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**MORPHOMETRIC AND ALLOZYMIC
CHARACTERISATION AND GENETIC VARIATION
IN THREE SPECIES OF *CHRYSICHTHYS* IN GHANA**

**BY
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**A THESIS SUBMITTED TO THE DEPARTMENT OF OCEANOGRAPHY AND
FISHERIES, UNIVERSITY OF GHANA, LEGON, IN PARTIAL FULFILMENT OF
THE REQUIREMENTS FOR THE AWARD OF THE MASTER OF PHILOSOPHY
DEGREE IN FRESHWATER BIOLOGY.**

AUGUST, 1996

DEDICATION

DEDICATED TO MR. AND MRS. JOE SUTHERLAND

VRA, AKOSOMBO.



ACKNOWLEDGEMENT

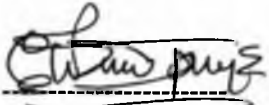
First and foremost, I thank the almighty God for His grace throughout the period of this work. I wish also to thank my Head of Department and Principal Supervisor Prof. C.J. Vanderpuye, and other members of the supervisory committee, Dr. E.K. Abban and Prof. Marian Ewurama Addy for their constructive criticisms and useful suggestions. I wish to state that Dr. E.K. Abban merits special mention for his immense contribution towards the completion of this work. My sincerest thanks go to the Institute of Aquatic Biology (IAB), of the Council for Scientific and Industrial Research (CSIR) in general, and the Director, Mr. Charles Biney in particular for the use of their facilities. My deepest gratitude goes to the technical support staff of the Fisheries Division (Messrs Abeka, Amedome and Anawoe) for their technical assistance. I wish to mention here that, Messrs Niampomah and Amegbe gave me much help on the computer. I also wish to thank the Librarian Mr. Kwofie and Mr. Asante, a Ph.D student at the Botany Department of the University of Ghana for their academic and moral support. Last but not the least, I wish to thank Sister Helen Dzureke, Clerk Grade I of the Department of Oceanography and Fisheries, for assisting in typing. I am also thankful to other persons not mentioned here, but whose contributions in one way or the other led to the completion of this work.

DECLARATION

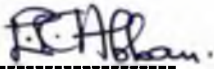
I, Michael Kwasi Dade, do hereby declare that this thesis consists entirely of my own work and that no part of it has been presented for another degree elsewhere.



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ABSTRACT

Chrysichthys species have been characterised by previous investigators. Most often, characterisation has been based on morphological and meristic characters. These characters may be modified by environmental factors, thus making them difficult to use in characterising species. There is the need therefore to refine or supplement taxonomy based on morphological and meristic characteristics. In the present study, variation in meristic counts and twelve body proportion variables in three species of the Catfish, *Chrysichthys* from two river basins (Volta and Densu) in Ghana were evaluated for their reliability in separating the species. Position of the longest dorsal soft fin ray and the number of branched pectoral fin rays were found to be stable and dependable in the identification of the three species. Body proportion values showed wide ranges which overlap so much that they do not give precise identification of species. In addition to the morphometric study, variation at 15 loci involving eleven proteins were studied by allozyme electrophoresis in each of the species to (i) identify loci that discriminate between species, (ii) estimate levels of genetic variation among *C. auratus*, *C. nigrodigitatus* and *C. maurus*, (iii) estimate phenetic relationships among populations and species, and (iv) indicate whether there are any significant differences in the genotypic frequencies of populations. Seven discriminating loci were found between *C. auratus* and either *C. nigrodigitatus* or *C. maurus*. At the loci investigated, genetic variation was generally low in all the species. It was highest in *C. auratus* and least in *C. nigrodigitatus* [Polymorphism, $P_{(1\% \text{ criterion})} = 0.178$ in *C. auratus*, 0.133 in *C. maurus* and 0.089 in *C. nigrodigitatus*; Heterozygosity, $H_e = 0.029$

in *C. auratus*, 0.016 in *C. maurus* and 0.009 in *C. nigrodigitatus*]. There were no significant genetic differences between populations within *C. auratus* and *C. nigrodigitatus* (average gene diversity between populations, D_{st} , = 0.001 in both species). Again based on loci screened, the closest species genetically were *C. nigrodigitatus* and *C. maurus* (Genetic identity, I , = 0.999) while the most distant species were *C. auratus* and *C. maurus* (I = 0.525). There were no significant changes in the genotypic frequencies of the populations (X^2_{05} ranges from 0.020 to 2.292 for polymorphic loci).

CHAPTER 1

INTRODUCTION

The genus *Chrysichthys* (Bleeker 1858) belongs to the fish family Bagridae. It has three subgenera: *Rheoglanis*, *Chrysichthys* and *Melanodactylus* (Risch, 1986). The genus *Chrysichthys* is discriminated from the other two genera by:

- (a) presence of short nasal barbels
- (b) small or medium adipose fin which is not rayed
- (c) 6 (rarely 5 or 7) soft dorsal fin rays (Roman, 1966)

Most species of *Chrysichthys* are found in freshwaters but a few occur in both fresh and brackish waters (Ezenwa, Odiete and Anyanwu, 1985). *Chrysichthys* species have been reported from practically all the river systems of tropical Africa, within latitude 25°N and 25°S from Tanzania in the east to Senegal in the west. Within this geographical range 40 species have been identified (Jayaram, 1966). Distribution of *Chrysichthys* species in West Africa is shown in Figure 1.

Important attributes of *Chrysichthys* species which makes them worth studying are their importance in the commercial fisheries of many West African countries, and their potential as a culturable fish. In many West African countries for example Ghana and Senegal, species of the genus *Chrysichthys* support thriving commercial fisheries, being an important food fish (Ikusemiju and Olaniyan, 1977). *Chrysichthys nigrodigitatus* for example, is considered as one of the fish species with a great potential for aquaculture in developing countries including Ghana. Its wide distribution (Figure 1) is also of tremendous

biological significance for the study of diversity within a species among other issues.

This work is aimed at contributing to the morphological and genetic characterization of *Chrysichthys* species. Proper identification of *Chrysichthys* species will enhance their study and exploitation as emphasised by Ferguson (1980). A study of the intraspecific systematics or population systematics of *Chrysichthys* species is also equally important. It plays a major role in the identification and conservation of unique genotypes of the fish species.

Though *Chrysichthys* species have been characterised by previous investigators (for example Vanderpuye 1981, Daget and Ittis 1965 and Boulenger 1911), characterisation has most often been based on morphological and meristic characters. However, these characters may be modified by environmental factors, thus making their systematic value less dependable (Vanderpuye, 1981). For example, Daget *et al.*, (1965) and Boulenger (1911) on evaluating the number of gill-rakers for its reliability in separating *C.nigrodigitatus* from the rest of the species, reported different ranges of gill-raker counts. Daget *et Ittis* (1965) reported a count of 16-18 below the first branchial arch, while Boulenger (1911) reported 12-17 for the same species. They therefore concluded that the systematic value of this character is as undependable as others. Vanderpuye (1981) also reported of overlap of ranges of gill-raker counts in four *Chrysichthys* species he studied. He also concluded that gill-raker counts were not very dependable in separating the species. Merrell (1981), also stated that populations of organisms, often in the process of adapting to local habitats, acquire some morphological modifications. These modifications may result in variation of traits within a species thereby affecting established limits of variation.

Over-reliance on morphological and meristic characters in species identification could therefore pose taxonomic problems. In Ghana for example, Vanderpuye (1981) and Loiselle (1972) identified four species of *Chrysichthys* (*C. auratus*, *C. walkeri*, *C. velifer* and *C. furcatus*) in the Volta lake based on morphology and meristics. Risch (1986a), cited in Goudswaard and Avoke (1993), however, identified only two (*C. auratus* and *C. nigrodigitatus*). This could be due to misidentification of species due to the absence of well defined distinguishing characters.

Problems associated with characterisation have often been resolved by the use of biochemical characters. Biochemical techniques have been employed to refine aspects of systematics for the past three decades. The advantages of using biochemical characters were recognised at the beginning of the century by Nuttall (1901) and Bateson (1913), cited in Ferguson (1980).

In this study, allozyme electrophoresis (with starch gel as medium) was used with the hope of confirming or contributing to refining taxonomy of the fishes studied. Technique of starch gel electrophoresis was introduced by Smithies (1955) and was first used in enzyme studies by Hunter and Markert (1957). Workers who used starch gel electrophoresis in attempts to refine systematics of fishes included Altukhov *et al.*, (1972), Aspinwal (1974) and Avise (1974). From the 1980's, the technique gained widespread use in resolving and refining systematic issues in fish. Ability to interpret and record allozymic data accurately depends greatly on knowledge of the protein category (i.e whether a protein is monomeric, dimeric or tetrameric) being stained. After electrophoresis, the pattern of enzymes observed, always in heterozygous individuals, depends on the number

of subunits in the protein molecules. In the case of monomeric enzymes, pattern observed in heterozygote individuals represents a simple combination of two different alleles. In the case of multimeric enzymes (dimeric or tetrameric) hybrid bands are formed in heterozygous individuals with the homomeric bands corresponding to those of homozygotes. In dimeric enzymes, heterozygous individuals display two homomeric and one heteromeric bands and thus show three bands. In tetrameric enzymes there are two homomeric and three heteromeric (hybrid) bands, producing typically a 5-banded pattern on the gel. These observable patterns are presented in Table 1. In the present study, data on allele frequencies permitted a discussion of genetic variation and taxonomic relationships among *Chrysichthys* populations and species. Phenetic relationships among the fishes were studied using the unweighted pair group arithmetic mean (UPGMA) method to generate dendrograms (Sneath and Sokal, 1973, cited in Ferguson, 1980).

Table 1 Diagrammatic representation of subunit structure patterns of enzymes on gel.

ENZYME-CATEGORY	ALTERNATIVE HOMOZYGOTE	HETEROZYGOTE
	a	b
MONOMERIC		
DIMERIC		
TETRAMERIC		

Note: In this representation, all enzymes have been allotted two alleles at a locus.

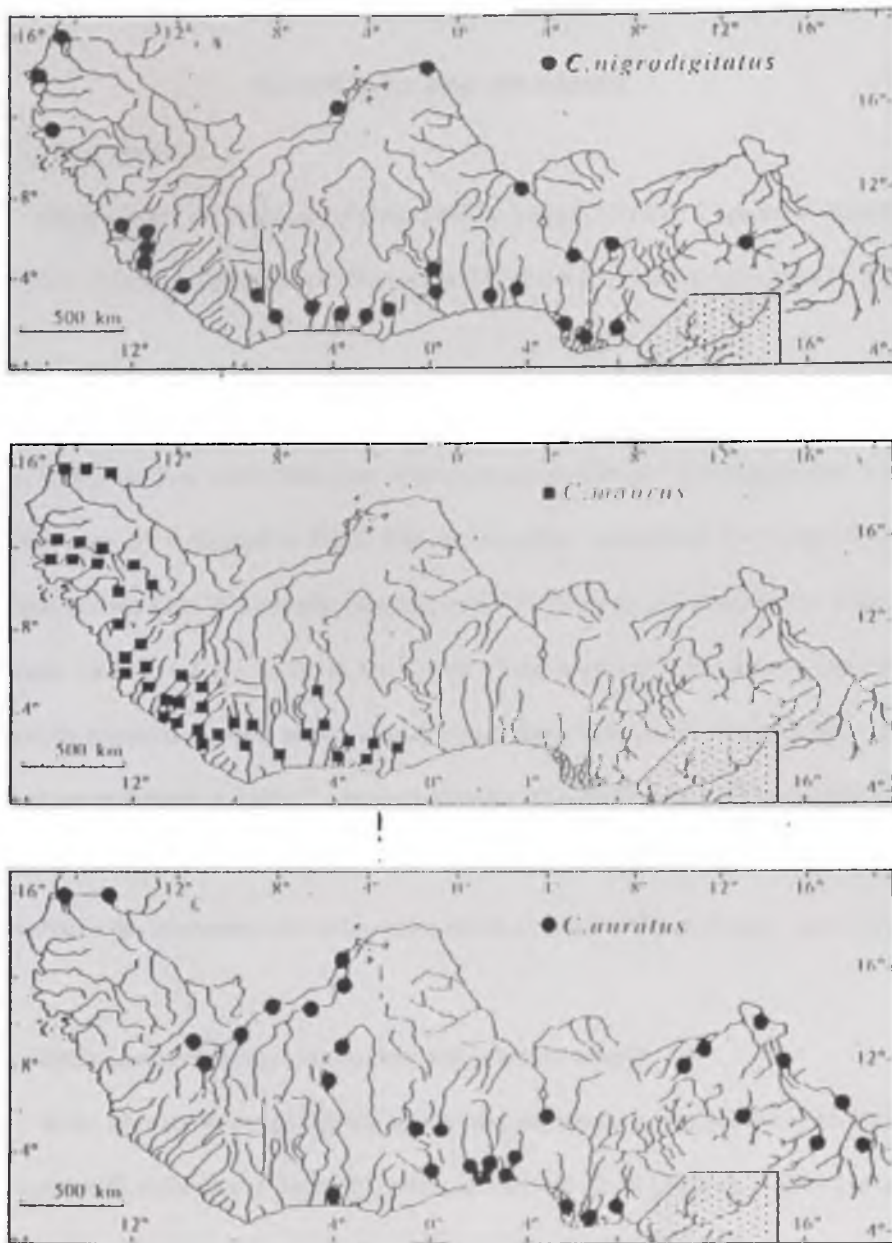


Fig.1 Geographical distribution of species of the genus *Chrysichthys* in West Africa. Source: Risch (1986b)

CHAPTER TWO

MATERIALS AND METHODS

2.1 Fishes studied

Fishes studied were species of *Chrysichthys* (Bleeker 1858): *C. auratus* (Geoffroy Saint Hilaire 1808), *C. nigrodigitatus* (Lacepede 1803) and *C. maurus* (Valenciennes 1839).

2.2 Fish sampling

Fishes studied were from two river systems in Ghana : The Densu and Volta. Sampling sites are indicated in Fig.2. The Volta system consists of the Volta river, its tributaries and the lake. In this study, sampling in the Volta basin was done in the lake and the lower reaches of the river. In the Densu river, sampling was done in the Weija reservoir(a dammed portion of the Densu river). Localities from where samples were obtained are indicated in Table 2. At each locality, 25 - 30 fresh individuals of fish were chosen at random from landings of local fishermen. Samples were stored on ice and transported to the laboratory where they were stored at about -30°C until they were needed.

2.3 Body proportion measurements and meristic counts

In the laboratory, morphological and meristic parameters were measured to identify specimens with reference to keys of Roman (1966) and Risch (1986a). Figure 3 shows demarcations of the various body parts measured. Major tools for the measurements were: a pair of calipers with 0.1 mm graduations, a magnifying glass, a pair of dividers, a ruler and

Table 2 Species studied and their sources

SPECIES	WATER BODY / LOCALITY
<i>C. auratus</i>	Volta Lake at Yeji
<i>C. auratus</i>	Volta Lake at Akosombo
<i>C. auratus</i>	Volta River at Battor
<i>C. nigrodigitatus</i>	Volta Lake at Yeji
<i>C. nigrodigitatus</i>	Densu River at Weija
<i>C. nigrodigitatus</i>	Volta River at Battor
<i>C. maurus</i>	Volta River at Battor

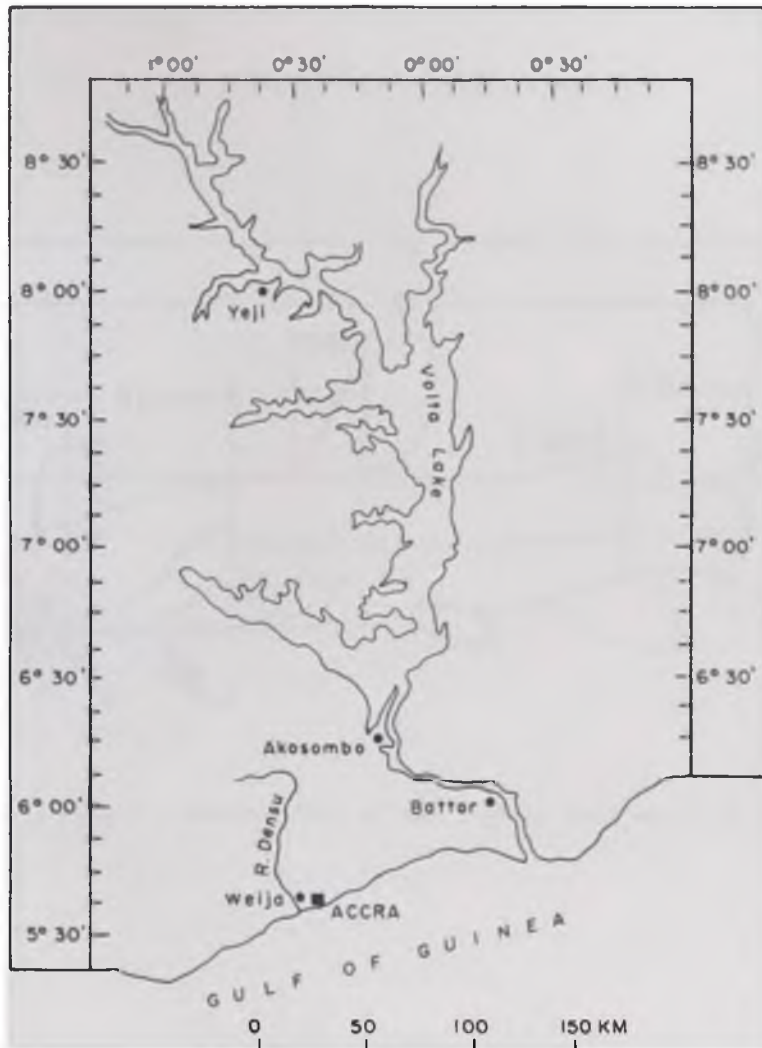


Fig.2. MAP SHOWING SAMPLING STATIONS

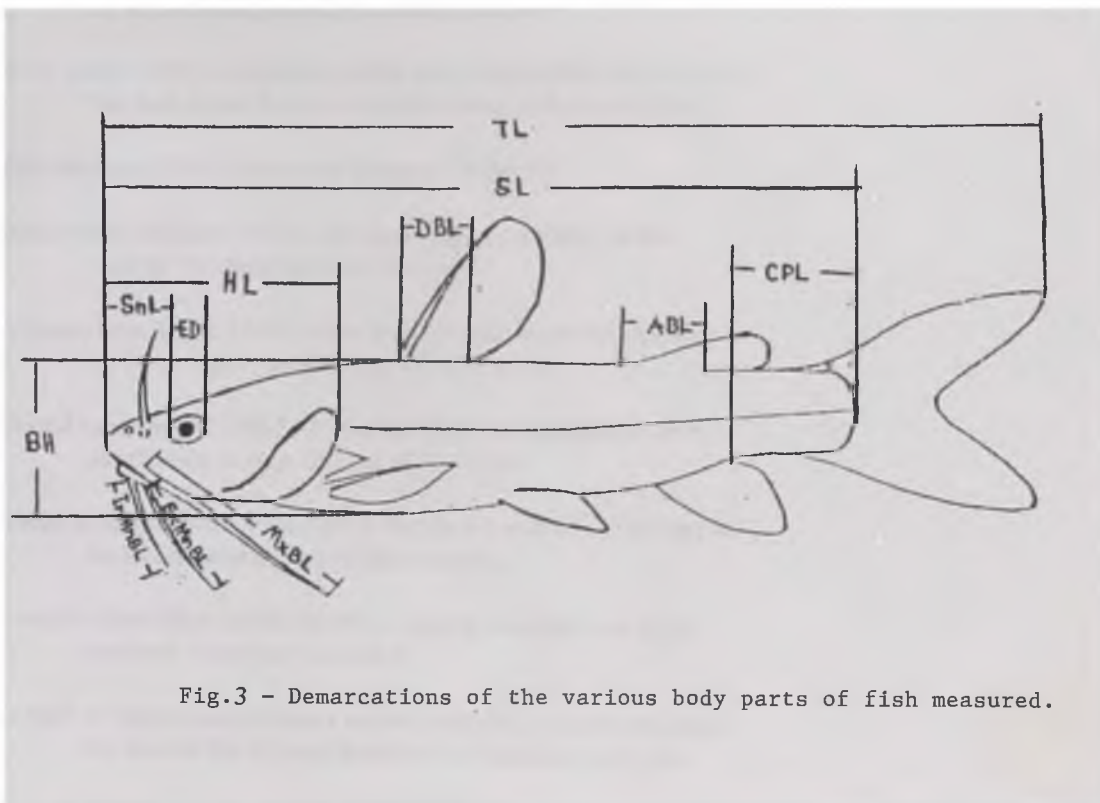


Fig.3 - Demarcations of the various body parts of fish measured.

LEGEND

Standard length (SL) - distance from the anterior end of the upper lip to the end of the vertebral column

Total length (TL) - length from the anterior end of upper lip to the end of caudal fin

Head length (HL) - a measure from the anterior end of the upper lip to the most posterior end of opercular

Body height (BH) - a measure of the body height from the base of the first dorsal fin ray vertically down to the base of fish.

Eye diameter (ED) - horizontal diameter of the iris

Interorbital distance (IOD) - the least width (diameter) of the roof of the skull between the eyes

Adipose base length (ABL) - horizontal length from the anterior to the posterior end of base of adipose fin

Dorsal base length (DBL) - horizontal distance between the first and the last fin rays of base of dorsal fin

Snout length (SnL) - a measure from the anterior end of the upper lip to the anterior end of the eye orbit

Length of maxillary barbel (MxBL) - length from the base of the maxillary barbel to its tip end

Length of internal mandibular barbel (InMnBL) - the length from the base of the internal mandibular barbel to its tip end

Length of external mandibular barbel (ExMnBL) - length from the base of the external mandibular barbel to its tip end

Length of caudal peduncle (CPL)- length from the posterior base of the anal fin to the central base of the caudal fin

a binocular microscope.

The following morphological measurements were taken :

Standard length (SL)

Total length (TL)

Head length (HL)

Body height (BH)

Eye diameter (ED)

Interorbital distance (IOD)

Adipose base length (ABL)

Dorsal base length (DBL)

Snout length (SnL)

Length of maxillary barbel (MxBL)

Length of internal mandibular barbel (InMnBL)

Length of external mandibular barbel (ExMnBL)

Length of caudal peduncle (CPL)

Meristic counts taken were:

Number of simple and branched rays of dorsal fin

Number of simple and branched rays of pectoral fin

Number of simple and branched rays of ventral fin

2.4 Starch gel electrophoresis

Soluble skeletal muscle proteins of fishes were subjected to electrophoresis in

hydrolysed potato starch media with the hope of identifying loci that may discriminate the species and provide some information on the population structure of the fishes studied.

(a) Preparation of Soluble skeletal muscle proteins

Weighed muscle pieces were crushed in a crucible together with equal volume of cold distilled water into a paste. The paste was transferred into test tubes and centrifuged at 4°C at approximately 4000 rev. min⁻¹ for 30 minutes. The supernatant was decanted into tubes, labelled and stored frozen as samples for later use in electrophoresis.

(b) Preparation of starch gel

A single gel contained 12.5% of hydrolysed potato starch in Continuous-Tris-Citrate (CTC) buffer, pH 8.0 (see buffer in Appendix 18). The mixture was heated in a Buchner flask held over a Bunsen burner flame with continuous swirling. Heating was stopped as soon as the first big bubble appeared at the bottom of the flask. The gel was quickly degassed using a vacuum pump, poured into a mould previously set, and covered with a glass plate. Gel was allowed to set and cooled at room temperature for about 3-4 hours after which it was incubated in a refrigerator for 3-12 hours.

(c) Loading of gel

A horizontal incision, about 4.0 cm from the lower end of the gel was made. The supernatant (from different samples) were adsorbed on strips of 0.33 mm Whatman chromatography paper and arranged along the upper cut surface of the gel. Specimens of

known proximate protein mobilities were included on new gels to indicate relative positions of new samples on gel. The cut surfaces of the gel were then pushed into place (with the samples between them). A spacer was pushed into the gel former together with the gel to ensure very close contact of samples to gel. The 'loaded' gel was placed over a buffer tray containing an electrode buffer [Continuous-Tris-Citrate (CTC) pH 8.0]. A wick was stretched gently over each end of the gel with enough of it immersed in the tray buffer. A thin polythene film was stretched over the gel to prevent dehydration of gel during electrophoresis and a glass plate placed over. Iced packs were then positioned on the glass plate as coolants.

(d) Electrophoresis

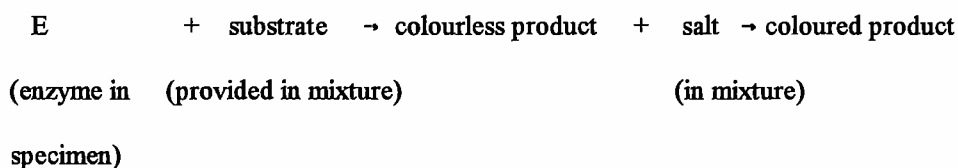
Buffer tray (with contents) was placed in a refrigerator and the terminals of tray connected to a power supply unit (negative terminal relatively nearer to samples). The ammeter and voltmeter were adjusted to about 50 amps and 160-200 volts respectively. The amperage and voltage readings were checked after 20 minutes to ensure that set values were constant. The duration for electrophoresis was between 4 to 5 hours depending on power supply conditions.

(e) Slicing of gel

After electrophoresis, the gel was trimmed, and the anodal end on the side of "specimen 1" cut off to indicate orientation of specimen prior to slicing. A Buchler gel slicer with a gauge of 2 mm was used to horizontally slice the gel into 2 mm slices.

(f) Staining of gel

A staining mixture produces bands on the general principle that a substrate (in the mixture) forms a colourless product with enzyme (in gel from the tissue sample). The initial product then couples with a salt (also in mixture) giving out coloured bands at positions where the enzyme(s) being stained for have migrated to during the electrophoresis of the samples.



Staining recipes used to stain enzymes were similar to those used by Shaw and Prasad (1970) (see Appendix 17). The slice of gel (cut surface up) was placed in a staining tray and the staining solution poured on them. Staining trays (containing the gel) were placed in a warm-air incubator at 37°C for enzymes to stain. Stain was washed off with tap water when the staining solution (yellowish in colour) began to turn blackish or when bands could be read on the gel, and a fixing solution added.

(g) Recording of allozymic data

Stained bands fade with time. Therefore record of patterns produced after electrophoresis and staining (i.e. banding patterns) were recorded diagrammatically for later analysis. Summary of proteins (enzymes) studied and number of loci screened are presented in Table 3.

Table 3 Proteins (enzymes) studied and number of loci screened.

Protein	Enzyme number	Protein abbreviation	Number of loci screened
Alcohol dehydrogenase	1.1.1.1	ADH	1
L- Lactate dehydrogenase	1.1.1.27	LDH	1
Malate dehydrogenase	1.1.1.37	MDH	2
Octanol dehydrogenase	1.1.1.73	ODH	1
Sorbitol dehydrogenase	1.1.1.14	SDH	2
Glycerol-3-phosphate dehydrogenase	1.1.1.8	G3PDH	1
Xanthine dehydrogenase	1.2.3.2	XDH	1
Malic enzyme	1.1.1.40	ME	2
Phosphoglucomutase	5.4.2.2	PGM	1
Glucose-6-phosphate isomerase	5.3.1.9	GPI	1
Isocitrate dehydrogenase	1.1.1.42	IDH	2

2.5 Analysis of data

2.5.1 Morphometric data

Means, Ranges and modes of twelve body characters of three species of *Chysichthys* were determined after morphological measurements. One-way Analysis of Variance (ANOVA) for proportions of selected characters was then performed to estimate differences in body characters of populations and species to assess significance of differences if any.

2.5.2 Electrophoretic data

(a) Allelic frequency

Results of allelic frequencies (from electrophoresis) provides an efficient data for the estimation of genetic differences between populations and species (Ferguson, 1980; Thorpe, 1982).

The frequency of an allele was estimated by the formula:

$$(2H + He) / 2N \quad (\text{Ferguson, 1980})$$

where H = number of homozygotes for that allele

He = number of heterozygotes for that allele

N = number of individuals examined

(b) Proportion of polymorphic loci in populations and species

The polymorphic state of an enzyme locus had been assessed on the basis of the frequency (f) of the most common allele. 1% and 5% criteria were considered here.

At 1% criterion, the most common allele with frequency less than 0.99 was



considered as polymorphic at each locus.

At 5% criterion, the most common allele with frequency less than 0.05 was considered as polymorphic at each locus.

Mean polymorphism per locus (P) was then calculated in each population at each criterion as:

$$P = \text{No. of polymorphic loci} / \text{No. of loci scored}$$

(Ferguson, 1980)

(c) Heterozygosity

Heterozygosity is considered a more reliable measure of population variability than polymorphism.

Expected heterozygosity per locus (H_e) according to Hardy-Weinberg was estimated by the formula:

$$H_e = 1 - \sum X_i^2$$

where X_i is the frequency of the i th allele at a locus

Mean heterozygosity per locus \bar{H}_e , was estimated as the sum of H_e over all loci divided by the total number of loci examined.

Observed heterozygosity (H), was the fraction of heterozygote individuals.

(d) Genetic Identity

Genetic identity (I) between two taxa was estimated by:

$$I = \sum x_i y_i / \sqrt{(\sum x_i^2 \sum y_i^2)} \text{ (Nei, 1972)}$$

where x_i and y_i are the frequencies of the i th allele in populations X and Y respectively.

Mean genetic identity (\bar{I}) is the mean over all loci studied. It was estimated by :

$$\bar{I} = I_{xy} / \sqrt{(I_x I_y)}$$

where I_{xy} , I_x and I_y are the arithmetic mean over all loci of $\sum x_i y_i$, $\sum x_i^2$ and $\sum y_i^2$ respectively.

(e) Genetic distance

Having obtained the I values for various pairs of taxonomic units, the genetic distance between pairs (D) was estimated by :

$$D = -\log_e I \text{ or } -\ln I$$

where I is the genetic identity between two taxonomic units.

(f) Construction of dendrogram

The unweighted pair group arithmetic mean (UPGMA) clustering method [Sneath and Sokal, (1973), as described by Ferguson, (1980)], pair-wise comparisons of genetic identities was used to generate the phenetic relationship among fishes based on allele frequency.

The initial step towards clustering among taxonomic units studied [Operational Taxonomic Units (OTU)] based on overall genetic 'similarities' or identities was to set out pair-wise genetic identities (0.0-1.0) in a matrix table. Then from the matrix, the two OTUs with the highest identity value (e.g. OTUs 1 and 2 in Table 13) were first clustered. The point at which the two OTUs were joined was with reference to the scale (Fig. 4), while the distance apart was arbitrary. The matrix was then reworked with OTUs 1 and 2 combined as a unit (OTU 1/2). In the new matrix, the identity between any OTU and OTU 1/2 was the

mean of the OTU's identity with OTU 1 and 2. This process was repeated until all OTUs were linked. The stepwise process of constructing the relationships is described by Ferguson (1980).

(g) Hardy-Weinberg analysis

Two methods were used here:

(i) Log likelihood χ^2 test (G test)

Genotypic frequencies were obtained from the allelic frequency values using the Hardy-Weinberg equation. The equation background indicates that for a two-allele polymorphism, where p and q represent the alleles, the genotypic frequencies would be p^2 , $2pq$ and q^2 . The difference between the observed and expected genotypic frequencies were tested for statistical significance using the log likelihood χ^2 test (G test).

$$G = 2 \sum \text{obs} \times \ln(\text{obs}/\text{exp}) = 2 [\sum \text{obs} \times \ln \text{obs} - (2.30259) \sum \text{obs} \times \log \text{exp}]$$

(ii) Wright's fixation index (F)

Wright's fixation index (F), which indicates deviations from Hardy-Weinberg expectations, was calculated as:

$$F = 1 - \text{observed heterozygosity} / \text{expected heterozygosity} \text{ or } 1 - H / H_e \text{ (Jain and Workman, 1967)}$$

Where H = Observed heterozygosity

H_e = Expected heterozygosity

CHAPTER 3

RESULTS AND DISCUSSION

3.1 MORPHOLOGICAL TAXONOMY

3.1.1 Frequency distribution of meristic characters

Frequency distribution of meristic characters studied among the *Chrysichthys* species are presented in Table 4. The table also shows counts recorded by previous workers on West Africa populations of the species (Roman, 1966; Risch, 1986a)

The results indicate that the number of dorsal rays in *C. auratus*, *C. nigrodigitatus* and *C. maurus* were consistently the same within and between species. The same applies to the pelvic rays (Table 4). The invariable states of the dorsal and pelvic fin rays were consistent with findings of Roman (1966) and Lowe-McConnell (1972). The pectoral fin rays did not show remarkable intraspecific variation. However, there were remarkable interspecific variations as indicated in Table 4. *Chrysichthys auratus* and *C. maurus* showed eight branched pectoral rays but *C. nigrodigitatus* apparently showed nine. Result obtained is compatible with those of Risch (1986a). He indicated that, there were populations of *C. maurus* that showed a higher percentage of specimens of eight branched rays on the pectoral fins in the Liberia - Ghana region. *C. nigrodigitatus* can therefore be distinguished from *C. maurus* and *C. auratus* on the basis of the number of branched pectoral fin rays (eight in *C. maurus* and *C. auratus* and nine in *C. nigrodigitatus*).

Table 4 Frequency distribution of meristic characters in three species of *Chrysiichthys* in Ghana.

Species	Water body / Locality	N	No. of dorsal fin ray		No. of pelvic fin ray		No. of pectoral fin ray		No. of branched pectoral fin ray counts in previous studies	
			II - 6	I - 5	I - 8	I - 9	Rmn	Rsh		
<i>C. auratus</i>	Volta lake / Yeji	26	26	26	26	0	0	8	8	
<i>C. auratus</i>	Volta lake / Akosombo	27	27	27	27	0	0	9	9	
<i>C. auratus</i>	Volta river / Bator	18	18	18	18	0	0	8 - 9	8 - 9	
<i>C. nigrodigitatus</i>	Volta lake / Yeji	18	18	18	0	18	0			
<i>C. nigrodigitatus</i>	River Densu / Weija	25	25	25	1	24	0			
<i>C. nigrodigitatus</i>	Volta river / Bator	26	26	26	0	26	0			
<i>C. maurus</i>	Volta river / Bator	20	20	20	20	0	0			

N = Sample size
Rmn = Roman (1966)
Rsh = Risch (1966)

Note: Number of unbranched fin rays are written in Roman numerals and number of branched in Arabic.

3.1.2 Means, Modes and Ranges of Body Proportion measurements

The means, modes and ranges of twelve body proportions for the three species of *Chrysichthys* determined from body measurement are presented in Table 5. Results show interpopulational and interspecific morphological variation. Body proportion values showed apparent wide ranges and overlapped among species. The extent of overlapping did not allow them to be used for species identification. This seems compatible with findings of Vanderpuye (1981). Seemingly wide range of body proportions in populations and species could be due to morphological modifications acquired in the process of adapting to their local habitats as emphasised by Merrell (1981).

3.1.3 Analysis of Variance of Body Proportion Variables

Presented in Appendices 15A, 15B and 15C are analyses of variance for each character in Table 5. A statistically significant amount of variation between species and between populations within species was found for the twelve body proportions. Results showed that among the *C. auratus* populations, four body proportions - ED/IOD, HL/BH, HL/ABL and SnL/ED were significantly different at $P < 0.001$. Among *C. nigrodigitatus* all the body proportion variables except ExMnBL/InMnBL were significantly different at $P < 0.001$. Among the three *Chrysichthys* species (*C. auratus*, *C. nigrodigitatus* and *C. maurus*), five body proportion variables - HL/ED, HL/ABL, BH/CPL, HL/DLRL and SL/HL were significantly different at $P < 0.001$. These body proportion characters could therefore be considered in the characterization of these populations and species.

Position of the longest dorsal fin ray and the number of branched pectoral fin rays

(appendices 1-7) have shown to be valuable in the identification of the three species. *C. nigrodigitatus* could be distinguished from *C. maurus* and *C. auratus* on the basis of the number of branched pectoral fin rays (nine in *C. nigrodigitatus* but eight in *C. auratus* and *C. maurus*). *Chrysichthys auratus* could be distinguished from *C. maurus* on the basis of position of the longest dorsal soft fin ray (first in *C. auratus* but second in *C. maurus*). Results obtained on meristic counts confirm the reliability of the keys used in the initial identification.

3.2 PROTEIN TAXONOMY

3.2.1 Loci scored

Base-line information on loci scored are provided below.

Results indicating scoring and the number of alleles observed at each locus were derived from allele frequencies (Table 10).

Alcohol dehydrogenase 1.1.1.1 (ADH). A single locus (*ADH-1**) was scored. Two alleles were observed. One was fixed for *C. nigrodigitatus* and *C. maurus* and the other for *C. auratus*. Allele common to *C. nigrodigitatus* and *C. maurus* had a relatively higher mobility compared to that of *C. auratus*. No heterozygotes were observed.

L-Lactate dehydrogenase 1.1.1.27 (LDH). A single locus (*LDH-A**) was scored. Two alleles were observed for *C. auratus* heterozygote individuals while homozygote individuals were fixed for the slower allele. A common allele was observed for both *C. nigrodigitatus* and *C. maurus*. The relative mobility of allele from *C. nigrodigitatus* and *C.*

Table 5

Ranges, Means and Modes of twelve Body proportions of three *Chrysichthys* species in Ghana.

Eye diameter / Interorbital distance

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.11-1.79	1.42	1.24	0.040
	V. Lake/Akosombo	27	1.33-1.92	1.68	1.87	0.029
	V. River/Battor	18	1.23-1.55	1.36	1.29	0.007
<i>C. nigro.</i>	V. Lake/Yeji	18	1.11-1.50	1.22	1.17	0.012
	R. Densu/Weiija	25	1.10-1.38	1.22	1.21	0.006
	V. River/Battor	28	1.34-1.84	1.70	1.80	0.016
<i>C. maurus</i>	V. River/Battor	20	1.20-1.77	1.38	1.33	0.024

Snout Length / Interorbital distance

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.64-1.97	1.86	1.90	0.010
	V. Lake/Akosombo	27	1.74-2.10	1.93	1.93	0.008
	V. River/Battor	18	1.69-1.98	1.89	1.95	0.007
<i>C. nigro.</i>	V. Lake/Yeji	18	1.65-1.97	1.83	1.93	0.013
	R. Densu/Weiija	25	1.26-1.78	1.52	1.51	0.022
	V. River/Battor	26	2.10-2.69	2.30	2.13	0.027
<i>C. maurus</i>	V. River/Battor	20	1.55-1.98	1.84	1.96	0.014

Species	Water Body/ Locality	Sample size (n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.36-1.73	1.56	1.51	0.011
	V. Lake/Akosombo	27	1.21-1.48	1.37	1.43	0.005
	V. River/Battor	18	1.27-1.79	1.48	1.31	0.028
<i>C. nigro.</i>	V. Lake/Yeji	18	1.39-1.80	1.55	1.53	0.016
	R. Densu/Weiija	25	1.09-1.38	1.25	1.32	0.005
	V. River/Battor	26	1.34-1.54	1.42	1.42	0.002
<i>C. maurus</i>	V. River/Battor	20	1.25-1.69	1.42	1.39	0.014

Head Length / Eye diameter

Species	Water Body/ Locality	Sample size (n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	3.09-3.86	3.51	3.69	0.043
	V. Lake/Akosombo	27	3.24-3.81	3.51	3.40	0.026
	V. River/Battor	18	3.24-3.98	3.67	3.77	0.050
<i>C. nigro.</i>	V. Lake/Yeji	18	3.53-4.25	3.95	3.99	0.039
	R. Densu/Weiija	25	3.27-3.96	3.68	3.78	0.044
	V. River/Battor	26	3.27-3.97	3.64	3.64	0.032
<i>C. maurus</i>	V. River/Battor	20	3.45-4.21	3.81	3.78	0.050

Head Length / Adipose base Length

Species	Water Body/ Locality	Sample size (n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	2.09-2.88	2.53	2.87	0.055
	V. Lake/Akosombo	27	2.42-2.97	2.73	2.89	0.023
	V. River/Battor	18	2.13-2.78	2.49	2.53	0.046
<i>C. nigro.</i>	V. Lake/Yeji	18	2.32-2.98	2.66	2.67	0.041
	R. Densu/Weiija	25	2.38-3.46	2.76	2.44	0.050
	V. River/Battor	26	2.70-3.58	3.04	2.82	0.050
<i>C. maurus</i>	V. River/Battor	20	2.33-3.21	2.67	2.50	0.089

Head Length / Maxillary barbel Length

Species	Water Body/ Locality	Sample size (n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.16-1.54	1.31	1.27	0.012
	V. Lake/Akosombo	27	1.05-1.45	1.24	1.20	0.013
	V. River/Battor	18	1.14-1.59	1.33	1.32	0.018
<i>C. nigro.</i>	V. Lake/Yeji	18	1.11-1.53	1.24	1.17	0.012
	R. Densu/Weiija	25	1.13-1.66	1.36	1.31	0.016
	V. River/Battor	26	1.11-1.33	1.24	1.23	0.004
<i>C. maurus</i>	V. River/Battor	20	1.13-1.59	1.33	1.31	0.013

Body Height / Caudal Peduncle Length

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.13-1.73	1.35	1.15	0.024
	V. Lake/Akosombo	27	1.10-1.55	1.40	1.48	0.012
	V. River/Battor	18	1.20-1.65	1.36	1.28	0.017
<i>C. nigro.</i>	V. Lake/Yeji	18	1.05-1.38	1.21	1.16	0.008
	R. Densu/Weiija	25	1.21-1.53	1.37	1.53	0.009
	V. River/Battor	28	1.11-1.39	1.23	1.17	0.007
<i>C. maurus</i>	V. River/Battor	20	1.11-1.68	1.33	1.22	0.035

Head Length / Longest dorsal ray Length

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	0.52-1.16	0.81	0.87	0.022
	V. Lake/Akosombo	27	0.51-1.33	0.84	0.95	0.040
	V. River/Battor	18	0.71-1.18	0.93	1.18	0.033
<i>C. nigro.</i>	V. Lake/Yeji	18	0.74-1.23	0.98	0.74	0.018
	R. Densu/Weiija	25	0.95-1.20	1.05	1.11	0.003
	V. River/Battor	26	0.73-1.08	0.94	1.01	0.007
<i>C. maurus</i>	V. River/Battor	20	0.87-1.28	1.04	1.22	0.015

External Mandibular barbel Length/Internal Mandibular barbel Length

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.29-1.81	1.52	1.62	0.030
	V. Lake/Akosombo	27	1.25-1.65	1.43	1.42	0.010
	V. River/Battor	18	1.26-1.76	1.47	1.55	0.022
<i>C. nigro.</i>	V. Lake/Yeji	18	1.18-1.63	1.47	1.49	0.013
	R. Densu/Weiija	25	1.20-1.67	1.44	1.29	0.016
	V. River/Battor	26	1.31-1.82	1.58	1.74	0.028
<i>C. maurus</i>	V. River/Battor	20	1.29-1.62	1.44	1.45	0.009

Standard Length / Head Length

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	3.03-3.59	3.30	3.43	0.023
	V. Lake/Akosombo	27	3.00-3.61	3.31	3.31	0.017
	V. River/Battor	18	3.13-3.60	3.36	3.45	0.015
<i>C. nigro.</i>	V. Lake/Yeji	18	3.26-3.71	3.51	3.51	0.014
	R. Densu/Weiija	25	3.41-3.88	3.66	3.72	0.011
	V. River/Battor	26	3.39-3.74	3.53	3.50	0.005
<i>C. maurus</i>	V. River/Battor	20	3.20-3.78	3.48	3.51	0.026

Snout Length / Eye diameter

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	1.10-1.62	1.33	1.15	0.026
	V. Lake/Akosombo	27	1.00-1.41	1.18	1.27	0.012
	V. River/Battor	18	1.23-1.59	1.38	1.43	0.013
<i>C. nigro.</i>	V. Lake/Yeji	18	1.12-1.74	1.51	1.56	0.026
	R. Densu/Weiija	25	1.04-1.45	1.25	1.04	0.015
	V. River/Battor	28	1.21-1.56	1.31	1.23	0.007
<i>C. maurus</i>	V. River/Battor	20	1.21-1.61	1.40	1.42	0.013

External Mandibular barbel Length / Head Length

Species	Water Body/ Locality	Sample size(n)	Range	Mean	Mode	SE
<i>C. auratus</i>	V. Lake/Yeji	26	0.38-0.53	0.45	0.44	0.002
	V. Lake/Akosombo	27	0.40-0.57	0.48	0.50	0.002
	V. Lake/Battor	18	0.38-0.52	0.45	0.46	0.002
<i>C. nigro.</i>	V. Lake/Yeji	18	0.39-0.54	0.46	0.46	0.002
	R. Densu/Weiija	25	0.35-0.52	0.43	0.35	0.003
	V. Lake/Battor	28	0.40-0.59	0.50	0.48	0.003
<i>C. maurus</i>	V. Lake/Battor	20	0.37-0.49	0.44	0.41	0.001

nigro = *nigrodigitatus* ; SE = Standard error

maurus (common to both) is between the faster and slower alleles of *C. auratus*. Heterozygotes were observed only in *C. auratus*.

Malate dehydrogenase 1.1.1.37 (sMDH). Two loci (*sMDH-A** and *sMDH-B**) were scored.

At *sMDH-A**, only one allele, common to all three species was observed. There were no heterozygotes.

At *sMDH-B**, two alleles common to all species (except *C. nigrodigitatus* from Battor) were observed for heterozygote individuals. Homozygote individuals were fixed for the slower allele. *C. nigrodigitatus* from Battor showed only one allele.

Octanol dehydrogenase 1.1.1.73 (ODH). A single locus (*ODH-1**) was scored. Two alleles were observed. One was fixed for *C. nigrodigitatus* and *C. maurus* and the other for *C. auratus*. Allele from *C. nigrodigitatus* and *C. maurus* was relatively faster than that from *C. auratus*. No heterozygotes were observed.

Malic enzyme (NAD) 1.1.1.40 (ME). Two loci (*ME-1** and *ME-2**) were scored. At each locus, only one allele, common to all three species was observed. No heterozygotes were observed.

Glucose-6-phosphate isomerase 5.3.1.9 (GPI). A single locus (*GPI-A**) was scored. Two alleles, common to all species except those from Yeji were observed for heterozygote

individuals. Homozygote individuals were fixed for the slower allele. Only one allele (the slower allele) was observed for *C. auratus* and *C. nigrodigitatus* from Yeji.

Phosphoglucomutase 5.4.2.2 (PGM). A single locus (*PGM-1**) was scored. Two alleles were observed. One was fixed for *C. nigrodigitatus* and *C. maurus* and the other for *C. auratus*. Allele from *C. auratus* was relatively faster than that from *C. nigrodigitatus* and *C. maurus*. No heterozygotes were observed.

Isocitrate dehydrogenase 1.1.1.42 (IDH). Two loci (*IDH-1** and *IDH-2**) were scored. At each locus, only one allele, common to all three species was observed. No heterozygotes were observed.

Sorbitol dehydrogenase (SDH). Two loci (*SDH-1**) and (*SDH-2**) were scored.

At *SDH-1**, two alleles were observed among the three species. One allele was fixed for *C. nigrodigitatus* and *C. maurus* and the other specific to *C. auratus*. The allele common to *C. nigrodigitatus* and *C. maurus* had a relatively faster mobility compared to that of *C. auratus*.

At *SDH-2**, only one allele, common to all three species was observed. No heterozygotes were observed.

Glycerol-3-phosphate dehydrogenase 1.1.1.8 G3PDH (GPD). A single locus (*G3PDH-1**) was scored. Two alleles were observed among the three species. One allele was

common to *C. nigrodigitatus* and *C. maurus* and the other specific to *C. auratus*. Allele common to *C. nigrodigitatus* and *C. maurus* was relatively faster than allele of *C. auratus*. No heterozygotes were observed.

Xanthine dehydrogenase (XDH). A single locus (*XDH-1**) was scored. Two alleles were observed among the three species. One allele was common to *C. nigrodigitatus* and *C. maurus* and the other specific to *C. auratus*. Allele common to *C. nigrodigitatus* and *C. maurus* was relatively faster than allele of *C. auratus*. No heterozygotes were observed.

3.2.2 Allozyme patterns of fish species at 15 loci

Allozyme patterns of the *Chrysichthys* species and populations compared at 15 enzymatic loci are presented in Table 6. Patterns were observed after starch gel electrophoresis. Allozyme patterns obtained here were considered as expression of taxonomic character states in the species and populations .

For Species comparison, each gene locus was considered as a taxonomic character and genotypes observed in individuals of a species as the 'range' of character expression within the species. Loci at which no differences in pattern were observed between populations and species have been grouped together. Two alleles and one heterozygote type were assumed at any variable locus as basic possible genotypes. Results provide an allozyme basis on which pair-wise separation of species may be carried out. Table 6 shows that all individuals of *C. auratus*, *C. nigrodigitatus* and *C. maurus* expressed the 'characters': *ME-1**, *ME-2**, *IDH-1**, *IDH-2**, *sMDH-A** and *SDH-2** in non variable forms at each locus. All the three species had

Table 6 Specific protein patterns as taxonomic character states

SPECIES	<i>C. auratus</i> Yei	<i>C. auratus</i> Akogombo	<i>C. auratus</i> Bator	<i>C. nigrodigitatus</i> Yei	<i>C. nigrodigitatus</i> Bator	<i>C. nigrodigitatus</i> Weia	<i>C. maurus</i> Bator
Locus							
ME - 1*							
ME - 2*							
IDH - 1*	---	---	---	---	---	---	---
IDH - 2*							
sMDH - A*							
SDH - 2*							
ADH - 1*							
SDH - 1*							
ODH - 1*	---	---	---	---	---	---	---
XDH - 1*							
G3PDH - 1*							
sMDH - B*	---	---	---	---	---	---	---
LDH - A*	---	---	---	---	---	---	---
PGM - 1*	---	---	---	---	---	---	---
GPI - A*	---	---	---	---	---	---	---

At each polymorphic locus, pattern represents heterozygote individuals. Homozygote individuals are fixed for the slower allele.

Table 7 Discriminating loci between pairs of *Chrysichthys* species (No. of loci screened = 15)

Species pair	Discriminating loci	Loci with significant differential allele frequency
<i>C. auratus</i> / <i>C. nigro.</i>	ADH = 1*, LDH = A*, SDH = 1*, PGM = 1*, ODH = 1*, XDH = 1*, G3PDH = 1*	none
<i>C. auratus</i> / <i>C. maurus</i>	ADH = 1*, LDH = A*, SDH = 1*, PGM = 1*, ODH = 1*, XDH = 1*, G3PDH = 1*	none
<i>C. nigro.</i> / <i>C. maurus</i>	none	none

nigro = *nigrodigitatus*

a common non-variable allele.

Seven loci (46.7%) display fixation of alternative allele between either *C. nigrodigitatus* or *C. maurus* and *C. auratus*. However, there were no discriminating loci between *C. nigrodigitatus* and *C. maurus*.

In the present study, loci at which each of a pair of species had alternate alleles were considered as 'discriminating loci' between the pair. It was also possible to identify loci which, though not discriminating, showed significant differential allele frequencies on which species identification could be based. Such loci have, here, been defined as those at which one of a pair of species had a frequency ≥ 0.90 for one allele while the other had a frequency ≤ 0.10 for the same allele.

Table 7, derived from Table 6, shows taxonomically important discriminating loci between pairs of *Chrysichthys* species.

3.2.3 Distribution of Polymorphic loci

Table 8 shows the distribution of polymorphism for enzyme loci investigated in all populations and species. The Table indicates that:

(a) Out of the fifteen loci screened, twelve loci (representing 80%) were monomorphic for all populations and species.

(b) Three loci (LDH-A*, MDH-B* and GPI-A*) were polymorphic in certain species and populations.

(i) LDH-A* was polymorphic for only *C. auratus*.

(ii) MDH-B* was polymorphic in *C. auratus* at all 3 localities: *C. maurus* population from

Table 8 Distribution of Polymorphic loci in Populations and Species of *Chrysichthys*

Locus	POPULATION					SPECIES
	<i>C. auratus</i> Akosombo Battor	<i>C. auratus</i> Yeji	<i>C. nigro</i> Waija	<i>C. nigro</i> Battor	<i>C. maurus</i> Battor	
ADH - 1*						
LDH - A*	++	+				++
MDH - A*						
MDH - B*	++	++	++		+	++
SDH - 1*						
SDH - 2*						
GPI - A*	+	++	++	+	++	+
PGM - 1*						
ODH - 1*						
IDH - 1*						
IDH - 2*						
XDH - 1*						
3PDH - 1*						
ME - 1*						
ME - 2*						

Criteria for Polymorphism(P) : + = 1% ; ++ = 5%
nigro. = *nigrodigitatus*

Battor and *C. nigrodigitatus* populations from 2 out of the 3 localities.

(iii) *GPI-A** was polymorphic in *C. maurus* from Battor, and also in *C. auratus* and *C. nigrodigitatus* at all localities except Yeji.

Considering *MDH-B** and *GPI-A** as 'Characters', being polymorphic for almost all populations and species could be comparable to certain morphological features found to overlap across populations and species in morphological taxonomy. Furthermore, specificity of polymorphism at *LDH-A** to only *C. auratus* can again be compared to morphological taxonomy where certain features are specific to particular species. This result suggests the existence of species-specific polymorphic loci. *GPI-A** was monomorphic for Yeji populations of *C. auratus* and *C. nigrodigitatus*. *MDH-B** was also monomorphic for *C. nigrodigitatus* population at Battor.

3.2.4 Polymorphism in populations and species

Estimated polymorphism per locus *P*, in populations and species, are presented in Table 9. At 5% criterion, *P* was 0.133 for *C. auratus* at Akosombo and Battor, and 0.067 for *C. auratus* at Yeji. For all populations of *C. nigrodigitatus* and also for *C. maurus* population at Battor, *P* was 0.067. Mean *P* values were 0.111 for *C. auratus* and 0.067 for both *C. nigrodigitatus* and *C. maurus*.

At 1% criterion, *P* was 0.200 for *C. auratus* at Akosombo and Battor, and 0.133 for *C. auratus* at Yeji. For *C. nigrodigitatus* at Yeji and Battor, *P* was 0.067, and 0.133 for *C. nigrodigitatus* at Wejja. For *C. maurus* at Battor *P* was 0.133. Mean *P* values were 0.178 for *C. auratus*, 0.133 for *C. maurus* and 0.089 for *C. nigrodigitatus*.

Table 9 Genetic variation in populations belonging to three species of *Chrysichthys* based on 15 loci with Wright's fixation index, F

Species	Water body/Locality	N	n	* P P (0.05), P (0.01)	H mean	S E	He mean	S E	Wright's fixation index, F
<i>C. auratus</i>	Volta lake at Yeji	27	15	0.067	0.133	0.077	0.022	0.066	-0.091
<i>C. auratus</i>	Volta lake at Akosombo	27	15	0.133	0.200	0.117	0.039	0.097	-0.205
<i>C. auratus</i>	Volta lake at Bator	15	15	0.133	0.200	0.071	0.027	0.064	-0.111
	Mean			0.111	0.178				
<i>C. nigrodigitatus</i>	Volta lake at Yeji	14	15	0.067	0.067	0.036	0.009	0.034	-0.111
<i>C. nigrodigitatus</i>	Volta lake at Bator	16	15	0.067	0.067	0.032	0.008	0.030	0.000
<i>C. nigrodigitatus</i>	R. Densu at Weija	25	15	0.067	0.133	0.042	0.012	0.039	-0.167
	Mean			0.067	0.089				
<i>C. maurus</i>	Volta lake at Bator	16	15	0.067	0.133	0.053	0.016	0.048	-0.125

N = Sample size
n = No. of loci screened
P = Polymorphism per population
H = Observed heterozygosity
Ha = Genic diversity (expected heterozygosity)
F = Wright's fixation index
* 0.05 = 5% criterion; 0.01 = 1% criterion

Nevo *et al.*, (1984) and Powell (1975) estimated P for fish to be 0.209 and 0.220 respectively. Values obtained in this study are below those obtained by Nevo *et al.*, (1984) and Powell (1975). This calls for further investigation.

3.2.5 Allele Frequencies, Expected and Observed Heterozygosities.

Allelic distribution and frequencies at fifteen loci of the three species of *Chrysichthys* (*C. nigrodigitatus*, *C. auratus* and *C. maurus*) from two river basins and a total of four localities [Yeji, Akosombo and Battor on the Volta system and Weija on the Densu river, (Fig.2)] are presented in Table 10. The Table also provides estimates of observed and expected heterozygosity per locus (H and He respectively) and their means.

Table 9 provides a summary of the means of observed and expected (calculated) heterozygosities and Wright's fixation index of the three *Chrysichthys* species. Expected heterozygosities (He) at all polymorphic loci were lower compared to their corresponding observed values (H). Negative values obtained for Wright's fixation index for all populations (except *C. nigrodigitatus* at Battor) is also an indication of excess observed heterozygosity. *Chrysichthys auratus*, *C. nigrodigitatus* and *C. maurus* showed mean heterozygosities of 0.029 ± 0.007 , 0.009 ± 0.002 and 0.016 respectively.

Estimates of variability (Polymorphism and Heterozygosity) of fish and other populations have been associated with various environmental characteristics. The adaptive significance of both polymorphism and heterozygosity have been reviewed in Nevo *et al.*, (1984) and Selander and Whittman (1983).

Heterozygosity is considered a more reliable measure of population variability than

polymorphism because heterozygosity estimates are independent of sample size (Gorman and Renzi, 1979; Nevo *et al.*, 1984). The mean observed heterozygosity (H) values were all below what would have been expected (0.074) for tropical, medium sized, regionally distributed mainland fishes according to Nevo *et al.*, (1984). The values were also lower than the mean value expected for tropical fishes generally (0.067) according to Nevo *et al.*, (1984).

In attempting to explain the unexpected low levels of heterozygosity, the ecology of the study area and body size of fish were considered. Association of low variability with isolated populations was shown in cave populations of the fish *Astyanax mexicanus* and in populations of the lizard, *Anolis spp.* on the south Bimini Island by Avise and Selander (1972) and Webster *et al.*, (1972) respectively. The populations investigated here could however not be considered isolated. Furthermore, if the influence of body size on heterozygosity was to be considered [the neutralist view that larger animals generally have smaller effective population size and lower variability levels (Kimura, 1983)], the estimated mean heterozygosity for medium sized fishes was 0.049. Only *C. auratus* at Akosombo (H = 0.047) has a closer heterozygosity value. Others fall below this value. Since the results obtained here cannot be sufficiently explained by the 'isolation and body size hypothesis', it was necessary to consider other factors.

A special feature of freshwater fishes which could be directly related to the low variability values obtained, could be their relic status and endemism. Lowe-McConnell (1987) revealed that some of the big fish families in Africa are representatives of archaic elements with relatives in Southern America. Considering the sources from which samples were obtained, the fishes could not be said to be endemic or relic. Nevo *et al.*, (1984) estimated

the mean heterozygosity for relic and endemic fish species to be 0.016. Though *C. maurus* species showed a heterozygosity value ($H_e = 0.016$) equal to that estimated by Nevo *et al.*, (1984), other factors could be responsible for this. The other species (*C. auratus* and *C. nigrodigitatus*) however, showed either a higher or lower value.

3.2.6 Observed and expected genotypic distribution

Observed and expected genotypic distributions, G-values and probabilities of deviations from Hardy-Weinberg distributions for loci scored are presented in Appendix 16. Table 11 shows G-Values for three polymorphic loci in the three *Chrysichthys* species. According to Hardy-Weinberg Law, in sexually outbreeding natural populations, the inherent random mating proportions of gametes ensures that observed proportions of heterozygosity in a population would not be distinctly different from the expected. Genotypic distributions (and G-values) at all polymorphic loci (*LDH-A**, *sMDH-B**, and *GPI-A**) indicate excess observed heterozygosities. These therefore suggest deviations from Hardy-Weinberg equilibrium at these loci. However, a test of statistical significance at χ^2_{05} revealed that the deviations are insignificant. There are therefore no significant changes in the genotypic frequencies of the fish populations and species investigated. This suggests populations of outbreeders.

3.2.7 Gene diversity among Populations

Average gene diversities among the fish populations are given in Table 12. The gene diversities in the total population (H_t) of *C. auratus*, *C. nigrodigitatus* and *C. maurus* were

Table 10 Allelic frequencies, expected and observed heterozygosity values of *Chrysichthys* populations and species in Ghana.

SPECIES	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. maurus</i>
LOCALITY	Yeji	Akosombo	Battor	Yeji	Battor	Weila	Battor	Battor	Battor
Locus	Allele								
<i>ADH - 1*</i>	<i>b</i>	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000
	<i>a</i>	1.000 (27)	1.000 (27)	1.000 (15)	0.000 (14)	0.000 (16)	0.000 (25)	0.000 (16)	0.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<i>LDH - A*</i>	<i>c</i>	0.037	0.148	0.033	0.000	0.000	0.000	0.000	0.000
	<i>b</i>	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000
	<i>a</i>	0.963 (27)	0.852 (27)	0.967 (15)	0.000 (14)	0.000 (16)	0.000 (25)	0.000 (16)	0.000 (16)
	H	0.074	0.296	0.067	0.000	0.000	0.000	0.000	0.000
He	0.071	0.252	0.064	0.000	0.000	0.000	0.000	0.000	
<i>sMDH - A</i>	<i>b</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	<i>a</i>	1.000 (27)	1.000 (27)	1.000 (15)	1.000 (14)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table 10 cont.

SPECIES	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. maurus</i>
LOCALITY	Yeji	Akosombo	Battor	Yeji	Battor	Yeji	Battor	Weija	Battor
Locus	Allele								
<i>sMDH-B</i>	<i>b</i>	0.148	0.185	0.067	0.071	0.071	0.000	0.080	0.031
	<i>a</i>	0.852 (27)	0.815 (27)	0.933 (15)	0.929 (14)	0.929 (14)	1.000 (16)	0.920 (25)	0.969 (16)
	H	0.296	0.370	0.133	0.143	0.143	0.000	0.160	0.067
	He	0.252	0.302	0.125	0.132	0.132	0.000	0.147	0.060
<i>SDH-1*</i>	<i>b</i>	0.000	0.000	0.000	1.000	1.000	1.000	1.000	1.000
	<i>a</i>	1.000 (27)	1.000 (27)	1.000 (15)	0.000 (14)	0.000 (14)	0.000 (16)	0.000 (25)	0.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<i>SDH-2*</i>	<i>b</i>	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	<i>a</i>	1.000 (27)	1.000 (27)	1.000 (15)	1.000 (14)	1.000 (14)	1.000 (16)	1.000 (25)	1.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table 10 cont.

SPECIES	<i>C. auratus</i>		<i>C. auratus</i>		<i>C. auratus</i>		<i>C. nigrodigitatus</i>		<i>C. nigrodigitatus</i>		<i>C. maurus</i>	
LOCALITY	Yeji	Akosombo	Battor	Yeji	Battor	Weija	Battor	Weija	Battor	Weija	Battor	
Locus	Allele											
IDH - 1*	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	a	1.000 (27)	1.000 (27)	1.000 (15)	1.000 (14)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
IDH - 2*	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	a	1.000 (27)	1.000 (27)	1.000 (15)	1.000 (14)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
XDH - 1*	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	a	1.000 (27)	1.000 (27)	1.000 (15)	1.000 (14)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (25)	1.000 (16)	
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	

Table 10 cont.

SPECIES	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. maurus</i>
LOCALITY	Yeji	Akosombo	Battor	Yeji	Battor	Weija	Battor	Battor
Locus	Allele							
<i>GPI-A*</i>	b	0.019	0.125	0.000	0.062	0.020	0.100	0.100
	a	0.981 (27)	0.875 (15)	1.000 (14)	0.938 (16)	0.980 (25)	0.900 (16)	0.900 (16)
	H	0.037	0.250	0.000	0.125	0.049	0.200	0.200
	He	0.037	0.219	0.000	0.116	0.039	0.180	0.180
<i>PGM-1*</i>	b	1.000	1.000	0.000	0.000	0.000	0.000	0.000
	a	0.000 (27)	0.000 (15)	1.000 (14)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000
<i>ODH-1*</i>	b	0.000	0.000	1.000	1.000	1.000	1.000	1.000
	a	1.000 (27)	1.000 (15)	0.000 (14)	0.000 (16)	0.000 (25)	0.000 (16)	0.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	He	0.000	0.000	0.000	0.000	0.000	0.000	0.000

Table 10 cont.

SPECIES	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. auratus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. nigrodigitatus</i>	<i>C. maurus</i>
LOCALITY	Yeji	Akosombo	Battor	Yeji	Battor	Weija	Battor	Battor
Locus Allele								
G3PDH - 1*	b	0.000	0.000	1.000	1.000	1.000	1.000	1.000
	a	1.000 (27)	1.000 (15)	0.000 (14)	0.000 (16)	0.000 (25)	0.000 (16)	0.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	H _e	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ME - 1*	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	a	1.000 (27)	1.000 (27)	1.000 (14)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	H _e	0.000	0.000	0.000	0.000	0.000	0.000	0.000
ME - 2*	b	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	a	1.000 (27)	1.000 (27)	1.000 (14)	1.000 (16)	1.000 (25)	1.000 (16)	1.000 (16)
	H	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	H _e	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	H̄	0.024	0.047	0.030	0.008	0.014	0.008	0.018
	H̄ _e	0.022	0.039	0.027	0.008	0.012	0.008	0.016

*At each locus allele having the lowest mobility is designated as 'a'

Figure in parentheses indicates number of individual examined

Table 11 G-values for three polymorphic loci in three species of *Chrysichthys* in the Volta and Densu basins in Ghana.

Species	Water body / locality	Sample size	G-value
LDH-A*			
<i>C. auratus</i>	Volta Lake / Yeji	27	0.077
<i>C. auratus</i>	Volta Lake / Akosombo	27	1.197
<i>C. auratus</i>	Volta river / Battor	15	0.036
SMDH-B*			
<i>C. auratus</i>	Volta Lake / Yeji	27	1.197
<i>C. auratus</i>	Volta Lake / Akosombo	27	2.292
<i>C. auratus</i>	Volta river / Battor	15	0.144
<i>C. nigrodigitatus</i>	Volta Lake / Yeji	14	0.153
<i>C. nigrodigitatus</i>	Densu Rriver / Weiija	25	0.348
<i>C. maurus</i>	Volta Rriver / Battor	16	0.033
GPI-A*			
<i>C. auratus</i>	Volta Lake / Akosombo	27	0.034
<i>C. auratus</i>	Volta River / Battor	15	0.638
<i>C. nigrodigitatus</i>	Volta River / Battor	16	0.132
<i>C. nigrodigitatus</i>	Densu River / Weiija	25	0.020
<i>C. maurus</i>	Volta Rriver / Battor	16	0.325

Tabulated $X^2_{.05} = 3.84$

Table 12 Analysis of gene diversity among populations based on
Fifteen loci in three species of *Chrysichthys*.

Species	Population	Ht	He	Dst
<i>C. auratus</i>	3	0.030	0.029	0.001
<i>C. nigro*</i>	3	0.010	0.009	0.001
<i>C. maurus</i>	1	0.016	0.016	

Ht = Gene diversity in the total population ($1 - \sum_j P_j^2$)

where P = mean allelic frequency per locus of all populations
within a species

He(Hst) = Average gene diversity in a population

Dst = Average gene diversity between populations (Ht = He + Dst)

(Nevo et al, 1983)

**nigro* = *nigrodigitatus*

0.030, 0.010, and 0.016 respectively.

The average gene diversity in a population (H_e) was highest in *C. auratus* (0.029); *C. maurus* and *C. nigrodigitatus* had values of 0.016 and 0.009 respectively. The results show a wide variation of gene diversities among the three species which suggest that these fish groups, very likely, have different 'basic' levels of variability.

Average gene diversity between populations (D_{st}) for both *C. auratus* and *C. nigrodigitatus* (0.001) indicates that for each species, interpopulational variation was minimal. However, intrapopulational variation, H_e , i.e. diversity among individuals in a population was relatively high (Table 12). Higher diversity within populations than between populations has also been reported for *Sphincterochila* (a land snail) by Nevo, Bar-el and Bar (1983). They recorded higher genetic diversities within populations than between populations in five species of *Sphincterochila* in Israel.

3.3 TAXONOMIC RELATIONSHIPS AMONG POPULATIONS AND SPECIES

3.3.1 Genetic identities and distances between populations and species

Genetic Identity (I) and Genetic distance (D) were calculated between each pair of populations or species for 15 loci based on the identity of genes (Nei, 1972). Results are presented in Table 13A and 13B.

The mean and range values of D between populations within species were as follows: for *C. auratus*, mean = 0.002; range = 0.001 - 0.003; for *C. nigrodigitatus*, mean = 0.001.

The following features emerged from the matrix of genetic distances:

(i) Genetic distance, D, between populations was low: an average of 0.002 for *C. auratus* and

Table 13 Genetic identity (I) above diagonal, and Distance (D) below diagonal , between A, populations of *Chrysichthys* and B, three species of *Chrysichthys* studied , based on fifteen loci

A											
Species	Water body/Locality	no.	1	2	3	4	5	6	7		
<i>C. auratus</i>	Volta lake at Yeji	1		0.998	0.998	0.524	0.527	0.527	0.525		
<i>C. auratus</i>	Volta lake at Akosombo	2	0.001		0.997	0.529	0.528	0.528	0.526		
<i>C. auratus</i>	Volta river at Baltor	3	0.002	0.003		0.525	0.526	0.525	0.525		
<i>C. nigrodigitatus</i>	Volta lake at Yeji	4	0.646	0.636	0.644		0.999	0.999	0.999		
<i>C. nigrodigitatus</i>	Volta river at Baltor	5	0.640	0.638	0.642	0.001		0.999	0.999		
<i>C. nigrodigitatus</i>	River Dansu at Weija	6	0.640	0.638	0.644	0.001	0.001		0.999		
<i>C. maunus</i>	Volta river at Baltor	7	0.644	0.642	0.644	0.001	0.001	0.001			
B											
Species	no.	1	2	3							
<i>C. auratus</i>	1		0.527	0.525							
<i>C. nigrodigitatus</i>	2	0.640		0.999							
<i>C. maunus</i>	3	0.644	0.001								

0.001 for *C. nigrodigitatus*. This indicates that for each species, the populations are not genetically very different.

(ii) Genetic distance between species is generally high; it is 0.640 between *C. auratus* and *C. nigrodigitatus*, and 0.644 between *C. auratus* and *C. maurus*. The closest pair of species genetically, on the basis of loci screened were *C. nigrodigitatus* and *C. maurus* ($D = 0.001$), whereas the most distant species are *C. auratus* and *C. maurus* ($D = 0.644$).

(iii) Populations within closer distance (i.e geographically closer) should not always be expected to have a lower genetic distance than populations of wider distance apart (i.e geographically distant populations). The present results suggest that geographically closer populations could show greater D's whereas geographically distant populations could show smaller D's. Battor and Akosombo populations of *C. auratus* separated by about 60 km showed $D = 0.003$, whereas Battor and Yeji populations separated by about 312 km showed $D = 0.001$. This result is comparable to that obtained by Nevo *et al.*, (1983) on species of the land snail *Sphincterochila*.

Very high similarity values obtained between populations within species (an average of 0.998 for *C. auratus* and 0.999 for *C. nigrodigitatus*) could possibly be attributed to the fact that the environments from which the fishes were obtained (three localities in the Volta System) were broadly similar, being within a limited geographical area (Trewavas and Irvine, 1947; Lowe-McConell, 1972). The extremely high genetic identity between *C. nigrodigitatus* and *C. maurus* suggests that these fishes are genetically close. The low genetic identity value between *C. auratus* and *C. nigrodigitatus* undoubtedly confirmed that these are two different species. Although the loci screened were limited (15), it should be noted that according to

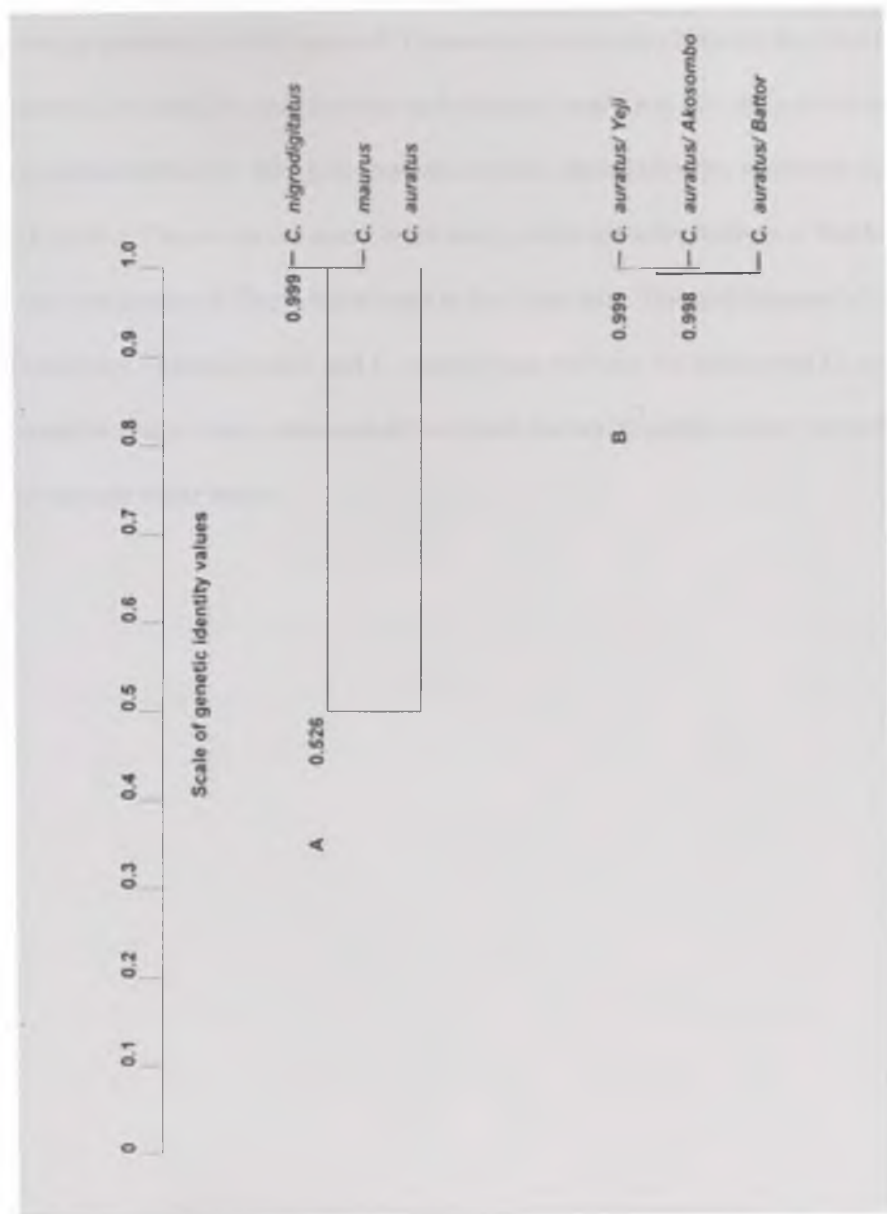
Avise (1975), genetic similarity values greater than 0.9 are associated with conspecifics, and values less than 0.9 occur between subspecies or species. (This has been widely used on molluscs like oysters and mussels). In the present study, the genetic identity values between each of the three populations of *C. nigrodigitatus* and *C. maurus* was 0.999. Based on the limits set by Avise above, the two are probably conspecifics. This is further strengthened by Table 7 where (a) of the 15 loci screened there were no discriminating loci between *C. nigrodigitatus* and *C. maurus* (b) the discriminating loci between *C. auratus* and *C. nigrodigitatus* were the same as those between the former and *C. maurus*. Whether or not *C. nigrodigitatus* and *C. maurus* are conspecifics could be established by screening more loci and/or conducting interbreeding experiments in another study.

3.3.2 Phenetic relationships among species and populations

Phenetic relationship among populations and species of *Chrysichthys* studied are presented in Figure 4. Figure 4A shows the relationships among the three *Chrysichthys* species. It indicates a closer relationship between *C. nigrodigitatus* and *C. maurus* than between either of them and *C. auratus*. Figure 4B shows the relationships among populations of *C. auratus*. Relationships among *C. nigrodigitatus* populations were not presented in a dendrogram because of the nature of the results. Very high genetic identities among populations within *C. auratus* and *C. nigrodigitatus* suggest very high level of similarity among populations. Closer relationship between fish populations might be due to ecological homogeneity at these localities (Trewavas and Irvine, 1947; Lowe-McConnell, 1972).

This work has revealed that though it is possible to characterise *Chrysichthys* species

Fig. 4 Phenetic relationships among A, *Chrysichthys* species and B, populations of *C. auratus*



on the basis of morphometrics, this method is not dependable as indicated by previous investigators. It has on the other hand confirmed its usefulness in refining systematics of fish. The inability to discriminate between *C. nigrodigitatus* and *C. maurus* could be due to the limited enzymes (protein) screened. Taxonomic relationships between the three *Chrysichthys* species produced by morphometry and allozymic analysis in this study is the same. The fish species identified by morphological and meristic characters were confirmed by biochemical characters. The protein taxonomy in this study corroborates the findings of Risch (1986a) that only two species of *Chrysichthys* occur in the Volta lake. The establishment of closer affinity between *C. nigrodigitatus* and *C. maurus* than between the former and *C. auratus* can be considered as a further refinement of the already known taxonomy of the *Chrysichthys* species in the two water basins.

SUMMARY

At least three species of *Chrysichthys* - *C. auratus*, *C. nigrodigitatus* and *C. maurus* exist in the Volta system and one species, *C. nigrodigitatus* in the Weija reservoir.

Position of the longest dorsal soft fin ray and the number of branched pectoral fin rays were confirmed as valuable characters in the identification and characterization of the three species.

Chrysichthys nigrodigitatus could be distinguished from *C. maurus* and *C. auratus* on the basis of the number of branched pectoral fin rays (nine in *C. nigrodigitatus* but eight in *C. auratus* and *C. maurus*) while *C. auratus* could be distinguished from *C. maurus* on the basis of position of longest dorsal soft fin ray (first in *C. auratus* and second in *C. maurus*).

Body proportion values showed seemingly wide ranges. Furthermore, ranges overlap across species so much that they do not give precise identification. However, five body proportions - HL/ED HL/ABL, BH/CPL, HL/DLRL, SL/HL were significantly different at $P < 0.001$ among the three species and could be considered in the characterization of the species.

Considering gene loci as taxonomic characters,

(a) all individuals of *C. auratus*, *C. nigrodigitatus* and *C. maurus* sampled expressed the 'characters'- *ME-1**, *ME-2**, *IDH-1**, *IDH-2**, *sMDH- A** and *SDH-2** in non-variable forms at each locus.

(b) Seven loci: *ADH-1**, *LDH-A**, *SDH-1**, *PGM-1**, *ODH-1**, *XDH-1** and *G3PDH-1**

were discriminating between *C. nigrodigitatus* or *C. maurus* and *C. auratus*.

Only three loci (*LDH-A**, *MDH-B** and *GPI-A**), (20%) out of the fifteen loci showed polymorphism.

(a) *LDH-A** was polymorphic in only *C. auratus*.

(b) *MDH-B** was polymorphic in *C. auratus* from all localities, *C. maurus* from Battor (the only locality studied for this species) and *C. nigrodigitatus* from all localities except Yeji.

(c) *GPI-A** was polymorphic in *C. maurus* from Battor, and also in *C. auratus* and *C. nigrodigitatus* at all localities except Yeji.

Genetic variation was generally low in all the species. It was highest in *C. auratus* and least in *C. nigrodigitatus*. [Polymorphism, P, (1% criterion) = 0.178 in *C. auratus*, 0.133 in *C. maurus* and 0.089 in *C. nigrodigitatus*; Heterozygosity, H_e , = 0.029 in *C. auratus*, 0.016 in *C. maurus* and 0.009 in *C. nigrodigitatus*.

There were no significant genetic differences between populations within *C. auratus* and *C. nigrodigitatus* (average gene diversity between populations, D_{st} , = 0.001 in both species).

There were no significant changes in the genotypic frequencies of populations and species (χ^2_{05} ranged from 0.020 to 2.292 for polymorphic loci).

Wright's fixation index, F, ranged from -0.205 to -0.091 in *C. auratus*; -0.167 to 0.000 in *C.*

nigrodigitatus and -0.125 in *C. maurus*.

Genetic distance between populations within species was very low: an average of 0.002 in *C. auratus* and 0.001 in *C. nigrodigitatus*.

The closest species genetically were *C. nigrodigitatus* and *C. maurus* (Genetic identity, $I = 0.999$) while the most distant species were *C. auratus* and *C. maurus* ($I = 0.525$).

Geographically closer populations could have greater genetic distances than geographically distant populations.

Morphological measurements and meristic counts

Appendix 1

Chrysiichthys auratus from the Volta lake at Yeji

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	ScL	MxBL	ExMnBL	InMsBL	FDLRL	DRL	CPL	No. of DFR	No. of PFR	No. of VFR
1	22.30	17.25	5.16	3.54	1.40	1.13	2.00	2.32	2.15	4.05	2.40	1.48	1	5.90	2.44	II - 6	I - 9	I - 5
2	22.50	17.20	5.40	3.29	1.40	1.26	2.20	2.34	2.09	3.80	2.28	1.40	1	5.88	2.30	II - 6	I - 9	I - 5
3	19.00	14.50	4.10	1.88	1.30	0.78	1.80	2.01	1.40	2.90	1.96	1.30	1	5.25	2.12	II - 6	I - 8	I - 5
4	20.50	15.10	4.35	2.75	1.30	0.83	1.94	2.20	1.53	3.51	1.90	1.40	1	6.60	2.40	II - 6	I - 8	I - 5
5	20.90	16.10	4.88	3.23	1.30	1.05	2.02	2.26	1.78	3.62	2.28	1.38	1	5.70	2.25	II - 6	I - 8	I - 5
6	21.60	16.50	4.92	3.80	1.44	0.95	1.95	2.45	1.62	3.90	2.12	1.47	1	5.90	2.40	II - 6	I - 8	I - 5
7	16.32	12.00	3.50	2.38	1.15	0.64	1.59	1.42	1.21	3.00	1.78	1.10	1	5.20	2.10	II - 6	I - 8	I - 5
8	16.50	12.50	3.65	2.10	1.18	0.66	1.40	1.68	1.30	3.01	1.94	1.12	1	4.00	1.78	II - 6	I - 8	I - 5
9	16.50	12.25	3.90	2.70	1.15	0.75	1.49	1.85	1.43	2.92	1.70	1.00	1	4.70	1.85	II - 6	I - 8	I - 5
10	16.30	12.35	3.65	2.18	1.00	0.64	1.30	1.60	1.26	3.15	1.80	1.20	1	3.82	1.80	II - 6	I - 8	I - 5
11	22.20	17.30	5.34	3.23	1.31	1.13	2.32	2.12	2.10	3.60	2.61	1.45	1	5.88	2.60	II - 6	I - 8	I - 5
12	18.40	13.72	4.05	2.87	1.12	0.70	1.70	1.75	1.46	3.19	1.80	1.00	1	4.65	2.04	II - 6	I - 8	I - 5
13	21.90	16.40	5.17	3.57	1.40	1.20	1.80	2.40	2.27	3.90	2.34	1.58	1	6.80	2.60	II - 6	I - 8	I - 5
14	16.50	12.15	3.74	2.76	1.16	0.66	1.50	1.92	1.30	2.50	1.58	0.90	1	4.20	1.60	II - 6	I - 8	I - 5
15	22.25	17.25	5.56	3.49	1.60	1.24	2.10	2.40	2.13	3.60	2.20	1.70	1	6.80	2.60	II - 6	I - 8	I - 5
16	24.20	18.50	5.56	3.57	1.44	1.19	1.94	2.70	2.19	4.10	2.32	1.64	1	8.00	2.50	II - 6	I - 8	I - 5
17	23.10	17.60	5.54	3.64	1.50	1.11	1.96	2.60	2.14	4.38	2.60	1.44	1	8.40	2.60	II - 6	I - 8	I - 5
18	21.10	16.00	4.50	2.80	1.35	0.84	1.80	2.30	1.61	3.62	2.00	1.40	1	5.10	2.40	II - 6	I - 8	I - 5
19	24.10	18.70	5.94	3.71	1.68	1.37	2.84	2.60	2.64	4.32	2.25	1.70	1	5.32	2.50	II - 6	I - 8	I - 5
20	18.90	13.90	4.05	2.59	1.20	0.83	1.60	1.75	1.40	3.50	1.84	1.30	1	6.80	2.10	II - 6	I - 8	I - 5
21	23.20	17.40	5.10	3.52	1.44	1.10	2.23	2.40	2.03	3.90	2.06	1.54	1	5.80	2.40	II - 6	I - 8	I - 5
22	21.35	18.96	6.25	3.90	1.76	1.30	2.60	2.64	2.53	5.20	3.20	2.20	1	7.80	2.40	II - 6	I - 8	I - 5
23	16.90	12.55	3.50	2.03	1.05	0.74	1.25	1.60	1.21	3.00	1.75	1.30	1	5.50	1.60	II - 6	I - 8	I - 5
24	27.50	20.20	6.56	4.08	1.76	1.35	2.28	2.74	2.57	4.62	3.00	2.10	1	8.90	2.96	II - 6	I - 8	I - 5
25	28.60	21.20	6.67	4.43	1.85	1.45	2.35	2.90	2.71	4.72	2.75	2.10	1	9.20	3.26	II - 6	I - 8	I - 5
26	22.10	16.00	4.89	2.61	1.48	1.04	2.10	2.42	1.95	3.90	2.24	1.72	1	8.60	2.50	II - 6	I - 8	I - 5

Appendix 2
Morphological measurements and meristic counts
***Chrysiichthys auratus* from Volta lake at Akosombo**

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	SnL	M _s BL	E _s MnBL	InMnBL	PDLRL	DLRL	CPL	No. of DFR	No. of PFR	No. of VFR
1	13.80	10.68	3.14	2.34	0.97	0.52	1.20	1.60	0.97	2.61	1.38	1.10	1	3.30	1.58	II - 0	I - 8	I - 5
2	14.50	11.20	3.37	2.42	0.90	0.61	1.14	1.50	1.14	2.60	1.49	1.15	1	3.59	1.81	II - 6	I - 8	I - 5
3	14.90	11.10	3.32	2.36	0.93	0.56	1.15	1.55	1.08	2.40	1.50	0.98	1	4.30	1.70	II - 6	I - 8	I - 5
4	13.71	10.69	3.37	2.43	0.99	0.59	1.23	1.50	1.13	2.38	1.40	0.93	1	3.40	1.72	II - 6	I - 8	I - 5
5	13.92	10.38	3.47	2.43	0.96	0.58	1.20	1.55	1.14	2.88	1.50	0.84	1	5.05	1.65	II - 6	I - 8	I - 5
6	14.55	11.02	3.37	2.63	0.95	0.60	1.20	1.48	1.19	2.80	1.70	1.21	1	4.70	1.85	II - 6	I - 8	I - 5
7	12.85	10.25	3.03	2.12	0.89	0.58	1.10	1.30	0.98	2.74	1.44	0.98	1	2.72	1.60	II - 6	I - 8	I - 5
8	13.34	10.20	3.08	2.18	0.88	0.57	1.12	1.40	1.04	2.50	1.58	1.23	1	3.15	1.60	II - 6	I - 8	I - 5
9	12.62	9.85	3.00	1.12	0.82	0.50	1.20	1.40	0.96	2.19	1.50	1.06	1	2.62	1.40	II - 6	I - 8	I - 5
10	15.55	11.90	3.50	2.68	0.92	0.69	1.23	1.88	1.24	3.02	1.50	1.12	1	4.80	1.85	II - 6	I - 8	I - 5
11	12.50	9.60	2.90	2.22	0.85	0.54	1.06	1.40	1.04	2.68	1.55	1.05	1	3.60	1.50	II - 6	I - 8	I - 5
12	15.12	11.40	3.51	2.43	1.02	0.53	1.35	1.63	1.09	2.80	1.74	1.16	1	5.80	1.98	II - 6	I - 8	I - 5
13	12.10	9.28	2.57	2.04	0.76	0.41	1.00	1.20	0.81	2.27	1.28	0.82	1	2.70	1.76	II - 6	I - 8	I - 5
14	12.29	8.92	2.81	2.04	0.82	0.44	1.00	1.29	0.97	2.41	1.49	1.09	1	5.50	1.48	II - 6	I - 8	I - 5
15	13.50	10.10	2.94	2.04	0.85	0.54	1.10	1.35	0.98	2.46	1.47	0.89	1	5.10	1.59	II - 6	I - 8	I - 5
16	11.55	9.16	2.79	2.08	0.20	0.45	0.98	1.30	0.85	2.60	1.60	1.10	1	3.95	1.43	II - 6	I - 8	I - 5
17	11.78	9.90	2.67	2.05	0.80	0.45	0.90	1.20	0.87	2.08	1.18	0.90	1	2.70	1.40	II - 6	I - 8	I - 5
18	14.10	10.50	2.95	2.07	0.90	0.47	1.22	1.40	1.02	2.82	1.48	1.12	1	3.35	1.88	II - 6	I - 8	I - 5
19	18.80	14.38	4.12	3.08	1.08	0.74	1.50	2.12	1.41	2.90	1.76	1.30	1	4.19	2.10	II - 6	I - 8	I - 5
20	16.62	12.73	3.77	2.78	1.10	0.53	1.41	1.68	1.32	3.02	1.70	1.12	1	4.10	1.84	II - 6	I - 8	I - 5
21	17.78	13.68	4.22	2.96	1.12	0.70	1.46	1.96	1.56	3.00	1.70	1.20	1	5.56	2.25	II - 6	I - 8	I - 5
22	16.60	13.24	4.00	2.80	1.08	0.73	1.60	1.90	1.53	3.50	2.18	1.40	1	3.00	2.02	II - 6	I - 8	I - 5
23	19.92	12.90	4.05	2.89	1.20	0.68	1.56	1.77	1.42	2.80	1.70	1.20	1	6.59	2.17	II - 6	I - 8	I - 5
24	16.00	11.86	3.68	2.95	1.00	0.73	1.30	1.70	1.27	3.06	2.02	1.40	1	4.50	1.90	II - 6	I - 8	I - 5
25	15.38	11.14	3.50	2.61	1.00	0.57	1.40	1.59	1.25	2.95	1.77	1.31	1	4.80	1.73	II - 6	I - 8	I - 5
26	17.12	12.96	4.15	2.81	1.20	0.66	1.50	1.60	1.35	3.11	1.64	1.20	1	5.40	1.90	II - 6	I - 8	I - 5
27	14.70	11.19	3.42	2.82	0.98	0.63	1.80	1.60	1.17	2.73	1.70	1.20	1	5.28	1.90	II - 6	I - 8	I - 5

Appendix 3 Morphological measurements and maristic counts

Chrysichthys auratus from Volta river at Battor

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	SeL	MaxBL	ExMnBL	InMnBL	PDRL	DRL	CPL	No. of DFR	No. of PFR	No. of VFR
1	23.60	18.00	5.22	3.39	1.36	0.96	1.88	2.53	1.66	3.90	2.23	1.63	1	4.60	2.30	11-6	1-8	1-5
2	19.60	15.90	4.61	3.44	1.26	0.98	1.85	2.10	1.80	2.90	2.10	1.32	1	3.90	2.60	11-6	1-8	1-5
3	20.25	15.10	4.45	3.03	1.18	0.86	1.76	1.98	1.45	3.71	1.86	1.46	1	3.78	2.41	11-6	1-8	1-5
4	23.50	17.10	5.25	3.26	1.36	1.00	1.98	2.38	1.95	3.34	2.00	1.48	1	4.55	2.72	11-6	1-8	1-5
5	20.80	16.10	4.57	3.08	1.40	1.00	2.04	2.30	1.73	3.42	2.20	1.42	1	1.30	2.40	11-6	1-8	1-5
6	29.10	21.70	6.70	4.00	1.68	1.30	2.46	3.20	2.57	5.20	2.82	2.24	1	8.80	2.95	11-6	1-8	1-5
7	19.40	14.50	4.35	3.00	1.12	0.86	1.85	2.00	1.68	3.60	2.00	1.30	1	6.10	2.30	11-6	1-8	1-5
8	21.60	16.20	4.90	3.28	1.30	0.96	2.30	2.40	1.70	4.20	2.10	1.22	1	5.70	2.22	11-6	1-8	1-5
9	19.80	15.45	4.93	2.84	1.52	0.98	2.08	2.10	1.90	3.58	1.88	1.46	1	4.25	2.10	11-6	1-8	1-5
10	32.00	25.50	7.92	4.42	2.12	1.70	3.05	5.42	3.32	5.54	3.70	2.36	1	10.00	3.28	11-6	1-8	1-5
11	22.40	17.70	5.45	3.20	1.50	1.08	2.20	2.38	2.00	4.10	2.38	1.86	1	7.30	2.62	11-6	1-8	1-5
12	30.60	24.10	7.30	4.90	1.85	1.50	2.64	3.44	2.95	5.80	3.70	2.50	2	8.40	3.80	11-6	1-8	1-5
13	14.30	11.40	3.24	2.55	0.88	0.68	1.50	1.66	1.28	2.80	1.70	1.10	1	4.10	2.00	11-6	1-8	1-5
14	16.00	12.30	3.70	2.70	1.02	0.72	1.50	1.75	1.30	2.40	1.62	0.92	1	5.20	2.16	11-6	1-8	1-5
15	15.20	12.50	3.70	2.80	1.00	0.73	1.46	1.80	1.38	2.80	1.70	1.15	1	3.90	1.70	11-6	1-8	1-5
16	14.28	11.45	3.18	2.40	0.98	0.68	1.48	1.60	1.30	2.80	1.66	1.11	1	4.06	1.92	11-6	1-8	1-5
17	16.16	12.45	3.67	2.80	1.02	0.70	1.42	1.72	1.34	2.70	1.64	1.08	1	3.96	1.72	11-6	1-8	1-5
18	23.42	17.98	5.20	3.36	1.40	0.99	1.90	2.48	1.82	3.85	2.20	1.60	1	4.48	2.24	11-6	1-8	1-5

Morphological measurements and meristic counts
Chrysichthys nigrodigitatus from the Volta lake at Yeji

Appendix 4

Sample no.	TL	SL	HL	BH	ED	IOD	ABL	DBL	SnL	MxBL	ExMnBL	InMnBL	PDLRL	DLRL	CPL	No. of DFR	No. of PFR	No. of VTR
1	26.80	20.10	5.48	3.58	1.42	1.21	2.10	2.80	2.00	4.70	2.51	1.68	2	5.70	3.10	11-6	1-9	1-5
2	26.50	20.10	5.90	3.85	1.48	1.20	2.00	2.90	2.33	4.74	2.60	1.71	2	5.70	3.09	11-6	1-9	1-5
3	25.70	19.50	5.51	3.95	1.47	1.19	2.08	2.72	2.01	4.40	2.22	1.50	2	6.10	3.10	11-6	1-9	1-5
4	26.00	20.00	5.70	3.70	1.34	1.20	1.95	3.00	2.16	4.30	2.78	1.72	2	6.70	2.80	11-6	1-9	1-5
5	25.50	19.20	5.18	3.58	1.42	1.08	2.10	2.54	2.02	3.95	2.30	1.50	2	4.28	2.95	11-6	1-9	1-5
6	24.10	17.45	4.80	3.33	1.16	0.99	1.65	2.60	1.91	3.90	2.20	1.42	2	6.50	2.88	11-6	1-9	1-5
7	22.70	16.40	4.66	3.05	1.32	0.88	1.95	2.34	1.70	3.90	2.10	1.48	2	5.10	2.70	11-6	1-9	1-5
8	32.80	25.60	7.46	5.20	1.88	1.69	2.78	3.85	2.80	6.70	3.85	2.45	2	7.50	4.10	11-6	1-9	1-5
9	23.60	16.90	4.79	2.94	1.45	0.93	1.80	2.42	1.80	4.00	2.20	1.58	2	5.20	2.80	11-6	1-9	1-5
10	26.50	20.35	5.66	3.82	1.42	1.17	1.90	2.60	1.85	4.60	2.90	1.95	2	6.20	3.09	11-6	1-9	1-5
11	29.60	21.70	6.12	4.05	1.58	1.44	2.45	3.29	2.46	5.35	3.30	2.05	2	6.85	2.93	11-6	1-9	1-5
12	27.50	21.30	5.87	4.07	1.42	1.26	2.32	3.05	2.38	4.82	2.55	1.80	2	6.00	3.30	11-6	1-9	1-5
13	28.55	22.10	6.44	4.45	1.60	1.40	2.35	3.30	2.55	4.20	2.52	2.13	2	6.30	3.40	11-6	1-9	1-5
14	26.50	20.30	5.87	3.65	1.56	1.38	2.20	2.89	2.41	5.00	2.90	1.70	2	5.70	3.14	11-6	1-9	1-5
15	26.00	20.40	6.30	3.56	1.60	1.22	2.62	2.76	2.38	4.62	2.61	1.70	2	5.50	3.08	11-6	1-9	1-5
16	33.30	23.70	6.89	3.83	1.70	1.32	2.50	3.43	2.50	5.82	3.60	2.70	2	7.00	3.52	11-6	1-9	1-5
17	18.10	14.10	4.22	2.68	1.15	0.82	1.82	1.98	1.60	3.80	2.00	1.40	2	3.85	2.10	11-6	1-9	1-5
18	30.70	24.10	7.00	3.94	1.70	1.50	2.50	3.14	2.95	4.95	3.10	1.90	2	5.70	3.60	11-6	1-9	1-5

Morphological measurements and meristic counts
Chrysichthys nigrodigitatus from Volta river at Bathor

Appendix 5

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	SgL	MxBL	Ex-MnBL	In-MsBL	PDLRL	DLRL	CPL	No. of DFR	No. of PFR	No. of VFR
1	18.90	14.00	4.00	2.68	1.10	0.69	1.24	1.90	1.50	3.25	2.00	1.15	2	3.85	2.40	II - 6	I - 9	I - 5
2	19.32	14.34	4.14	2.87	1.10	0.70	1.37	2.00	1.49	3.48	2.26	1.50	2	4.08	2.45	II - 6	I - 9	I - 5
3	16.31	11.69	3.28	2.40	0.88	0.49	1.08	1.52	1.14	2.52	1.80	1.21	2	3.20	1.88	II - 6	I - 9	I - 5
4	19.32	13.80	3.96	2.64	1.10	0.60	1.30	1.96	1.38	3.15	2.02	1.30	2	4.10	2.23	II - 6	I - 9	I - 5
5	26.80	19.00	5.32	3.65	1.42	0.92	1.58	2.70	1.96	4.40	2.20	1.60	2	7.25	3.00	II - 6	I - 9	I - 5
6	26.40	19.80	5.71	3.75	1.38	1.18	1.55	2.80	2.30	4.60	2.60	1.60	2	7.30	2.95	II - 6	I - 9	I - 5
7	27.10	19.90	5.36	3.91	1.12	1.15	1.76	2.80	2.04	4.70	2.90	1.75	2	7.00	3.50	II - 6	I - 9	I - 5
8	16.70	12.85	3.67	2.47	1.08	0.60	1.24	1.63	1.38	3.13	1.69	1.22	2	4.20	2.01	II - 6	I - 9	I - 5
9	24.90	17.40	4.65	3.48	1.21	0.80	1.72	2.30	1.76	4.05	2.18	1.32	2	5.80	2.98	II - 6	I - 9	I - 5
10	15.08	11.30	3.27	2.38	0.86	0.50	1.15	1.51	1.05	2.55	1.64	0.92	2	3.60	1.80	II - 6	I - 9	I - 5
11	20.50	15.05	4.16	2.76	1.20	0.70	1.42	2.07	1.48	3.26	2.00	1.22	2	4.10	2.48	II - 6	I - 9	I - 5
12	19.20	14.22	4.00	2.60	1.05	0.60	1.45	2.00	1.38	3.15	1.98	1.27	2	4.70	2.33	II - 6	I - 9	I - 5
13	14.39	10.40	2.95	2.14	0.78	0.46	1.00	1.45	1.00	2.26	1.65	0.98	2	3.19	1.72	II - 6	I - 9	I - 5
14	13.15	9.70	2.70	2.00	0.70	0.38	0.98	1.38	0.93	2.44	1.58	0.90	2	3.20	1.70	II - 6	I - 9	I - 5
15	19.10	14.08	4.07	2.87	1.08	0.55	1.30	1.98	1.48	3.12	1.64	1.25	2	3.95	2.20	II - 6	I - 9	I - 5
16	13.00	9.70	2.75	1.97	0.70	0.38	0.80	1.40	0.92	1.14	1.63	0.92	2	3.10	1.61	II - 6	I - 9	I - 5
17	25.70	19.50	5.51	3.95	1.47	1.19	1.80	2.72	2.01	4.40	2.22	1.50	2	6.10	3.10	II - 6	I - 9	I - 5
18	22.30	17.25	5.16	3.54	1.40	1.13	2.00	2.32	2.15	4.05	2.40	1.48	2	5.90	2.44	II - 6	I - 9	I - 5
19	19.00	14.50	4.10	1.83	1.30	0.78	1.90	2.01	1.40	2.90	1.96	1.30	2	5.25	2.12	II - 6	I - 9	I - 5
20	26.80	20.10	5.48	3.58	1.42	1.21	1.80	2.80	2.00	4.70	2.51	1.68	2	5.70	3.10	II - 6	I - 9	I - 5
21	22.20	17.30	5.34	3.23	1.31	1.13	2.32	2.12	2.30	3.60	2.61	1.45	2	4.60	2.60	II - 6	I - 9	I - 5
22	22.50	17.20	5.40	3.29	1.40	1.26	2.20	2.34	2.09	3.80	2.28	1.40	2	5.20	2.30	II - 6	I - 9	I - 5
23	26.00	20.00	5.70	3.70	1.34	1.20	1.95	3.00	2.16	4.30	2.78	1.72	2	5.10	2.80	II - 6	I - 9	I - 5
24	13.20	10.00	1.05	1.70	0.85	1.06	1.15	1.32	0.94	2.30	1.40	1.00	2	3.35	1.50	II - 6	I - 9	I - 5
25	19.90	12.00	3.50	2.38	1.15	0.64	1.59	1.42	1.21	3.00	1.78	1.10	2	5.30	2.10	II - 6	I - 9	I - 5
26	16.50	12.50	3.65	1.90	1.18	0.66	1.40	1.68	1.30	3.01	1.94	1.00	2	4.00	1.78	II - 6	I - 9	I - 5

Morphological measurements and meristic counts

Appendix 6

Chrysichthys nigrodigitatus from Densu river at Wejia

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	SaL	MxBL	ExMeBL	JaMeBL	PDLRL	DURL	CPL	No. of DFR	No. of PFR	No. of VFR
1	15.20	11.76	3.17	2.90	0.94	0.78	1.30	1.70	0.98	2.80	1.50	1.12	2	3.26	1.90	II - 6	I - 9	I - 5
2	16.68	12.70	3.41	3.00	0.96	0.84	1.16	1.88	1.14	2.80	1.42	1.10	2	3.35	1.96	II - 6	I - 9	I - 5
3	16.16	12.48	3.52	2.66	0.91	0.77	1.48	1.93	1.16	2.80	1.75	1.09	2	3.20	2.02	II - 6	I - 9	I - 5
4	17.38	13.06	3.37	2.73	0.97	0.82	1.25	2.00	1.05	2.48	1.57	1.10	2	3.36	2.06	II - 6	I - 9	I - 5
5	17.18	13.10	3.67	2.79	0.97	0.88	1.30	1.88	1.28	2.81	1.80	1.15	2	3.30	2.06	II - 6	I - 9	I - 5
6	17.10	13.00	3.52	2.78	1.00	0.78	1.30	1.90	1.14	2.81	1.20	0.82	2	3.35	2.10	II - 6	I - 9	I - 5
7	14.80	11.40	3.14	2.39	0.95	0.75	1.22	1.67	0.99	2.38	1.42	0.94	3	3.14	1.92	II - 6	I - 9	I - 5
8	16.10	12.36	3.27	2.61	1.00	0.77	1.18	1.70	1.16	2.50	1.39	0.91	2	3.19	1.92	II - 6	I - 9	I - 5
9	16.62	12.70	3.41	2.78	1.00	0.80	1.28	1.90	1.11	2.54	1.80	1.15	2	3.28	2.12	II - 6	I - 9	I - 5
10	16.40	12.45	3.31	2.80	0.90	0.78	1.21	1.80	1.10	2.54	1.70	1.02	2	3.50	2.10	II - 6	I - 9	I - 5
11	16.30	12.40	3.43	2.90	1.01	0.73	1.18	1.80	1.12	2.71	1.69	1.09	2	3.48	1.90	II - 6	I - 9	I - 5
12	16.75	12.81	3.44	2.66	0.97	0.75	1.26	1.90	1.17	2.36	1.53	0.97	2	3.30	2.20	II - 6	I - 9	I - 5
13	17.35	13.30	3.75	2.71	0.98	0.79	1.28	1.91	1.30	2.90	1.53	1.04	2	3.60	1.97	II - 6	I - 9	I - 5
14	15.60	11.75	3.21	2.52	0.86	0.63	1.10	1.60	1.08	1.12	1.25	0.90	2	3.24	1.83	II - 6	I - 9	I - 5
15	18.55	14.00	3.80	2.95	0.98	0.78	1.40	2.10	1.39	2.80	1.80	1.10	2	3.50	2.21	II - 6	I - 9	I - 5
16	17.30	13.32	3.58	2.78	0.92	0.77	1.38	1.82	1.33	2.73	1.57	1.08	2	3.60	2.08	II - 6	I - 9	I - 5
17	15.30	11.79	3.13	2.71	0.84	0.73	1.06	1.71	1.03	2.64	1.20	1.00	2	2.98	1.83	II - 6	I - 9	I - 5
18	15.20	11.00	3.10	2.64	0.82	0.68	1.27	1.60	1.00	2.10	1.08	0.80	2	2.88	1.73	II - 6	I - 9	I - 5
19	16.00	12.24	3.28	2.68	0.86	0.76	1.10	1.80	1.14	2.50	1.25	0.91	2	3.00	1.89	II - 6	I - 9	I - 5
20	16.20	12.61	3.40	2.68	0.90	0.77	1.17	1.85	1.17	2.17	1.20	0.92	2	3.30	2.05	II - 6	I - 9	I - 5
21	15.60	11.25	3.29	2.49	0.88	0.68	1.19	1.67	1.13	1.98	1.29	1.00	2	3.22	1.90	II - 6	I - 9	I - 5
22	17.30	13.18	3.67	2.97	0.94	0.84	1.26	1.87	1.32	2.35	1.30	1.02	2	3.31	2.20	II - 6	I - 9	I - 5
23	17.70	13.69	3.88	2.97	0.98	0.78	1.41	2.15	1.38	2.61	1.69	1.22	3	3.49	2.20	II - 6	I - 9	I - 5
24	17.40	13.66	3.77	3.11	0.96	0.78	1.48	2.02	1.33	2.83	1.52	1.15	2	3.50	2.30	II - 6	I - 9	I - 5
25	16.50	12.60	3.38	2.68	0.88	0.80	1.26	1.71	1.20	2.30	1.65	0.92	2	3.25	2.11	II - 6	I - 9	I - 5

Morphological measurements and meristic counts

Appendix 7

Chrysichthys maunus from Volta river at Bator

Sample no	TL	SL	HL	BH	ED	IOD	ABL	DBL	SoL	MsBL	ExMnBL	InMnBL	PDLRL	DLRL	CPL	No of DFR	No of PFR	No of VFR
1	29.10	23.60	6.73	3.96	1.68	1.38	2.20	3.00	2.71	5.14	3.30	2.15	2	5.50	3.60	11-6	1-8	1-5
2	26.50	20.40	5.40	3.78	1.38	1.15	2.16	2.61	2.00	4.30	2.50	1.61	2	5.70	3.10	11-6	1-8	1-5
3	22.80	16.50	4.65	3.07	1.23	0.92	1.91	2.40	1.76	3.60	2.00	1.52	2	5.10	2.60	11-6	1-8	1-5
4	24.80	18.90	5.10	3.66	1.30	0.90	1.59	2.60	1.73	3.62	2.10	1.50	2	5.30	3.00	11-6	1-8	1-5
5	20.15	15.00	4.16	3.00	1.10	0.80	1.49	2.10	1.48	3.15	2.00	1.40	3	4.65	2.30	11-6	1-8	1-5
6	29.08	23.65	6.92	4.12	1.62	1.36	2.16	3.00	2.69	5.21	3.28	2.18	2	5.54	3.62	11-6	1-8	1-5
7	27.80	21.42	5.84	4.66	1.32	1.20	2.21	2.64	2.25	4.68	2.56	1.70	2	5.68	3.15	11-6	1-8	1-5
8	21.90	16.20	4.50	3.08	1.19	0.90	1.80	2.28	1.72	4.00	1.96	1.49	2	5.15	2.58	11-6	1-8	1-5
9	25.30	19.10	5.60	3.80	1.35	1.12	1.86	2.62	1.74	4.10	2.16	1.60	2	5.32	3.00	11-6	1-8	1-5
10	20.90	16.22	5.10	3.96	1.21	0.91	1.61	2.23	1.54	3.92	2.10	1.45	2	4.70	2.36	11-6	1-8	1-5
11	19.30	13.90	4.08	2.67	1.12	0.81	1.50	1.82	1.59	3.20	1.84	1.04	2	4.20	2.22	11-6	1-8	1-5
12	14.40	11.50	3.54	2.50	1.00	0.75	1.52	1.82	1.26	2.74	1.50	1.04	2	2.90	1.85	11-6	1-8	1-5
13	16.70	12.15	3.66	2.55	0.98	0.76	1.48	1.78	1.39	2.30	1.55	1.10	2	3.60	2.08	11-6	1-8	1-5
14	16.00	12.45	3.57	2.72	0.96	0.74	1.50	1.76	1.35	2.54	1.32	1.02	2	3.40	2.00	11-6	1-8	1-5
15	18.90	14.10	3.94	2.90	1.00	0.82	1.60	2.10	1.44	2.82	1.75	1.12	3	4.30	2.42	11-6	1-8	1-5
16	18.00	13.30	4.16	3.13	1.16	0.83	1.60	1.90	1.60	3.50	1.88	1.46	2	3.90	1.95	11-6	1-8	1-5
17	19.00	15.00	4.35	3.40	1.26	0.82	1.84	2.05	1.60	3.12	2.02	1.42	2	3.40	2.05	11-6	1-8	1-5
18	17.40	13.50	4.00	2.87	1.14	0.86	1.60	1.90	1.45	3.05	1.82	1.00	2	3.50	2.00	11-6	1-8	1-5
19	16.68	12.10	3.62	2.52	0.96	0.72	1.45	1.74	1.36	2.28	1.54	1.06	2	3.54	2.06	11-6	1-8	1-5
20	16.56	12.60	3.74	2.86	1.04	0.78	1.50	1.84	1.44	2.85	1.74	1.20	2	3.96	1.74	11-6	1-8	1-5

Appendix 8 Body proportions of *Chrysichthys auratus* from the Volta lake at Yeji

Sample no	ED/IOD	SnL/IOD	HL/BH	HL/ED	HL/ABL	HL/MxBL	BHV/CPL	HL/DLRL	E _N M _B L/ _I nM _B L	SL/HL	SnL/ED	E _N M _B L/HL
1	1.24	1.90	1.46	3.69	2.58	1.27	1.45	0.87	1.62	3.34	1.54	0.47
2	1.11	1.66	1.64	3.86	2.45	1.42	1.43	0.92	1.63	3.19	1.49	0.42
3	1.67	1.92	1.69	3.15	2.27	1.41	1.15	0.78	1.51	3.54	1.15	0.48
4	1.57	1.84	1.58	3.35	2.24	1.24	1.15	0.66	1.36	3.47	1.18	0.44
5	1.24	1.70	1.51	3.75	2.42	1.35	1.44	0.86	1.65	3.30	1.37	0.51
6	1.52	1.71	1.39	3.42	2.52	1.26	1.47	0.83	1.44	3.35	1.13	0.43
7	1.56	1.89	1.47	3.50	2.20	1.17	1.13	0.67	1.62	3.43	1.21	0.51
8	1.79	1.97	1.73	3.09	2.60	1.21	1.18	0.91	1.73	3.42	1.10	0.53
9	1.53	1.91	1.44	3.39	2.62	1.34	1.46	0.83	1.70	3.14	1.24	0.44
10	1.56	1.96	1.67	3.65	2.81	1.16	1.21	0.96	1.50	3.38	1.26	0.49
11	1.16	1.85	1.65	3.66	2.30	1.48	1.24	0.97	1.80	3.24	1.44	0.49
12	1.00	1.94	1.41	3.62	2.38	1.37	1.41	0.87	1.80	3.39	1.21	0.44
13	1.17	1.89	1.45	3.69	2.87	1.33	1.37	0.76	1.48	3.17	1.62	0.45
14	1.76	1.97	1.36	3.22	2.49	1.49	1.73	0.89	1.76	3.25	1.12	0.42
15	1.29	1.72	1.59	3.48	2.65	1.54	1.34	0.82	1.29	3.10	1.33	0.40
16	1.21	1.84	1.56	3.86	2.87	1.36	1.42	0.70	1.41	3.32	1.52	0.42
17	1.35	1.93	1.52	3.69	2.83	1.26	1.40	0.66	1.81	3.18	1.42	0.47
18	1.61	1.92	1.61	3.33	2.50	1.24	1.17	0.88	1.42	3.55	1.19	0.44
19	1.23	1.93	1.60	3.54	2.09	1.38	1.48	0.89	1.32	3.15	1.60	0.38
20	1.45	1.69	1.56	3.38	2.53	1.16	1.23	0.60	1.42	3.43	1.17	0.45
21	1.31	1.85	1.45	3.54	2.29	1.31	1.46	0.88	1.34	3.41	1.41	0.40
22	1.35	1.95	1.60	3.55	2.40	1.20	1.63	0.80	1.45	3.03	1.44	0.51
23	1.75	1.64	1.72	3.33	0.80	1.17	1.27	0.64	1.35	3.59	1.15	0.50
24	1.30	1.90	1.61	3.73	2.88	1.42	1.38	0.74	1.43	3.08	1.46	0.46
25	1.28	1.87	1.51	3.61	2.84	1.41	1.16	0.73	1.31	3.18	1.46	0.41
26	1.42	1.88	1.71	3.30	2.33	1.25	1.14	0.57	1.30	3.27	1.31	0.46

Appendix 9 Body proportions of *Chrysichthys auratus* from Volta lake at Akosombo

Sample no	ED/ JOD	SnL/ JOD	HL/ BH	HL/ ED	HL/ ABL	HL/ MxBL	BH/ CPL	HL/ DLRL	ExMnBL/ IsMnBL	SL/ HL	SnL/ ED	ExMnBL/ HL
1	1.87	1.87	1.34	3.24	2.62	1.20	1.48	0.95	1.25	3.40	1.00	0.44
2	1.48	1.87	1.39	3.74	2.96	1.30	1.34	0.99	1.30	3.32	1.27	0.44
3	1.79	1.93	1.41	3.57	2.89	1.38	1.39	0.77	1.53	3.34	1.16	0.45
4	1.68	1.92	1.39	3.40	2.74	1.42	1.41	0.99	1.51	3.17	1.24	0.42
5	1.66	1.97	1.43	3.61	2.89	1.20	1.47	0.69	1.56	3.00	1.19	0.43
6	1.58	1.98	1.28	3.55	2.81	1.20	1.42	0.72	1.40	3.27	1.25	0.50
7	1.87	1.88	1.43	3.40	2.75	1.11	1.33	1.11	1.47	3.38	1.01	0.50
8	1.54	1.82	1.41	3.50	2.75	1.23	1.36	0.98	1.28	3.31	1.18	0.48
9	1.64	1.92	1.42	3.66	2.50	1.37	1.51	1.15	1.42	3.28	1.17	0.51
10	1.33	1.80	1.31	3.80	2.85	1.16	1.45	0.73	1.34	3.40	1.35	0.50
11	1.57	1.93	1.31	3.37	2.74	1.08	1.48	0.81	1.48	3.31	1.22	0.43
12	1.92	2.06	1.44	3.44	2.60	1.25	1.23	0.61	1.50	3.25	1.07	0.53
13	1.85	1.98	1.25	3.38	2.57	1.13	1.16	0.95	1.56	3.61	1.06	0.50
14	1.71	2.02	1.38	3.43	2.81	1.17	1.38	0.51	1.37	3.17	1.18	0.53
15	1.57	1.81	1.44	3.46	2.67	1.20	1.28	0.58	1.65	3.44	1.15	0.50
16	1.82	1.89	1.34	3.40	2.85	1.07	1.45	0.71	1.45	3.28	1.04	0.57
17	1.78	1.93	1.30	3.33	2.97	1.28	1.46	0.90	1.31	3.41	1.08	0.44
18	1.91	1.96	1.43	3.28	2.42	1.05	1.10	0.88	1.32	3.56	1.13	0.50
19	1.46	1.91	1.34	3.81	2.75	1.42	1.47	0.98	1.35	3.49	1.31	0.43
20	1.90	2.07	1.36	3.43	2.67	1.25	1.51	0.67	1.52	3.38	1.09	0.45
21	1.60	1.94	1.43	3.77	2.89	1.41	1.32	0.76	1.42	3.24	1.39	0.40
22	1.48	2.10	1.43	3.70	2.50	1.14	1.32	1.33	1.56	3.31	1.41	0.55
23	1.76	1.97	1.40	3.38	2.60	1.45	1.33	0.61	1.42	3.19	1.12	0.42
24	1.37	1.74	1.25	3.68	2.83	1.20	1.55	0.82	1.40	3.22	1.27	0.55
25	1.75	2.02	1.34	3.50	2.50	1.19	1.51	0.73	1.35	3.18	1.25	0.51
26	1.82	2.05	1.48	3.46	2.77	1.33	1.48	0.77	1.30	3.12	1.13	0.40
27	1.56	1.86	1.21	3.49	2.90	1.25	1.48	0.65	1.42	3.27	1.19	0.50

Appendix 10 Body proportions of *Chrysipterus auratus* from Volta river at Bator

Sample no	EL/IOD	SoL/ROD	HL/BH	HL/ED	HL/ABL	HL/MxBL	BH/CPL	HL/DLRL	ExMaBL/InMaBL	SL/HL	SoL/ED	ExMaBL/HL
1	1.42	1.94	1.21	3.84	2.78	1.34	1.47	1.13	1.37	3.45	1.37	0.43
2	1.29	1.84	1.34	3.66	2.49	1.59	1.32	1.18	1.59	3.45	1.43	0.46
3	1.28	1.69	1.47	3.77	2.53	1.20	1.26	1.18	1.27	3.39	1.23	0.42
4	1.29	1.95	1.61	3.86	2.65	1.57	1.20	1.15	1.35	3.26	1.43	0.38
5	1.40	1.73	1.48	3.26	2.24	1.33	1.28	0.86	1.35	3.52	1.24	0.48
6	1.29	1.98	1.68	3.98	2.72	1.28	1.36	0.76	1.26	3.24	1.53	0.42
7	1.30	1.95	1.45	3.88	2.35	1.21	1.30	0.71	1.54	3.33	1.50	0.46
8	1.35	1.77	1.49	3.77	2.13	1.17	1.48	0.86	1.72	3.31	1.31	0.43
9	1.55	1.94	1.74	3.24	2.37	1.38	1.35	1.16	1.29	3.13	1.25	0.38
10	1.25	1.95	1.79	3.74	2.60	1.43	1.35	0.79	1.57	3.22	1.57	0.47
11	1.39	1.85	1.70	3.63	2.47	1.32	1.22	0.75	1.28	3.25	1.33	0.44
12	1.23	1.97	1.49	3.95	2.77	1.26	1.29	0.87	1.48	3.30	1.59	0.51
13	1.29	1.88	1.27	3.68	2.16	1.16	1.28	0.79	1.55	3.52	1.45	0.52
14	1.46	1.81	1.37	3.63	2.47	1.54	1.25	0.71	1.76	3.32	1.27	0.44
15	1.37	1.89	1.32	3.70	2.53	1.32	1.65	0.95	1.48	3.38	1.38	0.46
16	1.44	1.91	1.28	3.24	2.15	1.14	1.30	0.78	1.50	3.60	1.33	0.52
17	1.46	1.91	1.31	3.60	2.58	1.36	1.63	0.93	1.52	3.39	1.31	0.45
18	1.41	1.84	1.55	3.71	2.74	1.35	1.50	1.16	1.38	3.46	1.30	0.42

Appendix 11 Body proportions of *Chrysichthys nigrodigitatus* from Volta lake at Yeji.

Sample no	ED/IOD	SnL/IOD	HL/BH	HL/ED	HL/ABL	HL/MxBL	BH/CPI	EL/DURL	ExMnBL/InMnBL	SL/HL	SnL/ED	ExMnBL/HL
1	1.17	1.65	1.53	3.86	2.61	1.17	1.15	0.96	1.49	3.67	1.41	0.46
2	1.23	1.94	1.53	3.99	2.95	1.24	1.25	1.04	1.52	3.41	1.57	0.44
3	1.24	1.69	1.39	3.75	2.65	1.25	1.27	0.90	1.48	3.54	1.37	0.40
4	1.12	1.80	1.54	4.25	2.92	1.33	1.32	0.74	1.62	3.51	1.61	0.49
5	1.31	1.87	1.45	3.65	2.47	1.31	1.21	1.21	1.53	3.71	1.42	0.44
6	1.17	1.93	1.44	4.14	2.91	1.23	1.16	0.74	1.55	3.64	1.65	0.46
7	1.50	1.93	1.53	3.53	2.39	1.19	1.13	0.91	1.42	3.52	1.20	0.45
8	1.11	1.66	1.43	3.97	2.68	1.11	1.27	0.99	1.57	3.43	1.49	0.52
9	1.11	1.93	1.63	3.88	2.66	1.20	1.05	0.92	1.39	3.53	1.24	0.46
10	1.21	1.69	1.48	3.99	2.98	1.23	1.24	0.91	1.49	3.60	1.30	0.51
11	1.17	1.71	1.51	4.03	2.50	1.14	1.38	0.89	1.61	3.55	1.62	0.54
12	1.13	1.89	1.44	4.13	2.53	1.22	1.23	0.98	1.42	3.63	1.68	0.43
13	1.14	1.82	1.45	4.03	2.74	1.53	1.31	1.02	1.18	3.43	1.55	0.39
14	1.13	1.75	1.61	4.19	2.67	1.17	1.16	1.03	1.34	3.51	1.72	0.49
15	1.31	1.95	1.77	3.94	2.40	1.36	1.16	1.15	1.54	3.24	1.56	0.41
16	1.29	1.89	1.80	4.05	2.76	1.18	1.09	0.98	1.33	3.44	1.56	0.52
17	1.40	1.95	1.57	3.67	2.32	1.11	1.28	1.10	1.43	3.34	1.39	0.47
18	1.13	1.97	1.78	4.12	2.80	1.41	1.09	1.23	1.63	3.44	1.74	0.44

Appendix 12 Body proportions of *Chrysichthys nigrodigitatus* from Volta river at Battor

Sample no	ED/IOD	SoL/IOD	HL/BH	HL/ED	HL/ABL	HL/MxBL	BH/CPL	HL/DiRL	ExMnBL/InMnBL	SL/HL	SoL/ED	ExMnBL/HL
1	1.59	2.17	1.49	3.64	3.23	1.23	1.12	1.04	1.74	3.50	1.36	0.50
2	1.45	2.13	1.44	3.76	3.02	1.19	1.17	1.01	1.51	3.46	1.35	0.55
3	1.80	2.33	1.37	3.73	3.04	1.30	1.28	1.03	1.49	3.56	1.30	0.55
4	1.83	2.30	1.50	3.60	3.05	1.26	1.19	0.97	1.55	3.48	1.25	0.51
5	1.54	2.13	1.46	3.75	3.37	1.21	1.22	0.73	1.38	3.57	1.38	0.41
6	1.80	2.28	1.49	3.40	2.96	1.17	1.23	0.87	1.39	3.50	1.28	0.46
7	1.34	2.20	1.34	3.84	2.70	1.15	1.17	0.80	1.65	3.74	1.45	0.47
8	1.72	2.10	1.37	3.80	2.84	1.28	1.32	0.91	1.78	3.46	1.22	0.50
9	1.71	2.11	1.50	3.47	2.93	1.28	1.11	1.01	1.64	3.62	1.23	0.48
10	1.75	2.30	1.54	3.81	2.76	1.27	1.12	0.85	1.56	3.56	1.31	0.50
11	1.70	2.17	1.38	3.78	2.95	1.30	1.24	0.92	1.68	3.53	1.28	0.56
12	1.84	2.45	1.35	3.86	2.75	1.11	1.18	0.84	1.76	3.59	1.33	0.58
13	1.82	2.69	1.42	3.77	3.13	1.30	1.30	1.03	1.31	3.46	1.37	0.40
14	1.84	2.42	1.40	3.67	3.44	1.29	1.22	0.89	1.77	3.53	1.23	0.59
15	1.71	2.27	1.39	3.30	2.78	1.14	1.32	0.88	1.80	3.48	1.21	0.58
16	1.50	2.20	1.40	3.97	3.06	1.32	1.20	1.08	1.32	3.50	1.47	0.41
17	1.70	2.30	1.42	3.27	3.07	1.25	1.38	0.98	1.64	3.39	1.26	0.48
18	1.60	2.50	1.46	3.52	3.03	1.12	1.26	0.90	1.82	3.50	1.56	0.55
19	1.74	2.13	1.35	3.70	2.82	1.23	1.33	0.89	1.79	3.45	1.23	0.54
20	1.80	2.40	1.43	3.76	3.35	1.27	1.15	0.93	1.74	3.65	1.33	0.53
21	1.81	2.68	1.40	3.41	3.22	1.29	1.27	0.95	1.66	3.52	1.24	0.54
22	1.78	2.51	1.42	3.54	3.58	1.19	1.15	0.99	1.40	3.52	1.27	0.45
23	1.74	2.31	1.44	3.65	3.09	1.33	1.39	0.99	1.52	3.45	1.23	0.48
24	1.75	2.20	1.36	3.59	3.08	1.23	1.37	0.97	1.36	3.57	1.26	0.43
25	1.70	2.13	1.41	3.46	2.82	1.32	1.17	0.88	1.37	3.59	1.25	0.44
26	1.72	2.28	1.36	3.64	3.08	1.22	1.16	1.05	1.57	3.50	1.33	0.48

Appendix 13 Body proportions of *Chrysichthys nigrodigitatus* from Densu river at Weija

Sample no	ED/IOD		SoL/IOD		HL/BH		HL/ED		HL/ABL		HL/MxBL		BIU/CPL		HL/DURL		ExMnBL/InMnBL		SL/HL		SoL/ED		ExMnBL/HL	
	IOD	ED	SoL	IOD	BH	HL	ED	ABL	MxBL	HL	CPL	DURL	InMnBL	ExMnBL	HL	SL	ED	InMnBL	ExMnBL	HL	ED	HL	HL	
1	1.21	1.26	1.09	1.13	2.44	1.13	1.53	0.97	13.40	3.71	1.04	0.47												
2	1.14	1.36	1.14	1.14	2.94	1.22	1.53	1.02	1.29	3.72	1.19	0.42												
3	1.18	1.51	1.32	1.26	2.38	1.26	1.21	1.10	1.61	3.55	1.27	0.50												
4	1.18	1.28	1.23	1.36	2.70	1.36	1.33	1.00	1.43	3.88	1.08	0.47												
5	1.10	1.45	1.32	1.31	2.82	1.31	1.35	1.11	1.57	3.57	1.32	0.49												
6	1.28	1.46	1.27	1.25	2.71	1.25	1.32	1.05	1.46	3.69	1.14	0.35												
7	1.27	1.32	1.31	1.31	2.57	1.32	1.24	1.00	1.51	3.63	1.04	0.45												
8	1.30	1.51	1.25	1.31	2.77	1.31	1.36	1.03	1.53	3.78	1.16	0.43												
9	1.25	1.39	1.23	1.34	2.66	1.34	1.31	1.04	1.57	3.72	1.11	0.52												
10	1.35	1.41	1.18	1.30	2.74	1.30	1.33	0.95	1.67	3.76	1.22	0.51												
11	1.38	1.53	1.18	1.27	2.91	1.27	1.53	0.99	1.55	3.62	1.11	0.49												
12	1.29	1.56	1.29	1.47	2.73	1.47	1.21	1.04	1.58	3.72	1.21	0.44												
13	1.24	1.64	1.38	1.29	2.93	1.29	1.38	1.04	1.47	3.55	1.33	0.41												
14	1.37	1.71	1.27	1.31	2.92	1.31	1.38	0.99	1.39	3.66	1.26	0.39												
15	1.26	1.78	1.29	1.36	2.71	1.36	1.33	1.09	1.64	3.68	1.42	0.47												
16	1.19	1.73	1.29	1.31	2.59	1.31	1.34	0.99	1.45	3.72	1.45	0.44												
17	1.15	1.41	1.15	1.19	2.95	1.19	1.48	1.05	1.20	3.77	1.23	0.38												
18	1.21	1.47	1.17	1.47	2.44	1.47	1.53	1.08	1.35	3.55	1.22	0.35												
19	1.13	1.50	1.22	1.31	2.98	1.31	1.42	1.09	1.37	3.73	1.33	0.38												
20	1.17	1.52	1.27	1.37	2.91	1.37	1.42	1.03	1.30	3.71	1.30	0.35												
21	1.29	1.66	1.32	1.66	2.76	1.66	1.31	1.20	1.29	3.41	1.28	0.39												
22	1.12	1.57	1.24	1.56	2.91	1.56	1.35	1.11	1.27	3.59	1.40	0.35												
23	1.26	1.77	1.31	1.49	2.75	1.49	1.35	1.11	1.39	3.53	1.41	0.44												
24	1.23	1.71	1.21	1.33	2.55	1.33	1.35	1.08	1.32	3.62	1.39	0.40												
25	1.10	1.50	1.28	1.30	2.61	1.30	1.48	1.01	1.45	3.56	1.36	0.44												

Appendix 14 Body proportions of *Chirochthys maurus* from Volta river at Battor

Sample no	EDV IOD	SnL/ IOD	HL/ BH	HL/ ED	HL/ ABL	HL/ MxBL	BH/ CPL	HL/ DLRL	ExMnBL/ InMnBL	SL/ HL	SnL/ ED	ExMnBL/ HL
1	1.22	1.96	1.69	4.00	3.06	1.31	1.10	1.22	1.53	3.51	1.61	0.49
2	1.20	1.74	1.43	3.91	2.50	1.26	1.22	0.95	1.55	3.78	1.56	0.46
3	1.50	1.91	1.51	3.78	2.43	1.29	1.18	0.91	1.32	3.51	1.43	0.43
4	1.44	1.92	1.39	3.92	3.21	1.41	1.22	0.96	1.40	3.71	1.33	0.41
5	1.38	1.85	1.39	3.78	2.79	1.32	1.30	0.89	1.43	3.61	1.35	0.48
6	1.24	1.98	1.68	4.12	3.20	1.33	1.14	1.24	1.50	3.42	1.60	0.47
7	1.20	1.88	1.25	4.06	2.64	1.20	1.48	1.03	1.51	3.67	1.56	0.44
8	1.49	1.91	1.46	3.78	2.50	1.13	1.19	0.87	1.32	1.60	1.45	0.44
9	1.21	1.55	1.47	4.15	3.01	1.36	1.27	1.05	1.35	3.41	1.29	0.39
10	1.33	1.69	1.29	4.21	3.16	1.30	1.68	1.07	1.45	3.22	1.27	0.41
11	1.38	1.96	1.53	3.64	2.72	1.28	1.20	0.97	1.47	3.41	1.42	0.45
12	1.33	1.68	1.42	3.54	2.33	1.29	1.35	1.22	1.44	3.25	1.26	0.42
13	1.53	1.83	1.44	3.73	2.47	1.59	1.23	1.02	1.41	3.32	1.42	0.42
14	1.62	1.82	1.31	3.72	2.38	1.41	1.36	1.05	1.29	3.49	1.41	0.37
15	1.22	1.76	1.36	3.94	2.46	1.40	1.20	0.92	1.56	3.58	1.44	0.44
16	1.40	1.93	1.33	3.59	2.60	1.19	1.61	1.07	1.29	3.20	1.38	0.45
17	1.77	1.95	1.28	3.45	2.36	1.39	1.66	1.28	1.42	3.45	1.27	0.46
18	1.40	1.69	1.39	3.51	2.50	1.31	1.44	1.14	1.62	3.38	1.21	0.41
19	1.50	1.89	1.44	3.77	2.50	1.59	1.22	1.02	1.45	3.62	1.42	0.43
20	1.33	1.85	1.31	3.60	2.49	1.31	1.64	0.94	1.45	3.37	1.38	0.47

PDLRL - Position of longest dorsal ray length

DLRL - Length of the longest dorsal ray

DFR - Dorsal fin ray

PFR - Pelvic fin ray

VFR - Ventral fin ray

Note : other abbreviations used in tables have been previously defined (refer page 10)

Appendix 15A.

Analysis of variance of twelve body proportion variables in *Chrysichthys auratus* from three localities on the Volta system in Ghana.

	Degrees Of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-value
ED/IOD***					
Between Populations within species	2	0.6733	24.0035	3.1317	1.30E-08
Within Populations	66	0.0280			
Total	68				
SnL/IOD*					
Between Populations within species	2	0.0409	4.8226	3.1317	0.0110
Within Populations	66	0.0085			
Total	68				
HL/BH***					
Between Populations within species	2	0.2396	18.4184	3.1317	4.05E-07
Within Populations	66	0.0130			
Total	68				
HL/ED*					
Between Populations within species	2	0.1764	4.6041	3.1317	0.0133
Within Populations	66	0.0383			
Total	68				

Appendix 15A cont.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
HL/ABL***					
Between Populations within species	2	0.4235	10.4027	3.1317	0.0001
Within Populations	66	0.0407			
Total	68				
HL/MxBL*					
Between Populations within species	2	0.0565	4.0534	3.1317	0.0217
Within Populations	66	0.0140			
Total	68				
BH/CPL^					
Between Populations within species	2	0.0146	0.8114	3.1317	0.4484
Within Populations	66	0.0180			
Total	68				
HL/D _r RL^					
Between Populations within species	2	0.0806	2.5550	3.1317	0.0851
Within Populations	66	0.0315			
Total	68				

Appendix 15A cont.

	Degrees Of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
ExMnBL/InMnBL*					
Between Populations within species	2	0.0531	2.6020	3.1317	0.0814
Within Populations	66	0.0204			
Total	68				
SL/HL^					
Between Populations within species	2	0.0216	1.1253	3.1317	0.3305
Within Populations	66	0.0192			
Total	68				
SnL/ED***					
Between Populations within species	2	0.2467	14.2453	3.1317	6.80E-06
Within Populations	66	0.0173			
Total	68				
ExMnBL/HL^					
Between Populations within species	2	0.0052	2.7279	3.1317	0.0725
Within Populations	66	0.0019			
Total	68				

Appendix 15B

Analysis of variance of twelve body proportion variables in *Chrysichthys nigrodigitatus* from two localities on the Volta system and one locality on the Weiija reservoir in Ghana.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
ED/IOD***					
Between Populations within species	2	1.9162	167.0653	3.1359	1.49E-26
Within Populations	66	0.0115			
Total	68				
SnL/IOD***					
Between Populations within species	2	3.8751	178.2291	3.1359	2.48E-27
Within Populations	66	0.0217			
Total	68				
HL/BH***					
Between Populations within species	2	0.4886	71.2881	3.1359	3.23E-17
Within Populations	66	0.0069			
Total	68				
HL/ED***					
Between Populations within species	2	0.5832	15.2162	3.1359	3.68E-06
Within Populations	66	0.1392			
Total	68				

Appendix 15B cont.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
HL/ABL***					
Between Populations within species	2	0.9088	19.0396	3.1359	2.96E-07
Within Populations	66	0.0477			
Total	68				

HL/MxBL***					
Between Populations within species	2	0.1037	9.7855	3.1359	0.0002
Within Populations	66	0.0106			
Total	68				

BH/CPL***					
Between Populations within species	2	0.1783	22.1162	3.1359	4.45E-08
Within Populations	66	0.0080			
Total	68				

HL/D_rRL***					
Between Populations within species	2	0.0758	8.8630	3.1359	0.0004
Within Populations	66	0.0085			
Total	68				

Appendix 15B cont.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
ExMnBL/InMnBL**					
Between Populations within species	2	0.1435	7.1666	3.1359	0.0015
Within Populations	66	0.0200			
Total	68				
SL/HL***					
Between Populations within species	2	0.1548	16.2050	3.1359	1.88E-06
Within Populations	66	0.0096			
Total	68				
SnL/ED***					
Between Populations within species	2	0.3806	25.7008	3.1359	5.57E-09
Within Populations	66	0.0148			
Total	68				
ExMnBL/HL***					
Between Populations within species	2	0.0310	11.6095	3.1359	4.78E-05
Within Populations	66	0.0027			
Total	68				

Appendix 15C

Analysis of variance of twelve body proportion

variables in three species of *Chrysichthys* in Ghana

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
ED/IOD*					
Between species	2	0.2292	4.3386	3.0536	0.0147
Within species	157	0.0528			
Total	159				
SnL/IOD[^]					
Between species	2	0.0279	0.4333	3.0536	0.6492
Within species	157	0.0644			
Total	159				
HL/BH**					
Between species	2	0.0991	5.0810	3.0536	0.0073
Within species	157	0.0195			
Total	159				
HL/ED***					
Between species	2	0.8286	17.1250	3.0536	1.87E-07
Within species	157	0.0484			
Total	159				

Appendix 15C cont.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
HL/ABL***					
Between species	2	1.0750	16.4323	3.0536	3.31E-07
Within species	157	0.0654			
Total	159				
HL/MxBL[^]					
Between species	2	0.0205	1.4525	3.0536	0.2371
Within species	157	0.0233			
Total	159				
BH/CPL***					
Between species	2	0.1559	8.7535	3.0536	0.0002
Within species	157	0.0178			
Total	159				
HL/D_LRL***					
Between species	2	0.4721	22.4031	3.0536	2.76E-09
Within species	157	0.0211			
Total	159				
ExMnBL/InMnBL[^]					
Between species	2	0.0393	1.8893	3.0536	0.1546
Within species	157	0.0208			
Total	159				

Appendix 15C cont.

	Degrees of freedom (df)	Mean square (MS)	Computed F	Tabular F	P-Value
SL/HL***					
Between species	2	1.0929	61.5063	3.0536	1.88E-20
Within species	157	0.0178			
Total	159				

SnL/ED**					
Between species	2	0.1248	5.3526	3.0536	0.0056
Within species	157	0.0233			
Total	159				

ExMnBL/HL[^]					
Between species	2	0.0060	2.3717	3.0536	0.0967
Within species	157	0.0025			
Total	159				

Levels of significance: *P < 0.05; **P < 0.01; ***P < 0.001;

[^]P > 0.05

Appendix 16 Observed (obs) and expected (exp) genotypic distributions, G - values and Probabilities of deviations from expected Hardy Weinberg distributions, for fifteen loci in three species of *Chrysichthys*.

<i>ADH - 1*</i>								
Genotypic distribution								
Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C. nigro.</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C. maurus</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

LDH - A***Genotypic distribution**

Species Locality	Water body/ size	Sample		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	25.00	2.00	0.00	0.077	<0.90
			exp.	25.039	1.924	0.037		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	20.00	7.00	0.00	1.197	<0.90
			exp.	19.599	6.809	0.591		
<i>C. auratus</i>	Volta river/ Battor	15	obs.	14.00	1.00	0.00	0.036	<0.90
			exp.	14.026	0.957	0.016		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C. nigro.</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C. maurus</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

*sMDH - A**
Genotypic distribution

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C. nigro.</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	25.00	0.00	0.00	0.00	>0.99
			exp.	25.00	0.00	0.00		
<i>C. maurus</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		

sMDH - B***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	20.00	7.00	0.00	1.197	<0.90
			exp.	19.599	6.809	0.591		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	17.00	10.00	0.00	2.292	<0.90
			exp.	17.934	8.142	0.924		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	13.00	2.00	0.00	0.144	<0.90
			exp.	13.057	1.875	0.067		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	12.00	2.00	0.00	0.153	<0.90
			exp.	12.038	1.847	0.071		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	<0.99
			exp.	16.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	21.00	4.00	0.00	0.348	<0.90
			exp.	21.160	3.680	0.160		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	15.00	1.00	0.00	0.033	<0.90
			exp.	15.023	0.961	0.015		

ODH - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105 *	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

SDH - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C.nigro.</i>	River Densu/ Wejja	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

SDH - 2***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C. nigro.</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	25.00	0.00	0.00	0.00	>0.99
			exp.	25.00	0.00	0.00		
<i>C. maurus</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		

GPI - A***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	26.00	1.00	0.00	0.034	<0.90
			exp.	25.984	0.999	0.010		
<i>C. auratus</i>	Volta river/ Battor	15	obs.	11.00	4.00	0.00	0.638	<0.90
			exp.	11.484	3.281	0.234		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C. nigro.</i>	Volta river/ Battor	16	obs.	14.00	2.00	0.00	0.132	<0.90
			exp.	14.078	1.861	0.062		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	24.00	1.00	0.00	0.020	<0.90
			exp.	24.010	0.980	0.010		
<i>C. maurus</i>	Volta river/ Battor	16	obs.	13.00	3.00	0.00	0.325	<0.90
			exp.	12.960	2.880	0.160		

PGM - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	0.00	0.00	27.00	0.00	>0.99
			exp.	0.00	0.00	27.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	0.00	0.00	27.00	0.00	>0.99
			exp.	0.00	0.00	27.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	0.00	0.00	15.00	0.00	>0.99
			exp.	0.00	0.00	15.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	25.00	0.00	0.00	0.00	>0.99
			exp.	25.00	0.00	0.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		

XDH - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

G3PDH - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C. auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C. auratus</i>	Volta Lake/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C. nigro.</i>	Volta Lake/ Yeji	14	obs.	0.00	0.00	14.00	0.00	>0.99
			exp.	0.00	0.00	14.00		
<i>C. nigro.</i>	Volta Lake/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		
<i>C. nigro.</i>	River Densu/ Weija	25	obs.	0.00	0.00	25.00	0.00	>0.99
			exp.	0.00	0.00	25.00		
<i>C. maurus</i>	Volta Lake/ Battor	16	obs.	0.00	0.00	16.00	0.00	>0.99
			exp.	0.00	0.00	16.00		

IDH - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	20	obs.	20.00	0.00	0.00	0.00	>0.99
			exp.	20.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	18	obs.	18.00	0.00	0.00	0.00	>0.99
			exp.	18.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	13	obs.	13.00	0.00	0.00	0.00	>0.99
			exp.	13.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C.nigro.</i>	Volta river/ Battor	13	obs.	13.00	0.00	0.00	0.00	>0.99
			exp.	13.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	19	obs.	19.00	0.00	0.00	0.00	>0.99
			exp.	19.00	0.00	0.00		
<i>C.maurus</i>	Volta river/ Battor	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		

IDH - 2***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	20	obs.	20.00	0.00	0.00	0.00	>0.99
			exp.	20.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	18	obs.	18.00	0.00	0.00	0.00	>0.99
			exp.	18.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	13	obs.	13.00	0.00	0.00	0.00	>0.99
			exp.	13.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C.nigro.</i>	Volta river/ Battor	13	obs.	13.00	0.00	0.00	0.00	>0.99
			exp.	13.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	19	obs.	19.00	0.00	0.00	0.00	>0.99
			exp.	19.00	0.00	0.00		
<i>C.maurus</i>	Volta river/ Battor	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		

ME - 1***Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C.nigro.</i>	Volta river / Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	25.00	0.00	0.00	0.00	>0.99
			exp.	25.00	0.00	0.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		

*ME - 2****Genotypic distribution**

Species	Water body/ Locality	Sample size		100/100*	100/105*	105/105*	G	P
<i>C.auratus</i>	Volta Lake/ Yeji	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta Lake/ Akosombo	27	obs.	27.00	0.00	0.00	0.00	>0.99
			exp.	27.00	0.00	0.00		
<i>C.auratus</i>	Volta river/ Battor	15	obs.	15.00	0.00	0.00	0.00	>0.99
			exp.	15.00	0.00	0.00		
<i>C.nigro.</i>	Volta Lake/ Yeji	14	obs.	14.00	0.00	0.00	0.00	>0.99
			exp.	14.00	0.00	0.00		
<i>C.nigro.</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		
<i>C.nigro.</i>	River Densu/ Weija	25	obs.	25.00	0.00	0.00	0.00	>0.99
			exp.	25.00	0.00	0.00		
<i>C.maurus</i>	Volta river/ Battor	16	obs.	16.00	0.00	0.00	0.00	>0.99
			exp.	16.00	0.00	0.00		

Appendix 17

ENZYME STAINING RECIPES

ADH

NAD	15 mg.
Tris-HCl (0.2M) pH 9.0	30 mls.
Iso-propanol	0.75 mls.
PMS	Trace
MTT	6 mg.

LDH

NAD	15 mg.
Sodium Lactate	1 ml.
Tris-HCl (0.2M) pH 9.0	30 mls.
PMS	Trace
MTT	7 mg.

IDH

Sodium Isocitric acid	50 mg.
MgCl ₂	10 mg.
NADP	4 mg.
Tris-HCl (0.2M) pH 9.0	30 mls.
PMS	Trace
MTT	7 mg.

MDH

L-Malic acid	150 mg.
NAD	10 mg.
Tris	600 mg.
H ₂ O	30 mls.
PMS	Trace
MTT	7 mg.

ME

DL Malic acid	60 mg.
NADP	10 mg.
MgCl ₂	10 mg.
Tris-HCl (0.2M) pH 9.0	30 mls.
PMS	Trace
MTT	7 mg.

ODH

NAD	15 mg.
Octanol	0.75 mls.
Tris-HCl (0.2M) pH 9.0	30 mls.
PMS	Trace
MTT	6 mg.

PGI

Fructose-6-Phosphate	20 mg.
NADP	4 mg.
MgCl ₂	20 mg.
G6PDH	50 ul.
Tris-HCl (0.2M) pH 9.0	30 mls.
PMS	Trace
MTT	7 mg.

PGM

Na-G-PO ₄	50 mg.
MgCl ₂	70 mg.
NADP	3 mg.
G6PDH	50 ul.
Tris-HCl (0.2M) pH 8.0	30 mls.
PMS	Trace
MTT	7 mg.

SDH

Sorbitol	150 mg.
NAD	15 mg.
MgCl ₂	10 mg.
Tris-HCl (0.2M) pH 8.0	30 mls.
PMS	Trace
MTT	7 mg.

XDH

Hypoxanthine	20 mg.
NAD	15 mg.
Tris-HCl (0.2M) pH 8.0	30 mls.
PMS	Trace
MTT	7 mg.

 α GPDH

NAD	15 mg.
EDTA	60 mg.
α -glycerophosphate	20 mg.
Tris-HCl (0.2M) pH 8.0	30 mls.
PMS	Trace
MTT	7 mg.

Appendix 18**BUFFERS (GEL AND ELECTRODE) USED IN ELECTROPHORETIC ASSAYS****Gel and Electrode Buffer Preparation**

11.98g of Citric acid was added to 30.29g of Tris[hydroxymethyl]-aminomethane. Distilled water was then added to make up to 1 litre.

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