71	71	SI			0.921*	23	(11)
43	43	SI			0.786*	23	(11)
58	58	SI			0.786*	23	(11)
24	24	12	1.000	1.000*	0.851*	61	(Si)
46	46	12	1.000	1.000*	0.851*	61	(Si)
61	61	SI			0.852*	66	(Si)
66	66	SI			0.852*	61	(SO)
25	25	13	1.000	1.000□	0.688*	69	(Si)
55	55	13	1.000	1.000*	0.688*	69	(Si)
26	26	SI			0.478*	54	(SO)
27	27	14	1.000	1.000*	0.669*	70	(SO)
47	47	14	1.000	1.000*	0.669*	70	(SO)
28	28	15	1.000	1.000*	0.893*	70	(Si)
48	48	15	1.000	1.000*	0.893*	70	(SO)
70	70	SI			0.893*	28	(15)
74	74	SI			0.813*	28	(15)
45	45	17	1.000	1.000*	0.565*	56	(SO)
63	63	17	1.000	1.000*	0.565*	56	(Si)
50	50	18	1.000	1.000*	0.573*	18	(8)
68	68	18	1.000	1.000*	0.573*	18	(6)
51	51	SI			0.644*	76	(SO)
52	52	SI			0.501*	18	(8)
60	60	SI			0.642*	27	(14)
65	65	SI			0.544*	27	(14)
67	67	19	1.000	1.000*	0.556*	50	(18)
79	79	19	1.000	1.000*	0.556□	50	(18)
73	73	SI			0.514*	18	(8)
78	78	SI			0.644*	51	(SO)

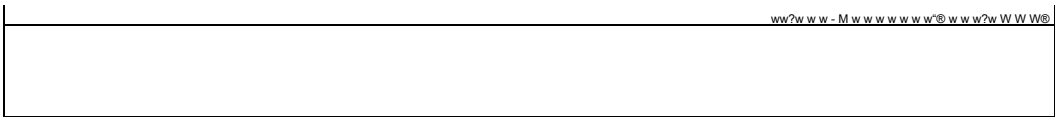
II 2SS EfffEggggggfEgEag5EfffEggEgI
22°->="!;SStt^ == r-SSS"" = == ^ = SSSSS»S">aSS"f-5»»«SSS""tStESfSSSSS3RS3SSS'""55S»SKS5SaS2

I? iII!ilIIIiil!!!!!!II!IillI111!111!IIIi!i!ilIiI11111!iillI11111IIT!li!iililiii

!!!!!!§!!!!!!! §!!!!!!§!!!! iii! I!!§1!!§1§§!§!111§§! I! 11181! i§ §§
iilililililililililS iiiiiillliliii §§§!! ilililililililililililil II 181111 ii §§
»».a>0, °g°°22,2s».;2s2s»»»cc:»i5es».



[IiH:?!s!; = llll = isfs46sSSs?SSSS5gf;aSs55SK.aS;S2SSCt:S2SSKa?3553SSSSRRSS"85S5SBgC
:~^S»SSS^5iSSSSKSri = K»<;sSfe»5?asSSR^SSf3\$"l2a^?iS' = BSSICtSSS'«SR?3SS'SSSSi:aa3SS?SE?!;KC



3!I!il!!!I!!!i!!i!l8111!IISiI!8!II!!IISSIIII!l!13!IIIIi!i!l!!!l11i!3!SIllIaiil

ii iiiiiiiiiiHiii itttiii §;; **m** iitifi! nsitSiSSS « H H !!
» iiiiiHiiHHH mm is! m wm hhhhhh a « u h

i 1 ii s **A** s I
2LS-S5ll = = SSlsl = §S"3SK?;s"a33SSStSS5ls5|F!SS = SSBSS2SP::SESSR5:SSi5S5SSSS5SssaS!??gS0SS
'~»S^ri~ = 2afiS-si.pig,2~SSKSS«Sj2CS = S33-25VRsga = giSK'S24KisS23RftS15SS5SRES3SSSSSS?SSSSS'

^CALCULATED DIVERSITY INDEX - 0.971		WordWj_iaval-0.875 TRUE DIVERSITY INDEX - 0.972					
No	Name	PhP- type	sim min	sim mean	sim max	to	PhP type
1	E COLI	1	0.984	0.989 ■	0.985 ?	60	(SI)
9	9	1	0.984	0.989 *	0.985 ?	60	(SI)
29	29	1	0.978	0.987 '	0.971 *	60	(SI)
49	49	1	0.971	0.988 *	0.973 *	60	(SI)
73	73	1	0.968	0.986 *	0.966 *	60	(SI)
78	78	1	0.964	0.988 *	0.968 *	60	(SI)
53	53	1	0.978	0.982 *	0.963 *	60	(SI)
57	57	1	0.964	0.976 *	0.966 '	60	(SI)
60	60	Si			0.985 7	1	(1)
2	MICROCO SP	2	0.984	0.989 *	0.980 7	25	(SI)
37	37	2	0.978	0.984 *	0.972 *	25	(SI)
31	31	2	0.972	0.985 *	0.965 *	25	(SI)
33	33	2	0.964	0.980 '	0.974 *	25	(SI)
39	39	2	0.964	0.975 ?	0.957 *	25	(SI)
25	25	Si			0.980 7	2	(2)
42	42	12	0.982	0.991 *	0.926 *	2	(2)
58	58	12	0.979	0.989 *	0.925 *	2	(2)
51	51	12	0.979	0.981 *	0.923 *	25	(SI)
24	CONTROL	10	0.997	0.997 *	0.950 '	56	(SI)
80	CONTROL	10	0.997	0.997 *	0.946 *	56	(SI)
56	CONTROL	Si			0.950 *	24	(10)
20	20	Si			0.874 *	25	(SI)
27	27	Si			0.884 *	51	(12)
8	CLOSTRIDIUM SP	7	0.983	0.988 '	0.955 '	16	(SI)
40	40	7	0.970	0.982 *	0.964 *	16	(SI)
65	65	7	0.970	0.977 *	0.964 *	16	(SI)
16	16	Si			0.964 *	40	(7)
17	17	SI			0.955 '	19	(SI)
19	19	SI			0.955 *	17	(SI)
72	72	SI			0.913 *	19	(SI)
35	35	SI			0.842 *	80	(10)
4	PSEUDO AEROG	4	0.986	0.986 ■	0.975 7	34	(11)
23	23	4	0.968	0.977 *	0.958 *	34	(11)
76	76	4	0.968	0.977 *	0.958 *	34	(11)
34	34	11	0.997	0.997 *	0.975 ?	4	(4)
68	68	11	0.997	0.997 *	0.969 *	4	(4)
14	14	9	0.985	0.985 *	0.965 *	4	(4)
18	18	9	0.985	0.985 *	0.966 *	4	(4)
74	74	Si			0.958 *	4	(4)
77	77	Si			0.890 *	4	(4)
5	PSEUDO FLUORE	Si			0.948 *	11	(SI)
11	11	Si			0.948 '	5	(SI)
64	64	Si			0.948 '	5	(SI)
67	67	SI			0.948 *	5	(SI)
71	71	SI			0.948 *	5	(SI)
28	28	SI			0.882 *	5	(SI)
12	12	SI			0.972 *	22	(SI)
22	22	SI			0.972 *	12	(SI)
43	43	Si			0.834 *	5	(SI)
36	36	Si			0.890 *	55	(SI)
55	55	Si			0.890 ■	36	(SI)
50	50	SI			0.866 *	11	(SI)
6	SALMONELLA TYPH	5	0.990	0.995 '	0.772 *	75	(13)
30	30	5	0.990	0.995 '	0.772 *	75	(13)
45	45	5	0.989	0.993 *	0.773 *	75	(13)
61	61	5	0.985	0.991 *	0.768 '	75	(13)
38	38	5	0.979	0.990 *	0.772 *	77	(SI)
46	46	5	0.982	0.992 *	0.748 *	77	(SI)
52	52	5	0.979	0.986 '	0.781 *	75	(13)
66	66	13	0.980	0.988 *	0.790 *	69	(SI)
70	70	13	0.972	0.984 *	0.811 *	69	(SI)
75	75	13	0.988	0.991 '	0.788 *	69	(SI)
79	79	13	0.972	0.981 *	0.795 *	69	(SI)
69	69	Si			0.811 *	70	(13)
7	STREPTOCO FAE	6	0.982	0.994 '	0.959 ■	62	(SI)
15	15	6	0.980	0.993 *	0.958 *	62	(SI)
59	59	6	0.982	0.994 '	0.959 *	62	(SI)
47	47	6	0.975	0.989 *	0.951 *	62	(SI)
54	54	6	0.975	0.980 *	0.930 *	62	(SI)
62	62	Si			0.959 *	7	(6)
10	10	a	1.000	1.000 *	0.927 *	21	(SI)
13	13	8	1.000	1.000 *	0.927 *	21	(SI)
21	21	SI			0.927 *	10	(8)
26	26	Si			0.875 '	32	(SI)
32	32	Si			0.875 '	26	(SI)
41	41	SI			0.800 *	34	(11)
3	KLEBSIELLA PNEU	3	0.979	0.989 *	0.972 *	48	(SI)
63	63	3	0.981	0.989 *	0.970 *	48	(SI)
44	44	3	0.979	0.980 *	0.946 *	48	(SI)
48	48	Si			0.972 *	3	(3)

PHENOTYPES In aXu*tl/ - IdentUly level - 0.975
 *CALCULATED DIVERSITY INDEX - 0.877 TRUE DIVERSITY INDEX - 0.976

No	Name	PhP. type	sim min	mean	aim max	to nr	PhP type
1.	STREPTOCO FAE		0.987	0.993 *	0.793 *	9	(Si)
53.	53	1	0.984	0.990 *	0.785 *	9	(Si)
60.	60	1	0.979	0.990 *	0.743 *	9	(so)
62.	62	1	0.979	0.991 *	0.782 *	9	(SO)
71.	70	1	0.976	0.989 *	0.780 *	9	(Si)
76.	75	1	0.978	0.988 *	0.747 *	9	(SO)
79.	78	1	0.976	0.980 *	0.843 *	9	(SO)
9.	9	Si					(1)
4.	PSEUDO AEROG	3	1.000	1.000 *	0.912 *	36	(SO)
14.	14	3	1.000	1.000 *	0.912 *	36	(SO)
45.	45	3	1.000	1.000 *	0.912 *	36	(Si)
61.	61	3	1.000	1.000 *	0.912 *	36	(SO)
68.	67	3	1.000	1.000 *	0.912 *	36	(SO)
36.	36	Si			0.912 *	4	(3)
50.	50	12	1.000	1.000 *	0.901 *	4	(3)
69.	68	12	1.000	1.000 *	0.901 *	4	(3)
72.	71	Si			0.922 *■	78	(Si)
78.	>7	Si			0.922 *	72	(SO)
19.	19	Si			0.910 *	30	(SO)
30.	30	Si			0.910 *	19	(SO)
5.	MICROCO SP	4	0.990	0.991 *	0.960 *	64	(10)
15.	15	4	0.980	0.989 *	0.949 *	64	(10)
22.	22	4	0.976	0.987 *	0.946 *	64	(10)
29.	29	4	0.976	0.982 *	0.949 *	64	(10)
40.	40	10	0.984	0.990 *	0.944 *	70	(14)
56.	56	10	0.983	0.989 *	0.946 *	70	(14)
64.	63	10	0.983	0.984 *	0.960 *	5	(4)
70.	69	14	1.000	1.000 *	0.946 *	56	(to)
74.	73	14	1.000	1.000 *	0.946 *	56	(10)
34.	34	Si			0.894 *	5	(4)
12.	12	Si			0.793 *	34	(SO)
8.	CLOSTRIDIUM	6	0.983	0.989 *	0.983 *	28	(so)
75.	74	6	0.983	0.989 *	0.983 ?	28	(so)
18.	18	6	0.983	0.989 *	0.960 *	28	(SO)
51.	51	6	0.983	0.989 *	0.960 *	28	(SO)
28.	28	Si			0.983 ?	8	(6)
13.	13	Si			0.979 ?	8	(6)
44.	44	Si			0.960 *	13	(so)
24.	CONTROL	8	0.993	0.993 *	0.952 *	81	(SO)
43.	CONTROL	8	0.993	0.993 *	0.945 *	81	(so)
25.	25	Si			0.968 *	25	(SO)
81.	CONTROL	Si			0.968 *	25	(Si)
21.	21	Si			0.903 *	25	(so)
31.	31	9	1.000	1.000 *	0.882 *	8	(6)
59.	59	9	1.000	1.000 *	0.882 *	8	(6)
3.	PSEUDO FLOURE	Si			0.900 *	43	(SO)
43.	43	Si			0.900 ■	3	(SO)
37.	37	Si			0.882 *	8	(6)
35.	35	Si			0.833 *	3	(so)
41.	41	Si			0.820 *	3	(SO)
80.	79	Si			0.833 *	3	(SO)
7.	ECOLI	5	0.997	0.998 *	0.940 *	16	(7)
33.	33	5	0.997	0.998 *	0.940 *	16	(7)
42.	42	5	0.998	0.998 *	0.938 *	16	(7)
54.	54	5	0.997	0.998 *	0.938 *	16	(7)
57.	57	5	0.997	0.998 *	0.938 *	16	(7)
16.	16	7	1.000	1.000 *	0.940 *	7	(5)
17.	17	7	1.000	1.000 *	0.940 *	7	(5)
27.	27	Si			0.938 *	7	(5)
52.	52	Si			0.772 *	30	(Si)
2.	SALMONELLA PARA	2	0.989	0.996 *	0.821 *	10	(Si)
47.	47	2	0.989	0.996 *	0.821 *	10	(Si)
55.	55	2	0.989	0.996 *	0.821 *	10	(SO)
23.	23	2	0.992	0.994 *	0.823 *	10	(SO)
38.	38	2	0.989	0.990 *	0.829 *	63	(13)
10.	10	Si			0.951 *	63	(13)
63.	63	13	1.000	1.000 *	0.951 *	10	(SO)
65.	64	13	1.000	1.000 *	0.951 *	10	(Si)
58.	58	Si			0.945 *	10	(Si)
6.	KLEBSIELLA PNEU	Si			0.8G3 *	20	(SO)
46.	4G	11	1.000	1.000 *	0.854 *	6	(Si)
73.	72	11	1.000	1.000 ■	0.854 *	6	(Si)
11.	11	Si			0.845 *	6	(Si)
26.	26	Si			0.845 *	6	(Si)
32.	32	Si			0.845 *	6	(SO)
39.	39	Si			0.845 *	6	(Si)
87.	66	Si			0.845 *	6	(Si)
20.	20	Si			0.967 *	49	(SO)
49.	49	Si			0.967 *	20	(SO)
66.	65	Si			0.920 *	77	(SO)
77.	7G	Si			0.920 *	66	(Si)

PHENOTYPES to akuaos/ CALCULATED DIVERSITY INDEX - 0.982		Identity level -0.975 TRUE DIVERSITY INDEX - 0.977					
No	Name	PHP-type	sim min	sim mean	sim max	to nr	PHP type
1.	STREPTOCO FAE	1	1.000	1.000 *	0.959 *	20	(S)
31.	31	1	1.000	1.000 *	0.959 *	20	(S)
20.	20	SI			0.959 '	1	(1)
26.	26	SI			0.958 *	1	(1)
10.	10	SI			0.957 *	1	(1)
59.	59	SI			0.957 '	1	(1)
16.	16	SI			0.957 '	1	(1)
40.	40	SI			0.957 '	1	(1)
35.	35	SI			0.958 *	1	(1)
72.	72	SI			0.957 *	1	(1)
3.	MICROCO SP	3	0.984	0.994 *	0.983 ?	67	(14)
47.	47	3	0.984	0.994 '	0.983 ?	67	(14)
81.	80	3	0.984	0.994 *	0.983 ?	67	(14)
42.	42	3	0.978	0.990 *	0.977 ?	67	(14)
77.	76	3	0.972	0.986 *	0.971 '	67	(14)
57.	57	3	0.972	0.980 *	0.964 *	67	(14)
67.	67	14	1.000	1.000 *	0.983 ?	3	(3)
74.	73	14	1.000	1.000 *	0.983 ?	3	(3)
70.	69	SI			0.981 ?	3	(3)
79.	78	SI			0.982 ?	3	(3)
24.	CONTROL	SI			0.945 *	48	(12)
48.	CONTROL	12	1.000	1.000 ■	0.945 *	24	(SO)
82.	CONTROL	12	1.000	1.000 *	0.945 *	24	(SO)
73.	72	SI			0.879 ■	24	(SO)
7.	CLOSTRIDIUM	6	1.000	1.000 *	0.878 '	39	(SO)
65.	65	6	1.000	1.000 *	0.878 '	39	(SI)
39.	39	SI			0.878 '	7	(6)
30.	30	SI			0.869 '	7	(6)
49.	49	SI			0.927 '	53	(SI)
53.	53	SI			0.927 *	49	(SI)
61.	61	13	1.000	1.000 ■	0.927 *	49	(SI)
63.	63	13	1.000	1.000 *	0.927 *	49	(SO)
2.	PSEUDO AEROG	2	0.984	0.992'	0.909 *	23	(SO)
18.	18	2	0.984	0.992 *	0.909 *	23	(SO)
43.	43	2	0.984	0.992 ■	0.909 '	23	(SI)
75.	74	2	0.984	0.992 *	0.909 *	23	(SO)
11.	11	2	0.972	0.985 *	0.894 '	46	(SO)
78.	77	2	0.972	0.985 *	0.894 *	46	(SI)
54.	54	2	0.972	0.981 *	0.902 *	23	(SI)
23.	23	SI			0.909 *	2	(2)
46.	46	SI			0.903 *	2	(2)
21.	21	10	1.000	1.000 *	0.896 *	2	(2)
69.	68	10	1.000	1.000 *	0.896 *	2	(2)
371.	37	SI			0.834 *	21	(10)
8.	SHIGELLA DYSEN	7	0.992	0.993 *	0.945 *	33	(SO)
22.	22	7	0.989	0.992 *	0.948 ■	33	(SI)
13.	13	7	0.989	0.991 *	0.937 *	33	(SI)
33.	33	SI			0.948 ■	22	(7)
9.	SALMONELLA TYPH	8	0.985	0.992 *	0.986 ?	56	(9)
45.	45	8	0.980	0.989 *	0.983 ?	56	(9)
41.	41	8	0.980	0.983 *	0.970 *	56	(9)
17.	17	9	0.981	0.986 *	0.968 *	9	(8)
56.	56	9	0.991	0.991 '	0.986 ?	9	(8)
66.	66	9	0.981	0.986 *	0.968 *	9	(8)
29.	29	SI			0.935 *	45	(8)
51.	51	SI			0.935 *	45	(8)
4.	KLEBSIELLA PNEU	4	0.998	0.999 *	0.972 *	12	(SO)
60.	60	4	0.998	0.999 *	0.972 *	12	(SI)
62.	62	4	0.998	0.999 *	0.972 ■	12	(SO)
52.	52	4	0.998	0.998 *	0.968 *	12	(SI)
12.	12	SI			0.972 *	4	(*)
44.	44	SI			0.972 *	4	(4)
58.	58	SI			0.918 *	4	(4)
64.	64	SI			0.874 '	58	(SO)
19.	19	SI			0.845 ■	4	(4)
71.	70	SI			0.845 *	4	(4)
6.	PSEUDO FLUORE	SI			0.948 *	15	(SO)
15.	15	SI			0.948 *	6	(SI)
25.	25	4 Si			0.948 *	6	(SI)
28.	28	SI			0.948 *	6	(SI)
50.	50	SI			0.914 *	8	(SO)
34.	34	SI			0.966 '	55	(SI)
55.	55	SI			0.960 *	34	(SI)
5.	ECOLI	5	1.000	1.000 ■	0.985 ?	27	(11)
76.	75 '	5	1.000	1.000 *	0.985 ?	27	(11)
27.	27	11	0.987	0.987 *	0.985 ?	5	(5)
32.	32	11	0.987	0.987 *	0.945 *	5	(5)
14.	14	SI			0.938 *	5	(5)
38.	38	SI			0.938 *	5	(5)
80.	79-	SI			0.939 *	5	(5)
36.	36	SI			0.938 *	5	(5)
68.	68	SI			0.604 ■	55	(SI)

Anunak 8 d.

PHENOTYPES in akumall/ Identity tetra - 0.975
CALCULATED DIVERSITY INDEX - 0.875 TRUE DIVERSITY INDEX - 0.676

No	Name	PhP- type	in In	aim mean	sim	to nr	PhP type
1.	STREPTOCO FAE	1	1.000	1.000 *	0.958 *	18	(SI)
32.	32	1	1.000	1.000 *	0.958 *	18	(SI)
12.	12	SI			0.957 *	1	(1)
16.	16	SI			0.955 *	12	(SI)
18.	18	SI			0.958 *	1	(1)
29.	29	SI			0.957 *	1	(1)
22.	22	SI			0.957 *	1	(1)
44.	44	SI			0.957 *	1	(1)
25.	25	SI			0.957 *	1	(1)
2.	PSEUDO FLUORE	2	0.991	0.991 *	0.991 ?	15	(9)
0.	9	2	0.991	0.991 *	0.980 ?	15	(9)
15.	15	9	0.992	0.992 *	0.991 ?	2	(2)
28.	28	9	0.992	0.992 *	0.985 *	2	(2)
38.	38	SI			0.928 *	2	(2)
3.	PSEUDO AEROG	3	0.984	0.992 *	0.970 *	41	(SI)
80.	79	3	0.984	0.992 *	0.970 *	41	(SI)
63.	63	3	0.984	0.984 *	0.951 *	41	(SO)
41.	41	SI			0.970 *	3	(3)
46.	46	SI			0.970 *	3	(3)
57.	57	SI			0.966 *	3	(3)
47.	47	12	0.983	0.983 *	0.896 *	3	(3)
61.	61	12	0.983	0.983 *	0.900 *	41	(SI)
54.	54	SI			0.901 *	3	(3)
50.	50	SI			0.898 *	3	(3)
37.	37	SI			0.868 *	24	(SI)
52.	52	SI			0.917 *	78	(SO)
78.	77	SI			0.917 *	52	(SO)
69.	69	16	0.992	0.996 *	0.917 *	78	(SO)
71.	70	16	0.992	0.996 *	0.917 *	78	(SI)
75.	74	16	0.992	0.992 *	0.910 *	78	(SO)
7.	CLOSTRIDIUM	7	1.000	1.000 *	0.850 *	46	(13)
53.	53	7	1.000	1.000 *	0.850 *	48	(13)
17.	17	10	0.984	0.984 *	0.926 *	65	(15)
23.	23	10	0.984	0.984 *	0.926 *	65	(15)
65.	65	15	0.983	0.997 *	0.926 *	17	(10)
74.	73	15	0.969	0.979 *	0.918 *	17	(10)
79.	78	15	0.969	0.976 *	0.901 *	17	(10)
24.	CONTROL	SI			0.960 *	48	(13)
48.	CONTROL	13	0.976	0.976 *	0.960 *	24	(SO)
81.	CONTROL	13	0.976	0.976 *	0.955 *	24	(SO)
31.	31	SI			0.880 *	17	(10)
33.	33	11	1.000	1.000 *	0.815 *	66	(14)
38.	38	11	1.000	1.000 *	0.815 *	66	(14)
49.	49	SI			0.936 *	59	(SO)
59.	59	SI			0.938 *	49	(SO)
64.	64	U	0.969	0.983 *	0.807 *	33	(11)
68.	68	14	0.969	0.981 *	0.793 *	33	(11)
66.	68	14	0.973	0.982 *	0.819 *	49	(SO)
77.	76	14	0.984	0.989 *	0.826 *	59	(SO)
73.	72	14	0.969	0.978 *	0.850 *	49	(SO)
4.	KLEBSIELLA PNEU	4	1.000	1.000 *	0.973 *	39	(SO)
60.	60	4	1.000	1.000 *	0.973 *	39	(SO)
39.	39	SI			0.973 *	4	(4)
11.	11	SI			0.938 *	4	(4)
21.	21	SI			0.938 *	4	(4)
43.	43	SI			0.938 *	4	(4)
34.	34	SI			0.968 *	67	(SO)
67.	67	SI			0.968 *	34	(SI)
6.	ENTEROBACTER AERO	8	0.992	0.992 *	0.728 *	39	(SI)
56.	56	6	0.992	0.992 *	0.799 *	39	(so)
5.	E COLI	5	0.980	0.993 *	0.939 *	76	(SI)
19.	19	5	0.979	0.991 *	0.941 *	76	(SO)
27.	27	5	0.979	0.991 *	0.941 *	76	(SI)
14.	14	5	0.976	0.988 *	0.940 *	51	(SI)
35.	35	5	0.976	0.988 *	0.941 *	55	(SI)
70.	70	5	0.970	0.989 *	0.935 *	51	(SI)
72.	71	5	0.970	0.989 *	0.935 *	51	(SI)
30.	30	5	0.972	0.985 *	0.937 *	51	(SO)
62.	62	5	0.970	0.975 *	0.919 *	76	(SO)
51.	51	SI			0.940 *	14	(5)
76.	75	SI			0.941 *	19	(5)
55.	55	SI			0.941 *	35	(5)
8.	PROTEUS MIRA	8	0.990	0.992 *	0.932 *	42	(SI)
40.	40	8	0.990	0.992 *	0.932 *	42	(SI)
10.	10	8	0.978	0.983 *	0.930 *	42	(SI)
13.	13	8	0.978	0.983 *	0.873 *	42	(SI)
20.	20	8	0.978	0.983 *	0.930 *	42	(SI)
26.	28	8	0.978	0.983 *	0.930 *	42	(SI)
42.	42	SI			0.932 *	8	(0)
45.	45	SI			0.928 *	42	(SI)
58.	58	SI			0.591 *	50	(so)

IDENTITY INDEX - 0.975
 LGULATED DIVERSITY INDEX - 0.956 TRUE DIVERSITY INDEX - 0.853

No	Name	PhP-type	mln	aim-mean	sim	to	PhP-type
1.	STREPTOCO FAE	1	0.992	0.997 *	0.959 *	179	(SI)
26	26	1	0.990	0.996 *	0.960 *	167	(SI)
98	93	1	0.992	0.997 *	0.959 *	179	(SI)
103.	103	1	0.992	0.997 *	0.959 *	179	(SI)
110.	STREPTOCO FAE	1	0.992	0.997 *	0.959 *	179	(SI)
133.	79	1	0.992	0.997 *	0.959 *	179	(SI)
39.	39	1	0.991	0.995 *	0.972 *	140	(SI)
12.	12	1	0.988	0.992 *	0.959 *	167	(SI)
20.	20	1	0.933	0.991 *	0.952 *	159	(SO)
24.	24	1	0.987	0.993 *	0.980 7	179	(SO)
33.	33	1	0.984	0.991 *	0.984 7	173	(SO)
36.	36	1	0.984	0.991 *	0.984 7	167	(SO)
181.	77	1	0.983	0.990 *	0.953 7	119	(SO)
167.	63	Si			0.984 ?	36	(I)
171.	67	Si			0.957 *	1	(I)
119.	15	Si			0.958 *	12	(I)
159.	55	Si			0.959 *	26	(I)
173.	69	Si			0.984 7	33	(I)
123.	24	Si			0.952 *	179	(SO)
179.	75	Si			0.980 7	24	(I)
140.	36	Si			0.972 *	39	(I)
112.	CITROBAC AMA	26	1.000	1.000 *	0.930 ■	128	(SO)
123.	19	26	1.000	1.000 ■	0.930 *	128	(SO)
6.	MICROCO SP	6	0.991	0.994 *	0.926 *	161	(27)
68.	68	6	0.991	0.994 *	0.926 *	161	(27)
111.	MICROCO SP	6	0.991	0.994 *	0.926 *	161	(27)
76.	76	6	0.985	0.990 *	0.891 *	161	(27)
90.	90	6	0.930	0.988 *	0.922 *	161	(27)
129.	25	6	0.980	0.988 *	0.922 7	161	(27)
113.	9	6	0.980	0.988 *	0.922 *	161	(27)
133.	29	6	0.980	0.988 *	0.922 *	161	(27)
161.	57	27	0.983	0.992 *	0.926 7	6	(6)
168.	64	27	0.983	0.992 *	0.926 *	6	(6)
166.	62	27	0.983	0.983 *	0.901 *	6	(6)
57.	57	18	1.000	1.000 *	0.815 *	161	(27)
73.	73	18	1.000	1.000 *	0.815 *	161	(27)
18.	18	9	0.981	0.996 7	0.983 7	63	(20)
50.	50	9	0.981	0.996 *	0.983 ?	63	(20)
59.	59	9	0.981	0.996 *	0.983 7	63	(20)
77.	77	9	0.981	0.996 *	0.983 7	63	(20)
105.	BACILLUS	9	0.981	0.996 *	0.983 7	63	(20)
127.	23	9	0.981	0.996 *	0.983 7	63	(20)
141.	37	9	0.981	0.996 *	0.983 7	63	(20)
65.	65	9	0.979	0.994 *	0.977 7	63	(20)
134.	30	9	0.976	0.992 *	0.976 7	63	(20)
121.	17	9	0.969	0.982 *	0.962 *	63	(20)
170.	66	9	0.969	0.979 *	0.969 *	63	(20)
63.	63	20	1.000	1.000 *	0.983 7	18	(9)
130.	26	20	1.000	1.000 *	0.983 7	18	(9)
32.	CONTROL	12	0.975	0.981 *	0.965 *	72	(22)
184.	CONTROL	12	0.982	0.984 *	0.982 7	104	(22)
152.	CONTROL	12	0.975	0.979 *	0.973 7	104	(22)
72.	CONTROL	22	0.997	0.997 *	0.979 ?	184	(12)
104.	CONTROL	22	0.997	0.997 *	0.982 7	184	(12)
56.	56	17	1.000	1.000 *	0.892 *	152	(12)
137.	33	17	1.000	1.000 *	0.892 *	152	(12)
41.	41	13	0.933	0.996 *	0.983 ?	47	(15)
69.	69	13	0.983	0.996 *	0.983 7	47	(15)
117.	13	13	0.983	0.900 *	0.983 7	47	(15)
120.	16	13	0.983	0.996 *	0.983 7	47	(15)
75.	75	13	0.981	0.992 *	0.959 *	47	(15)
125.	21	13	0.975	0.992 *	0.975 7	47	(15)
61.	61	13	0.975	0.981 *	0.984 7	53	(15)
47.	47	15	0.984	0.984 1	0.983 7	41	(13)
53.	53	15	0.984	0.984 *	0.984 7	61	(13)
3.	PSEUDO FLUORE	3	0.980	0.993 *	0.965 *	9	(SI)
164.	60	3	0.980	0.993 *	0.965 *	9	(SI)
169.	65	3	0.980	0.993 *	0.965 *	9	(SI)
34.	34	3	0.974	0.987 *	0.952 7	9	(SI)
33.	38	3	0.974	0.979 *	0.893 7	9	(SO)
9.	9	SI			0.065 *	3	(3)
85.	35	25	1.000	1.000 *	0.874 *	38	(3)
92.	92	25	1.000	1.000 *	0.874 *	38	(3)
42.	42	SI			0.896 *	49	(SI)
62.	62	SI			0.903 *	54	(SI)
49.	49	SI			0.903 *	54	(SO)
54.	54	SI			0.903 *	49	(SO)
4.	PSEUDO AEROG	4	0.985	0.995 *	0.986 7	132	(11)
25.	35	4	0.985	0.995 *	0.906 7	132	(11)
44.	44	4	0.985	0.995 *	0.906 7	132	(11)
60.	60	4	0.985	0.995 *	0.986 7	132	(11)
108.	PSEUDO AEROG	4	0.985	0.995 *	0.986 ?	132	(11)

Appendix - 8 F

PHENOTYPES In aka*oilg/ ^CALCULATED DIVERSITY INDEX - 0.978		Identity toval - 0.975 TRUE DIVERSITY INDEX - 0.978					
No Nama	PhP- *im tpa mln	*im mean	sim max	to nr	PhP lypo		
1.	BACILLUS	1	0.983	0.989 *	0.941 *	56	(SI)
13.	13	1	0.978	0.986 *	0.927 *	56	(SI)
35.	35	1	0.976	0.979 *	0.924 *	56	(SO)
32.	CONTROL	SI		0.969 *	0.969 *	80	(SO)
60.	CONTROL	SI		0.969 *	0.969 *	32	(SO)
56.	CONTROL	SI		0.962 *	0.962 *	32	(SO)
44.	44	SI		0.892 *	0.892 *	1	(1)
18.	16	SI		0.905 *	0.905 *	47	(SO)
24.	24	SI		0.882 *	0.882 *	18	(SO)
26.	26	SI		0.882 *	0.882 *	18	(SO)
47.	47	SI		0.932 *	0.932 *	56	(SO)
55.	55	SI		0.914 *	0.914 *	47	(SO)
57.	57	SI		0.922 *	0.922 *	68	(SO)
66.	66	SI		0.922 *	0.922 *	57	(SO)
5.	PSEUDOMONAS	4	1.000	1.000 *	0.912 *	21	(9)
10.	10	4	1.000	1.000 *	0.912 *	21	(9)
17.	17	4	1.000	1.000 *	0.912 *	21	(9)
21.	21	9	1.000	1.000 *	0.912 *	5	(4)
52.	52	9	1.000	1.000 *	0.912 *	5	(4)
30.	30	SI		0.903 *	0.903 *	5	(4)
23.	23	SI		0.912 *	0.912 *	5	(4)
69.	69	SI		0.903 *	0.903 *	5	(4)
25.	25	10	1.000	1.000 *	0.909 *	5	(4)
33.	33	10	1.000	1.000 *	0.909 *	5	(4)
36.	38	10	1.000	1.000 *	0.909 *	5	(4)
43.	43	10	1.000	1.000 *	0.909 *	5	(4)
50.	50	12	0.996	0.956 *	0.906 *	64	(SO)
54.	54	12	0.992	0.994 *	0.906 *	64	(SO)
56.	56	12	0.992	0.994 *	0.914 *	64	(SO)
64.	64	SI		0.914 *	0.914 *	58	(12)
45.	45	11	1.000	1.000 *	0.855 *	24	(SO)
49.	49	11	1.000	1.000 *	0.855 *	24	(SO)
3.	KLEBSIELLA PNEU	3	0.993	0.999 *	0.918 *	41	(SO)
40.	40	3	0.998	0.999 *	0.918 *	41	(SO)
48.	40	3	0.998	0.999 *	0.918 *	41	(SO)
79.	79	3	0.998	0.998 *	0.917 *	41	(SO)
41.	41	SI		0.918 *	0.918 *	3	(3)
72.	72	SI		0.874 *	0.874 *	41	(SO)
59.	59	SI		0.845 *	0.845 *	3	(3)
65.	65	SI		0.845 *	0.845 *	3	(3)
6.	SALMONELLA TYPH	5	1.000	1.000 *	0.934 *	63	(SI)
60.*	60	5	1.000	1.000 *	0.934 *	63	(SO)
63.	63	SI		0.935 *	0.935 *	74	(SO)
74.	74	SI		0.935 *	0.935 *	63	(SO)
66.	66	13	1.000	1.000 *	0.933 *	6	(5)
76.	76	13	1.000	1.000 *	0.933 *	6	(5)
70.	70	SI		0.934 *	0.934 *	6	(5)
7.	STAPYLOCOCCUS AMR	6	0.995	0.998 *	0.923 *	78	(SO)
36.	36	6	0.995	0.998 *	0.923 *	78	(SO)
75.	75	6	0.995	0.995 *	0.918 *	78	(SO)
76.	76	SI		0.923 *	0.923 *	7	(6)
53.	53	SI		0.761 *	0.761 *	46	(SO)
6.	STREPTOCOCCUS FAE	7	0.995	0.997 *	0.957 *	29	(SO)
27.	27	7	0.995	0.997 *	0.957 *	29	(SO)
11.	11	7	0.996	0.997 *	0.948 *	29	(SO)
12.	12	7	0.995	0.997 *	0.959 *	34	(SO)
14.	14	7	0.995	0.997 *	0.959 *	34	(SO)
34.	34	SI		0.959 *	0.959 *	12	(7)
48.	46	SI		0.939 *	0.939 *	11	(7)
29.	29	SI		0.957 *	0.957 *	8	(7)
39.	39	SI		0.953 *	0.953 *	29	(SO)
51.	51	SI		0.922 *	0.922 *	8	(7)
62.	62	SI		0.772 *	0.772 *	6	(5)
2.	E COLI	2	0.988	0.996 *	0.945 *	28	(SO)
20.	20	2	0.988	0.996 *	0.945 *	28	(SI)
42.	42	2	0.988	0.996 *	0.945 *	28	(SO)
67.	67	2	0.988	0.996 *	0.945 *	28	(SO)
9.	9	2	0.989	0.994 *	0.943 *	73	(SO)
37.	37	2	0.992	0.993 *	0.944 *	73	(SI)
31.	31	2	0.984	0.993 *	0.943 *	73	(SI)
15.	15	2	0.984	0.989 *	0.934 *	28	(SO)
73.	73	SI		0.945 *	0.945 *	2	(2)
71.	71	SI		0.939 *	0.939 *	2	(2)
26.	28	SI		0.945 *	0.945 *	2	(2)
77.	77	SI		0.943 *	0.943 *	37	(1)
4.	PROTEUS MIRA	SI		0.748 *	0.748 *	16	(SI)
16.	16	SI		0.748 *	0.748 *	4	(SI)
19.	19	8	1.000	1.000 *	0.693 *	16	(SI)
22.	22	8	1.000	1.000 *	0.693 *	16	(SI)
61.	61	SI		0.671 *	0.671 *	23	(SO)

Appendix figure

Identity level - 0.978 W:
TRUE DIVERSITY INDEX = 0.989

PHENOTYPES in akulaIM/ _CALCULATED DIVERSITY INDEX - 0.990		Identity level - 0.978 W: TRUE DIVERSITY INDEX = 0.989					
No	Name	PhP type	sim min	sim mean	sim max	to nr	PhP typ@
1.	E COLI	1	1.000	1.000 *	0.945 *	75	(SI)
65.	65	1	1.000	1.000 *	0.945 *	75	(SI)
70.	70	1	1.000	1.000 *	0.945 *	75	(SI)
75.	75	SI			0.945 *	1	(1)
29.	29	SI			0.939 *	1	(1)
19.	19	SI			0.938 *	1	(1)
35.	35	SI			0.939 *	1	(1)
79.	79	SI			0.927 *	1	(1)
2.	BACILLUS	SI			0.903 *	55	(SI)
55.	55	SI			0.906 *	59	(SI)
45.	45	SI			0.890 *	2	(SI)
51.	51	SI			0.890 *	2	(SO)
42.	42	13	1.000	1.000 *	0.882 *	32	(10)
47.	47	13	1.000	1.000 *	0.882 *	32	(10)
58.	58	SI			0.876 *	2	(SO)
32.	CONTROL	10	0.990	0.990 *	0.875 *	4	(3)
80.	CONTROL	10	0.990	0.990 *	0.890 *	4	(3)
63.	63	SI			0.876 *	2	(SI)
37.	37	SI			0.910 *	59	(SI)
59.	59	SI			0.910 *	37	(SI)
60.	60	SI			0.882 *	2	(SO)
4.	MICROCO LUT	3	1.000	1.000 *	0.897 *	72	(SO)
68.	68	3	1.000	1.000 *	0.897 *	72	(SO)
72.	72	SI			0.897 *	4	(3)
74.	74	SI			0.892 *	4	(3)
10.	10	SI			0.874 *	4	(3)
21.	21	SI			0.870 *	4	(3)
5.	PSEUDO AEROG	4	0.996	0.998 *	0.975 *	14	(0)
11.	11	4	0.995	0.998 *	0.974 *	14	(9)
39.	39	4	0.996	0.998 *	0.975 *	14	(9)
22.	22	4	0.995	0.996 *	0.970 *	14	(9)
14.	14	9	0.978	0.978 *	0.975 *	5	(4)
43.	43	9	0.978	0.978 *	0.909 *	5	(4)
28.	28	SI			0.897 *	11	(4)
55.	55	SI			0.901 *	5	(4)
33.	33	SI			0.897 *	11	(4)
9.	SHIG SONNEI	8	0.989	0.989 *	0.949 *	20	(SO)
67.	67	8	0.989	0.994 *	0.936 *	20	(SO)
71.	71	8	0.989	0.994 *	0.936 *	20	(SO)
20.	20	SI			0.949 *	9	(8)
15.	15	SI			0.942 *	9	(8)
54.	54	SI			0.938 *	15	(SI)
27.	27	SI			0.874 *	4	(3)
3.	KLEBSIELLA PNEU	2	1.000	1.000 *	0.863 *	25	(SI)
30.	30	2	1.000	1.000 *	0.863 *	25	(SI)
25.	25	SI			0.863 *	3	(2)
24.	24	SI			0.854 *	3	(2)
16.	16	SI			0.845 *	3	(2)
36.	36	SI			0.845 *	3	(2)
18.	18	SI			0.845 *	3	(2)
64.	64	SI			0.812 *	45	(SI)
6.	SALMONELLA TYPH	5	0.995	0.996 *	0.933 *	41	(SO)
12.	12	5	0.993	0.995 *	0.956 *	48	(SO)
17.	17	5	0.993	0.994 *	0.934 *	41	(SI)
48.	48	SI			0.956 *	12	(5)
41.	41	SI			0.934 *	17	(5)
77.	77	SI			0.823 *	17	(5)
8.	PROTEUS MIRA	7	1.000	1.000 *	0.932 *	78	(SO)
69.	69	7	1.000	1.000 *	0.932 *	78	(SI)
78.	78	SI			0.932 *	8	(7)
73.	73	SI			0.930 *	8	(7)
49.	49	14	1.000	1.000 *	0.761 *	16	(SO)
61.	61	14	1.000	1.000 *	0.761 *	16	(SI)
7.	STREPTOCO FAE	6	0.997	0.999 *	0.959 *	57	(SI)
62.	62	6	0.997	0.999 *	0.959 *	57	(SI)
66.	66	6	0.997	0.999 *	0.959 *	57	(SI)
76.	76	6	0.997	0.999 *	0.978 *	50	(SO)
50.	50	SI			0.978 *	78	(6)
57.	57	SI			0.959 *	7	(6)
23.	23	SI			0.951 *	31	(SI)
31.	31	SI			0.958 *	7	(6)
26.	26	SI			0.939 *	23	(SI)
13.	13	SI			0.570 *	78	(SO)
34.	34	11	1.000	1.000 *	0.935 *	38	(SI)
44.	44	11	1.000	1.000 *	0.935 *	38	(SI)
38.	38	SI			0.935 *	34	(11)
40.	40	12	1.000	1.000 *	0.719 *	3	(2)
46.	46	12	1.000	1.000 *	0.719 *	3	(2)
52.	52	15	1.000	1.000 *	0.661 *	21	(SI)
53.	53	15	1.000	1.000 *	0.661 *	21	(SI)

292

PHENOTYPES In akwiliS/
*CALCULATED DIVERSITY INDEX - 0.091Appendix - On
Identity level - 0.975
TRUE DIVERSITY INDEX - 0.991

No	Nam#	PhP- typa	»im min	»im mean	»im max	to nr	PhP type
1.	BACILLUS	SI			0.907 *	48	(SI)
77.	77	SI			0.890 *	1	(SO)
61.	81	SI			0.893 *	48	(SO)
45.	45	9	1.000	1.000 *	0.883 *	80	(SO)
51.	51	9	1.000	1.000 *	0.863 *	80	(SO)
82.	62	9	1.000	1.000 *	0.863 *	80	(SO)
2.	CLOSTRIDIUM	1	1.000	1.000 *	0.905 *	79	(SO)
53.	53	1	1.000	1.000 *	0.905 *	78	(SO)
79.	79	SI			0.903 *	2	(1)
70.	70	SI			0.879 *	79	(so)
48.	CONTROL	SI			0.959 *	80	(SO)
80.	CONTROL	SI			0.959 *	48	(SO)
59.	59	SI			0.884 *	80	(SO)
38.	38	SI			0.882 *	2	(1)
8.	PSEUDO AEROG	5	1.000	1.000 *	0.915 *	68	(SO)
25.	25	5	1.000	1.000 *	0.915 *	68	(SO)
49.	49	5	1.000	1.000 *	0.915 *	68	(SO)
68.	68	SI			0.915 *	6	(5)
24.	24	SI			0.909 *	6	(5)
37.	37	SI			0.903 *	6	(5)
14.	14	SI			0.896 *	6	(5)
60.	60	SI			0.912 *	6	(5)
72.	72	SI			0.896 *	6	(5)
43.	43	8	0.990	0.990 *	0.964 *	54	(SI)
75.	75	8	0.990	0.990 *	0.950 *	54	(SO)
54.	54	SI			0.964 *	43	(8)
58.	58	SI			0.926 *	43	(8)
65.	65	SI			0.887 *	58	(SO)
5.	PROTEUS MIRA	4	1.000	1.000 *	0.932 *	11	(SO)
41.	41	4	1.000	1.000 *	0.932 *	11	(so)
47.	47	4	1.000	1.000 *	0.932 *	11	(SI)
35.	35	SI			0.932 *	5	(<)
19.	19	SI			0.931 *	5	(4)
30.	30	SI			0.931 *	5	(4)
11.	11	SI			0.968 *	23	(so)
23.	23	SI			0.968 *	11	(SO)
17.	17	sr			0.935 *	23	(SO)
64.	64	SI			0.929 *	11	(SO)
3.	ECOLI	2	0.995	0.998 *	0.940 *	22	(so)
27.	27	2	0.995	0.998 *	0.940 *	22	(so)
67.	67	2	0.995	0.998 *	0.940 *	22	(so)
10.	10	2	0.995	0.995 *	0.940 *	28	(so)
29.	29	SI			0.940 *	10	(2)
74.	74	SI			0.939 *	3	(2)
34.	34	SI			0.940 *	10	(2)
71.	71	SI			0.938 *	3	(2)
38.	38	SI			0.940 *	10	(2)
22.	22	SI			0.940 *	3	(2)
7.	SALMONELLA TYPH	6	1.000	1.000 *	0.934 *	9	(SO)
44.	44	6	1.000	1.000 *	0.934 *	9	(SI)
9.	9	SI			0.934 *	7	(6)
18.	18	SI			0.934 *	7	(6)
28.	28	SI			0.934 *	7	(6)
16.	16	SI			0.933 *	7	(6)
32.	32	7	1.000	1.000 *	0.934 *	7	(6)
50.	50	7	1.000	1.000 *	0.934 *	7	(6)
69.	69	SI			0.945 *	42	(SO)
42.	42	SI			0.946 *	56	(SO)
58.	58	SI			0.946 *	42	(SO)
73.	73	SI			0.945 *	42	(SO)
63.	63	SI			0.946 *	42	(SO)
78.	78	SI			0.914 *	63	(SI)
8.	STREPTOCO FAE	SI			0.959 *	13	(SO)
13.	13	SI			0.959 *	8	(SI)
28.	28	SI			0.959 *	8	(SO)
52.	52	SI			0.957 *	8	(SI)
40.	40	SI			0.957 *	8	(SO)
33.	33	SI			0.957 *	8	(SO)
21.	21	SI			0.959 *	13	(SO)
4.	KLEBSIELLA PNEU	3	1.000	1.000 *	0.863 *	31	(so)
15.	15	3	1.000	1.000 *	0.863 *	31	(SO)
20.	20	3	1.000	1.000 *	0.863 *	31	(SO)
78.	78	3	1.000	1.000 *	0.863 *	31	(SO)
31.	31	SI			0.863 *	4	(3)
12.	12	SI			0.845 *	4	(3)
39.	39	SI			0.845 *	4	(3)
48.	48	10	1.000	1.000 *	0.834 *	57	(11)
55.	55	10	1.000	1.000 *	0.834 *	57	(1)
57.	57	11	1.000	1.000 *	0.834 *	46	(10)
66.	66	11	1.000	1.000 *	0.834 *	46	(10)

Appendix 81

No	Name	PhP-type	sim mln	Jm mean	sim max	to	PhP type
1.	BACILLUS SP	1	1.000	1.000 ■	0.912 *	41	(SI)
53.	52	1	1.000	1.000 *	0.912 ■	41	(SI)
co.	79	1	1.000	1.000 ■	0.912 *	41	(SI)
41.	CONTROL	SI			0.955 ■	81	(SI)
81.	CONTROL	SI			0.955 *	41	(SI)
57.	CONTROL	SI			0.937 *	81	(SI)
2.	CLOSTRIDIUM	2	0.983	0.994 *	0.905 *	60	(SI)
31.	31	2	0.983	0.994 *	0.905 *	60	(SI)
64.	63	2	0.983	0.994 *	0.905 *	60	(SI)
59.	58	2	0.903	0.983 *	0.913 *	60	(SI)
60.	59	SI			0.913 *	59	(2)
70.	69	SI			0.883 *	41	(SI)
7.	PSEUDO AEROG	7	0.984	0.990 *	0.975 ?	16	(SI)
55.	54	7	0.984	0.990 *	0.975 ?	16	(SI)
25.	25	7	0.970	0.981 *	0.964 *	16	(SI)
79.	78	7	0.970	0.979 *	0.955 ■	16	(SI)
16.	16	SI			0.975 ?	7	(7)
24.	24	SI			0.970 ?	7	(7)
39.	38	SI			0.970 *	7	(7)
50.	49	SI			0.966 ■	7	(7)
5.	MICROCO SP	5	0.984	0.993 *	0.848 ' .	41	(SI)
58.	57	5	0.984	0.993 *	0.848 ' .	41	(SI)
63.	62	5	0.984	0.993 *	0.848 * .	41	(SI)
66.	65	5	0.972	0.989 *	0.827 * .	81	(SI)
73.	72	5	0.972	0.989 *	0.827 * .	81	(SI)
65.	64	5	0.972	0.979 *	0.840 * .	81	(SI)
12.	12	SI			0.834 * .	21	(SI)
21.	21	SI			0.034 * .	12	(SI)
3.	E COLI	3	0.983	0.992 *	0.928 ' .	36	(SI)
68.	67	3	0.983	0.992 *	0.928 * .	36	(SI)
78.	77	3	0.983	0.992 *	0.928 * .	36	(SI)
76.	75	3	0.982	0.990 *	0.925 * .	36	(SI)
75.	74	3	0.980	0.990 *	0.922 ' .	36	(SI)
13.	13	3	0.989	0.992 *	0.941 * .	36	(SI)
23.	23	3	0.980	0.987 * .	0.935 ' .	29	(SO)
38.	37	3	0.980	0.987 ■	0.935 ' .	29	(SI)
44.	43	3	0.982	0.987 ' .	0.935 * .	29	(SO)
36.	35	SI			0.941 * .	13	(3)
29.	29	SI			0.935 * .	23	(3)
4.	KLEBSIELLA PNEU	4	1.000	1.000 *	0.938 ' .	27	(SI)
40.	39	4	1.000	1.000 *	0.938 * .	27	(SI)
54	53	4	1.000	1.000 *	0.938 ' .	27	(SI)
27.	27	SI			0.938 * .	4	(4)
33.	33	10	1.000	1.000 *	0.938 * .	4	(4)
34.	34	10	1.000	1.000 *	0.938 * .	4	(4)
20.	20	SI			0.865 * .	4	(4)
15.	15	SI			0.845 * .	4	(4)
11.	11	SI			0.845 * .	4	(4)
49.	48	11	1.000	1.000 *	0.847 ' .	56	(SI)
51.	50	11	1.000	1.000 *	0.847 * .	56	(SI)
56.	55	SI			0.847 * .	49	(11)
6.	PROTEUS MIRA	6	0.990	0.993 *	0.748 * .	69	(SI)
18.	18	6	0.990	0.993 *	0.748 * .	69	(SO)
42.	41	6	0.986	0.991 *	0.754 * .	69	(SI)
14.	14	6	0.978	0.990 *	0.753 * .	69	(SO)
32.	32	6	0.978	0.990 *	0.753 * .	69	(SO)
47.	46	6	0.976	0.990 *	0.760 * .	69	(SI)
10.	10	0	0.076	0.983 ■	0.742 * .	69	(SI)
69.	68	SI			0.760 * .	47	(6)
8.	SALMONELLA TYPH	8	0.995	0.997 *	0.007 * .	67	(13)
19.	19	0	0.991	0.994 *	0.787 * .	71	(SI)
28.	28	0	0.991	0.994 *	0.016 ' .	67	(13)
35.	34	0	0.991	0.994 *	0.800 * .	67	(13)
46.	45	0	0.991	0.992 ' .	0.823 * .	67	(13)
67.	66	13	1.000	1.000 ■	0.823 * .	46	(S)
74.	73	13	1.000	1.000 *	0.823 * .	46	(B)
71.	70	SI			0.787 * .	19	(8)
9.	STREPTOCO FAE	9	0.994	0.997 ' .	0.975 ?	61	(SI)
17.	17	9	0.991	0.995 *	0.972 * .	61	(SO)
30.	30	9	0.993	0.997 *	0.974 ' .	61	(SI)
37.	36	9	0.994	0.997 *	0.975 ?	61	(SI)
22.	22	9	0.993	0.997 *	0.979 ?	61	(SI)
52.	51	9	0.990	0.994 *	0.981 ?	61	(SI)
26.	26	9	0.969	0.994 *	0.979 ?	61	(SI)
43.	42	9	0.990	0.992 *	0.972 * .	61	(SI)
48.	47	9	0.989	0.993 *	0.960 * .	61	(SI)
61.	60	SI			0.931 ?	52	(9)
62.	61	12	1.000	1.000 *	0.026 ' .	48	(9)
72.	71	12	1.000	1.000 ■	0.826 * .	40	(9)
45.	44	SI			0.746 * .	30	(SI)
77.	70	SI			0.717 * .	21	(SI)

Appendix 83

PHENOTYPES In akuset12/ CALCULATED DIVERSITY INDEX - 0.929		Idonlly level - 0.975 TRUE DIVERSITY INDEX - 0.926				
No Name	PhP- aim type min	sim mean	*im max	to nr	PhP type	
t. STREPTOCO FAE	1	0.065	0.995 *	0.980 ?	41	(SI)
26. 26	1	0.983	0.994 *	0.976 ?	41	(SI)
70. 70	1	0.985	0.985 *	0.980 ?	41	(SI)
39. 39	1	0.964	0.993 *	0.976 ?	41	(SI)
12. 12	1	0.079	0.990 *	0.973 *	41	(SI)
20. 20	1	0.975	0.989 *	0.966 *	41	(SI)
24. 24	1	0.979	0.991 *	0.973 *	41	(SI)
33. 33	1	0.979	0.989 *	0.973 *	41	(SI)
36. 36	1	0.979	0.989 *	0.973 *	41	(SI)
51. 51	1	0.975	0.981 *	0.956 *	41	(SI)
41. 41	SI			0.980 7	1	(1)
60. 60	SI			0.980 7	1	(1)
2. SALMONELLA TYPH	2	0.976	0.992 *	0.651 *	31	(4)
57. 57	2	0.978	0.982 *	0.651 *	31	(4)
64. 64	2	0.976	0.992 *	0.651 *	31	(-)
22. 22	2	0.971	0.989 *	0.668 *	31	(J)
15. 15	2	0.968	0.984 *	0.636 *	37	(5)
30. 30	2	0.977	0.986 *	0.656 *	37	(5)
44. 44	2	0.978	0.984 *	0.651 *	31	(4)
53. 53	2	0.968	0.979 *	0.625 *	31	(4)
65. 65	2	0.977	0.985 *	0.688 *	31	(4)
3. PSEUDO FLUORE	3	0.980	0.990 *	0.965 *	9	(sr)
45. 45	3	0.980	0.990 *	0.965 *	9	(SI)
34. 34	3	0.974	0.985 *	0.962 7	55	(SO)
33. 38	3	0.974	0.978 *	0.952 *	48	(SO)
48. 48	SI			0.961 *	3	(3)
55. 55	SI			0.982 7	34	(3)
9. 9	SI			0.965 *	3	(3)
6. MICROCO SP	6	0.991	0.997 *	0.847 *	32	(10)
42. 42	6	0.991	0.997 *	0.847 *	32	(10)
72. 72	6	0.991	0.997 *	0.847 *	32	(10)
61. 61	6	0.985	0.993 *	0.839 *	32	(10)
46. 46	6	0.985	0.989 *	0.827 *	32	(10)
18. 18	SI			0.903 *	32	(10)
32. CONTROL	10	1.000	1.000 *	0.903	18	(SI)
80. CONTROL	10	1.000	1.000 *	0.903 *	16	(SI)
4. PSEUDO AEROG	4	0.984	0.992 *	0.986 7	16	(SI)
35. 35	4	0.984	0.992 *	0.966 7	16	(SI)
43. 43	4	0.984	0.992 *	0.986 7	16	(SI)
31. 31	4	0.974	0.987 *	0.972 *	16	(SI)
59. 59	4	0.974	0.987 *	0.972 *	16	(SI)
52. 52	4	0.972	0.980 *	0.970 *	16	(SO)
10. 10	4	0.972	0.979 *	0.967 *	16	(SI)
16. 16	SI			0.966 7	4	(4)
25. 25	SI			0.977 7	4	(4)
49. 49	SI			0.945 *	16	(SO)
5. PROTEUS MIRA	5	0.990	0.996 *	0.748 *	67	(12)
56. 56	5	0.990	0.996 *	0.748 *	67	(12)
17. 17	5	0.986	0.994 *	0.748 *	67	(12)
37. 37	5	0.986	0.989 *	0.731 *	61	(6)
7. KLEBSIELLA PNEUM	7	0.993	0.996 *	0.627 *	21	(9)
19. 19	7	0.993	0.996 *	0.627 *	21	(9)
27. 27	7	0.990	0.995 *	0.629 *	58	(11)
62. 62	7	0.990	0.994 *	0.656 *	21	(9)
79. 79	7	0.990	0.995 *	0.625 *	21	(9)
65. 68	7	0.986	0.994 *	0.612 *	58	(11)
13. 13	7	0.984	0.991 *	0.622 *	21	(9)
23. 23	7	0.984	0.991 *	0.628 *	58	(11)
73. 73	7	0.984	0.989 *	0.628 *	58	(11)
a. E COLI	8	0.991	0.997 *	0.618 *	67	(12)
40. 40	6	0.991	0.997 *	0.618 *	67	(12)
63. 63	8	0.991	0.997 *	0.618 *	67	(12)
69. 69	6	0.991	0.997 *	0.618 *	67	(12)
11. 11	8	0.988	0.995 *	0.627 *	67	(12)
SO. 50	8	0.988	0.995 *	0.627 *	67	(12)
14. 14	8	0.988	0.995 *	0.592 *	48	(SO)
75. 75	8	0.988	0.995 *	0.592 *	48	(SO)
29. 29	8	0.985	0.993 *	0.625 *	67	(12)
47. 47	8	0.985	0.993 *	0.625 *	67	(12)
66. 66	8	0.985	0.989 *	0.621 *	48	(SO)
21. 21	9	1.000	1.000 *	0.954 *	58	(11)
54. 54	9	1.000	1.000 *	0.954 *	58	(H)
76. 76	9	1.000	1.000 *	0.954 *	58	(11)
58. 58	11	1.000	1.000 *	0.954 *	21	(9)
71. 71	11	1.000	1.000 *	0.954 *	21	(9)
28. 28	SI			0.520 *	16	(SO)
67. 67	12	1.000	1.000 *	0.748 *	5	(5)
77. 77	12	1.000	1.000 *	0.748 *	5	(5)
74. 74	13	1.000	1.000 *	0.738 *	31	(4)
78. 78	13	1.000	1.000 *	0.738 *	31	(4)

Appendix 8k

No	Name	PhP- type	sim	sim mean	aim	lo nr	PhP type
1	BACILLUS	1	0.983	0.996 *	0.864 *	48	(15)
26.	26	1	0.983	0.996 *	0.864 *	48	(15)
35.	35	1	0.983	0.996 *	0.864 *	48	(15)
53.	53	1	0.983	0.996 *	0.864 *	40	(15)
41.	41	1	0.977	0.992 *	0.852 *	9	(9)
39.	39	1	0.977	0.992 *	0.856 *	23	(11)
32.	32	Si			0.854 ■	80	(15)
8.	CONTROL	15	0.997	0.997 *	0.874 *	51	(9)
80.	CONTROL	15	0.997	0.997 *	0.871 *	51	(9)
9.	CLOSTRIDIUM	9	0.983	0.994 *	0.983 7	23	(11)
17.	17	9	0.983	0.994 *	0.983 7	23	(11)
45.	45	9	0.983	0.994 *	0.983 7	23	(11)
51.	51	9	0.981	0.992 *	0.959 *	23	(11)
37.	37	9	0.981	0.983 *	0.984 7	29	(11)
23.	23	11	0.984	0.984 *	0.983 7	9	(9)
29.	29	11	0.984	0.984 *	0.984 7	37	(9)
8.	MICROCO SP	8	0.984	0.993 *	0.854 *	80	(15)
44.	44	8	0.984	0.993 *	0.854 *	80	(15)
52.	52	8	0.978	0.989 *	0.830 *	80	(15)
66.	66	8	0.972	0.985 *	0.833 *	80	(15)
10.	10	8	0.972	0.979 *	0.831 *	80	(15)
33.	33	13	1.000	1.000 *	0.804 *	48	(15)
49.	49	13	1.000	1.000 *	0.804 *	48	(15)
5.	PSEUDO AERO	5	0.986	0.994 *	0.975 ?	24	(12)
20.	20	5	0.986	0.994 *	0.975 7	24	(12)
36.	36	5	0.986	0.994 *	0.975 7	24	(12)
46.	46	5	0.985	0.992 *	0.987 7	47	(SO)
11.	11	5	0.985	0.989 *	0.964 *	24	(12)
65.	65	5	0.985	0.989 *	0.964 *	24	(12)
47.	47	Si			0.987 7	46	(5)
28.	28	Si			0.975 7	46	(5)
24.	24	12	1.000	1.000 *	0.975 7	5	(5)
31.	31	12	1.000	1.000 *	0.975 7	5	(C5)
60.	60	16	1.000	1.000 *	0.774 *	41	(1)
75.	75	16	1.000	1.000 *	0.774 *	41	(1)
2.	ECOLI	2	0.991	0.997 ■	0.729 *	33	(13)
43.	43	2	0.991	0.997 *	0.729 *	33	(13)
71.	71	2	0.991	0.997 *	0.729 *	33	(13)
13.	13	2	0.984	0.994 *	0.726 *	33	(13)
53.	59	2	0.984	0.994 *	0.726 *	33	(13)
55.	55	2	0.988	0.995 *	0.726 *	33	(13)
67.	67	2	0.990	0.995 *	0.729 *	33	(13)
77.	77	2	0.982	0.989 *	0.694 *	33	(13)
62.	62	2	0.982	0.989 *	0.728 *	33	(13)
3.	KLEBSIELLA PNEU	3	0.993	0.996 *	0.719 *	18	(SO)
19.	19	3	0.993	0.996 *	0.719 *	18	(Si)
73.	73	3	0.993	0.996 *	0.719 *	18	(SO)
27.	27	3	0.990	0.995 *	0.714 *	18	(Si)
57.	57	3	0.992	0.995 *	0.723 *	18	(SO)
69.	69	3	0.988	0.994 *	0.707 *	10	(SO)
15.	15	3	0.984	0.990 *	0.707 *	18	(Si)
21.	21	3	0.984	0.992 *	0.714 *	18	(Si)
64.	64	3	0.984	0.992 *	0.714 *	18	(Si)
4.	PROTEUS MIRA	4	0.980	0.997 *	0.748 *	6	(6)
40.	40	4	0.990	0.997 *	0.748 *	6	(6)
59.	59	4	0.990	0.997 *	0.748 *	6	(6)
50.	50	4	0.986	0.995 *	0.748 *	6	(6)
70.	70	4	0.986	0.995 *	0.747 ■	6	(6)
56.	56	4	0.986	0.988 *	0.729 *	66	(3)
6.	PROTEUS VULG	6	0.991	0.996 *	0.748 *	4	(4)
16.	16	6	0.991	0.996 *	0.748 *	4	(4)
72.	72	6	0.991	0.996 *	0.748 *	4	(4)
54.	54	6	0.979	0.988 *	0.746 *	4	(4)
78.	78	6	0.979	0.988 *	0.746 *	4	(4)
7.	STREPTOCO FAE	7	1.000	1.000 *	0.727 *	29	(11)
14.	14	7	1.000	1.000 *	0.727 *	29	(11)
74.	74	7	1.000	1.000 *	0.727 *	29	(11)
79.	79	7	1.000	1.000 *	0.727 *	29	(11)
12.	12	Si			0.650 *	61	(17)
18.	18	Si			0.896 *	25	(SO)
38.	38	Si			0.903 *	30	(so)
25.	25	Si			0.903 *	30	(Si)
30.	30	Si			0.903 *	25	(Si)
61.	61	17	1.000	1.000 *	0.803 *	18	(Si)
68.	68	17	1.000	1.000 *	0.803 *	18	(Si)
22.	22	10	1.000	1.000 *	0.838 *	42	(14)
63.	63	10	1.000	1.000 ■	0.838 *	42	(14)
42.	42	14	1.000	1.000 *	0.830 ■	22	(10)
76.	76	14	1.000	1.000 *	0.038 *	22	(10)
34.	34	Si			0.788 *	22	(10)

Appendix B1

PHENOTYPES In akuio114/ CALCULATED DIVERSITY INDEX - 0.961		Identity level ■ 0.975 TRUE DIVERSITY INDEX - 0.959				
No Nam*		PhP- sim type mln	sim mean	sim max	lo nr	PhP typ*
1.	ECOU	1	0.991	0.996 *	0.729 *	59 (SI)
40.	49	1	0.991	0.996 *	0.729 *	59 (SI)
14.	14	1	0.969	0.994 *	0.754 *	59 (SI)
18.	18	1	0.988	0.994 *	0.726 *	59 (SI)
27.	27	1	0.888	0.994 *	0.726 *	59 (SO)
58.	56	1	0.990	0.995 *	0.730 *	59 (SO)
24.	24	1	0.985	0.991 ■	0.726 *	59 (SO)
37.	37	1	0.985	0.991 *	0.709 *	38 (SO)
47.	47	1	0.985	0.990 *	0.734 *	59 (SI)
33.	33	1	0.985	0.989 *	0.735 *	38 (SO)
3.	MICROCOCCLUS LUT	3	0.983	0.993 *	0.983 7	34 (SO)
50.	50	3	0.983	0.993 *	0.983 7	34 (SO)
65.	65	3	0.983	0.993 *	0.983 7	34 (SO)
22.	22	3	0.969	0.985 *	0.969 *	34 (SO)
13.	13	3	0.969	0.980 *	0.960 *	34 (SO)
34.	34	SI			0.983 ?	3 (3)
74.	74	SI			0.888 *	3 (3)
9.	BACILLUS	9	0.996	0.997 *	0.914 *	32 (13)
45.	45	9	0.996	0.997 *	0.914 *	32 (13)
68.	68	9	0.996	0.997 *	0.899 *	32 (13)
77.	77	9	0.996	0.997 *	0.899 *	32 (13)
32.	CONTROL	13	1.000	1.000 *	0.914 *	9 (8)
80.	CONTROL	13	1.000	1.000 *	0.914 *	9 (9)
79.	79	SI			0.883 *	3 (3)
59.	59	SI			0.824 *	74 (SO)
8.	CLOSTRIDIUM	8	0.984	0.993 *	0.979 7	23 (SI)
31.	31	8	0.984	0.993 *	0.979 7	23 (SO)
52.	52	8	0.989	0.993 ■	0.972 *	23 (SO)
43.	43	8	0.984	0.986 *	0.962 *	23 (SO)
23.	23	SI			0.979 7	8 (8)
39.	39	SI			0.979 7	6 (8)
12.	12	11	1.000	1.000 *	0.948 *	42 (SO)
17.	17	11	1.000	1.000 *	0.948 *	42 (SO)
42.	42	SI			0.948 *	12 (11)
63.	63	SI			0.771 *	12 (11)
5.	PSEUDO AEROG	5	0.996	0.998 *	0.912 *	76 (SO)
15.	15	5	0.996	0.998 *	0.912 *	76 (SO)
57.	57	5	0.996	0.998 *	0.912 *	76 (SO)
70.	70	5	0.996	0.998 *	0.912 *	76 (SO)
21.	21	5	0.996	0.997 *	0.905 *	76 (SO)
67.	67	5	0.996	0.997 *	0.905 *	76 (SO)
76.	76	SI			0.912 *	5 (5)
71.	71	SI			0.780 *	21 (5)
38.	38	SI			0.771 *	71 (SO)
11.	11	10	1.000	1.000 *	0.762 *	54 (SO)
25.	25	10	1.000	1.000 *	0.762 *	54 (SO)
2.	KLEBSIELLA PNEU	2	1.000	1.000 *	0.957 *	41 (SO)
29.	29	2	1.000	1.000 *	0.957 *	41 (SO)
48.	48	2	1.000	1.000 *	0.957 *	41 (SI)
41.	41	SI			0.957 *	2 (2)
10.	10	SI			0.938 *	2 (2)
40.	40	SI			0.938 *	2 (2)
54.	54	SI			0.938 *	2 (2)
62.	62	SI			0.938 *	2 (2)
18.	16	SI			0.927 *	2 (2)
64.	64	SI			0.921 *	2 (2)
4.	PROTEUS MIRA	4	0.990	0.997 *	0.744 *	75 (15)
26.	26	4	0.990	0.997 *	0.748 *	75 (15)
66.	66	4	0.990	0.997 *	0.748 *	75 (15)
69.	69	4	0.990	0.990 *	0.742 *	75 (15)
6.	SALMONELLA TYPH	6	0.986	0.994 *	0.807 *	58 (SI)
35.	35	6	0.986	0.994 *	0.807 *	58 (SO)
60.	60	6	0.983	0.991 *	0.800 *	58 (SO)
53.	53	6	0.971	0.985 *	0.766 *	58 (SO)
19.	19	6	0.971	0.982 *	0.788 *	58 (SI)
58.	58	SI			0.807 *	6 (6)
7.	STREPTOCO FAE	7	0.994	0.999 *	0.793 *	20 (12)
30.	30	7	0.992	0.998 *	0.792 *	20 (12)
51.	51	7	0.994	0.999 *	0.793 *	20 (12)
55.	55	7	0.994	0.999 *	0.793 *	20 (12)
61.	61	7	0.994	0.999 *	0.793 *	20 (12)
44.	44	7	0.992	0.994 *	0.748 *	20 (12)
20.	20	12	0.991	0.991 *	0.793 *	7 (7)
36.	36	12	0.991	0.991 *	0.734 *	7 (7)
28.	28	SI			0.553 ■	71 (SI)
46.	46	SI			0.688 *	75 (15)
72.	72	14	1.000	1.000 *	0.683 *	47 (1)
73.	73	14	1.000	1.000 *	0.683 *	47 (1)
75.	75	15	0.998	0.993 *	0.748 *	4 (4)
70.	78	15	0.998	0.993 *	0.721 *	4 (4)

Appendix 8-m

HENOTYPES in akuse1_15/ Identity Ioval - 0.975
 U.CULATED DIVERSITY INDEX * 0.941 TRUE DIVERSITY INDEX = 0.937

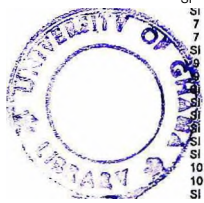
No	Name	PhP- typ*	sim min	sim mean	*bn max	(0 nr	PhP typo
1.	BACILLUS	i	0.983	0.996 *	0.884'	48	(SI)
15.	15	i	0.983	0.996 *	0.884'	48	(SI)
28.	28	1	0.983	0.996 *	0.884'	48	(SI)
67.	67	1	0.983	0.996 *	0.884'	48	(SI)
36.	36	1	0.976	0.992 *	0.868'	48	(SI)
21.	21	i	0.976	0.982 T	0.858'	48	(SI)
5.	MICROCO SP	5	0.991	0.996 *	0.926'	41	(13)
62.	62	5	0.991	0.996 *	0.926'	41	(13)
73.	73	5	0.991	0.996 *	0.926'	41	(13)
65.	65	5	0.980	0.988 *	0.922'	41	(13)
72.	72	5	0.980	0.988 *	0.922'	41	(13)
41.	41	13	1.000	1.000 *	0.926'	5	(5)
56.	56	13	1.000	1.000	0.926	5	(5)
24.	CONTROL	12	0.994	0.994 *	0.935'	48	(SI)
80.	CONTROL	12	0.994	0.994 *	0.947'	48	(SI)
48.	CONTROL	SI			0.947'	80	(12)
20.	20	11	1.000	1.000	0.864'	65	(5)
29.	29	11	1.000	1.000 *	0.864'	65	(5)
7.	PSEUDO FLUORE	7	1.000	1.000 *	0.948'	14	(10)
35.	35	7	1.000	1.000 *	0.948'	14	(10)
50.	50	7	1.000	1.000	0.948'	14	(10)
71.	71	7	1.000	1.000 *	0.948'	14	(10)
14.	14	10	1.000	1.000 *	0.948'	7	(7)
54.	54	10	1.000	1.000 *	0.948'	7	(7)
66.	66	SI			0.912'	7	(7)
58.	58	15	1.000	1.000 *	0.815'	41	(13)
64.	64	15	1.000	1.000 *	0.815'	41	(13)
69.	69	16	1.000	1.000 *	0.756'	36	(1)
76.	76	16	1.000	1.000 *	0.756'	36	(1)
2.	CITROBAC FREU	2	0.998	0.999 *	0.545'	75	(8)
43.	43	2	0.998	0.999 *	0.545'	75	(8)
53.	53	2	0.998	0.999 *	0.545'	75	(8)
12.	12	2	0.993	0.997'	0.533'	75	(8)
17.	17	2	0.993	0.997'	0.540'	75	(8)
3.	ECOLI	3	0.995	0.998 *	0.729'	58	(15)
32.	32	3	0.995	0.998 *	0.729	58	(15)
49.	49	3	0.995	0.998 *	0.729'	58	(15)
73.	73	3	0.995	0.998 *	0.729'	58	(15)
10.	10	3	0.992	0.995 *	0.726'	58	(15)
19.	19	3	0.989	0.994'	0.726'	58	(15)
39.	39	3	0.989	0.994'	0.726'	58	(15)
25.	25	3	0.989	0.993 *	0.695'	58	(15)
4.	KLEBSIELLA PNEU	4	0.987	0.996 *	0.627'	69	(16)
23.	23	4	0.987	0.996 *	0.627'	69	(16)
13.	13	4	0.984	0.995 *	0.623'	69	(16)
16.	16	4	0.981	0.993'	0.610'	69	(16)
26.	26	4	0.981	0.993'	0.625'	69	(16)
30.	30	4	0.984	0.994 *	0.614'	69	(16)
33.	33	4	0.984	0.993'	0.629'	69	(16)
38.	38	4	0.990	0.995 *	0.656'	69	(16)
45.	45	4	0.982	0.990 *	0.679'	69	(16)
60.	60	4	0.981	0.986 *	0.685'	69	(16)
74.	74	4	0.982	0.990 *	0.628'	69	(16)
6.	PSEUDO AEROG	6	0.984	0.992 *	0.985 ?	52	(SI)
31.	31	6	0.984	0.992 *	0.985 ?	52	(SI)
11.	11	6	0.970	0.990 *	0.982 ?	52	(SI)
18.	18	6	0.979	0.990 *	0.982 ?	52	(SI)
-22.	22	6	0.975	0.987 *	0.975 ?	52	(SI)
27.	27	6	0.975	0.987 *	0.975 ?	52	(SI)
37.	37	6	0.975	0.985 *	0.975 ?	52	(SI)
34.	34	6	0.972	0.979 *	0.972'	52	(SI)
44.	44	6	0.972	0.979 *	0.966'	52	(SI)
52.	52	SI			0.985 7	6	(6)
59.	59	SI			0.985 7	6	(6)
8.	SALMONELLA TYPH	8	0.990	0.995 *	0.772'	70	(17)
47.	47	8	0.990	0.995 *	0.772'	70	(17)
40.	40	8	0.987	0.994 *	0.709'	70	(17)
57.	57	8	0.987	0.994 *	0.709'	70	(17)
75.	75	8	0.987	0.989 *	0.759'	70	(17)
70.	70	17	1.000	1.000 *	0.772'	8	(8)
79.	79	17	1.000	1.000 *	0.772'	8	(8)
9.	STREPTOCO FAE	9	0.998	0.999 *	0.527'	61	(SI)
63.	63	9	0.998	0.999 *	0.527'	61	(SI)
68.	68	9	0.998	0.999 *	0.532'	61	(SI)
77.	77	9	0.998	0.998 *	0.518'	61	(SI)
42.	42	SI			0.940	61	(SI)
61.	61	SI			0.940'	42	(SI)
46.	46	14	0.998	0.999 *	0.833'	61	(SI)
55.	55	14	0.998	0.999 *	0.833'	61	(SI)

Appendix

PHENOTYPES in akuseiv/ CALCULATED DIVERSITY INOEX - 0.988		Identity level ■ 0.975 TRUE DIVERSITY INDEX ■ 0.989					
No	Name	PhP- typo	sim mln	im mean	sim	lo nr	PhP type
1.	STREPTOCO FAE	1	1.000	1.000 ■	0.958 *	30	(SI)
52.	52	1	1.000	1.000 *	0.958 *	30	(SI)
62.	62	1	1.000	1.000 *	0.958 *	30	(SI)
67.	67	1	1.000	1.000 *	0.958 *	30	(SI)
75.	75	1	1.000	1.000 *	0.958 *	30	(SI)
14.	14	SI			0.957 *	1	(1)
41.	41	SI			0.958 *	1	(D)
30.	30	SI			0.958 *	1	(1)
35.	35	SI			0.957 *	1	(1)
56.	56	SI			0.957 *	1	(1)
7.	CLOSTRIDIUM	6	1.000	1.000 *	0.882 *	29	(SI)
68.	68	6	1.000	1.000 *	0.882 *	29	(SI)
29.	29	SI			0.882 *	7	(6)
73.	73	SI			0.874 *	79	(SI)
79.	79	SI			0.874 *	73	(SO)
53.	53	SI			0.796 *	7	(C6)
2.	SALMONELLA PARA	2	0.986	0.993 *	0.942 *	37	(SI)
46.	48	2	0.986	0.993 *	0.942 *	37	(SO)
49.	49	2	0.986	0.986 *	0.959 *	44	(SO)
44.	44	SI			0.959 *	49	(2)
61.	61	SI			0.941 *	2	(2)
37.	37	SI			0.942 *	2	(2)
58.	53	SI			0.940 *	2	(2)
39.	39	SI			0.932 *	51	(SO)
51.	51	SI			0.952 *	49	(2)
4.	PROTEUS MIRA	SI			0.932 *	12	(SO)
12.	12	SI			0.932 *	4	(SO)
19.	19	SI			0.928 *	12	(SO)
21.	21	SI			0.930 *	4	(SI)
3.	PSEUDO AEROG	3	1.000	1.000 *	0.915 *	26	(SO)
42.	42	3	1.000	1.000 *	0.915 *	26	(SO)
69.	69	3	1.000	1.000 *	0.915 *	26	(SO)
77.	77	3	1.000	1.000 *	0.915 *	26	(SO)
28.	26	SI			0.915 *	3	(3)
17.	17	SI			0.909 *	3	(3)
18.	18	SI			0.909 *	80	(SO)
22.	22	SI			0.890 *	18	(SO)
34.	34	SI			0.898 *	38	(SO)
38.	38	SI			0.898 *	34	(SO)
57.	57	8	1.000	1.000 *	0.910 *	76	(SO)
65.	65	8	1.000	1.000 *	0.910 *	76	(SO)
76.	76	SI			0.910 *	57	(8)
74.	74	SI			0.797 *	80	(SI)
10.	10	SI			0.933 *	23	(SO)
33.	33	SI			0.926 *	10	(SO)
23.	QONTROL	SI			0.952 *	48	(SI)
48.	CONTROL	SI			0.966 *	80	(SI)
80.	CONTROL	SI			0.966 *	48	(SO)
15.	15	SI			0.902 *	10	(SO)
28.	28	SI			0.892 *	10	(SO)
40.	40	SI			0.917 *	33	(SO)
55.	55	SI			0.862 *	33	(SO)
5.	KLEBSIELLA PNEU	4	1.000	1.000 ■	0.863 ■	64	(SO)
71.	71	4	1.000	1.000 *	0.863 *	64	(SO)
45.	45	SI			0.854 *	5	(4)
13.	13	SI			0.845 *	5	(4)
24.	24	SI			0.845 *	5	(4)
60.	60	SI			0.845 *	5	(4)
64.	64	SI			0.953 *	72	(SI)
72.	72	SI			0.953 *	64	(SO)
66.	66	SI			0.906 *	72	(SI)
6.	ECCOU	5	0.995	0.999 *	0.945 *	16	(SI)
25.	25	5	0.995	0.999 *	0.945 *	16	(SO)
36.	38	5	0.995	0.999 *	0.945 *	16	(SI)
70.	70	5	0.995	0.999 *	0.945 *	16	(SO)
9.	9	5	0.995	0.995 *	0.943 *	16	(SI)
16.	18	SI			0.945 *	6	(5)
31.	31	SI			0.939 *	6	(5)
20.	20	SI			0.938 *	6	(5)
47.	47	SI			0.936 *	31	(SI)
78.	78	SI			0.940 *	9	(5)
50.	50	SI			0.894 *	9	(5)
8.	CITROBAC DIV	7	0.979	0.979 *	0.891 *	32	(SO)
27.	27	7	0.979	0.979 *	0.882 *	32	(SI)
32.	32	SI			0.891 *	8	(7)
43.	43	SI			0.870 *	8	(7)
11.	11	SI			0.732 *	49	(2)
54.	54	SI			0.748 *	21	(SI)
59.	50	SI			0.803 *	63	(SI)
S3.	63	SI			0.803 *	63	(SI)

Appendix 80

	PhP-type	sim min	sim moan	tim max	to nr	PhP type
1. STREPTOCO FAE	1	1.000	1.000 *	0.957 *	28	(SI)
26. 26	t	1.000	1.000 *	0.957 *	28	(SI)
26. 28	Si			0.957 *	1	(1)
40. 40	Si			0.957 *	1	(1)
34. 34	Si			0.957 *	1	(1)
61. 61	Si			0.954 *	34	(SO)
60. 60	Si			0.872 *	61	(SI)
39. 39	Si			0.856 *	1	(1)
2. BACILLUS	Si			0.890 *	18	(SI)
38. 38	Si			0.876 *	2	(SI)
18. 18	Si			0.894 *	27	(SI)
27. 27	Si			0.894 *	18	(SI)
31. 31	Si			0.805 *	2	(SI)
3. CLOSTRIDIUM	2	1.000	1.000 *	0.899 *	54	(SI)
49. 49	2	1.000	1.000 *	0.899 *	54	(SI)
54. 54	Si			0.899 *	3	(2)
72. 72	Si			0.803 *	3	(2)
65. 65	Si			0.863 *	3	(2)
9. 9	Si			0.908 *	15	(SO)
15. 15	Si			0.908 *	9	(SO)
19. 19	Si			0.869 *	15	(SO)
29. 29	Si			0.890 *	9	(SO)
22. 22	Si			0.887 *	9	(SO)
32. CONTROL	Si			0.945 *	80	(SO)
80. CONTROL	Si			0.945 *	32	(SO)
6. PROTEUS MIRA	5	1.000	1.000 *	0.931 *	63	(SO)
53. 53	5	1.000	1.000 *	0.931 *	63	(SO)
79. 79	5	1.000	1.000 *	0.931 *	63	(SO)
56. 56	Si			0.930 *	6	(5)
63. 63	Si			0.931 *	6	(5)
71. 71	Si			0.931 *	6	(5)
73. 73	Si			0.925 *	56	(SO)
78. 78	Si			0.878 *	3	(2)
66. 66	Si			0.933 *	75	(SO)
75. 75	Si			0.933 *	66	(SO)
4. E COLI	3	1.000	1.000 *	0.939 *	21	(SO)
44. 44	3	1.000	1.000 *	0.939 *	21	(SO)
21. 21	Si			0.939 *	4	(3)
62. 62	Si			0.939 *	4	(3)
35. 35	Si			0.938 *	4	(3)
30. 30	Si			0.938 *	4	(3)
11. 11	Si			0.938 *	4	(3)
16. 16	Si			0.935 *	11	(SO)
5. KLEBSIELLA PNEU	4	1.000	1.000 *	0.863 *	14	(SO)
43. 43	4	1.000	1.000 *	0.863 *	14	(SI)
10. 10	Si			0.854 *	5	(4)
50. 50	Si			0.845 *	5	(4)
41. 41	Si			0.910 *	47	(SI)
47. 47	Si			0.910 *	41	(SI)
52. 52	Si			0.891 *	41	(SI)
58. 58	Si			0.900 *	64	(SI)
64. 64	Si			0.900 *	58	(SO)
7. PSEUDO AEROG	Si			0.903 *	20	(SI)
20. 20	Si			0.903 *	7	(SO)
12. 12	Si			0.896 *	7	(SO)
17. 17	8	1.000	1.000 *	0.896 *	7	(SI)
36. 36	8	1.000	1.000 *	0.898 *	7	(SI)
33. 33	Si			0.926 *	48	(SI)
48. 48	Si			0.926 *	33	(SO)
8. SALMONELLA PARA	6	1.000	1.000 *	0.941 *	55	(SO)
42. 42	6	1.000	1.000 *	0.941 *	55	(SI)
77. 77	6	1.000	1.000 *	0.941 *	55	(SI)
46. 46	Si			0.940 *	8	(6)
59. 59	Si			0.941 *	8	(6)
55. 55	Si			0.941 *	8	(6)
68. 68	Si			0.940 *	8	(6)
13. 13	7	1.000	1.000 *	0.803 *	24	(9)
23. 23	7	1.000	1.000 *	0.803 *	24	(9)
14. 14	Si			0.967 *	24	(9)
24. 24	Si	1.000	1.000 *	0.967 *	14	(SO)
45. 45	Si	1.000	1.000 *	0.967 *	14	(SO)
37. 37	Si			0.896 *	24	(9)
57. 57	Si			0.780 *	20	(SI)
25. 25	Si			0.556 *	24	(9)
51. 51	Si			0.534 *	52	(SI)
67. 67	Si			0.922 *	78	(SI)
76. 76	Si			0.922 *	87	(SI)
69. 1169	10	1.000	1.000 *	0.000 *	8	(6)
70. 1170	10	1.000	1.000 *	0.000 *	8	(6)
74. 74	Si			0.700 *	61	(SO)



Appendix Q-P

PHENOTYPES in akusetv3/ Identity level = 0.875
 *CALCULATED DIVERSITY INDEX * 0.989 TRUE DIVERSITY INDEX * 0.989

No	Name	PhP- typo	tim min	tun mean	aim max	lo nr	PhP type
1.	STREPTOCO FAE	i	1.000	1.000 *	0.959 ■	66	(Si)
36.	36	i	1.000	1.000 *	0.959 *	66	(Si)
44.	44	i	1.000	1.000 *	0.959 *	66	(Si)
66.	66	Si			0.959 *	1	(D)
68.	68	Si			0.957 *	1	(1)
34.	34	13	1.000	1.000 *	0.957 *	1	(1)
42.	42	13	1.000	1.000 *	0.957 *	1	(1)
74.	74	Si			0.958 *	1	(O)
S.	ECOU	5	0.995	0.997 *	0.945 *	21	(Si)
30.	30	5	0.995	0.997 *	0.945 *	21	(Si)
35.	35	5	0.995	0.997 *	0.943 *	21	(SO)
43.	43	5	0.995	0.997 *	0.943 *	21	(Si)
21.	21	Si			0.945 *	5	(5)
13.	13	Si			0.939 *	5	(5)
58.	58	22	1.000	1.000 *	0.940 *	35	(5)
97.	50	22	1.000	1.000 *	0.940 *	35	(5)
63.	63	26	1.000	1.000 ■	0.940 *	35	(5)
64.	84	26	1.000	1.000 *	0.940 *	35	(5)
102.	55	26	1.000	1.000 *	0.940 *	35	(5)
51.	51	17	1.000	1.000 *	0.940 *	35	(5)
90.	43	17	1.000	1.000 ■	0.940 *	35	(5)
8.	CLOSTRIDIUM	8	1.000	1.000 *	0.883 *	40	(15)
25.	25	8	1.000	1.000 *	0.883 *	40	(15)
40.	40	15	1.000	1.000 *	0.891 *	87	(so)
48.	48	15	1.000	1.000 *	0.891 *	87	(SO)
81.	81	Si			0.922 *	87	(SO)
87.	87	Si			0.922 *	81	(SO)
33.	33	12	1.000	1.000 *	0.879 *	96	(27)
41.	41	12	1.000	1.000 *	0.879 *	96	(27)
65.	65	Si			0.976 7	96	(27)
72.	72	27	0.986	0.986 *	0.956 *	65	(SO)
96.	49	27	0.986	0.986 *	0.976 7	65	(Si)
7.	PSEUDO CAV	7	1.000	1.000 *	0.944 *	64	(SO)
49.	49	7	1.000	1.000 ■	0.944 *	64	(SO)
62.	62	7	1.000	1.000 *	0.944 *	64	(SO)
88.	41	7	1.000	1.000 *	0.944 *	64	(SO)
64.	64	Si			0.944 *	7	(7)
55.	55	20	1.000	1.000 *	0.930 *	64	(SO)
94.	47	20	1.000	1.000 *	0.930 *	64	(SO)
101.	54	Si			0.930 *	7	(7)
12.	12	Si			0.876 *	7	(7)
24.	CONTROL	Si			0.893 *	59	(23)
54.	54	19	1.000	1.000 *	0.893 *	45	(SO)
93.	46	19	1.000	1.000 *	0.893 *	45	(SO)
45.	45	Si			0.894 *	59	(23)
59.	59	23	1.000	1.000 *	0.894 *	45	(Si)
98.	51	23	1.000	1.000 *	0.894 *	45	(SO)
23.	23	10	0.997	0.997 *	0.931 *	38	(14)
32.	32	10	0.997	0.997 *	0.930 *	38	(14)
38.	38	14	1.000	1.000 ■	0.931 *	23	(10)
39.	39	14	1.000	1.000 ■	0.931 *	23	(10)
47.	47	14	1.000	1.000 *	0.931 *	23	(10)
27.	27	Si			0.929 *	32	(10)
17.	17	Si			0.935 *	26	(SO)
26.	26	Si			0.935 *	17	(SO)
20.	20	Si			0.933 *	17	(SO)
3.	PSEUDO AEROG	3	1.000	1.000 *	0.912 *	14	(SO)
19.	19	3	1.000	1.000 *	0.912 *	14	(so)
22.	22	Si			0.896 *	3	(3)
9.	9	Si			0.922 *	14	(SO)
14.	14	Si			0.922 *	9	(SO)
75.	75	Si			0.905 *	6	(6)
6.	CAMPYLOBACTER	6	1.000	1.000 *	0.907 *	60	(24)
52.	52	6	1.000	1.000 *	0.907 *	60	(24)
91.	44	6	1.000	1.000 *	0.907 *	60	(24)
60.	60	24	1.000	1.000 *	0.907 *	6	(6)
99.	52	24	1.000	1.000 *	0.907 *	6	(6)
86.	88	Si			0.905 *	6	(6)
71.	71	Si			0.844 *	59	(23)
2.	SALMONELLA PARA	2	1.000	1.000 *	0.942 *	11	(9)
29.	29	2	1.000	1.000 *	0.942 *	11	(9)
37.	37	2	1.000	1.000 *	0.942 *	11	(9)
48.	48	2	1.000	1.000 *	0.942 *	11	(9)
11.	11	9	1.000	1.000 *	0.942 *	2	(2)
31.	31	9	1.000	1.000 *	0.942 *	2	(2)
53.	53	18	1.000	1.000 *	0.941 *	2	(2)
79.	79	18	1.000	1.000 *	0.941 *	2	(2)
92.	45	18	1.000	1.000 ■	0.941 *	2	(2)
76.	76	Si			0.941 *	2	(2)
15.	15	Si			0.940 *	2	(2)
Rtt	Wl	1fl	i non	i nnn *	ft clln *	>=	1fl

Appendix 4
 PHENOTYPES in aJcisonv4/ Identity level: 0.975
 *CALCULATED DIVERSITY INDEX = 0.995 TRUE DIVERSITY INDEX - 0.995

No	Nama	PhP- typ*	min	sim mean	sim	to	PhP typ*
1.	ECOLI	1	1.000	1.000 *	0.972 *	58	(Si)
51.	51	1	1.000	1.000 *	0.972 *	58	(Si)
58.	58	Si			0.972 *	1	(1)
26.	26	Si			0.939 *	1	(1)
62.	62	Si			0.942 *	58	(Si)
37.	37	Si			0.939 *	1	(1)
9.	9	6	1.000	1.000 *	0.970 *	60	(Si)
33.	33	6	1.000	1.000 *	0.970 *	60	(Si)
60.	60	Si			0.970 *	9	(6)
30.	30	Si			0.938 *	1	(1)
55.	55	Si			0.945 *	1	(t)
65.	65	12	1.000	1.000 *	0.842 *	62	(Si)
70.	70	12	1.000	1.000 *	0.842 *	62	(Si)
2.	KLEBSIELLA PNEU	2	1.000	1.000 *	0.918 *	54	(Si)
66.	66	2	1.000	1.000 *	0.918 *	54	(SO)
54.	54	Si			0.918 *	2	(2)
27.	27	Si			0.854 *	2	(2)
12.	12	Si			0.845 *	2	(2)
36.	36	Si			0.845 *	2	(2)
49.	49	Si			0.845 *	2	(2)
47.	ENTEROBACTER CLOA	Si			0.954 *	64	(11)
64.	64	11	1.000	1.000 *	0.954 *	47	(SO)
68.	68	11	1.000	1.000 *	0.954 *	47	(SO)
73.	73	Si			0.891 *	64	(11)
75.	75	Si			0.827 *	64	(11)
3.	PSEUDO AERO	Si			0.903 *	40	(SO)
40.	40	Si			0.903 *	3	(SO)
53.	53	Si			0.896 *	3	(SO)
14.	14	8	0.996	0.996 *	0.885 *	7	(SO)
42.	42	8	0.996	0.996 *	0.890 *	7	(SO)
74.	74	Si			0.817 *	53	(Si)
39.	39	Si			0.874 *	45	(SO)
45.	45	Si			0.896 *	3	(SO)
4.	PSEUDO CAV	3	1.000	1.000 *	0.935 *	25	(SO)
20.	20	3	1.000	1.000 *	0.935 *	25	(SO)
25.	25	Si			0.935 *	4	(3)
16.	16	Si			0.927 *	4	(3)
31.	31	Si			0.927 *	4	(3)
7.	MICROCO SP	Si			0.890 *	78	(Si)
21.	21	Si			0.893 *	7	(SO)
23.	CONTROL	10	0.980	0.980 *	0.962 *	78	(SO)
48.	CONTROL	10	0.980	0.980 *	0.976 ?	78	(SO)
78.	CONTROL	Si			0.976 ?	48	(10)
11.	11	7	0.999	0.999 *	0.891 *	7	(Si)
46.	46	7	0.999	0.999 *	0.890 *	7	(SO)
67.	67	Si			0.852 *	70	(Si)
17.	17	Si			0.857 *	7	(SO)
72.	72	Si			0.843 *	17	(Si)
6.	STREPTOCO FAE	5	1.000	1.000 *	0.959 *	15	(Si)
71.	71	5	1.000	1.000 *	0.959 *	15	(SO)
15.	15	Si			0.959 *	6	(5)
18.	18	Si			0.957 *	6	(5)
10.	10	Si			0.957 *	6	(5)
28.	28	Si			0.957 *	6	(5)
50.	50	Si			0.957 *	6	(5)
34.	34	Si			0.957 *	6	(5)
22.	22	Si			0.988 *	6	(5)
59.	59	Si			0.957 *	6	(5)
44.	44	Si			0.958 *	6	(5)
76.	76	Si			0.957 *	6	(5)
19.	19	9	1.000	1.000 *	0.932 *	57	(Si)
61.	61	9	1.000	1.000 *	0.932 *	57	(Si)
57.	57	Si			0.932 *	19	(0)
43.	43	Si			0.931 *	19	(9)
52.	52	Si			0.931 *	19	(9)
5.	SALMONELLA PARA	4	1.000	1.000 *	0.941 *	8	(SO)
24.	24	4	1.000	1.000 *	0.941 *	8	(SO)
8.	e	Si			0.941 *	5	(4)
13.	13	Si			0.940 *	5	(4)
29.	29	Si			0.941 *	5	(4)
35.	35	Si			0.941 *	5	(4)
41.	41	Si			0.888 *	29	(SO)
32.	32	Si			0.722 *	63	(SO)
38.	38	Si			0.665 *	56	(so)
56.	56	Si			0.745 *	37	(Si)
63.	63	Si			0.751 *	49	(SO)
69.	69	13	1.000	1.000 *	0.591 *	53	(SO)
77.	77	13	1.000	1.000 *	0.591 *	53	(SO)

297

Appendix 3x-
 PHENOTYPES In aKusevS/
 Identity level - 0.975
 *CALCULATED DIVERSITY INDEX ■ 0.994 TRUE DIVERSITY INDEX ■ 0.994

No	Name	PhP- type	rr-	■tm mean	sim max	to nr	PhP type
1.	BACILLUS	Si			0.918 *	80	(8)
57.	57	Si			0.908 *	1	(Si)
75.	75	Si			0.895 *	1	(Si)
66.	66	Si			0.890 *	1	(Si)
2.	CLOSTRIDIUM	1	1.000	1.000 *	0.882 ■	10	(S.)
59	59	1	1.000	1.000 *	0.882 *	10	(Si)
15.	15	Si			0.882 .	2	(1)
70.	70	Si			0.878 .	2	(1)
10.	10	Si			0.912 ' .	53	(Si)
53.	53	Si			0.912 .	10	(Si)
24.	CONTROL	8	0.976	0.976 *	0.900 *	55	(Si)
80.	CONTROL	6	0.976	0.976 *	0.923 *	55	(Si)
55.	55	Si			0.923 .	80	(8)
46.	46	Si			0.823 .	2	(1)
78.	78	Si			0.865 *	24	(8)
63.	63	Si			0.882 *	1	(Si)
6.	PSEUDO AEROG	5	1.000	1.000 *	0.903 ■	26	(Si)
38.	38	5	1.000	1.000 *	0.903 *	26	(Si)
48.	48	5	1.000	1.000 *	0.903 .	26	(SO)
26.	26	Si			0.903 *	6	(5)
17.	17	Si			0.896 *	6	(5)
11.	11	7	1.000	1.000 *	0.896 *	6	(5)
32.	32	7	1.000	1.000 *	0.896 *	6	(5)
58.	58	Si			0.834 *	11	(7)
7.	SALMONELLA PARA	6	1.000	1.000 *	0.945 *	16	(SO)
40.	40	6	1.000	1.000 *	0.945 *	16	(SO)
9.	9	Si			0.944 *	7	(6)
18.	18	Si			0.945 *	7	(6)
22.	22	Si			0.944 *	7	(6)
27.	27	Si			0.943 .	7	(6)
33.	33	Si			0.933 *	27	(SO)
42.	42	10	1.000	1.000 *	0.935 *	56	(SO)
49.	49	10	1.000	1.000 *	0.935 *	56	(Si)
56.	56	Si			0.935 *	42	(10)
45.	45	Si			0.927 *	42	(10)
65.	65	Si			0.936 *	69	(SO)
69.	69	Si			0.936 *	65	(SO)
3.	E COLI	2	1.000	1.000 *	0.939 *	12	(SO)
73.	73	2	1.000	1.000 ■	0.939 *	12	(SO)
12.	12	Si			0.939 *	3	(2)
20.	20	Si			0.939 *	3	(2)
37.	37	Si			0.939 *	3	(2)
79.	79	Si			0.939 *	3	(2)
31.	31	Si			0.938 *	3	(2)
28.	28	Si			0.938 *	3	(2)
5.	PROTEUS MIRA	4	1.000	1.000 *	0.934 *	34	(SO)
36.	36	4	1.000	1.000 ■	0.934 *	34	(SO)
34.	34	Si			0.934 *	5	(4)
23.	23	Si			0.931 *	5	(4)
14.	14	Si			0.932 *	5	(4)
39.	39	Si			0.931 *	5	(4)
18.	18	Si			0.932 *	5	(4)
68.	68	14	1.000	1.000 *	0.823 .	39	(SO)
74.	74	14	1.000	1.000 *	0.823 .	39	(SO)
41.	41	9	1.000	1.000 *	0.756 *	58	(SO)
52.	52	9	1.000	1.000 *	0.756 *	58	(SO)
44.	44	12	1.000	1.000 *	0.793 *	57	(Si)
47.	47	12	1.000	1.000 *	0.793 *	57	(Si)
4.	KLEBSIELLA PNEU	3	1.000	1.000 *	0.863 *	76	(SO)
51.	51	3	1.000	1.000 *	0.863 *	76	(SO)
60.	60	3	1.000	1.000 *	0.863 *	76	(SO)
21.	21	Si			0.854 *	4	(3)
30.	30	Si			0.845 *	4	(3)
67.	67	Si			0.845 *	4	(3)
71.	71	Si			0.845 *	4	(3)
72.	72	Si			0.967 *	76	(Si)
73.	73	Si			0.967 *	72	(so)
77.	77	St			0.908 *	76	(SO)
8.	STREPTOCO FAE	Si			0.955 *	29	(Si)
29.	29	Si			0.955 *	8	(SO)
13.	13	Si			0.952 *	8	(SO)
19.	19	Si			0.952 *	8	(SO)
25.	25	Si			0.953 *	a	(Si)
35.	35	Si			0.953 *	8	(Si)
50.	50	13	1.000	1.000 *	0.957 *	54	(SO)
62.	62	13	1.000	1.000 *	0.957 *	54	(SO)
54.	54	Si			0.957 *	50	(13)
61.	61	Si			0.957 *	50	(13)
43.	43	11	1.000	1.000 *	0.735 *	3	(2)
64.	64	11	1.000	1.000 *	0.735 *	3	(2)

Appendix 9

Data on Rainfall and Temperature from the following synoptic stations, representing values for the study areas as supplied by the Meteorological Services Department.

(Courtesy; Water Research Institute)

Accra Rainfall (mm)												
Monthly Totals (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	0.0	50.3	59.0	86.2	246.1	126.3	68.7	38.8	15.0	7.0	15.5	839.2
1997	2.8	0.0	185.2	269.4	135.7	353.3	4.6	9.5	112.0	48.7	64.5	1223.6
1998	0.0	8.7	1.5	25.2	178.5	35.9	0.5	13.4	208.9	14.1	14.6	513.6
1999	19.4	38.6	6.8	47.1	53.1	327.3	19.4	30.6	26.8	8.4	2.4	641.8
Mean	5.6	24.4	63.1	107.0	153.4	210.7	23.3	23.1	90.7	19.6	24.3	804.4

Accra Temperature (°C)												
Monthly Means (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	28.4	28.7	28.8	28.9	27.7	26.5	25.7	25.2	25.8	27.3	28.2	28.1
1997	28.4	29.1	28.1	27.7	27.3	26.1	25.1	25.3	27.2	27.7	28.1	28.1
1998	28.5	30.1	30.7	30.5	28.5	27.3	26.3	25.9	26.7	27.5	28.6	28.2
1999	28.1	28.5	28.9	28.7	28.5	27.0	25.9	25.7	25.8	26.9	28.1	28.6
Mean	28.4	29.1	29.1	29.0	28.0	26.7	25.8	25.5	26.4	27.4	28.3	28.3

Akuse Rainfall (mm)												
Monthly Totals (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	1.3	55.5	144.3	161.2	338.2	121.2	217.6	86.6	50.8	205.1	24.4	2.1
1997	5.6	1.5	139.5	147.0	214.0	360.4	128.5	9.5	22.2	108.3	93.9	38.2
1998	10.0	8.8	33.7	21.3	301.9	221.6	31.1	12.8	68.3	314.7	71.6	15.8
1999	7.9	43.2	97.2	89.9	56.5	302.6	191.3	144.0	85.3	75.2	94.6	6.7
Mean	6.2	27.3	103.7	104.9	227.7	251.5	142.1	63.2	56.7	175.8	71.1	15.7

Akuse Temperature (°C)												
Monthly Means (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996								26.1	26.9	27.9	28.5	28.5
1997	29.5	29.9	29.7	28.8	28.3	27.4	26.3	26.8	28.2	28.6	28.7	28.5
1998	28.3	31.3	31.9	32.1	29.7	28.5	27.5	27.1	28.3	28.3	29.1	28.4
1999	29.1	29.3	30.3	29.1	28.2	27.0	26.1	26.1	26.7	27.2	27.7	27.3
Mean	29.0	30.2	30.6	30.0	28.7	27.6	26.6	26.7	27.7	28.0	28.5	28.1

Appendix 9 (cont'd)

Data on Rainfall and Temperature from the following synoptic stations, representing values for the study areas as supplied by the Meteorological Services Department.

(Courtesy; Water Research Institute)

Kumasi Rainfall (mm)												
Monthly Totals (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	3.7	80.2	72.2	111.8	145.7	106.0	202.7	109.6	72.5	81.8	2.8	51.9
1997	53.7	33.0	138.0	296.7	218.7	250.3	73.4	59.0	96.3	162.2	11.1	11.3
1998	51.8	26.6	35.9	267.4	183.3	188.3	56.5	75.6	74.7	76.5	23.5	31.7
1999	61.3	25.9	109.9	217.0	101.7	217.9	202.6	114.1	135.2	204.3	39.0	0.0
Mean	42.6	41.4	89.0	223.2	162.4	190.7	133.8	89.6	94.7	131.2	19.1	23.7

Kumasi Temperature (°C)												
Monthly Means (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	26.7	27.9	27.8	27.8	27.5	26.0	25.4	25.0	25.1	25.8	27.7	26.7
1997	27.0	28.5	28.5	26.9	27.0	25.8	24.8	24.6	25.9	26.9	27.3	27.3
1998	27.4	28.8	30.2	29.1	27.8	26.5	25.5	24.6	25.8	26.5	27.9	27.3
1999	27.9	27.8	28.1	27.3	27.2	26.5	25.5	25.1	25.1	25.6	26.9	27.3
Mean	27.3	28.3	28.7	27.8	27.4	26.2	25.3	24.8	25.5	26.2	27.5	27.2

Tema Rainfall (mm)												
Monthly Totals (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	0.0	60.7	101.2	291.0	175.2	165.4	78.8	39.3	10.9	0.8	31.4	0.0
1997	0.0	0.0	122.5	177.0	262.3	450.1	40.5	5.4		158.2	32.5	46.3
1998	0.0	12.6		12.0	135.4	60.9	4.7	2.4	6.9	82.7	5.6	11.7
1999	29.2	83.2	13.4	55.7	48.8	169.3	41.7	5.2	28.5	29.7	7.0	3.5
Mean	7.3	39.1	79.0	133.9	155.4	211.4	41.4	13.1	15.4	67.9	19.1	15.4

Tema Temperature (°C)												
Monthly Means (1996 - 1999)												
Year	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
1996	27.6	28.4	28.4	28.6	28.0	26.9	25.9	25.3	25.0	26.7	27.8	27.4
1997	27.3	28.4	27.9	27.7	27.3	26.3	24.7	24.5	26.5	27.3	27.8	28.0
1998	28.2	29.3	30.0	29.7	27.2	27.1	25.8	25.0	26.0	27.4	28.7	28.4
1999	27.3	28.0	28.1	28.1	27.4	26.3	25.1	24.5	25.3	26.6	27.4	27.3
Mean	27.6	28.5	28.6	28.5	27.5	26.7	25.4	24.8	25.7	27.0	27.9	27.8

ACKNOWLEDGEMENT

I am grateful to all the people who have helped me and made this work possible in one or way or another.

I am most grateful to Prof (Emeritus) G. C. Clerk, my supervisor, for his willingness to accept me in his laboratory to undertake this work, and for his tremendous support. I am also grateful to the Head of Botany Department, Prof. G. T. Odamtten, for his advice and support.

My gratitude goes to the Director-General of the Council for Scientific and Industrial Research (CSIR) of Ghana, Prof. W. S. Alhassan, the Director of Water Research Institute of the CSIR, Dr. C. A. Biney, and the Head of Division of Environmental Biology and Health, Ms J. C. Ofori, for provision of the necessary resources without which this study will not have been possible.

I recognise with appreciation the efforts of Prof. (Emeritus) Tord Holme, who arranged for my visit to the Microbiology and Tumourbiology Centre (MTC), Karolinska Institute, Sweden as a guest researcher during the early part of this study. I am grateful to Prof. Roland Mollby and his team at MTC, Karolinska Institute, most especially Dr. Inger Kuhn, who introduced me to the typing of bacteria using the PhenePlate (PhP) system. I am also grateful for the equipment and bacterial strains supplied to facilitate the use of the PhP system in Ghana by Mollby group. I am indebted to the Swedish Institute for supporting my stay in Sweden.

I am grateful to the staff of the Public Health Reference Laboratory, Korle Bu Teaching Hospital, Accra for the use of their laboratory and for the provision of reference strains of pathogenic bacteria; the staff of the Fisheries Department, Greater Accra and Ashanti Regions for the trips and introduction to the fish farms; the staff of Volta Basin Research Project, Akosombo office, for laboratory use; the staff of Botany Department, University of Ghana, for their assistance; the staff of ARDEC, Water Research Institute, Akosombo, for laboratory use; and, the staff of the Environmental Biology and Health Division, Environmental Chemistry Division

and Fisheries Division of the Water Research Institute for their numerous help during this study.

I recognize with appreciation the encouragement given by the following people during doubtful periods; Mrs Joyce Ampofo, Dr. Zhian Bian, MTC, Karolinska Institute, Sweden, Dr. I. K. Asante, Mr. Ted Annang, Mr. G. Ameka and Mr. J. Adomako (all of the Botany Department, University of Ghana), Dr (Mrs.) M. Enstua-Mensah, Mr. H. Dankwa, Dr. E. K. Abban, Dr. A. Opoku, Mr. A. A. deGraft Johnson, Dr. M. Ocran, Mr Godwin Amegbe, Mrs Wilhermina Tetteh, Mr. Sena Niampoma, Mr. Seth Acquaye and Mr. J. S. Amakye (all of Water Research Institute).

The fish farmers and their families, of the study areas, whose understanding and patience made this study possible are acknowledged.

REFERENCES

1. ALLEN, G.H., BUSCH, R.A. and A.W. MORTON (1979). Preliminary bacteriological studies on wastewater-fertilized marine fishponds. Humboldt Bay, California Bay, California. *In*: ADVANCES IN AQUACULTURE (Ed. by T.V.R. Pillay and W.A. Dill) FISHING NEWS BOOKS, OXFORD, ENGLAND, and 492 - 498.
2. ALLEN, G. H. and B. HEPHER (1969). Recycling of wastes through aquaculture and constraints to wider application. *In*: Advances in aquaculture (Ed. by T.V.R. Pillay and W.A. Dill) FISHING NEWS BOOKS, OXFORD, ENGLAND, and 478 - 487.
3. ALMEIDA, L.J., da SILVA and Y.M. FREITAS (1968). Microorganisms from some tropical fish diseases. J. FISH. RES. BD. CANADA 25: 197 201.
4. AMERICAN PUBLIC HEALTH ASSOCIATION (1995). Standard methods for the examination of water and wastewater, 19th ed. American Public Health Association, Washington, D.C.
5. AXELROD, H.R. and L.P. SCHULTZ (1969). Handbook of tropical aquarium fishes. THE PUBLICATIONS, JERSEY CITY, N.Y. 70p.
6. BALARIN, J.D. (1979). Tilapia, a guide to their biology and culture in Africa. UNIVERSITY OF STIRLING. UNITED KINGDOM.
7. BALARIN, J.D. (1988). National reviews for aquaculture development in Africa, 18 Ghana. F.A.O FISH CIRC. (770.18): 121p.
8. BARDACH, J.E., J.H RYTHER, and W.O McLARNEY (1972). Aquaculture: the farming and husbandry of freshwater and marine organisms. WILEY INTERSCIENCE, NEW YORK. 868p.

9. BAYOUMI, A.R. and M.T KHALIL (1988). Tilapia fisheries in Lake Manzala, Egypt. BULLETIN OF INSTITUTE OF OCEANOGRAPHY AND FISHERIES **14**, 87-99.
10. BEUCHART, L.R. (1996). Pathogenic microorganisms associated with fresh produce. JOURNAL OF FOOD PROTECTION **59**, 206-216.
11. BINEY, C. A. (1982). Preliminary surveys on the state of pollution of the coastal environment of Ghana. OCEANOL. ACTA 4 SUPPL. (Vol. Spec.) 39 - 43.
12. BISWAS, S. (1969). Thermal changes in the Volta Lake at Ajena. *In*: Man-made Lakes. The Accra symposium. Edited by Letitia E. Obeng. CSIR. GHANA UNIVERSITIES PRESS, ACCRA. 103 - 109.
13. BLACKWOOD, C.M. (1978). Microbiological quality of fishery products - role and environment, Canada. Fisheries Inspection Branch. CANADIAN INSTITUTE OF FOOD SCIENCE AND TECHNOLOGY JOURNAL **1**, A42 - A49.
14. BONN, E.W. and B.J. FOLLIS (1967) Effects of hydrogen sulfide on channel catfish, *Ictalurus punctatus*. TRANS. AMER. FISH. SOC., **96**, 31-36.
15. BOYD, C.E. (1981) Water quality in warmwater fish ponds. AGRICULTURAL EXPERIMENT STATION, AUBURN UNIVERSITY, AUBURN, 359p.
16. BUCK, D.H., R.J BAUR, and C.R. ROSE (1979). Experiments in recycling swine manure in fish ponds, p.489-492. *In*: T.V.R. PILLAY AND W.M.A. DILL (eds) ADVANCES IN AQUACULTURE. FISHING NEWS BOOK LTD, FARMHAM, SURREY, ENGLAND.
17. BULLOCK, G.L. (1964). *Pseudomonadctles* as fish pathogens. DEVELOPMENT IN INDUSTRIAL MICROBIOL. **5**: 101-108.

18. BULLOCK, G.L., D.A. CONROY, and S.F. SNIESZKO (1971). Diseases of fishes, p. 000 - 000. *In*: S.F. Snieszko and H.R. Axelrod [ed.] Book 2A: BACTERIAL DISEASES OF FISHES. THE PUBLICATIONS, JERSEY CITY, N.J.
19. CALDREICH, E.E. and N.A. CLARKE (1966). Bacterial pollution indicators in the intestinal tract of freshwater fish. *J. APPL. MICROBIOL.* 41: 429-437.
20. CHEESBROUGH, M. (1994). Medical Laboratory Manual for Tropical Countries. Vol. II: *Microbiology*. TROPICAL HEALTH TECHNOLOGY & BUTTER WORTH-HEINEMANN.
21. CHEN, P. H. and S.T. HSU (1986). PCB poisoning from toxic rice-bran oil in Taiwan. *In*: PCB and the environment, Vol. III (Ed. by J.S. Waid). CRC PRESS, BOCA RATON, FLORIDA, 22-37.
22. COHEN, J. and H.I. SHUVAL (1973). Coliforms, faecal coliform and streptococci as indicators of water pollution. *WATER AIR SOIL POLLUT.* 2: 85-95.
23. COPE, O.B. (1964). Sport fishery investigations. *In*: The effects of pesticides on fish and Wildlife. U.S. FISH. WILD. SER. CIRC. 226, 51 - 63.
24. COWAN, S.T. and J. LISTON (1994). The nature of bacterial identification schemes. *In*: BERGEY'S MANUAL OF DETERMINATIVE BACTERIOLOGY 9TH EDN. (J. G. HOLT, N. R. KRIEG, P.H.A. SNEATH, J. T. STALEY AND S. T. WILLIAMS EDS.) WILLIAMS & WILKINS, BALTIMORE, MARYLAND, USA . 3 - 5 .
25. CUELIN, A. (1962). Polluted waters and the contamination of fish. *FISH FOOD* 2: 481-500.
26. DHSS (1991). The bacteriological Examination of Drinking Water Supplies 1982. PUBLIC HEALTH LABORATORY SERVICE, LONDON, HMSO.

27. DENYOH, F.M.K. (1985). Status of Aquaculture in Freetown. PROC. WORKSHOP ON VILLAGE LEVEL AQUACULTURE DEVELOPMENT IN AFRICA. 3p.
28. DOWNING, K.M. and J.C. MERKENS (1955). The influence of dissolved oxygen concentrations on the toxicity of un-ionized ammonia to rainbow trout (*Salmo gairdneri* Richardson) ANN. APPL. BIOL., 43, 243 - 246.
29. van DUIJN, J.C. (1973). Diseases of fishes. 3rd ed. BUTTERWORTH Co. LTD. LONDON. 372p.
30. EDWARDS, P., C. POLPRASERT and K.L. WEE. (1987). Resource recovery and health aspects of sanitation. AIT RESEARCH REPORT, 205, 324p.
31. EIFAC (EUROPEAN INLAND FISHERIES COMMISSION). (1973). Water quality criteria for European freshwater fish. Report on ammonia and inland fisheries. WATER RES., 7, 1011 - 1022.
32. ENTZ, B. (1969). Observation on the limnochemical conditions of the Volta Lake. In: Man-made Lakes. The Accra symposium. Edited by Letitia E. Obeng. CSIR. GHANA UNIVERSITIES PRESS, ACCRA. 110-115.
33. EVISON, L.M. and A. JAMES (1973). A comparison of the distribution of intestinal bacteria in British and African water sources. APPL. BACTERIOL. 36: 109-118.
34. FAO (1990). Source book for inland fishery resources of Africa: 2 CIFA Tech. PAPER No. 18.2 ROME FAO. 41 lp.
35. FAPOHUNDA, A.O., K.W. MacMILLAN, D.L. MARSHALL and W.M. WAITES (1994). Growth of selected cross-contaminating bacterial pathogens on beef and fish at 15 and 35°C. JOURNAL OF FOOD PROTECTION 57, 337-340.

36. FINEGOLD, S.M. and E.J. BARON (1986). Methods for identification of etiologic agents of infectious disease. *In: Bailey and Scott's Diagnostic Microbiology*. 7th Edn. C.V MOSBY COMPANY. ST. LOUIS, MISSOURI; 63146.
37. FRAZIER, W. C. C. (1958). Food Microbiology. TATA MCGRAW-HILL PUBLISHING CO. LTD. BOMBAY, INDIA.
38. GANAPATI, S.V. (1969). A major Man-made Lake in South India. *In: Man-made Lakes. The Accra symposium. Edited by Letitia E. Obeng.* CSIR. GHANA UNIVERSITIES PRESS, ACCRA. 57 - 72.
39. de GUZMAN, M.R. and H. CHIA (1978). The uses of pig manure in Taiwan. FFTC EXTENSION BULLETIN No. **104**, TAIPEI, TAIWAN.
40. GRIMALDI, E., G. PEDUZZI, G. CARICCHOLI and E. SPREAFICO (1973). Diffusa infezione branchiale da funghii altrribuite al genere *Branchiomyces* Plehn (*Phycomycetes saprolegniales*) a carico dellittiofuana di laghi situati a novde a sud delle Alpi. MEM. INST. ITAL. IDRIOBIOL 30, 61 - 96.
41. HANNAY, C. L. and I. L. NORTON (1947). Enumeration, isolation and study of faecal streptococci from river water. PROC. SOC. APPL. BACTERIOL. I; 39 - 45.
42. HAQUE, M.A., K. OHKI, M. KIKUCHI and O. KOHASHI (1994). Contact hemolysin production by strains of enteroaggregative *Escherichia coli* isolated from children with diarrhoea. JOURNAL OF CLINICAL MICROBIOLOGY **32**, 1109 - 1111.
43. HENEGBRY, M.S., GORDEN, R.W. and D.H. BUCK (1988). Bacterial populations in the gut of the silver carp (*Hypophthalmichthys molitrix*) PROG. FISH CULT., 50: 86 - 92.
44. HOLT, S. J. (1969). The food resources of the ocean. SCIENTIFIC AMERICAN **221**; 178 - 194.



45. HOLT, J. G., N. R. GRIEG, P H. A. SNEATH and S. T. WILLIAMS (1994).
Bergey's Manual of Determinative Bacteriology 9th Edn. WILLIAMS &
WILLIAMS. BALTIMORE, MARYLAND, USA.
46. HOPKINS, K.D., E.M. CRUZ, M.L. HOPKINS, and K.C. CHONG (1980).
Optimum manure loading rates in tropical freshwater fish ponds receiving
untreated piggery wastes, p. 15-29. *In*: ICLARM-CLSU integrated animal-
fish farming project: poultry-fish and pig-fish trials. ICLARM TECH. REP
2. INTERNATIONAL CENTER FOR LIVING AQUATIC RESOURCES
MANAGEMENT, MANILA AND THE FRESHWATER AQUACULTURE
CENTER, CENTRAL LUZON STATE UNIVERSITY, NUEVA ECIJA,
PHILIPPINES.
47. ISHAK, M. M. (1986). Development of fish farming in Egypt: cage and pen
(enclosure) culture. INTERNATIONAL DEVELOPMENT RESEARCH
CENTER AND INSTITUTE OF OCEANOGRAPHY AND FISHERIES
REPORT. No 4 (phase 2).
48. JANSSEN, W.A. (1970). Fish as potential vectors of human bacterial diseases,
p. 248 - 290. *In*: S.F. Snieszko [ed.]. A Symposium on diseases of fish and
shellfish. AMER. FISH. SOC. SPEC. PUBL. 5 WASHINGTON, D.C.
49. KABATA, Z. (1985). Parasites and diseases of fish cultured in the tropics.
LONDON AND PHILADELPHIA, Taylor and Francis (ed).
50. KHALIL, M. T. and H.A. HUSSEIN (1997). Use of waste water for
aquaculture: an experimental field study at a sewage-treatment plant,
Egypt. AQUACULTURE RESEARCH, 28, 859 - 865.
51. KORZENIEWSKI, K. and J. KORZENIEWSKA (1982). Changes in the
composition and physiological properties of the bacterial flora of water and
bottom sediments in Lake Letowo caused by intensive trout culture.
POLSKIE ARCH. HYDROBIOL, 29(3-4), 671 - 682.

52. KUHN, I., G. ALLESTAM, T.A. STENSTROM and R. MOLLBY (1991). Biochemical fingerprinting of water coliform bacteria a new method for measuring the phenotypic diversity and for comparing different bacterial populations. APPL. ENVIRON. MICROBIOL 57 (11): 3171 3177.
53. KUHN, I. and R. MOLLBY (1993). The PhP RS system A simple microplate method for studying coliform bacterial populations. J. MICROBIOL METHODS 17: 255 - 259.
54. MARY, P.P (1977). Studies on the gastrointestinal microflora of the mullet *Liza dussumeiei* (Valenciennes) Ph.D. Thesis CAS IN MARINE BIOL. ANNAMALAI UNIV. 122p.
55. MASON, C. F. (1991). Heavy metals and organochlorines. *In* Biology of Freshwater pollution. LONGMAN SC. & TECH. 169 - 186.
56. MORIARTY, D.J.W. (1976). Quantitative studies on the bacteria and algae in the food of the mullet *Mugil cephalus* L., and the prawn *Metapenaeus bennettiae* (Tack and Dali). J. EXP. MAR. BIOL. ECOL. 22: 131 143.
57. MUNRO, A. L. S. (1982). The pathogenesis of bacterial diseases of fish. *In*: Microbial diseases of fish (Ed. R. J. Roberts) ACADEMIC PRESS. INC., LONDON, p. 132.
58. NAUEN, C.C. (1983). Compilation of legal limits for hazardous substances in fish and fishery products. FAO, ROME, ITALY.
59. NEWMAN, J.T., B.J. CONSENZA and J.D. BUCK (1972). Aerobic microflora of the bluefish (*Pomatomus saltatrix*) intestine. JOURNAL OF THE FISHERIES RESEARCH BOARD OF CANADA 29, 333 336.
60. NYANTENG, V.K. (1981). Trends in fish prices and implications for the development of the fishing industry. FAO/UNDP(CEAF)/TECH 181/33: 25p.

61. ODUM, W.E. (1968). The ecological significance of fine particles selection by the striped mullet, *Mugil cephalus*. LIMNOL. OCEANOGR. 13: 92 - 98.
62. OGBONDEMINU, F.S. (1993). The occurrence and distribution of enteric bacteria in fish and water of tropical aquaculture ponds in Nigeria. JOURNAL OF AQUACULTURE IN THE TROPICS.8, 61 - 66.
63. OLAYEMI, A.B., O. ADEDAYO and A.O. OJO (1991). Microbial flora of six freshwater fish species from Asa River, Ilorin, Nigeria. REVISTA DE BIOLOGIA TROPICAL 39, 165 - 167.
64. OWUSU-FRIMPONG, M. (1989). A survey of fish farming practices in southern Ghana. INSTITUTE OF AQUATIC BIOLOGY, ACCRA. IAB 120. 33p.
65. PARKS, R.W., E. SCARSBROOK, and C.E. BOYD (1975). Phytoplankton and water quality in a fertilized fish pond. AUBURN UNI. AGR. EXP. STA. CIRC., 224, 16p.
66. PENNINGS, C.M., R.C. SEITZ, H. KARCH, and H.G. LENARD (1994). Hemolytic-anemia in association with *Escherichia coli* 0157 infection in two sisters. EUROPEAN JOURNAL OF PEDIATRICS 153, 656 - 658.
67. PILLAY, T.V.R. (1992). Sources and utilization of water. Water and waste water use. *In*: Aquaculture and the Environment. Halsted Press: an Imprint of John Wiley and Sons, Inc. New York Toronto p. 49.
68. PILLAY, T.V.R. (1990). Aquaculture: Principles and Practices. FISHING NEWS BOOKS, Oxford, UK 575p.
69. PILLAY, T.V.R, DUTTA, S.N. and S. RAJAGOPAL. (1954). The *Vibrio* flora of fishes, water and silt in the Hooghly estuary, with reference to cholera endemicity. AL ASSOC. BULL., ALL-INDIA INSTITUTE OF HYGIENE AND PUBLIC HEALTH, CALCUTTA, 1 - 5 .

70. PINCHOT, B. G. (1973). Marine farming. SCIENTIFIC AMER. **225**; 238 - 244.
71. POWERS, E.M., C. AY, and O.B. ROWLEY (1970). Bacteriology of dehydrated space foods. BACTERIOL. PROC. A84: 13.
72. RAJ, H. D. (1969). Cell cultures and mycoplasmas. TEX. REP. BIOL. MED. **23**: 285
73. RAJ, H. and LISTON, J. (1961). Survival of bacteria of Public Health significance in frozen sea foods. FOOD TECHNOLOGY 6: 421 - 433.
74. RAO, D.U., N.H. PARHAD, C.S. RAO and K.S. RAO (1968). Coliform as indicators of faecal contamination. ENVIRON. HEALTH. **10(1)** :21.
75. RHEINHEIMER, G. (1976). The influence of physical and chemical factors on aquatic micro-organisms. *In*: Aquatic Microbiology. JOHN WILEY & SONS. 79 - 105.
76. ROBERTS, R.T (1978). Neoplasia of fishes. *In*: FISH PATHOLOGY, ed. R.J. Roberts (1st Edn), p. 232. LONDON.
77. RUDOLFS, W., L. FALK, and R.A. RAGOTSKIE (1950). Literature review on the occurrence and survival of enteric, pathogenic and relative organisms in soil, water, sewage and sludge on vegetation. SEWAGE IND. WASTE 22. 1261p.
78. RYTHER, J. H. and G. C. MATTHIESSEN (1969). Aquaculture: its status and potential. OCEANUS **14**: 2 - 14.
79. SALLE, A.J. (1964). Fundamental principles of bacteriology. 5th ed. MCGRAW-HILL BOOK CO., NEW YORK. 50p.
80. SCHOTISSEK C. and E.R. NAYLOR (1988). Fish farming and influenza pandemis. NATURE 331, 215.

81. SERA, H. and Y. ISHIDA (1972). Bacterial flora in the digestive tracts of marine fish. II. Changes of bacterial flora with time lapse after ingestion of diet. BULL. JPN. SOC. SCI-FISH. 38: 633.
82. SHEWAN, J.M. (1970). Bacteriological standards for fish and fishery products. CHEMISTRY AND INDUSTRY. 6: 193 197
83. SHIRANEE, P., NATARAJAN, P. and R. DHERENDRAN (1993). The role of gut and sediment bacterial flora in the nutrition of cultured pearl spot (*Etroplus saratensis*, Bloch). THE ISRAEL JOUR. OF AQUACUL. BAMIDGEH **45(2)**: 45 - 58.
84. SMITH, D.R. (1985). Aquaculture training manual. FISHING NEWS BOOKS LTD., ENGLAND. 135p.
85. SPECK, M. L. (1976). Compedium of methods for the microbiological examination of foods American Public Health Association, Intersociety/Agency Committee on Microbiological Methods for Foods. R. DONNELLY & SONS CO. CRAWFORDSVILLE, USA. 11 - 94.
86. STATGRAPHICS PLUS (1995). Multiple-Sample Comparison Analysis. MANUGISTICS INC. NEW YORK. 50p.
87. STATUTORY ORDERS and REGULATIONS (1955). The food and drug act and regulations 2: 1673 1806.
88. SWINGLE, H. S. (1969). Methods of analysis for waters, organic matter and pond bottom soils used in fisheries research. AUBURN UNIVERSITY, AUBURN, ALABAMA, 119p.
89. TABAK, H.H., C.W. CHAMBERS and P.W. KABBLER (1964). Microbial metabolism of Aromatic compounds. I. Decomposition of phenolic compounds and aromatic hydrocarbons by phenol-adapted bacteria. BACTERIOL. REV. **23**, 97 - 108.

90. THATCHER, F.S. (1963). The microbiology of specific frozen foods in relation to public health: Report of an international committee. J. APPL. BACTERIOL. **26**: 266 - 285.
91. THATCHER, F.S., and D.S. CLARK (1968). Their significance and methods of enumeration. *In*: Microorganisms in food. UNIVERSITY OF TORONTO PRESS, CANADA, p.107 - 114
92. THIMANN, K. V. (1964). Das leben der Bakterien. JENA FISCHER. 875p.
93. TIEWS, K. (1981). Aquaculture in heated effluent and recirculation systems, Vol. I. SCHRIFTEN DER BUNDESFORSCHUNGSANSTALT FUR FISCHEREI, HAMBURG, 59 61.
94. TODD-SANFORD (1969). Bacteriologic application to diagnosis. *In* Clinical Diagnosis by Laboratory Methods. Vol. II. W. B. SAUNDERS CO. 1423 — 1484.
95. TWEDT, R.M., P.L. SPAULDING and H.E. HALL (1969). Morphological, cultural, biochemical and serological comparison of Japanese strains of *Vibrio parahaemolyticus* with related cultures isolated in the United States. J. BACTERIOL. **98**: 511 518
96. UTSUNOMIYA, A., D. ELIO, A. REYES, E. CASTRO, E. RODRIGUEZ, C. TRESS, J. De-CORZO, E. HANNOVER, A. KAI, K. TAMURA and N. HIGA (1995). Major enteropathogenic bacteria isolated from diarrheal patients in Bolivia: a hospital base study. MICROBIOLOGY AND IMMUNOLOGY **39**, 845 - 851.
97. WANG, B. (1985). Ecological Wastewater Treatment and Utilization Systems in China, Effluents + Water Treatment Journal (EWTJ), **25 (5)**: 189 - 192.

98. WANG, B. (1987). The development of ecological Wastewater Treatment and Utilization Systems (EWTUS) in China. WAT. SCI. TECHNOL. 19: 51-63.
99. WHO (1989). Health guidelines for the use of wastewater in agriculture and aquaculture. WHO Technical Report Series No, 778. WORLD HEALTH ORGANIZATION, GENEVA.
100. WHETSTONE, G.A., H.W. PARKER, and D.M. WELLS (1974). Study of current and proposed practices in animal waste management. EPA 430/9-74-003. United States Environmental Protection Agency, Washington, DC.
101. WOYNAROVICH, E. (1980). Raising ducks on fish ponds. *In*: Integrated Agriculture Aquaculture farming systems (Ed. by R.S.V. Pullin and Z.H.Shahadeh). ICLARM CONF. PROC., 4: 129 - 134.
102. WOYNAROVICH, E. (1979). The feasibility of combining animal husbandry with fish-farming, with special reference to duck and pig production, p. 203-208. *In*: T.V.R. PILLAY AND W.M.A. FAMHAM, SURREY, ENGLAND.