DEVELOPMENT OF HIGH-YIELDING AND STABLE MAIZE (*Zea mays* L.) HYBRIDS TOLERANT TO ACID SOILS OF THE TROPICAL HUMID FOREST ZONES OF CAMEROON

By

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DECLARATION

I hereby declare that except for references to work of other researchers, which have been duly cited, this work is my original research and that neither part nor whole has been presented elsewhere for the award of a degree.

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ABSTRACT

Maize is the most important cereal produced in the Bimodal Humid Forest Zone (BHFZ) of Cameroon. Yield of the crop in the BHFZ is very low because of the negative impact of soil acidity especially Al toxicity on plant growth. Liming increases soil pH levels reduces the level of Al saturation and boost the productivity but it is costly and unavailable. Therefore, it becomes necessary to explore more sustainable and affordable ways of increasing yield of the crop. The objective of the present study was to identify high-yielding and stable maize hybrids tolerant to acid soils. A Participatory Rural Appraisal (PRA) was conducted in the BHFZ to identify farmer constraints to maize production and varietal preferences. Results indicated that farming is undertaken by the youth with maize being the most important cereal crop. Maize is grown for home consumption and for cash. Slash and burn associated with fallow systems were the predominant land management practices. The main constraints affecting maize production are low soil fertility, high cost of fertilizer, use of poor quality seeds, lack of improved varieties, and poor post-harvest handling and preservation methods. Farmers' were willing to adopt new and improved maize varieties. Farmers' preferred traits in improved maize varieties were high yield, good quality grain, soft and sweet taste, early maturity, pest and disease resistance. A genetic diversity study was conducted on thirty hybrid parental materials used to assess the variability among them using agronomic traits and molecular markers. These lines (13 from IRAD, 14 from CIMMYT and three from IITA) were evaluated in acid soil environments from 2013 to 2014. Fresh leaf samples of the 30 lines were collected at 14 days old and genotyped using 200 SNP markers. As results, the local inbred lines had flint and indented kernel, with a yellow color. Most of them had primary –secondary tassel type with reddish color. The inbred lines were grouped into two main clusters containing four groups with different levels of stress tolerance.

Cluster I from the molecular characterization contained all the introduced inbred lines and most of the locally adapted lines subdivided into 16 sub-clusters. Cluster II had two Acid Tolerant Population (ATP) lines. There was low variability between Acid Tolerant Population (ATP) lines and introduced lines. The performance of 121 genotypes were subsequently evaluated in 12 environments made of acid soil and control soil conditions using a simple lattice design (11 x 11). Fifteen high-yielding hybrids were identified in these environments. All these hybrids out-yielded the best hybrid check variety by equal or more than 10%. Heritability estimates of all the traits recorded in acid soil environments was lower under acid than in control soil conditions. Yield reduction due to Al toxicity ranged from 2 to 69%. Then, the general and specific combining abilities of 112 hybrids and their parents were estimated using line by tester mating design. The results showed that Al tolerance for grain yield was under both additive and non-additive gene action with the non-additive gene action predominating. Four distinct heterotic groups were identified under acid soil and across environments. In control environments, two heterotic groups were identified. Cam Inb gp1 17 and 9450 were the best testers in control and across environments while 4001 was the best under acid soil environments. The yield stability study of 121 genotypes was carried out across nine environments using a lattice square design (11x11). The study environments were grouped into three mega-environments. Eight hybrids were the most high-yielding and stable hybrids across environments and could be potential hybrids for release after on-farm and multi-locational trials. Almost all these hybrids had at least one introduced parent suggesting that the introduction of inbred lines was effective to the development of high-yielding and stable maize hybrids under acid soil conditions.

DEDICATION

To my grandfather (Temgoua Ibo), my father (Tandzi Pierre), my mother (Tchofack Veronique), my ants (Tagne Marie Pascale, Tonleu Thérèse, Ngoune Odile), my daughters (Lynn Christie, Ange Veronica, Carine), all my brothers and sisters.

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LIST OF ABBREVIATIONS

ACDIC	Citizens Association for the Defense of collective interests
Al	Aluminum
AMMI	Additive Main effect and Multiplicative Interaction
BHFZ	Bimodal Humid Forest Zone
Ca	Calcium
CEMAC	Central African Economic and Monetary Community
CIMMYT	International Maize and Wheat Improvement Center
ECEC	Effective Cation Exchange Capacity
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistical databases
GCA	General Combining Ability
GGE	Genotype plus Genotype by Environment interaction
IITA	International Institute of Tropical Agriculture
IRAD	Institute of Agricultural Research for Development
Mg	Magnesium
Ca	Calcium
P	Phosphorus
SCA	Specific Combining Ability
SNP	Single Nucleotide Polymorphisms
USDA	United States Department of Agriculture
WFC	Web Feature Service

CHAPTER ONE

GENERAL INTRODUCTION

1.1 Background

Maize is the principal crop and major staple food in most African and South American countries (Denic *et al*., 2008). It is estimated that about 70% of the maize produced in sub-Saharan Africa is for human consumption (WFC, 2002). Every part of the maize plant has economic value: the grain, leaves, stalk, tassel, and cob can all be used to produce a large variety of food and non-food products (IITA, 2009). About 95% of the gain in production since 1961 have come from increasing yields, except in Africa, where about half the gains have come from expanding the area of cultivation (Pardey and Beintema, 2001).

In Cameroon, maize is the most widely cropped and consumed cereal crop. It is mainly cropped by resource poor farmers. Recently, it has become a cash crop and, therefore, an important source of income. Maize is the source of a large number of industrial products in addition to its use as human food and animal feed. Diversified uses of maize include corn starch, corn oil, baby corns and popcorns. Maize is used as raw material for industries such as breweries and oil-mills. The average yield of maize in Cameroon is very low (1.8 t/ha) and has remained constant over years (Aroga *et al.*, 2001; Ngoko *et al.*, 2002). ACDIC (2010) reported the average yield of maize produce ranged from 0.8 – 1 t/ha. The annual maize production was estimated at 1,647 036 tons in 2013 (FAOSTAT, 2013). However, this production is not sufficient to meet the demand of the population. In 2008, the quantity of maize flour imported was estimated to 24,815 tons (FAOSTAT, 2011) and this continue to increase until to date.

1.2 Maize production constraints in the Bimodal Humid Forest Zone of Cameroon

The Bimodal Humid Forest Zone (BHFZ) of Cameroon is a mid-altitude plateau 300-600 m above sea level with a Sub-Equatorial Congo-Guinea climate characterized by four seasons: two rainy seasons from March to June and from September to November; and two dry seasons from December to Febuary and from July to August (Njomgang *et al.*, 2010). The rainfall is between 1500 and 2000 mm and has contributed to leached the soil from basic cations such as Ca, Mg, K and Na rendering the soil more acidic dominated by the acidic cations Al and H (Njomgang *et al.*, 2010). Over the past decades, farmers' interest in maize production has increased, and maize has become a cash crop like coffee and cocoa, and is now an important source of income (Nguimgo *et al.*, 2003; Hauser *et al.*, 2006). There is an increasing demand for the crop because of its use as feed in animal production and in the brewing industry. The annual demand of maize for human consumption and animal feed in Cameroon was estimated to 870,000 and 320,000 tons, respectively (Etoundi and Dia, 2008). Maize production in Cameroon has been increasing steadily from an estimated 966,000 metric tonnes in 2004 (USDA, 2013) to 1,647 036 tons in 2013 (FAOSTAT, 2013). These increases have mainly been due to increases in area harvested (832400 ha) rather than yield increase per unit area (0.8 – 1t/ha). The BHFZ, by virtue of its bimodal rainfall pattern holds promise for increasing the output for maize if the main fertility constraint of low soil pH can be solved.

1.3 Maize breeding programs for acid tolerance

In neutral or basic soils, Al is found in insoluble divalent and monovalent forms of Al-oxides or Al-hydroxides, but the soluble trivalent Al^{3+} ion is the dominant element in acidic soils (Kochian and . 1995; Krill *et al.*, 2010). The Al^{3+} disrupts many physiological processes in plants through both apoplastic and symplastic interactions inducing inhibition of root growth as the primary symptom of Al toxicity (Delhaize and Ryan, 1995; Krill *et al.*, 2010). The reduction in root growth and function leads to a decrease in yield and increases susceptibility to other stresses, primarily drought and mineral deficiencies, due to the limited capacity of roots to absorb sufficient water and mineral nutrition from the soil (Krill *et al.*, 2010).

Five maize open pollinated varieties (OPVs) from Cameroon were reported to have some level of tolerance to soil acidity (The et *al.*, 2001). Three of these (ATP-SR-Y, ATP-S4 SYN Y and ATP SYN I-W) have been found to give 13% increase in grain yield over local varieties in the humid forest area of Cameroon (The *et al.*, 2001). In addition, two best cross hybrids (ATP-SR-Y x 87036 and ATP S_5 Syn y x 9450) have been identified as good genotypes for Al induced soil acidity in the humid forest area based on their yield under stress environments (4.04 and 5.01 t/ha) (Tandzi, 2005). But, only ATP SR Y is the acid tolerant open-pollinated variety released and commercialized in Cameroon (The, 2000).

1.4 Problem Statement / justification

Maize, the main cereal produced in the BHFZ of Cameroon, is constrained by acidic soils. According to Etoundi and Dia, (2008) maize does not only occupy an important place in the different functions of agricultural production in Cameroon but it is the most consumed cereal in the country. The soils in this region are mainly Oxisols with high weathering intensity (Njomgang *et al.*, 2010). The exchangeable bases have been washed out leaving Al^{3+} and H+ cations to predominate the exchange complex culminating in the formation of acid soils. The high levels of acidity (pH ranging between 3.8 and 5) coupled with a high Al saturation of 40 to 80% have led to Al toxicity as well as deficiencies in other nutrients such of Ca and Mg and P

(Nounamo *et al.*, 2002). Acid soils cover 75% of arable land area with Al toxicity account for 40-80% or 1-2 t/ha reduction in grain yield (Bindzi, 1987; Nwaga *et al.*, 2004). Yield losses of 60% has been reported in acid tolerant population (ATP SR Y) (The *et al.*, 2001).

Many attempts have been made to amend the acid soils of the BHFZ of Cameroon. Methods such as the use of wood ash and agricultural liming have been employed in the control of acid soils of the BHFZ. Application of wood ash at 4 t/ha has been used so far but it is not sustainable and practicable due to the vast nature of the acid soils of the BHFZ (Mbah *et al.*, 2010). However, the effect of lime on the soil of Cameroon has contributed to lower its pH, as compare to that of Guadeloupe where exchangeable Al decreased significantly. This is because of the very high levels of exchangeable Al in the Cameroonian soils which have to be displaced by the Ca from the lime. To be effective, higher quantity of lime will have to be applied per unit area. The application of lime in agriculture is expensive and beyond the means of the resource poor small scale farmers of the BHFZ. The amendment is also not readily available in the country. Lime usage is also not environmentally friendly and has so far had only a temporary effect (The *et al.*, 2001). The land use systems and production strategies adopted by farmers depend on the interaction between biophysical and socio-economic resources available to them (Kenga *et al.*, 2002). It is only through characterization and diagnostic surveys at different households that better understandings of environment in which farmers operate and their constraints could be obtained for accurate targeting of appropriate technologies and policies.

Any attempt at resolving the low yield of maize on acid soils of Cameroon would have to focus on sustainability vis-à-vis affordability for the farmer. Breeding for acid soil-tolerant maize cultivars may be the solution to the problem. Acid tolerant cultivars provide an environmentally friendly, inexpensive, and long term solution to sustainable crop production on acid soils

(Granados *et al.*, 1993; Welcker *et al.*, 2005). Attempts have been made at breeding maize tolerant to Al toxicity (The *et al.*, 2005; The *et al.*, 2006). Some OPVs, (ATP) are somewhat tolerant to acid soils. However these ATP varieties still show yield losses up to 60% when cropped on acid soil conditions (The et al., 2006). There is a need of reducing yield loss due to soil acidity especially Al toxicity and increasing yield productivity per unit area. This could be done through the development of maize hybrids under stress environments. However, no single cross hybrids tolerant to acid soils has been developed and released in the country yet. The BHFZ covers an area of 21.7 million hectares with different levels of acidity in the soil. Any hybrid developed for the zone must be stable within a wide range of Al toxicity soil environments. It is therefore incumbent for hybrids tolerant to acid soils with good yield stability to be developed for the Bimodal Humid Forest Zone.

Farmer's perceptions about maize varieties, their constraints and preferences have to be established and included in the breeding program. The national breeding program has obtained a number of inbred lines from CIMMYT, IITA and other African breeding programs. However, little is known about the morphological and the molecular characterization of the Cameroonian lines, the heterotic relationship between the local and the introduced inbred lines in general and specifically in lower pH. It is therefore important to get more information on the available inbred lines, to understand the heterotic relationship between these lines from different origins and to appreciate the yield stability of maize genotypes across environments.

1.5. Objectives

The aim of the study is to develop high-yielding and stable maize hybrids tolerant to acid soils with toxic level of Aluminium.

The specific objectives are to:

i. Identify constraints to maize production from the farmers' perceived point of view and maize traits preferred by farmers
ii. Determine morphological and molecular trait variation among inbred lines under acid soil conditions
iii. Determine performance of hybrids under acid and control soil conditions and determine the correlation between yield and other related traits.
iv. Estimate the combining abilities, the gene action and classify inbred lines into heterotic groups
v. Evaluate yield stability of maize genotypes across environments.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Biology of maize

Maize (Zea mays *L.*) belong to the family of Graminae (Poacea) commonly called grass family (Hitchcock and Chase, 1971). The base chromosome number for *Zea* is 2n = 2x = 20 (Mandal, 2014). Maize is a monoecious and wind pollinated plant, whereby about 95% of cross pollination and about 5% of self-pollination are usually possible (Mandal, 2014). On average 21,000 pollen grains could be produced for each kernel on an ordinary ear with 1000 kernels (O.E.C.D., 2003). A tassel produces at least 2000 pollen grains for each silk of a ear of 1000 silks (Aylor *et al.*, 2003). A normal ear may have an average of 500 to 600 kernels. Pollen grain viability is for about 12-18 hours in cool environment and thereafter they may be killed in few hours by heat or desiccation (Mandal, 2014). Pollination must be completed within 3 - 4 hours after removal of anthers to ensure viability of pollen (Mandal, 2014). Corn in the field sheds pollen for around 13 days (O.E.C.D., 2003). An average temperature of 20 – 24°C is optimum, and the temperature should not sink below 14°C at night whereas the minimum for germination is 8°C (Rudelsheim and Smets, 2011). A radical starts developing 2-3 days after sowing, and the primary roots are almost fully developed at emergence. Maize constitutes an important source of carbohydrates, protein, vitamin B, and minerals (calcium, magnesium, phosphorous, iron). Maize protein is deficient in two essential amino acids, lysine and tryptophan. These two amino acids can only be obtained from food as they cannot be metabolically synthesized (Kassa *et al.*, 2013).

2.2 Importance of maize

Maize (*Zea mays* L.) is one of the most important staple foods in the world. Maize is cropped originally in Central America and it is now distribute to the rest of the world because of its ability to grow in diverse climates. The total maize production in the world was 984.37 million tons in 2013 and an estimated 985.39 million tons is to be produced in 2014 (USDA, 2014). The world maize production from 2014 to 2015 is estimated at 985.39 million metric tons (U.S.D.A., 2014). The greatest maize producer, the United States of America (USA), shared 40% of the total world production in 2004 and has reached the national record of 10.06 tons of dry grain per hectare on the area of 30 million hectares (Radosavljevic *et al.*, 2010). The whole continent of Africa contributes only 7% of the global production (FAOSTAT, 2011). In developing countries, 30% of maize produced is used for direct human consumption.

2.3 Maize production constraints

About 95 percent of the gains in production since 1961 have come from increasing yields, except in Africa where about half the gains have come from the expansion of cropping land (Pardey and Beintema, 2001). The average grain yield of a maize crop in the tropics is 1.8 tons/ha, as compared to the global average of 4.2 tons/ha (Xu and Crouch, 2008).

Despite the high yield of improved hybrids, maize production faces environmental constraints which could be classified into biotic and abiotic stresses. The biotic constraints include diseases and pests that are of a global nature and occur in most maize growing environments. Examples are leaf blights, leaf rusts, leaf spots, stalk rots and ear rots. Diseases that are of regional economic importance in the tropics include for Asia - downy mildews, which are also spreading to some parts of Africa and the Americas. For Africa - maize streak virus and the parasitic weed Striga and for Latin America - maize stunt and tar spot (Xu and Crouch, 2008).

2.4 Abiotic constraints

2.4.1 Drought

Drought is one of the most serious abiotic factors limiting crop production worldwide. Change in global climate increases the need for better adaptation and breeding for improved drought tolerance in crops. Maize is one of the most sensitive crops to drought despite the fact that it is a C4 plant, with high photosynthetic rate and relatively low transpiration rate (Anđelković *et al.*, 2012). Drought tolerance or resistance in native plant species is often defined as survival, but in crop species it must be defined in terms of productivity (Saba *et al.*, 2001). The effects of soil properties on water availability also influence nutrient availability because water is essential for chemical reactions, biological activity, and the transport and absorption of nutrients by roots (Stevens *et al.*, 2002). Different studies have been done in drought stress environments on maize selection (Badu-Apraku *et al.*, 2005; Moradi *et al.*, 2012; Badu-Apraku *et al.*, 2013; Ifie, 2013).

2.4.2 Salinity

Soil salinity is one of the major environmental stresses that adversely affect plant growth and development. Effects of salinity on crop productivity are more severe in arid and semiarid regions where rainfall is limited and there are high evapo-transpiration, high temperature, poor water quality, and poor soil management practices (Azevedo Neto *et al.*, 2006). Salinity has reached a level of 19.5% of all irrigated-land and 2.1% of dry-land agriculture worldwide (Carpıcı *et al.*, 2009).

2.4.3 Low nitrogen and low phosphorus

Nitrogen is a vital plant nutrient and a major yield determining factor required for maize production (Shanti *et al.*, 1997; Onasanya *et al.*, 2009). Nitrogen is a component of protein and nucleic acids and when it is sub-optimal, growth is reduced. Its availability in sufficient quantity throughout the growing season is essential for maize growth. It is also a characteristic constituent of proteins and an integral component of many other compounds essential for plant growth processes including chlorophyll and many enzymes (Onasanya *et al.*, 2009). The maximum N uptake occurs during the month prior to tasseling and silking and significant amounts of N are transferred from leaf tissue to grain during the grain-fill process (Alley *et al.*, 2009). In Africa, N fertilizer supply is limited, N fertilizer is very expensive and/or unavailable when required by poor farmers therefore low-N-tolerant cultivars are highly desirable (Bänzinger and Cooper, 2001; Chen *et al.*, 2013).

Phosphorus is one of the 17 essential nutrients required for plant growth as well as all energy mediated processes in plants (Raghothama and Karthikeyan, 2005). It is the second most important macronutrient next to nitrogen in limiting crop growth (Balemi and Negisho, 2012). The low availability of phosphorus is due to the fact that it readily forms insoluble complexes with cation such as aluminum and iron under acidic soil condition and with calcium and magnesium under alkaline soil conditions whereas the poor P fertilizer recovery is due to the fact that the P applied in the form of fertilizers is mainly adsorbed by the soil, and is not available for plants lacking specific adaptations (Balemi and Negisho, 2012).

2.4.4 Acid soils

Acid soil is defined as soils with pH < 5.5 in the top layer (Von Uexkull and Mutert, 1995; Dalovic *et al.*, 2012). Among the critical soil chemical properties affecting soil nutrient availability is soil pH which is a measure of the acidity or alkalinity. Soil acidity is determined by the amount of hydrogen (H^+) activity in soil solution and influenced by edaphic, climatic, and biological factors. High rainfall affects the rate of soil acidification depending on the rate of water percolation through the soil profile. Soil acidification is intensified by the removal of cations through the harvesting of crops and by acid precipitation from polluted air (Ulrich *et al.*, 1980; Hede *et al.*, 2001). Organic matter decay forming carbonic acid and other weak acids also contributes in the acidification process. Generally, a decrease in soil pH increases availability of cations, especially essential micronutrients, Fe, Mn, Cu and Zn (Gupta *et al.*, 2013). Acid soils limit crop production on 30-40% of the world's arable land and up to 70% of the world's potentially arable land (Hede *et al.*, 2001). Acid soils covered 3,950 million ha or 30% of global arable land (Von Uexkull and Mutert, 1995; Dalovic *et al.*, 2012). Poor fertility of acid soils is due to a combination of mineral toxicities (Aluminum, Manganese and Iron) and deficiency caused by leaching or decreased availability of P, Ca, Mg and some other micronutrients, especially Mo, Zn and B (Gupta *et al.*, 2013).

Toxic levels of metals in soils may be caused by natural soil properties or by agricultural, manufacturing, mining, and waste disposal practices. Acid soils occur mainly in two global belts: the Northern belt, with a cold, humid temperate climate, and the Southern tropical belt, with warm and humid conditions (Von Uexkull and Mutert, 1995; Dalovic *et al.*, 2012).

At Ebolowa, soils are deep to very deep, well drained, brownish yellow to brown, characterized by a very low pH (3.8 to 5) and a high clay which of up to 80% in the topsoil (Nounamo and Yemefack, 2000). They are strongly weathered soils in which edaphic constraints such as acidity, high exchangeable Aluminium and low basic cation ratio, have been identified as the main limiting factors to sustained permanent cropping systems (Yemefack *et al.*, 2002). About 65 to 70% of these soils are Oxisols (Yemefack *et al.*, 2002). Soil pH, exchangeable Al, organic carbon, available P, base and Al saturations, exchangeable Ca and Effective Cation Exchangeable Capacity (ECEC) significantly change with the land-use systems (Agoumé and Birang, 2009).

2.4.4.1 Aluminium toxicity

Aluminium (Al) toxicity is one of the major factors constraining crop production on 67% of the total acid soil area in the world (Abate *et al.*, 2013). Acid soils have high contents of H^+ and low contents of essential plant nutrients, primarily P and Ca, which are limiting factors for high and stable yields of cultivated cereal crops (Dalovic *et al.*, 2012). Generally, Aluminum is not regarded as an essential element for plant growth, but in some conditions, low concentrations can increase growth or produce other desirable effects (Silva, 2012). For instance it can correct or prevent P toxicity in the case of Al-tolerant maize (Silva, 2012). Some agricultural practices, such as crop removal from the farm, leaching of nitrogen below the plant root zone, inappropriate use of nitrogenous fertilizers, and build-up in organic matter, cause further acidification of agricultural soils (Silva, 2012).

Strong subsoil acidity (Al toxicity) reduces plant rooting depth, increases susceptibility to drought, and decreases the use of subsoil nutrients (Foy *et al.*, 1978). Visible effects of soluble

Al on plant tops are a secondary effect of reduced nutrient uptake. Symptoms include those similar to deficiencies of Ca, Mg, Fe, and P. These are probably a result of decreased root proliferation, reduced root activity and reduction in uptake of water with an increased sensitivity to drought. Root growth inhibition may be directly/indirectly responsible for the loss of plant production (Silva, 2012). At soil pH values at or below 5, toxic forms of Al dissolve into the soil solution, inhibiting root growth and function and thus reducing crop yield. The determination of the content of available Al (exchangeable and in the soil solution) is essential for an evaluation of the risk of plant production on acid soils, where Al can occur in concentrations toxic to plants and microorganisms (Dalovic *et al.*, 2012).

2. 5 Conventional breeding for abiotic constraints

The tolerance to mineral elements can be defined as the ability of a plant to grow better, produce more dry matter, and develop fewer deficiency symptoms when grown at low or toxic levels of the mineral element. Alternatively, it can be defined as the ability of a genotype to produce higher yield in a soil that has a deficiency or toxicity of a particular element compared to a standard genotype (Graham *et al.*, 2002).

Improving grain yield is the major objective in maize breeding. Selection and breeding have always been conducted to achieve high yield and better quality of crops under stressful conditions (Niu *et al.*, 2012). Grain yield and its response to stress are highly complex traits involving a long-term interaction between the environment and plant characteristics and regulatory pathways at different scales of organization (Araus *et al.*, 2012). Greater grain yield of newer Argentinean maize hybrids was mainly related to an increased harvest index (Echarte *et al.*, 2013). The trait most frequently associated with genetic yield improvement in maize under stress conditions is delayed leaf senescence or ‘‘stay green’’ (Duvick, 1997b; Nguyen and Blum, 2004). Al-tolerant genotypes should produce higher shoot and root weight with higher nutrient efficiency ratio (NER) for P, Ca, Mg, and Fe at 41% Al saturation (Baligar *et al.*, 1997). The application of 4 t/ha of wood ash lime significantly increased yield of maize grown under acid soils (Mbah *et al.*, 2010).

Valuable traits may be combined in a selection index which is, in a way, a quantitative translation of the ideotype concept (Araus *et al.*, 2010; Moradi *et al.*, 2012). In another study, anthesis-silking interval (ASI) under drought has become shorter in modern hybrids, and selection has possibly led to an increase in the growth of spikelets, ears and a reduction in final spikelet number (Bänziger *et al.*, 2000). Moreover, a reduction of leaf senescence during grain filling has been one the most visually and distinctive traits between older and newer hybrids (Duvick *et al.*, 2004). For instance, N-efficient maize cultivars bred in a low-N environment showed increased yield of 11% under high-N conditions and 14% under low-N conditions. Increasing maize nitrogen use efficiency under low-N supply while maintaining the yield potential under high-N conditions is therefore feasible (Chen *et al.*, 2009). In tropical maize, the indirect pressure of selection to reduce tassel size by selecting for increased grain production has had relatively modest effects on tassel size. Therefore, tropical inbred lines usually still possess a relatively large tassel, which may eventually have a negative effect on the development of ear and silk when the supply of photo assimilates is limited by drought stress (Araus *et al.*, 2012).

In 1998, the International Cooperation with Developing Countries (INCO) project titled fitting maize into cropping systems on acid soils of the tropics was established. In the project, Brazil (EMBRAPA), Columbia (CIAT/CIMMYT International Network), Cameroon (IRAD) and Guadeloupe (INRA) worked in collaboration on the selection of maize inbred lines, hybrids and composites varieties adapted to acid soil environments (Welcker, 2000). Breeders from Latin America, Africa, and Europe exchanged advanced genetic materials and evaluated them in a wide range of acid soil environments (Welcker *et al.*, 2005). Conventional breeding methods associated with different mating designs were applied to study the combining ability, the heritability and the gene effects linked to acidity tolerance. In Cameroon, some maize synthetic and top crosses varieties have been identified with different levels of tolerance with good performance on acid and non-acidic soil and expressed small relative grain yield lost due to soil acidity of the soil (The, 2000). From this project, the acid tolerant open-pollinated population ATP SR Y was released (The, 2000). Exotic germplasms were constantly introgressed into local germplasm (Youmbi *et al.*, 2005). Plants with short Anthesis-Silking Interval (ASI) have been used by breeders as selection criteria for stress tolerance in maize (Granados *et al.*, 1993; Youmbi *et al.*, 2005). Recurrent selection has increased maize yields in acid soils even though major genotype x environment interactions complicated selection (Welcker *et al.*, 2005). Some of these studies estimated general or specific combining abilities or otherwise approximated breeding potential. Grain yield, plant height and days to male flowering have been the full season traits assessed for sensitivity to Al (Kochian *et al.*, 2009). Aluminum exclusion is related to the ability of plants to excrete organic acids (predominantly citric acid and oxalate in maize) and phenolics. The most important mechanisms of aluminum tolerance are soil alkalinization, aluminum complexation and aluminum compartmentation (Kochian *et al.*, 2004). Alkalinization of the rhizosphere relies on the fact that toxic Aluminum species become less available with increasing pH (Kochian *et al.*, 2004).

2.5.1 Line x tester mating design

The line by tester mating design is one of the mating designs mainly used in private breeding programs. This design has been extensively used to estimate general combining ability (GCA) and specific combining ability (SCA) variances and their effects (Kempthorne, 1957). It is also used in understanding the nature of gene action involved in the expression of economically important quantitative traits. The mating design involves "l" lines and "t" testers. All of the lines are crossed to each of the testers and thus, "l" x "t" full sib progenies is produced. These progenies resulting from line x tester mating, along with or without the parents, can be tested in a replicated trial using suitable field design (Alarmelu *et al.*, 2010). Line by tester mating design developed by Kempthorne (1957) provides reliable information on the general and specific combining abilities effects of parents and their hybrid combinations (Gowda *et al.*, 2013). The design has been widely used in maize breeding by several workers and continues to be applied in quantitative genetic studies in maize (Sharma *et al.*, 2004).

2.5.2 Combining abilities

The concept of combining ability is important in designing plant breeding programs. It is especially useful to compare the performance of lines in hybrid combinations. Combining ability or productivity in crosses is defined as the ability of parents to combine so that favorable genes/characters are transmitted to their progenies (Panhwar *et al.*, 2008). Combining ability analysis is useful to assess the potential value of inbred lines and it also helps in identifying the nature of gene action involved in various quantitative characters. This information is essential for formulating hybrid breeding program (Gowda *et al.*, 2013). There are two types of combining ability: general and specific, that has been recognized in quantitative genetics. Specific combining ability is defined as the deviation in the performance of hybrids from the expected productivity based upon the average performance of lines involved in the hybrid combination; while general combining ability is defined as average performance of a line in a series of crosses (Panhwar *et al.*, 2008). General combining ability is due to genes which are largely additive in their effects and specific combining ability is due to the genes with dominance or epistatic effects (Sprague and Tatum, 1942).

In low and high stresses, the specific combining ability effects (SCA) of some tropical maize germplasm have been found to be significant, showing that the non-additive genetic effects were the most important, making the selection of parent pairs with breeding potential possible (Vagno de Souza *et al.*, 2009). Since the development of new cultivars through continuous process of hybridization, information on combining ability of new inbreds have become essential. The nature and magnitude of gene action is an important factor in developing an effective breeding program (Gowda *et al.*, 2013). For instance, the evaluation of hybrids and parental lines by Asif et al. (2007) showed that none of the cross combination exhibited desirable significant SCA effects for all the characters.

2.5.3 Heterosis, heterotic pattern and heterotic group

Hybrid vigor or heterosis is the phenomenon in which progeny of crosses between inbred lines or pure bred populations are better than the expected average of the two populations or inbred lines for a particular trait (Kwena, 2008). Heterosis observed in various crosses is the average expression of heterosis of the hybrids formed by crossing a sample of genotypes from each of the two populations (Hallauer and Miranda, 1988). The manifestation of heterosis usually depends on genetic divergence of the two parental varieties. Information on heterosis and heterotic groups is important in the development of high performance hybrids and improvement of populations from collections. Heterosis is credited for large increase in production per unit area, thus sparing large amounts of land for other uses such as environmentally benign nature preserve (Duvick, 1997a).

According to Goff (2011) the dominance and over-dominance theories remain the best models to explain heterosis, especially for single gene or single trait heterosis and are not mutually exclusive while the epistasis which is the interaction between different genes, explain hybrid vigor. Maize grain yield in the United States of America has increased by about 100 kg / ha / year or 2% per year from the start of large-scale adoption of hybrids by maize growers in the late 1930s until the first decade of the 21^{st} century and about 75% of the yield improvement has been attributed to genetic gain (Tollenaar and Lee, 2006). Germplasm are thus classified into specific heterotic groups or patterns depending on their similarity in combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups (Kwena, 2008). Heterosis and combining ability is a prerequisite for developing a good economically viable hybrid maize variety (Izhar and Chakraborty, 2013).

To systematically exploit heterosis in hybrid breeding program, the concept of heterotic groups and patterns was suggested (Reif *et al.,* 2005).The term heterotic pattern refers to a specific pair of two heterotic groups, which express high heterosis and consequently high hybrid performance in their cross." The concept of heterotic patterns includes the subdivision of the germplasm available in a hybrid breeding program in at least two divergent populations, which are improved with inter-population selection methods (Reif *et al.*, 2005). Conventional methods, based on testcross data, have been widely used to estimate heterosis between populations or inbred lines and group them into heterotic groups or patterns (Menkir *et al.*, 2003; Welcker *et al.*, 2005; Badu-Apraku *et al.*, 2013; Qurban *et al.*, 2014).

In most private sectors, breeders develop their heterotic groups by using elite inbred lines as testers. The general process is to cross two inbreds with different desirable traits but which both combine well with an elite tester. The F1 of this self-cross is to produce a source population from which new inbreds will be developed. The new inbreds are selected by evaluating hybrids between them and the tester. Any tester hybrids that outperform the best commercial check hybrid by 10% or more are advanced and the new inbred is classed into an anti-tester heterotic group (Mikel and Dudley, 2006). Heterotic groups in dent corn have been subdivided into Iowa Stiff Stalk Synthetic (BSSS) and non- BSSS (Lu and Bernardo, 2001). In practice, commercial corn hybrids consist of crosses of two unrelated inbreds each derived from different families or heterotic groups; there is much less diversity within heterotic groups, but diversity increases on pooling germplasm from different heterotic groups (Mikel, 2008).

Vasal *et al.* (1992) assigned inbred lines to heterotic groups using the traditional method of specific combining ability. Lines in genetically different heterotic groups are usually identified by positive SCA effects between them while inbred lines in the same heterotic group have a tendency to exhibit negative SCA effects when crossed (Vasal *et al.*, 1992).

2.5.4 Grain yield stability and genotype by environment (G x E) interaction

Crop yield potential was defined as the yield of a cultivar when grown in environments to which it is adapted with nutrients and water non limiting and with pests, diseases, weeds, lodging, and other stresses effectively controlled (Evans, 1993). Hence, a more functional definition of yield potential is the yield obtained when an adapted cultivar is grown with the minimal possible stress that can be achieved with best management practices (Cassman, 1999). Improvements in maize stress tolerance have contributed to an increase in grain yield (GY). Grain yield in maize is determined by kernel number per plant (KNP) and kernel weight (KW) (Cerrudo *et al.*, 2012). Yield improvement has been associated with increased in stress tolerance and heterosis, but the nature of the enhanced stress tolerance remains elusive. Yield improvement is the result of changes underlying physiological processes (Tollenaar and Lee, 2006).

The *et al*. (2001) showed that the application of lime except in the first year resulted in a significant increase in maize grain yield of both the tolerant (82%) and particularly the susceptible maize cultivar (208%). The application of lime corresponded to a significant decrease in exchangeable Al and significant increase in pH and available Ca and Mg contents of the soil (The *et al*., 2001). The yield gaps among the same genotypes evaluated under stress and non-stress environments are attributed mainly to limitations imposed by acid soil infertility, and to a lesser extent to limited water supply and to production constraints such as lack of disease and pest control (Murata *et al.*, 2013). Nutrient stresses (both deficiencies and toxicities) are largely responsible for poor plant growth and lower nutrient use efficiency in acid soils (Murata *et al.*, 2003).

Environment is the sum total of physical, chemical and biological factors (Nath *et al.*, 2013). Genotype × environment interactions (GEI) are of major importance to plant breeders in developing improved genotypes because they cause difficulties in selecting genotypes evaluated in diverse environments. When G×E interaction is significant, its cause, nature, and implications must be carefully considered because it reduces the correlation between phenotypic and genotypic values, and has been shown to hinder the selection progress (Khalil *et al.*, 2011). Grain yield, is quantitative in nature and routinely exhibits genotype x environment interactions and necessitates genotype evaluation in multi-environments trials in the advanced stages of selection (Singh *et al.*, 2009; Kandus *et al.*, 2010). The GxE interaction allows the classification of genotypes by their behavior in two different situations, either stable or adapted to a particular environment in terms of the yield or some other interesting agronomic feature (Kandus *et al.*, 2010; Badu-Apraku *et al.*, 2011a; Adu *et al.*, 2013; Jorge de Oliveira *et al.*, 2014).

By partitioning yield components of hybrids into linear and non-linear components, Singh *et al.*(2009) found that both were responsible for expression of the traits. However, the linear component was larger in magnitude than the non-linear component suggesting that variation in the performance of different cultivars could be predicted. The evaluation of G × E interaction gives an idea of stability of the population (Nath *et al.*, 2013). Significant achievement in crop production may be possible by breeding varieties for their stability for yield and yield components (Singh *et al.*, 2009b; Lal *et al.*, 2010). Varietal mean yield over all environments and regression coefficients have been used to classify the cultivars specially adopted at poor and better yielding environments and for their general adaptability. Average phenotypic stability has been denoted by a regression coefficient of unit $bi = 1$ (Finlay and Wilkinson, 1963). A cultivar with $bi < 1$ has above average stability, $bi > 1$ has below average stability and $bi = 0$ has absolute phenotypic stability which means a constant gain in all environments (Finlay and Wilkinson, 1963). It has also been found that the variety with the smallest mean value would be the one that contributes the least to variety × location interactions and thus would be considered as the most stable genotype in the tests (Nath *et al.*, 2013).

Additive Main Effects and Multiplicative Interaction (AMMI) analysis is one of the popular parametric but multivariate methods to predict adaptation and stability of cultivars. The usefulness of the method to be applied to some different crops has been noted by many researchers (Gauch and Zobel, 1996b; Asfaw *et al.*, 2009; Bose *et al.*, 2014; Jorge de Oliveira *et al.*, 2014).

The GGE biplot has been recognized as an innovative methodology in biplot graphic analysis in plant breeding. Fan *et al.* (2007) showed that the GGE biplot was a useful tool for identifying locations that optimized hybrid performance and for making better use of limited resources available for maize testing programs (Fan *et al.*, 2007). The GGE biplot graphically displays genotype main effect plus G×E of multi-environment trials in a way that facilitates visual evaluation of cultivars and mega-environment identification (Yan *et al.*, 2007).

2.6 Genetic diversity in maize

Genetic diversity is the average sequence divergence between any two individuals for a given loci (Ahmad *et al.*, 2010). The strategies used in maize breeding programs are frequently characterized by a decrease of genetic diversity in the pool of germplasms and an increase in the genetic evenness in cereal production (Lee, 1998; Morales *et al.*, 2010). This might cause important problems, particularly sensitivity to new diseases and/or a decreased tolerance to high temperatures or drought (Duvick, 1989). Genetic knowledge of germplasm diversity among local populations has a significant impact on the improvement of plants, not only on a valuable source of useful traits but also on a bank of highly adapted genotypes (Barcaccia *et al.*, 2003). DNA polymorphism assays are powerful tools for characterizing and studying germplasm resources (Powell *et al.*, 1996; Okumus, 2007). The knowledge of genetic diversity and relationships among flint inbred lines would help reduce genetic vulnerability and broaden the genetic base of crops in national improvement programs (Hallauer *et al.*, 1988; Morales *et al.*, 2010). In Cameroon, several inbred lines and others maize varieties have been developed at the Institute of

Agricultural Research for Development showing different level of tolerance to some environmental stresses. For instance the ATP SR Y which is the Acid Tolerant Population developed (The *et al*., 2000), released and commercialized so far.

2. 7 Participatory breeding

The rapid rural appraisal (RRA) has spread since its development in the 1980s and has evolved into participatory rural appraisal (PRA) in the 1990s (Chambers, 1994). Worldwide, participatory rural appraisals (PRAs) have been used to solicit farmers' views on various agricultural resource management options necessary to ensure household food security and improvement in their welfare (Chambers, 1992). PRA describes a growing family of approaches and methods to enable local people to share and analyze their knowledge of life and conditions, to plan and to act (Chambers, 1992). Over the past years, several local varieties have been developed by breeders that have been reported to possess some level of resistance to ear rots (Schjøth *et al.*, 2008; Mukanga *et al.*, 2011). Participatory methods include mapping and modeling, transect walks, matrix scoring, seasonal calendars, trend and change analysis, well-being, wealth ranking and grouping, and analytical diagramming (Chambers, 1994). Understanding the maize production constraints could be useful in designing an effective breeding program that does not only incorporates the constraints but improves other agronomic traits as well (Mukanga *et al.*, 2011). Odendo *et al*. (2002) used PRA to solicit farmers' views on the selection of varieties they planted, and reported that earliness and high yield were the most important traits to farmers. Similarly, Nkongolo *et al*. (2008) also used farmer participatory tools to access farmers' indigenous knowledge of the major characteristics of sorghum landraces and reported that farmer characterization of sorghum varieties had allowed for the selection of landraces that had outperformed already existing varieties.

In the North and Extreme North province of Cameroon, the rural appraisal survey on the basis of the following aspects, crop and livestock husbandry, land, labor and climatic conditions revealed that, with high population growth and large numbers of rainfall deficit years have encouraged intensification of arable farming and heightened the competition between grazing and cropping systems (Kenga *et al.*, 2002). Cameroonian population lives in the rural environment where agriculture is the main activity (Etoundi and Dia, 2008). Products from the agricultural activities serve for on-farm consumption and source of income (Manu *et al.*, 2014).

CHAPTER THREE

3.0 FARMERS' PERCEPTION ON MAIZE PRODUCTION IN THE HUMID FOREST AREA OF CAMEROON

3.1 Introduction

Maize productivity in sub-Saharan Africa as in Cameroon is low due to the variable production environment, stress and limited access to essential inputs (Banziger and Meyer, 2002). Maize (*Zea mays* L.) production in Cameroon is mainly in the hands of resource-poor farmers. Poor scale farmers grow the crop in highly variable and stress-prone environments (Banziger and Meyer, 2002).

It is believed that some better cultivars have not been adopted even when available because farmers' preferences were generally not considered in the breeding process. In most cases, commercial breeders fail to consider the special and unique preferences of small-scale farmers in rural areas, possibly because breeders are not aware of them (Banziger and Cooper, 2001; Derera, 2007). According to (Bänziger *et al.*, 2004), regional programs have a tendency to focus their breeding goals on the requirements of the commercial farming sector. Effective breeding should be based on clear identification of farmers' perceived constraints and their preferences for cultivars through interactive breeding and research. Most of the breeders have focused more on increasing yields in control, agronomically well-managed conditions and farmers perceive little advantage in growing these varieties because they are not designed for their needs (Reeves and Cassaday, 2002) and sometime because they are not aware on the existence of the improved variety. For effective breeding, farmers' preferences for varieties should be clearly identified through researcher-farmer interaction and collaboration (Sibiya *et al.*, 2013). As breeders involve farmers in their breeding programs, they learn more about the most important selection criteria of male and female farmers for the cultivars preferred in the rural cropping systems environments (Danial *et al.*, 2007). This encourages the use of locally adapted cultivars resulting in less dependence on foreign materials. Such a strategy has resulted in selection and development of new wheat, barley, common bean, quinoa, potato and maize cultivars in various part of the world (Danial *et al.*, 2007). It has therefore become clear that breeders must be well acquainted with the farmer preferences such as the requirements for specific agronomic, storage, processing and marketing traits if adoption rate is expected to be high (Danial *et al.*, 2007).

The Bimodal Humid Forest Zone (BHFZ) of Cameroon has in the recent past seen the integration of maize into the cropping system. This has largely been due to the high demand for the crop especially the fresh green cob in the administrative capital, Yaoundé, and the high return on the crop per unit area compared to the traditional root crops. However most of the soils in this zone are acidic, decreasing the yields (Njomgang *et al.*, 2010). The Acid Tolerant Population (ATP) introduced to the area decreases in yield when grown in the acid soils (The *et al.*, 2006). With the farmers' inability to correct acidity of the soils by applying agricultural lime, it has become imperative to develop acid tolerant hybrids which are also high-yielding. These hybrid varieties must have the ability of growing well in terms of yield stability in most of the soils of the BHFZ. To develop successful hybrids, it is necessary for the researcher to identify the farmers' preferences in terms of their ideal maize variety and also their specific needs vis-à-vis the cropping of the crop.

A participatory rural appraisal (PRA) including focus group discussion in the South Region of Cameroon was carried out, the objectives were to:

- Elucidate farmer perceptions on maize cultivars
- Identify farmers' needs and constraints on maize production
- Solicit suggestions and interventions for promoting sustainable production of maize.

3.2 Materials and Methods

3.2.1 Study site

The study was conducted in the Bimodal Humid Forest Zone (BHFZ) of Cameroon which covered three regions out of 10 in the country. Five villages (Asso'osseng, Biyeyem, Djop, Ndengue and Nkoemvone) were inveolved in the study. Annual rainfall is 1800 mm with bimodal distribution (The *et al.*, 2001). The soils are Oxisols and typically Kandiudox. These soils are highly weathered and dominated by kaolinitic clay with high Aluminium (Al) toxicity (The *et al.*, 2005). The study site mainly has forest vegetation with mixed cropping as the main farming system. The crops grown include cocoa, maize, groundnut, cassava and yam. The villages were selected based on the possession of acidic nature of the soils and where maize is a mojor cereal crop cultivated there.

3.2.2 Sampling procedure and data collection

A multidisciplinary research team comprising of a Plant Breeder, (the principal investigator), a social scientist, a facilitator, an agricultural extension officer, three students at the Masters level from the University of Yaounde and SupAgro Institute of Montpellier, France.

The selection of the households within each of the five villages was done through random sampling of farmers who were cropping maize either as a sole crop or as a mixed crop in the studied area, their willingness and availability to cooperate with the research team. For the focus group discussion, 10 farmers were randomly selected from each of the five villages to form the main focus group of 50 people. These farmers were subdivided into five groups. For socio-cultural reasons, there were some men in the five villages who were not prepared to mix with their female counterparts for the focus group discussion. An entirely male group had to be created to serve their needs while the other four groups were a mixture of males and females. Contact was established with the group via telephone and or government zonal extension agent.

The focus group discussion was done using the format below as guidelines in developing a questionnaire:

- Introduction and purpose of the meeting
- Presentation of research team
- Presentation of the representative of farmers in the village
- Questions on farming system(s)
- Questions on crop production with more emphases on maize cropping
- Questions on the difficulties encountered in farming
- Questions on marketing, labor and expectations including other comments.

A recorder was discretely used during the group discussion to facilitate information gathering. In addition, illustrated charts were used to help elicit farmers' preferences, difficulties and their geographical location. The questionnaire was translated into local language to help farmer understanding. Occasionally, there was a need to use translators to clarify doubts. This was either done by a research team member or a participant from the farmers' group.

Although a leader guided the discussion, other scientists could intervene at any moment to particular information that may have been overlooked. The zonal extension agent was the key informant that took part in the discussion. He gave, when necessary, additional information for those farmers who were not able to provide. Care was taken to avoid people monopolizing the discussion because of their wealth status or their leadership role. Plate 3.1 shows some pictures of the focus group discussions.

Plate 3.1: Focus groups discussion at Ebolowa (a, b, c and d)

The group discussions involved listing of production constraints, varieties grown and identifying the preferred traits of maize cultivars. In the focus group discussions, individuals and group members would at times be asked to write their contributions before a group oral discussion. Additional relevant data were also collected from secondary sources which included published and unpublished literature about agriculture production in the study areas.

A structured questionnaire was prepared based on the information gathered from the focus group discussions. A questionnaire (Appendix 3.1) was drafted to elicit individual household information in each village. Individual interviews were used to assess thoughts, opinions, and feelings of individual farmers of the humid forest area of Cameroon during the period from April to May 2013. A total of 178 farmers were individually interviewed.

3.2.3 Data analysis

The qualitative data were analyzed using descriptive statistics to characterize the sample households in terms of different socioeconomic and biophysical features. While the quantitative data analyses were performed using least square means of the Statistical Package for Social Scientists (SPSS) version 17. Descriptive statistics, Stata software for modelization and mean comparisons were used for data collected in each village followed by comparisons among villages. Ranking, scoring and pair wise scoring were used in each of the focus groups.

3.3 Results

3.3.1 Focus group discussion

Farmers were randomly selected to list the five most pertinent problems of farming which were characterized (Table 3.1). The weight of each problem was estimated by attributing the coefficient 1 to 5 to the best five pertinent problems with the coefficient 5 attributed to the main difficulty encountered.

Farmers ranked change in weather as the most important constraint followed by post-harvest decay and weeds problems (Table 3.1). Pests and diseases were reported to be the least important (rank 10). All the constraints were grouped into biotic and abiotic problems (Figure 3.1). The expression of abiotic constraints was higher at Asso'ooseng, Nkoemvone, Ndjop and Ndengue.

Table 3. 1 : Farmers' production constraints and their classification in order of priorities

Problem	Weight	Ranking
Change in weather	22	1
Conservation problem (post-harvest problem)	17	2
Weeds control	13	3
Market problem	12	4
Maize shelling problem	10	5
Poor soils (set-aside)	**9**	**6**
High cost and lack of fertilizers	9	7
Field road management problem (infrastructure problem)	5	8
Unawareness on improved and adapted seeds	5	9
Pests and diseases	3	10

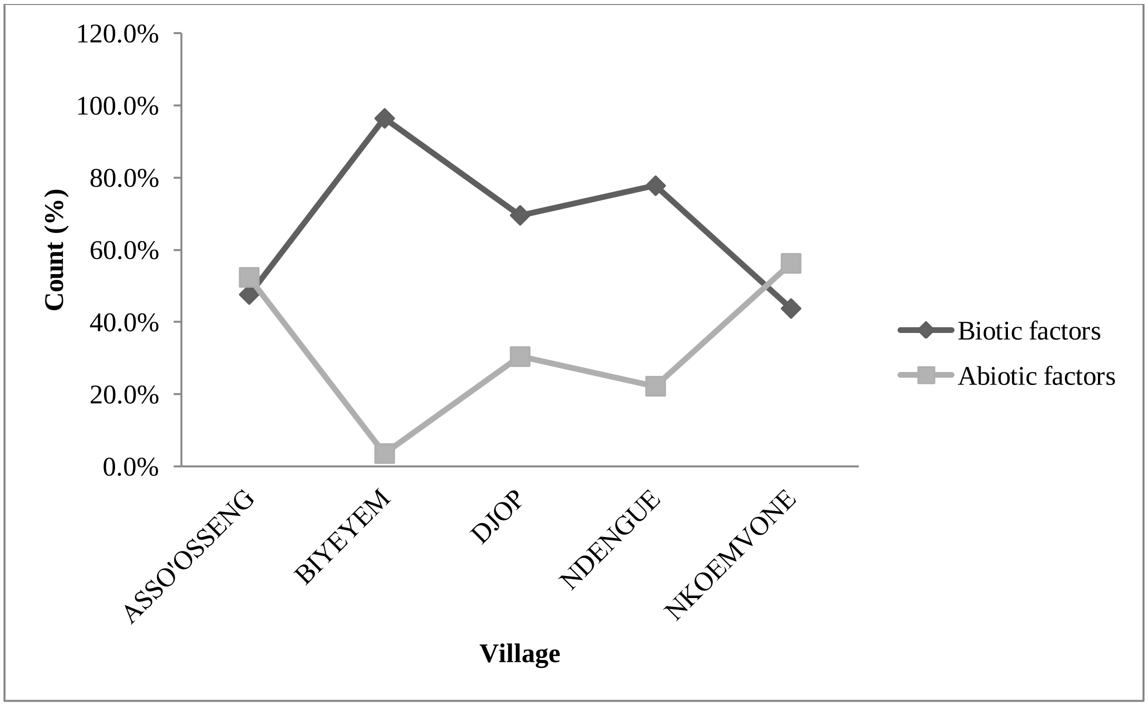
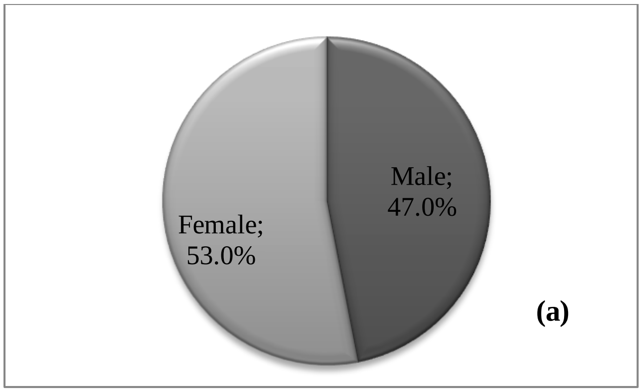


Figure 3.1: Major constraints to maize production

3.3.2 Individual interviews

3.3.2.1 Farmer characteristics

The sample of farmers from Ebolowa was composed of 53% women and 47% of men. At individual village level, there were more women than men in Asso'osseng and Djop (Figure 3.2).



Farmers' distribution according to gender (a)

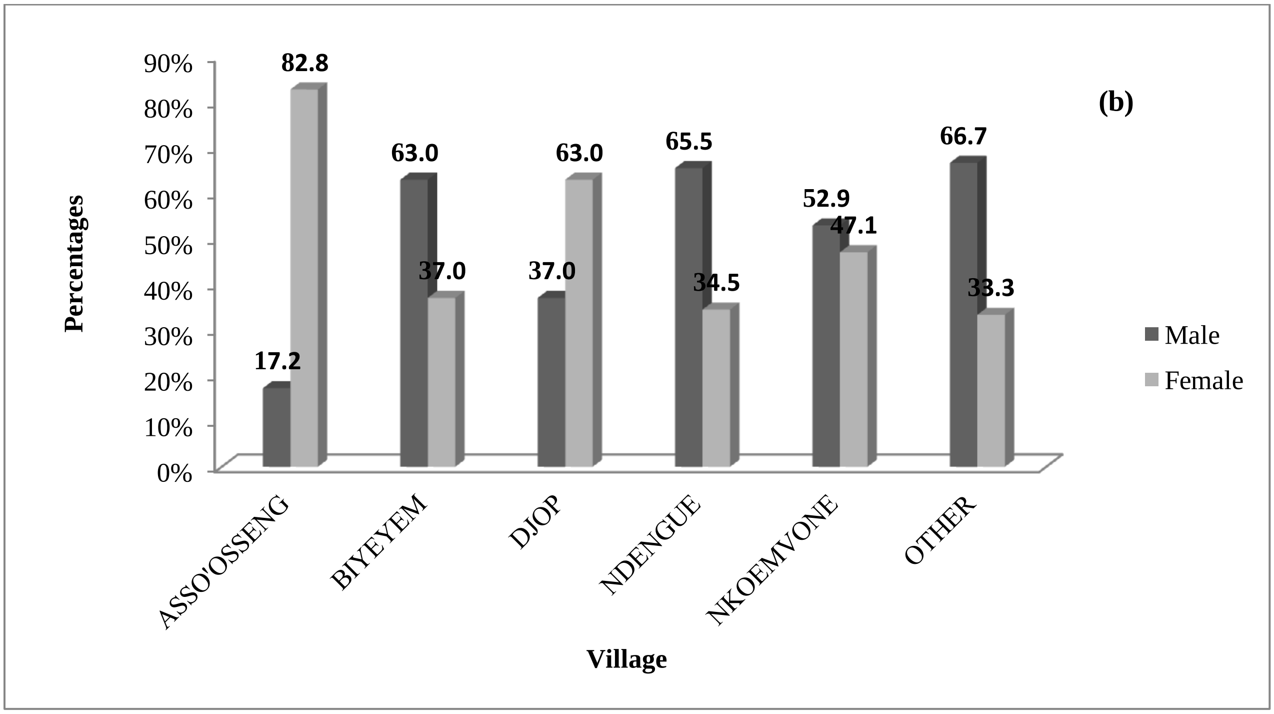


Figure 3.2: Farmers' distribution according to gender (a); and gender per village (b)

Farmers were also classified according to their age per village and to their level of schooling (Table 3.2). Many (43.8%) farmers were between 31 – 45 years old while 34.4% of farmers were between 46-65 years old. At Biyeyem, there were no farmers less than 30 years and over 65 years old. The highest level of study achieved by farmers was secondary school and 56.9% of them had reached that level (Table 3.3). None of the female farmers reached the tertiary school.

Table 3.2: Farmers' distribution according to the age per village (%)

Characteristics	**Villages**					
	Asso'osseng	**Biyeyem**	**Djop**	**Ndengue**	**Nkoemvone**	**Overall**
Age of farmer						
< 30 years	17.2	0.0	40.7	13.8	17.6	18.8
31 – 45 years	20.7	56.5	44.4	48.3	58.8	43.8
46 – 65 years	55.2	43.5	14.8	34.5	17.6	34.4
>65 years	6.9	0.0	0.0	3.4	5.9	3.1
Level of studies						
No formal education	10.3	4.0	0.0	10.3	0.0	5.4
Primary	51.7	16.0	51.9	34.5	23.5	36.2
Secondary	37.9	80.0	48.1	51.7	70.6	**56.9**
Tertiary (University)	0.0	0.0	0.0	3.4	5.9	1.5

Table 3.3: Farmers' characteristics according to the level of instruction per gender (%)

	Gender		
	Male	Female	Overall
Age of farmer			
< 30 years old	18.7	18.5	18.6
31 – 45 years old	50.5	43.2	47.1
46 – 65 years old	29.7	34.6	32.0
> 65 years old	1.1	3.7	2.3
Level of studies			
No formal education	4.3	3.7	4.0
Primary	22.8	42.7	32.2
Secondary	63.0	53.7	58.6
Tertiary (University)	9.8	0.0	5.2

The chi square ($\chi 2$) of age of farmer was significant at 5% while the chi square of the level of studies of farmer was significant at 1% (Table 3.4).

Table 3.4: Chi square of some characters coming from the survey

	Farmer sex				
	df	χ^2 cal.	χ^2 read	P-value	Significance
Age of farmer	3	7.82	7.82	0.05	*
Level of education	3	14.26	7.82	0.003	**

**: significant at 5%; **: significant at 1%* *Independence: The null hypothesis is that the response category is independent of the treatment group. The alternate hypothesis is that there is some sort of (ill defined) association.*

3.3.2.2 Farmers activities

The main activity practiced in all the five villages was agriculture involving 178 farmers (Figure 3.3). The distribution of farmers based on their main activity per village (Table 3.5). At Asso'osseng and Nkoemvone, 2.4% and 17.9% of farmers were temporary workers in the Research Institute. Few of them manage small businesses (2.4% at Asso'osseng, 3.3% at Ndengue and 7.7% at Nkoemvone) while most of them farmed (Table 3.5).

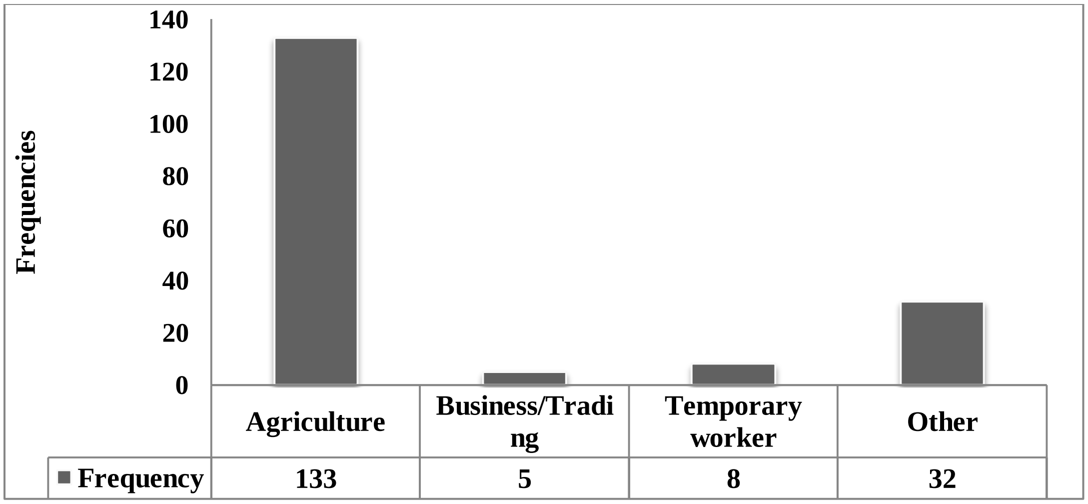


Figure 3.3: Sample distribution of farmers according to their main activity

Table 3.5: Sample distribution according to the main activity by village (%)

		Main activity				TOTAL
		Agriculture	Business/Trading	Temporary	Other	
VILLAGE	ASSO'OSSENG	70.7	2.4	2.4	24.4	100.0
	BIYEYEM	93.3	0.0	0.0	6.7	100.0
	DJOP	96.4	0.0	0.0	3.6	100.0
	NDENGUE	96.7	3.3	0.0	0.0	100.0
	NKOEMVONE	43.6	7.7	17.9	30.8	100.0
	OTHER	30.0	0.0	0.0	70.0	100.0
	ALL	**74.7**	**2.8**	**4.5**	**18.0**	**100.0**

3.3.2.3 Type of crops grown in different villages

There was a diversity of crops grown in the villages. Among them, maize, cassava, cocoyam (macabo), groundnut, cocoa and sweet potato were the most important (Figure 3.4). Rice and sorghum were not widely grown in that part of the country.

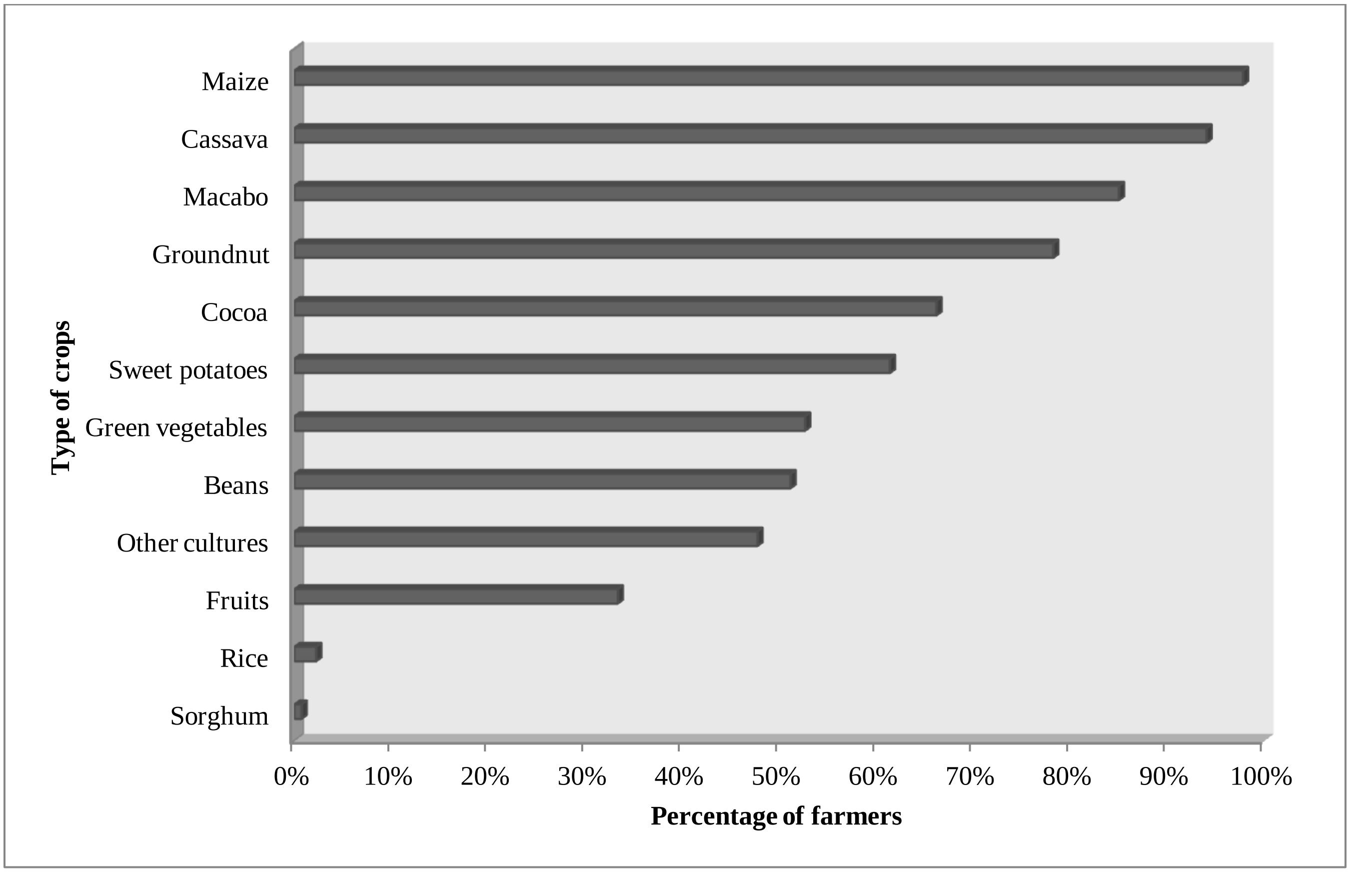


Figure 3.4: Distribution of farmers based on their village and the type of crop

The most important cereal produced in all the villages was maize with an average of 97.7% of farmers producing it. Only 3.4% of farmers grew rice at Asso'osseng, 3.4% at Ndengue and 5.9% at Nkoemvone. Sorghum was grown at Ndengue by 3.4% of farmers (Table 3.6). Vegetables as beans (51.1%), groundnut (78.2%) and green vegetables (52.6%) were produced.

Table 3.6: Farmers' distribution according to type of crops by village (%)

		Village						
		ASSO'OSSENG	BIYEYEM	DJOP	NDENGUE	NKOEMVONE	OTHER	**ALL**
Cereal	Maize	96.6	96.4	100.0	100.0	94.1	100.0	**97.7**
	Rice	3.4	0.0	0.0	3.4	5.9	0.0	**2.3**
	Sorghum	0.0	0.0	0.0	3.4	0.0	0.0	**0.8**
Vegetable	Beans	62.1	42.9	51.9	51.7	47.1	33.3	**51.1**
	Groundnut	79.3	35.7	88.9	100.0	88.2	100.0	**78.2**
	Green vegetables	75.9	7.1	59.3	69.0	52.9	33.3	**52.6**
Tuber	Cassava	93.1	89.3	92.6	96.6	100.0	100.0	**94.0**
	Sweet potatoes	69.0	33.3	55.6	89.7	64.7	0.0	**61.4**
	Macabo	93.1	71.4	96.3	89.7	76.5	33.3	**85.0**
Cocoa		65.5	57.1	55.6	93.1	58.8	33.3	**66.2**
Fruit		51.7	3.6	40.7	53.6	11.8	0.0	**33.3**
Other crops		58.6	46.4	11.5	72.4	52.9	0.0	**47.7**

3.3.2.4 Agricultural and production system used by farmers

In all the villages, most farmers (72.5%) practiced intercropping system (Table 3.7). Only 22.9% grew maize per field during a given agricultural season (69% of men and 31% of women) while 4.6% of farmers practiced relay cropping (100% of men) (Figure 3.5). In all the villages, farmers mainly practiced rain fed agriculture (94.5% of farmers) while few (4.7%) used irrigation system (Table 3.7).

Table 3.7: Agricultural system used and type of maize variety grown by farmers (%)

	Villages					
	Asso'osseng	**Biyeyem**	**Djop**	**Ndengue**	**Nkoemvone**	Total
System used						
Monoculture (maize only)	18.5	28.6	37.0	20.7	5.9	22.9
Intercropping	81.5	53.6	59.3	79.3	94.1	72.5
Relay cropping	0.0	17.9	3.7	0.0	0.0	4.6
Provenance of water for crop						
Rain	92.3	96.2	92.3	100.0	88.2	94.5
Irrigation	0.0	0.0	0.0	0.0	0.0	0.0
Rain and irrigation	0.0	3.8	0.0	0.0	0.0	0.8
Maize varieties grown						
ATP SR Y	17.2	3.6	7.4	0.0	14.3	7.8
CMS 8704	31.0	96.4	81.5	85.7	57.1	71.3
CMS 8501	44.8	10.7	11.1	0.0	21.4	17.1
CLH 101	10.3	0.0	18.5	0.0	7.1	7.0
CLH 103	0.0	0.0	3.8	0.0	7.1	2.3
Local variety	62.1	92.9	65.4	95.8	64.3	72.7
Other variety	11.1	0.0	0.0	0.0	46.7	16.4

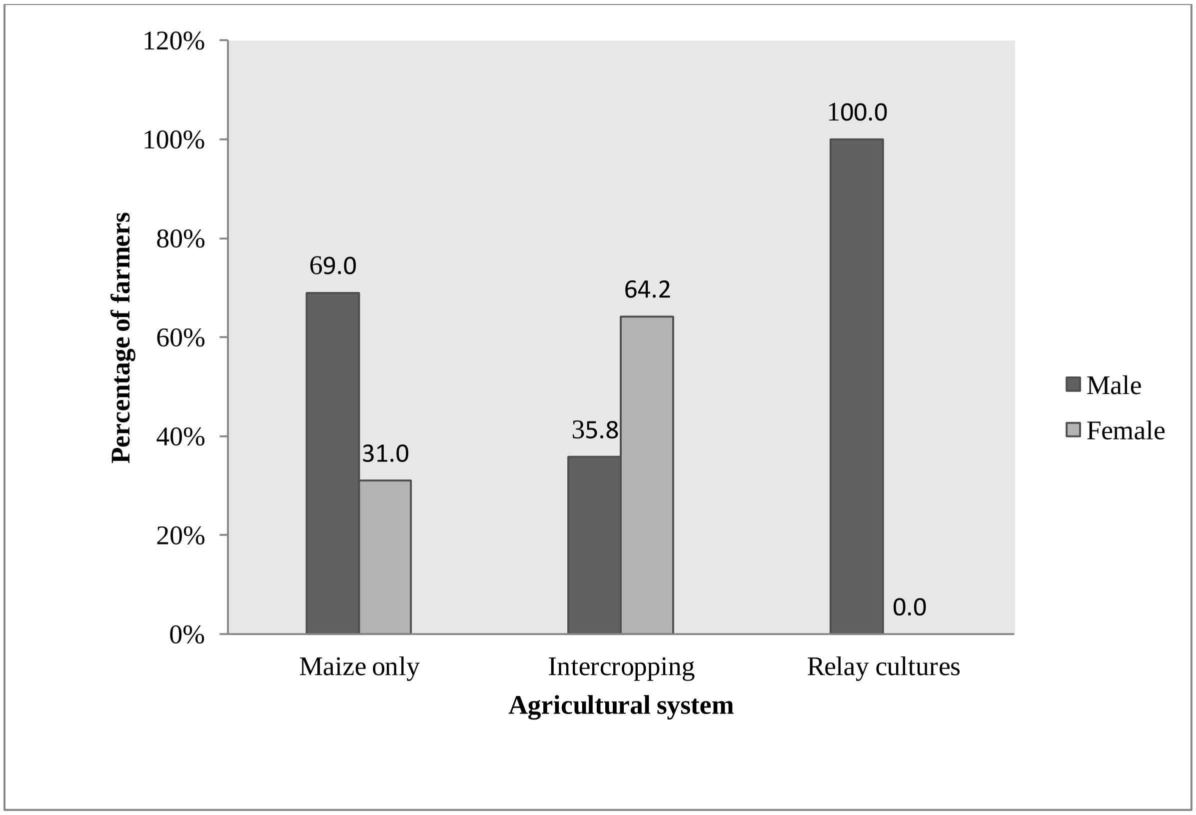


Figure 3.5: Farmers' distribution according to the agricultural system by gender

3. 3.2.5 Maize varieties used as seed

Some improved maize varieties developed at the Institute of Agricultural Research for Development (IRAD) were grown. Among them were the most acid tolerant population adapted in the South Region of the country (ATP SR Y). Most farmers preferred their local variety, compared to the improved genotypes (71.3% of farmers grew it). Few farmers (7.8%) grew the ATP SR Y (Table 3.7). Moreover at Ndengue village, 17.1% of farmers grew CMS 8501 which is a white open-pollinated variety. Most of the farmers did not grow the single cross hybrids like CLH 101(7% of the farmers) and CLH 103 (2.3% of the farmers) (Table 3.7).

3.3.2.6 Sources of maize seed

Almost sixty percent (60%) of farmers bought their seed from the local market, 37% of them used saved seeds and only 17% of farmers bought seed from the Research Institute (Table 3.8).

Table 3.8: Farmers' distribution according to the sources of seed (%)

		Seed's provenance		
		Research Institute (IRAD)	**Local Market**	**Personal seed**
VILLAGE	ASSO'OSSENG	10.7	39.3	53.6
	BIYEYEM	14.3	82.1	25.0
	DJOP	14.8	44.4	40.7
	NDENGUE	6.9	69.0	24.1
	NKOEMVONE	47.1	64.7	52.9
	OTHER	33.3	66.7	0.0
	ALL	**16.7**	**59.8**	**37.1**

3.2.2.7 Criteria that determine the choice of farmers' maize seed variety

Farmers chose their variety based on 3 criteria (Tables 3.9 and Table 3.10): the consumption purpose; the commercialization and the availability of seed. The best three criteria on maize seed preferences listed by farmers were: sweet taste (68.9%), high-yielding (72.6%) and seeds availability (50.9%). Most of the men (72.5%) preferred the sweet taste in maize and 66.1% of female preferred that trait (Table 3.10). More men (82.4%) preferred high-yielding varieties compared to females (64.3%). Similarly with availability of seeds, men (56.9%) were more concerned than females (44.6%).

Table 3.9: Farmers' seed selection criteria across villages

	VILLAGE				
	ASSO'OSSE NG	DJOP / BIYEYEM	NDENG UE	NKOEMVO NE	Overal l
Seed color	36.0%	31.3%	30.0%	58.3%	35.2%
High yield	42.3%	83.3%	80.0%	83.3%	72.6%
Sweet taste	42.3%	77.1%	70.0%	91.7%	68.9%
Good adaptation	11.5%	10.4%	75.0%	58.3%	28.3%
Pest and disease resistant	30.8%	20.8%	80.0%	33.3%	35.8%
Kernel size	15.4%	6.3%	35.0%	41.7%	17.9%
Early maturity	34.6%	27.1%	70.0%	58.3%	40.6%
Seed availability	30.8%	50.0%	75.0%	58.3%	50.9%
Grain quality	11.5%	29.2%	65.0%	50.0%	34.0%

Table 3.2: Farmers' seed selection criteria based on gender

	Gender					
	Male		Female		ALL	
	Number	%	Number	%	Number	%
Seed color	15	29.4	23	41.8	38	35.8
High yield	42	82.4	36	64.3	78	72.9
Good taste (sweet tasting)	37	72.5	37	66.1	74	69.2
High yield under non fertile soils	17	33.3	13	23.2	30	28.0
Pests and diseases resistant	16	31.4	22	39.3	38	35.5
Good size of grain produce	9	17.6	10	17.9	19	17.8
Late variety	3	5.9	5	8.9	8	7.5
Early variety	22	43.1	22	39.3	44	41.1
Seed availability	29	56.9	25	44.6	54	50.5
Grain quality produce	18	35.3	19	33.9	37	34.6
Other	6	11.8	4	7.1	10	9.3

3.3.2.8 Farmers view about soil fertility on their farms

During the individual interviews, a question was asked about the view of farmers concerning the fertility of the soil in the village (Table 3.11). Almost sixty-four percent (64%) of the farmers responded that they had fertile soil while 23% of farmers reported that the soil on their farms was not fertile and only 13% of them with 18% of the female farmers and 7% of male farmers did not know the status of their soil (Table 3.12).

Table 3.11: Farmers' views about soil fertility on their farms based on gender

	Gender					
	Male		Female		ALL	
	Number	%	Number	%	Number	%
Do you have fertile soil?						
Yes	39	69.6	39	59.1	78	63.9
No	13	23.2	15	22.7	28	23.0
Don't know	4	7.1	12	18.2	16	13.1
Strategies used to overcome soil infertility						
Lying fallow	38	79.2	46	83.6	84	81.6
Chemical fertilizer	12	25.0	8	14.5	20	19.4
Organic fertilizer	3	6.3	5	9.1	8	7.8
Improved variety	6	12.5	5	9.1	11	10.7
Other	5	10.4	6	10.9	11	10.7
Uses of maize						
Consumption	/	21.7	/	25.0	/	23.3
Commercialization	/	40.2	/	35.0	/	37.8
Other	/	38.0	/	40.0	/	39.0

Table 3.12: Farmers' views about soil fertility and their coping strategies across villages

	VILLAGE						ALL
	ASSO'OSSENG	BIYEYEM	DJOP	NDENGUE	NKOEMVONE	OTHER	
Do you have fertile soil?							
Yes	28.6	87.5	81.8	86.2	41.2	0.0	64.2
No	50.0	12.5	18.2	6.9	23.5	33.3	22.8
Don't know	21.4	0.0	0.0	6.9	35.3	66.7	13.0
Strategies							
Lying fallow	62.5	100.0	88.0	96.0	50.0	50.0	81.6
Chemical fertilizer	33.3	5.9	4.0	4.0	70.0	100.0	19.4
Organic fertilizer	20.8	0.0	4.0	0.0	20.0	0.0	7.8
Improved variety	25.0	0.0	4.0	0.0	40.0	0.0	10.7

3.3.2.9 Strategies used by farmers to overcome poor soil fertility

To overcome the problem of soil infertility, 82% of farmers practiced fallow system of cropping (Table 3.12). At Biyeyem and Ndengue, farmers did not use organic fertilizer but a high rate of organic fertilizer was applied at Asso'osseng (20.8%) and Nkoemvone (20.0%). Chemical fertilizer was highly used at Nkoemvone (70.0%).

3.3.2.10 Uses of products from the farm

Farmers mainly grew maize for home consumption, for commercialization and for other use like animal feed. Therefore, 23% of farmers produced maize for consumption, 38% of them produced for commercialization and 39% produced for other uses (Table 3.11).

3.3.2.11 Advice received by farmers on agricultural techniques

Forty-six percent of farmers (46%) received advice from the Research Institute (IRAD) which is located at Nkoemvone, Non-Governmental Organizations (NGO) and the Tertiary education level (Table 3.13). However, 34% of farmers received advice from the ministry (MINADER) while 35% of farmers received their advice from friends and other farmers.

Table 3.13: Origin of advises received by farmers based on village

		MINADER (post officer, …)	IRAD / NGO / universities	Development agencies (PACA, IITA, CIRAD, ICRAF…)	Friend (other farmers / growers)	Media and other
VILLAGE	ASSO'OSSENG	28.6	52.4	15.0	45.0	5.0
	BIYEYEM	47.6	52.4	4.8	28.6	4.8
	DJOP	50.0	12.5	25.0	12.5	0.0
	NDENGUE	38.1	14.3	4.8	42.9	4.8
	NKOEMVONE	21.4	64.3	7.1	35.7	3.6
	OTHER	28.6	71.4	42.9	28.6	0.0
	ALL	34.0	46.2	11.4	35.2	3.8

3.3.2.12 Information needed by farmers to enhance their productivity

To improve the production per unit area of cropping land, 52% farmers needed information on soil fertility management, 62% of farmers needed information on crop diseases and pest damages, 34% on marketing, 58% on credit and 70% needed information on finance and improved seeds (Table 3.14).

Table 3.14: Information needed by farmers to improve their production per gender

	Gender:					
	Male		Female		ALL	
	Number	%	Number	%	Number	%
Soil fertility management	45	48.9	40	54.8	85	51.5
Crop diseases and pests	53	57.6	50	68.5	103	62.4
Marketing	37	40.2	19	26.0	56	33.9
Credit and finance	59	64.1	36	49.3	95	57.6
Improved seed	67	72.8	48	65.8	115	69.7
Other information	2	2.2	1	1.4	3	1.8

3.4 Discussion

Poor soil fertility was among the six best problems listed by farmers in the BHFZ. According to Njomgang *et al.* (2010), soil acidity is a major constraint in the humid forest area of Cameroon and this acidity is mainly due to Al toxicity. The soils in this region are of poor fertility due to a combination of Al toxicity and deficits caused by leaching or decreased availability of P, Ca, Mg and some other micronutrients, especially Mo, Zn and B (Gupta *et al.*, 2013). As a consequence, the productivity of the crop is reduced significantly. Farmers mentioned the change of weather among the major problems facing. The weather has become unpredictable. The raining seasons are no more following exactly the calendar of cropping seasons. This is a general constraint affecting the world and is not specific to the study environment.

In the present research, 47% of farmers were between 31 to 45 years old followed by 32% of them between 46 to 65 years old indicating that young people were involved in agricultural activities. This result might be because of the 1990's economic crises in Cameroon, which made the Government to reduce by half the number of youth employed. Consequently, most of these youths had become self-employed and agriculture, especially maize production, was one of their target areas because of the wide consumption of the crop. Additionally, about 55% of the Cameroonian population lives in the rural environment with agriculture as main activity (Etoundi and Dia, 2008).

In the present study, 59% of farmers reached the secondary school while only 4% were found not to be educated at all. The government policy in the country is to provide education to everyone. The primary and secondary schools were built in almost all the villages which are far from the towns. The public primary school is free of charge to children allowing resource constraint families to send their children to school. This reflects the level of education observed among the farmers. Male farmers were more educated than female meaning that girls stopped going to school very early and started with the farming activity especially when they gave birth. The female farmers started farming earlier than males and stopped during their old age (after 65 years) while most men stopped early (when they are 46 to 65 years old). The age and the level of study of farmers in the survey area depend on their gender. More women were involved in farming than men in this region of the country. This could be explained by a higher number of women than men in those areas. This result matched with those of Ayuk and Arrey (2003) on the size of population which was approximately 16.5 million inhabitants, 51% was composed of women and only 49% of men. Among women, 65% of them lived in the rural areas.

The principal crops produced in most of the villages were: maize, cassava, macabo, groundnut, cocoa, sweet potato, green leaves, beans, other crops (such as plantain, banana, yam, pepper), fruits, rice and sorghum. This result is similar to that of Pamo (2008) which stated that subsistence food crops grown in the Southern Region were comprised of taro, yams, cassava, rice, banana, plantain, maize, potatoes, roots and tubers, avocado, beans, okra, and were traded largely outside the cash economy. Farmers were forced to abandon cocoa or coffee plantations for other income – generating opportunities such as food crops (Ngo Nkot *et al.*, 2013). Among the cereals produced, maize is the most important (98%) and has become one of their cash crops.

The agricultural system used by smallholders was based on traditional slash-and-burn agriculture or shift cropping. In this system, farmers slashed the forest vegetation, burned the biomass and then cropped before abandoning the land to fallow. According to Degrande and Duguma (2000) and Asaah *et al*. (2011), the length of the fallow varied from about three years in high population areas with relatively fertile soils to over ten years where population density was low and soil acidity was a major constraint. This technique improved the nutrients elements of plants in the soil. The problems of low productivity and food security had been attributed to slash and burn cropping systems (Kotto-Same *et al.*, 2000). The change in land covered impacts the exchange of water and energy between the soil, vegetation and the atmosphere. These changes can alter atmospheric circulation and thermodynamics, affecting rainfall patterns and surface temperatures.

In the present study, farmers first preferred their local maize landraces "*Obeng bo'o and Zole*", because of the good taste and smooth grain, but they recognized that those local varieties had long period of maturity with low yield per hectare estimated at 0.8 t/ha (ACDIC, 2014). They liked hybrids mostly for commercial purpose. Up to now, 73% of the farmers prefer to grow their local variety compared to the improved variety (71.3% of CMS 8704 and 7.8% farmers grow ATP SR Y). One of the reasons explaining the negative effect of the adoption of improved varieties was their custom also because older farmers tend to stick to their old production techniques and were usually less willing to accept change. Similar result was reported by Kafle (2010). In the present study, young people were associated with a higher risk-taking behavior than the elderly. Therefore, they could easily accept change and adopt improved varieties if these varieties are available. Some farmers did not produce the improved maize variety especially the acid tolerant composite ATP SR Y which was the most adapted to the area. This was because of the non-availability of the seeds. Moreover, the sweet tasting quality of the OPV (CMS 8704) was why some of the farmers grow this improved variety. Because of the sweetness, the cobs were sold when fresh, boiled or roasted. Additionally, farmers usually eat or sale fresh maize because of the post-conservation challenges. This was because of the high moisture in dried maize which is due to the water content in the air in the humid forest zone, the conservation of dried maize becomes therefore difficult to handle.

The bimodal humid forest zone of Cameroon experiences a very high rainfall regime. The huge quantity of water is washed away the soil surface or deep into the soil profile. In the process, water washes away almost all the essential plant nutrients (Ca, K, P, Mg) from the soil increasing the level of Al toxicity in the soil. This was one of the main causes of Al toxicity in that region. Farmers did not know much about the fertility of their soil even though they used some agricultural systems (like shifting cultivation, intercropping, fallow) to overcome the problem of soil infertility, pests and diseases management and weed control. Similarly, Gegrande and

Diguma (2000) reported that farmers in the humid lowland zone of Cameroon did not perceive soil fertility to be a major problem on their land because of their ignorance.

At the beginning of the agricultural campaign, most of the farmers bought maize seeds from the local market, some of them used the remnant seeds or the seeds that they kept from the previous season, and few farmers bought their seeds from the Research Institute when available. Meanwhile, most farmers could use improved seeds if they were aware of their existence and if the seeds were available and largely spread in the market. This could be the role of the seed companies which are not yet spread in the country. Farmers (95%) predominantly grew maize and they displayed strong preferences for local varieties due to their perceived superior quality traits such as grain size, good taste and white flour. This implied that breeding for acid tolerance should aim at developing maize cultivars that will not be only acid tolerant but also possess farmer's preferred traits. Additionally, the use of improved variety will make the yield increase compared to the utilization of the local variety. Therefore, the practice of good agricultural system and the use of improved seed will make maize yield increase significantly and will raise farmers' income considerably.

3.5 Conclusions

This study examined small – scale farmers' perceptions on maize varieties, production constraints, and preferences for stress tolerant improved cultivars. The results show that many young people were involved in farming activity. Farmers usually grew maize for home use and for sale. They produced maize as a source of income. Whereas maize production is facing different constraints in the region including the problem of low production per unit area, low soil fertility, high cost of fertilizers, post-harvest conservation of maize and weeds control are prevalent. The practice of appropriate agricultural system associated with the utilization of improved and adapted varieties could significantly increase the yield of maize under farmer field area. Smallholder farmers in that area of the country prefer high-yielding maize varieties tolerant to low soil fertility, which produce good quality grain, soft and sweet tasting, and which are pests and diseases resistant with short maturation period if possible. If such hybrid maize could be developed by breeders, farmers would be willing to adopt it.

CHAPTER FOUR

4.0 MORPHOLOGICAL AND MOLECULAR CHARACTERIZATION OF SELECTED MAIZE (*Zea mays* L.) INBRED LINES UNDER ACID SOIL CONDITIONS

4.1 Introduction

Maize (*Zea mays* L.) is cropped in a wider range of conditions than wheat and rice because of its greater adaptability (Udaykumar *et al.*, 2013). Several million people in the developing world consume maize as a staple food deriving their protein and energy requirements from it (Yadav and Singh, 2010). Concerted and intensive efforts are required to develop climate-change-resilient maize cultivars while accelerating the yield growth, without which the outcome will be hunger and food insecurity for millions of poor consumers of maize (Prasanna, 2012). Maize has enormous genetic diversity that offers incredible opportunities for genetic enhancement despite the environmental challenges. There is no lack of favorable alleles in the global maize germplasm that contribute to higher yield, abiotic stress tolerance, disease resistance or nutritional quality improvement. However, these desirable alleles are often scattered over a wide array of landraces or populations (Prasanna, 2012).

Different methodologies have been used to characterize genetic diversity in the maize germplasm including morphological characters, pedigree analysis, heterosis and the detection of variation at the DNA level using markers (Udaykumar *et al.*, 2013). The advent of molecular genetics has enhanced selection accuracy for quantitative traits by incorporating molecular information into genetic improvement programs (Tang and Li, 2006). Analysis of genetic diversity and of relationships among the elite breeding materials can significantly aid in crop improvement. In maize, this information is useful in planning for hybrid and line development, assigning lines to heterotic groups and in plant variety protection (Yuan *et al.*, 2002; Yadav and Singh, 2010).

In the recent past, there has been an increase in the cultivation of maize in the Humid Forest zone of Cameroon. This zone had hither to been put to tree crop cultivation due to the high rainfall. The acidic nature of the zone is, however, a limiting factor to the production of the crop as yield is always sub optimal. To increase the livelihood of farmers in the zone and to minimize deforestation, it has become necessary to intensify the production of the crop by increasing output per unit area. This has called for breeding techniques which focus on varieties which will be adapted to the acid soils and not necessarily amending the soils to increase pH to the optimal range, There must therefore, be a concerted effort to improve on inbred lines for the Humid forest zone of Cameroon. Morphological and molecular studies of inbred lines have not yet been undertaken under acid soils of the Humid Forest Zone of country. For an effective and efficient national maize breeding program in the Cameroon, there is an urgent need to gather useful information in this regard.

The objectives of the present study were to:

- Assess maize inbred lines for variation in morphological traits
- Assess maize inbred lines for variation in molecular traits.

4.2 Materials and methods

4.2.1 Morphological characterization

4.2.1.1 Plant material

On station evaluation of thirty inbred lines were carried out in native acid soil at Nkoemvone from 2013 to 2014 cropping season. Fourteen of these lines came from CIMMYT, three from IITA and the other thirteen from the Institute of Agricultural Research for Development (IRAD). The origin of these lines and their respective unique characteristics are presented in Table 4 1.

Table 4.1: Maize inbred lines used in the study

Lines	Code	Origin	Characteristics
4001	1	IITA	Tolerant to low N
88069	2	IRAD	Good root volume
9450 (1)	3	IITA	Temperate adapted
ATP 32	4	IRAD	Acid soil tolerant
ATP 50	5	IRAD	Acid soil tolerant
ATP S5 31Y - 2	6	IRAD	Acid soil tolerant
ATP S6 20Y - 1	7	IRAD	Acid soil tolerant
ATP S6 31Y-2	8	IRAD	Acid soil tolerant
ATP S6 31Y-BB	9	IRAD	Acid soil tolerant
ATP S8 26Y - 2	10	IRAD	Acid soil tolerant
ATP S8 30Y - 2	11	IRAD	Acid soil tolerant
ATP S9 30Y - 1	12	IRAD	Acid soil tolerant
ATP S9 36Y - 1	13	IRAD	Acid soil tolerant
CI gp1 17	14	IRAD	Tolerant and P efficient
CI gp1 17 (F)	15	IRAD	/
CLA 135	16	CIMMYT	Susceptible
CLA 183	17	CIMMYT	Acid soil tolerant
CML 304	18	CIMMYT	Susceptible
CML 332	19	CIMMYT	Susceptible
CML 434	20	CIMMYT	Acid soil tolerant
CML 435	21	CIMMYT	Acid soil tolerant
CML 437	22	CIMMYT	Acid soil tolerant
CML 439	23	CIMMYT	Acid soil tolerant
CML 479	24	CIMMYT	Acid soil tolerant
CML 486	25	CIMMYT	Acid soil tolerant
CML 533	26	CIMMYT	Acid soil tolerant
CML 534	27	CIMMYT	Acid soil tolerant
CML 535	28	CIMMYT	Acid soil tolerant
D300-17	29	CIMMYT	Acid soil tolerant
KU 1414	30	IITA	Tolerant to low N

4.2.1.2 Physiography of experimental sites and field layout

The evaluations were carried out at one of the stations of IRAD at Nkoemvone in Ebolowa, the Southern Region of Cameroon. Nkoemvone village is located 25 km from the city of Ebolowa and, 180 km from the main research station at Yaounde. The altitude is 615 m above sea level with geographic coordinates of 12° 24 E, 2° 40 N (The *et al.*, 2006). The average temperature is 24 °C and the annual rainfall is 1800 mm with a bimodal distribution (The *et al.*, 2001). The soil has been classified as Kandiudox with high Al toxicity (The et al., 2001, 2005, 2006). At Ebolowa, soil is highly weathered and acidic with a soil pH in water of about 4.2 and saturation of 79.8%. In general, this tropical rainforest is dominated by nutrient-poor soils, in spite of the tremendous amount of forest biomass (Yemefack *et al.*, 2005). The main farming system is cocoa, maize, groundnut, cassava intercrop.

The inbred lines were evaluated at two locations in two seasons. After initial land preparation which involved stumping and ploughing, the genotypes were sown in the field in alpha lattice design (10 x 3). Each year, site and treatment (acid soil and control) was considered as one environment. Each genotype was planted in single row of 4 m long in two replications. Rows spacing was 0.75 m apart and the hill spacing on the same row was 0.50 m. Three seeds were planted per hill and 10 days after emergence, plants were thinned to 2 per hill for a total density of 53,333 plant/ha.

Weeds were controlled by the use of herbicides. The field trial received the recommended rate of fertilizer in split application, which consist of a basal dose of 37 N, 24 P_2O_5 and 14 K_2O kg/ha applied 7 days after planting and the remaining 126 kg N/ha applied 30 days after planting (The *et al.*, 2005).

4.2.1.3 Data collection

4.2.1.3.1 Morphological characterization of inbred lines

Data were recorded on number of days to anthesis (number of days when 50% of the plant in the experimental unit shade pollen), number of days to silking (number of days when 50% of the plants in the experimental unit show silk), plant height (cm), and ear height. Plant aspect was scored on a scale of 1 to 5 (with 1 being very good height, good ear height and good size) and 5 (being very poor height, very low or very high ear height, poor plant size), ear aspect (rated from 1 to 5 where 5 corresponded to the very bad aspect of grain and 1 to the very good ear aspect). Seed moisture content, plant stand at harvest, number of ears at harvest and grain yield was also taken. At harvest, grain yield (GY) was measured on a whole plot basis following standard CIMMYT procedure and was adjusted to 15% moisture using the formula below

GY (t/ha) = [Grain Weight (kg/plot) x 10 x (100-MC) / (100-15) / (Plot Area)]

Where MC = Grain Moisture Content (CIMMYT, 1985)

And plot area = row length * 0.75 (4*0.75 = 3m).

Vegetative plant data was taken outlined by the 'Descriptors for maize' (IBPGR, 1991): Rating of total leaf surface, number of leaves above the uppermost ear including ear leaf after milk stage, root lodging two weeks before harvest, stalk lodging two weeks before harvest, sheath pubescence at flowering, tassel type at milk stage (primary, primary-secondary and primary-secondary-tertiary), days to ear leaf senescence, total number of leaves per plant after flowering, leaf orientation after flowering (erect; pendant), presence of leaf ligule after flowering, (Present =1 and Absent =0), tassel size after milk stage (Small, Medium, Large).

After harvest, ear data were recorded using all ears on at least 20 representative plants per accession on: kernel row arrangement (regular, irregular, straight, spiral), kernel type (floury, semi-floury, with an external layer of hard endosperm, dent, semi-dent, intermediate between dent and flint but closer to dent, semi-flint, flint with a soft cap, flint, pop, sweet, opaque 2/QPM, tunicate, waxy), kernel color (white, yellow, purple, variegated, brown, orange, mottled, white cap, red), shape of upper surface of kernel (shrunken, indented, level, rounded, pointed, strongly pointed).

4.2.1.3.2 Molecular characterization of maize genotypes

Fresh leaf samples of 30 maize genotypes were collected, packed and sent in double wells per genotype to Laboratory of the Government Chemist (LGC) Genomics for genotyping. Young leaves were harvested from 14 day old seedlings from two plants per inbred line. Four samples of six millimeter leaf discs were taken from each inbred line and placed in a 96 well plate. The 96 well plates containing the leaf samples were sealed with a perforated heat seal and sent to LGC Genomic for genotyping. The sampling was carried out following the protocol of the Kbioscience leaf sampling kit. The genotyping was conducted using the KAPS method with 200 SNP markers. The details on the principle and procedure of the DNA assay are available at http://www.kbioscience.co.uk/reagents/KASP.

4.2.2 Data analysis

4.2.2.1 Morphological characterization

The analysis of variance (ANOVA) was performed using the PROC GLM in SAS version 9.2. The blocks were nested within replication by environments and replications within environments were treated as random factors and the genotype as fixed (Akinwale *et al.*, 2014). The statistical model used for the combined analysis is as follows:

$$Yijkg = \mu + Ei + Bk(ij) + Gg + EGig + \varepsilon ijkg$$

Where Yijkg is the observed measurement for the gth genotype grown in the environment i, in the block k in replicate j; μ is the; grand mean; Ei is the main effect of environment; Bk(ij) is the effect of block nested within replicate j by environment i; Gg is the effect of the genotype; EGig is the interaction effect between genotype and environment, and $\varepsilon ijkg$ is the error term.

A dendrogram was generated through Statistica 6 graphics software for field data.

4.2.2.2 Molecular characterization

DARwin5 software was used for the tree construction from the molecular markers and the factorial plots using field data results (http://darwin.cirad.fr/darwin).

4.3 Results

4.3.1. Morphological characterization of the tassel, silk and leaf of lines from IRAD

The characters were observed on each line at the flowering stage (Table 4.2). The tassel was mainly of the primary – secondary type (found in 80% of the lines), except for line ATP S6 31Y-2 which had primary type and ATP S6 31Y BB which had the primary – secondary – tertiary type (Table 4.2) The sheath pubescence was mainly intermediate except for ATP 32, ATP S6 31Y-2, ATP S9 36Y BB and 4001 which had dense sheath pubescence. Most of the tassels were reddish but some were greenish. Seven lines had large tassels while three lines (4001, ATP S8 30Y-2 and ATP S6 31Y BB) had medium tassel size and ATP 50 had small size of the tassel.

Four inbred lines had dense compact type of the tassel, two lines had dense semi-compact structure, three lines had dense spread structure, one line (ATP 50) had semi spread structure and Cam Inb gp1 17 had spread structure of the tassel. Eight lines had pendant leaf orientation whilst three lines (ATP 50, ATP S8 30Y-2 and ATP S9 36Y BB) had erect leaf orientation. Most of the silk were reddish while four lines had whitish green silks. Three lines (88069, ATP S9 30Y-1 and ATP S6 31Y BB) had the leaf ligules (Table 4.3).

Table 4.2: Morphological characteristics of maize genotypes

Genotype	Tassel type	Sheath pubescence	tassel color	Tassel size	silk color	Tassel criteria	Leaf orientation
ATP 32	Primary-secondary	Dense	reddish	Large	reddish	dense semi-compact	Pendant
ATP 50	Primary-secondary	Intermediate	reddish	Large	reddish	semi spread	Erect
ATP S6 31Y-2	Primary	Dense	whitish greenish	Small	reddish	dense spread	Pendant
ATP S6 31Y-BB	Primary-secondary	Intermediate	reddish	Medium	whitish	dense compact	Pendant
ATP S8 26Y-2	Primary-secondary-tertiary	Intermediate	greenish reddish	Large	whitish	dense spread	Pendant
ATP S8 30Y-2	Primary-secondary	Intermediate	reddish	Medium	reddish	dense compact	Erect
ATP S9 30Y-1	Primary-secondary	Intermediate	reddish	Large	reddish	semi-compact	Pendant
ATP S9 36Y-BB	Primary-secondary	Dense	whitish green	Large	whitish green	dense semi-compact	Erect
88069	Primary-secondary	Intermediate	reddish green	Large	whitish green	dense and spread	Pendant
Cam Inb gp1 17	Primary-secondary	Intermediate	whitish greenish	Large	whitish green	spread	Pendant
4001	Primary-secondary	Dense	greenish	Medium	reddish	dense compact	Pendant

Table 4.3: Other morphological characteristics of lines

Genotype	Presence of leaf ligules (1 if present and 0 if not)	Number of ramification of tassel		
		Primary	Secondary	Tertiary
ATP 32	0	11	2	1
ATP 50	0	10	2	1
ATP S6 31Y-2	0	9	2	0
ATP S6 31Y-BB	1	11	3	0
ATP S8 26Y-2	0	11	1	0
ATP S8 30Y-2	0	9	1	0
ATP S9 30Y-1	1	12	1	0
ATP S9 36Y-BB	0	13	2	0
88069	1	9	0	1
Cam Inb gp1 17	0	10	2	1
4001	0	8	3	0
Mean		10	2	0.4

4.3. 2 Kernel character of lines from IRAD

All the lines had yellow, flint kernels and with an indented shape on the upper surface (Table 4.4). The kernel arrangement of rows on the cob was regular for most of the lines, irregular for ATP S9 36Y BB, ATP S8 26Y-2 and ATP S6 31Y-2. The arrangement of kernels on the cob was spiral for 4001 (Table 4 4).

Table 4.4: Kernel characteristics of different inbred lines

Genotype	Kernel color	Kernel arrangement	Kernel type	Shape of upper surface of kernel
ATP 32	yellow	regular	flint	indented
ATP 50	yellow	regular	flint	indented
ATP S6 31Y-2	yellow	irregular	flint	indented
ATP S6 31Y-BB	yellow	regular	flint	indented
ATP S8 26Y-2	yellow	irregular	flint	indented
ATP S8 30Y-2	yellow	regular	flint	indented
ATP S9 30Y-1	yellow	irregular	flint	indented
ATP S9 36Y-BB	yellow	regular	flint	indented
88069	yellow	regular	flint	indented
Cam Inb gp1 17	yellow	regular	flint	indented
4001	yellow	spiral	flint	indented

4.3.3 Agronomic performance of inbred lines

4.3.3.1 Mean square of quantitative traits

The analysis of variance for the yield and other related traits for all the 30 inbred lines (inbred lines from IRAD, CIMMYT and IITA) showed highly significant differences ($P<0.001$) for yield, plant aspect, ear aspect, ears harvested, plants harvested, ear height, plant height and day to anthesis. The ears per plant was significant at $P<0.05$ while the days to silk, the anthesis-silking interval and the plant stand showed significant differences among genotypes at $P<0.01$ (Table 4.5).

Table 4.5: Analysis of variance for various quantitative traits in maize inbred lines

Source	df	Yield (t/ha)	pltasp	earasp	epp	earhar	pltha	Earhgt (cm)	Pltght (cm)	Asi (day)	Silk (day)	Anthe (day)	pltstd
Environment	3	6.4**	33***	23***	0.01NS	212***	311***	5381***	1420NS	113***	5811***	6299***	589***
Block (rep*envir)	9	2.6**	0.3 NS	1.1***	0.03 NS	19.5*	14.6 NS	231.5 NS	1085 NS	2.8 NS	23 NS	12 NS	21 NS
Genotype	29	4.1***	0.9***	1***	0.07*	31***	26***	517***	2291***	5**	32**	27***	26.8**
Geno x Envir	87	2.5***	0.4 NS	0.4NS	0.06*	23***	17**	224NS	836NS	2NS	13NS	11NS	17*
Error	108	1.2	0.36	0.3	0.04	10.8	9.7	190	620	2.7	16.5	8.7	11.8

Envir = environment, Geno = genotype (Inbred lines), df= degree of freedom, pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earght = ear height, pltght = plant height, asi = anthesis-silking interval, pltstd = plant stand, NS = non-significant, * = significant at P<0.05, ** = significant at P<0.01, *** = significant at P<0.001.

4.3.3.2 Mean performance of quantitative traits of lines under acid soil

The overall mean yield recorded was 1.4 t/ha (Table 4 6). Seven genotypes yielded more than the overall mean under acid soil condition: Cml 535, Cam Inb gp1 17 (F), ATP 50, ATP S8 26Y-2, ATP S6 31Y-BB, ATP S5 31Y-2 and 88069. The mean of the plant aspect and ear aspect were 3.1 and 2.9 respectively. One ear per plant was recorded for all the lines. The mean ear height of the lines was 70.6 cm with a mean plant height of 159 cm. The silk emergence averaged 68 days to come out while the average pollen shedding was 67 days.

Table 4.6: Mean values for quantitative traits recorded on maize lines grown on acid soils

Line	pltstd	Anthe	silk	Asi	plthght	earhgt	plthar	earhar	epp	earasp	pltasp	Yield (t/ha)
4001	7.8	67.6	68	1	141.9	72.5	7.9	8.3	1	3.4	3.6	1.4
4444	7.8	70.5	72	2	108.1	45.6	6.4	5.8	1	4.1	4.3	0.4
88069	9.3	70	72	2	116.3	62.5	7.5	6.8	1	3.6	3.5	1.7
9450	5.6	70.3	73	3	111.9	60	5.1	5.3	1	3.8	3.8	0.7
ATP S5 31Y-2	12.1	65.6	69	3	133.6	59.8	10.3	10.3	1	3.6	3.3	1.6
ATP S6 20Y-1	8.4	69.1	72	3	111.1	54.8	7.5	6.1	0.8	3.9	3.6	1.1
ATP S6 21Y-2	10	68.1	70	2	123.1	60	9	8.8	1	3.6	3.3	1
ATP S6 31Y-BB	11.8	63.8	66	2	151.9	80.6	11.1	9.3	0.8	3.1	2.9	3.1
ATP S8 26Y-2	8.9	67.1	70	3	140.5	66.3	8.3	7.3	0.8	3.5	3.3	1.5
ATP S8 30Y-3	7.8	67.1	70	3	114.6	66.3	7.1	6	0.9	3.9	3.5	1.1
ATP S9 30Y-1	7.8	64.9	66	1	154.4	69.4	6.9	6	0.9	3.1	3.5	1.2
ATP S9 36Y-BB	9.4	67.8	71	3	113.1	58.1	7	5.4	0.7	3.9	3.4	1
ATP-32	7.6	71.8	74	3	116.3	53.1	6.5	4.9	0.8	4.3	4.4	0.5
ATP-50	9.3	68.3	70	2	133.8	64.4	8.9	8.3	0.8	3.5	3.3	2.5
Cam Inb gp1 17 (F)	12.5	66.5	69	2	140.3	70	11.8	12	1	3.1	3.7	3.1
Cla 135	7.3	66.5	68	2	140.8	60	8.5	8.2	1	3.9	3.4	1.3
Cla 183	9.6	68.6	71	2	121.1	61.1	8.8	7.8	1	3.8	4	1.1
Cml 304	7.1	69.1	72	2	120.6	58.7	7.9	7.3	0.9	3.7	3.5	1.4
Cml 332	7.1	70.6	73	2	102.5	59.4	6.6	5.6	0.9	4.3	4	1
Cml 357	8	67.8	70	3	128.5	60.7	8.9	8.1	1	3.6	3.4	1.6
Cml 434	5.5	66.3	69	3	120.5	55	3.9	3.9	1	3.8	3.4	0.5
Cml 435	7.4	66.8	68	2	115.3	61.6	6.6	6.5	1.2	4.1	3.6	1.1
Cml 437	6.6	70.3	72	1	112.6	62.3	6	5.8	1	4	3.5	0.9
Cml 439	6.6	66.6	70	4	107.8	46.3	5.6	4.6	0.9	4.1	3.5	0.8
Cml 479	8.6	67.9	68	0	148.1	66.9	7.8	7.3	1	3.6	2.9	2.1
Cml 533	7.4	69	72	3	134	72.9	6.3	6.1	1	3.7	3.7	0.9
Cml 534	12	66.8	68	2	159.1	70.6	11.1	11.8	1.1	2.9	3.1	2.4
Cml 535	10.4	66.2	69	2	152	66.3	9.4	9.3	1	3.4	3.2	2.4
D300-17	8	69.7	72	3	94.3	45.6	7	6.5	0.9	3.8	3.5	1.2
Ku 1414	7.9	68.3	70	2	127.4	59.8	7.6	6.4	1	4	3.6	0.9
Mean	8.5	67.9	70	2	126.5	61.7	7.8	7.2	1	3.7	3.5	1.4
lsd	3.4	2.9	4	1.6	24.6	13.6	3	3.2	0.2	0.6	0.6	1.1

df= degree of freedom, pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earght = ear height, pltght = plant height, asi = anthesis-silking interval, pltstd = plant stand, lsd = least significant difference.

4.3.3.3 Correlation among agronomic traits

Yield was highly significant and positively correlated ($P < 0.01$) with plant stand, plant height, ear height, plants harvested, ears harvested and ears per plant. Moreover, it gave negative and highly significant correlation with ear aspect and plant aspect. It expressed negative and significant ($P < 0.05$) correlation with anthesis-silking interval. Yield had negative correlation with days to anthesis and days to silk but the correlation was not significant for any of the lines (Table 4.7).

Table 4.7: Correlation among agronomic traits

	pltstd	anthe	silk	asi	plthght	earght	plthar	earhar	epp	earasp	pltasp	Yield
pltstd												
anthe	-0.38**											
silk	-0.43**	0.98**										
asi	-0.27**	-0.10	0.07									
plthght	0.4**	-0.3**	-0.4**	-0.3**								
earght	0.30**	-0.5**	-0.5**	0.06	0.73**							
plthar	0.9**	-0.3**	-0.36**	-0.2**	0.43**	0.34**						
earhar	0.81**	-0.2**	-0.2**	-0.2**	0.44**	0.38**	0.9**					
epp	-0.03	0.026	0.01	-0.093	0.14	0.166*	0.003	0.36**				
earasp	-0.68**	0.57**	0.6**	0.27**	-0.58**	-0.47**	-0.6**	-0.6**	-0.13			
pltasp	-0.6**	0.741**	0.774**	0.17*	-0.4**	-0.4**	-0.6**	-0.5**	-0.1	0.8**		
Yield	0.616**	-0.03	-0.06	-0.17*	0.45**	0.37**	0.71**	0.83**	0.26**	-0.5**	-0.4**	

pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, earhar = ear harvested, pltha = plant harvested, earght = ear height, pltght = plant height, asi = anthesis-silking interval, pltstd = plant stand, * = significant at P<0.05, ** = significant at P<0.01.

4.3.3.4 Principal Component analysis

The first principal component explained 43.3% of the total variation among the genotypes while the second one accounted for 18.5%. The highest eigen value was 7.4 from the principal component 2 whilst PC1 gave 5.2 (Table 4.8 and Figure 4.1). Plant stand (pltstd), plants harvested (plthar), ears harvested (earhar), ear aspect (earasp), plant aspect (pltasp) and yield were the major discriminatory traits associated with PC I.

Table 4.8: Principal components (PCs) for multi-genic traits of maize genotypes

Traits	PC I	PC II
Eigen value	5.2	2.2
Cum. Eigen value	5.2	7.4
Total variance (%)	43.3	18.5
Cumulative variance	43.3	61.8
	Factor loadings	
	Factor 1	Factor 2
Pltstd	**0.82**	-0.36
Anthe	-0.65	-0.64
Silk	-0.66	-0.62
asi	-0.32	0.12
Plthght	0.52	0.32
earhgt	0.54	0.32
plthar	**0.82**	-0.43
earhar	**0.78**	-0.57
epp	0.03	-0.27
earasp	**-0.81**	-0.37
pltasp	**-0.80**	-0.07
Yield	**0.65**	-0.59

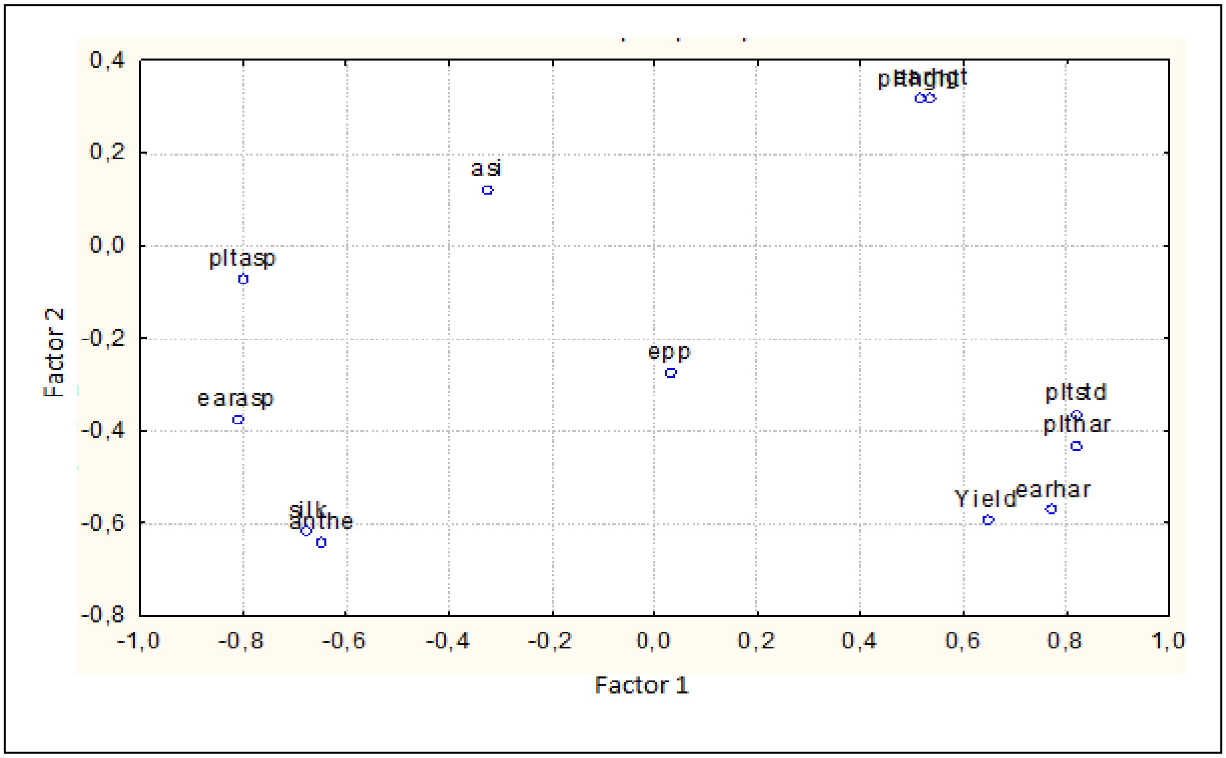


Figure 4.1: Scatter plot of the two factors extracted from the principal components.

4.3.3.5 Grouping of inbred lines based on field data

The mean value of 12 quantitative characters of 30 inbred lines was subjected to dissimilarity analysis. The matrix dendrogram was constructed to provide general view on the grouping of genotypes (Figure 4.2). The minimum genetic distance was recorded between Ku 1414 and ATP S9 36Y BB with a value of 0.00003 and the maximum was found between Cam Inb gp1 17 (F) and 4444 with a value of 3.55. Cluster analysis gave two major clusters (Table 4.9). The first major cluster was composed of three sub-clusters. The first sub-cluster contained 3 lines from IRAD and 4 introduced lines. The second sub-cluster had 3 lines from IRAD and 4 introduced lines. The third sub-cluster had 5 lines from IRAD and 5 introduced lines. The second major cluster contained 2 introduced inbred lines and 3 local lines. The introduced lines were distributed over the groups.

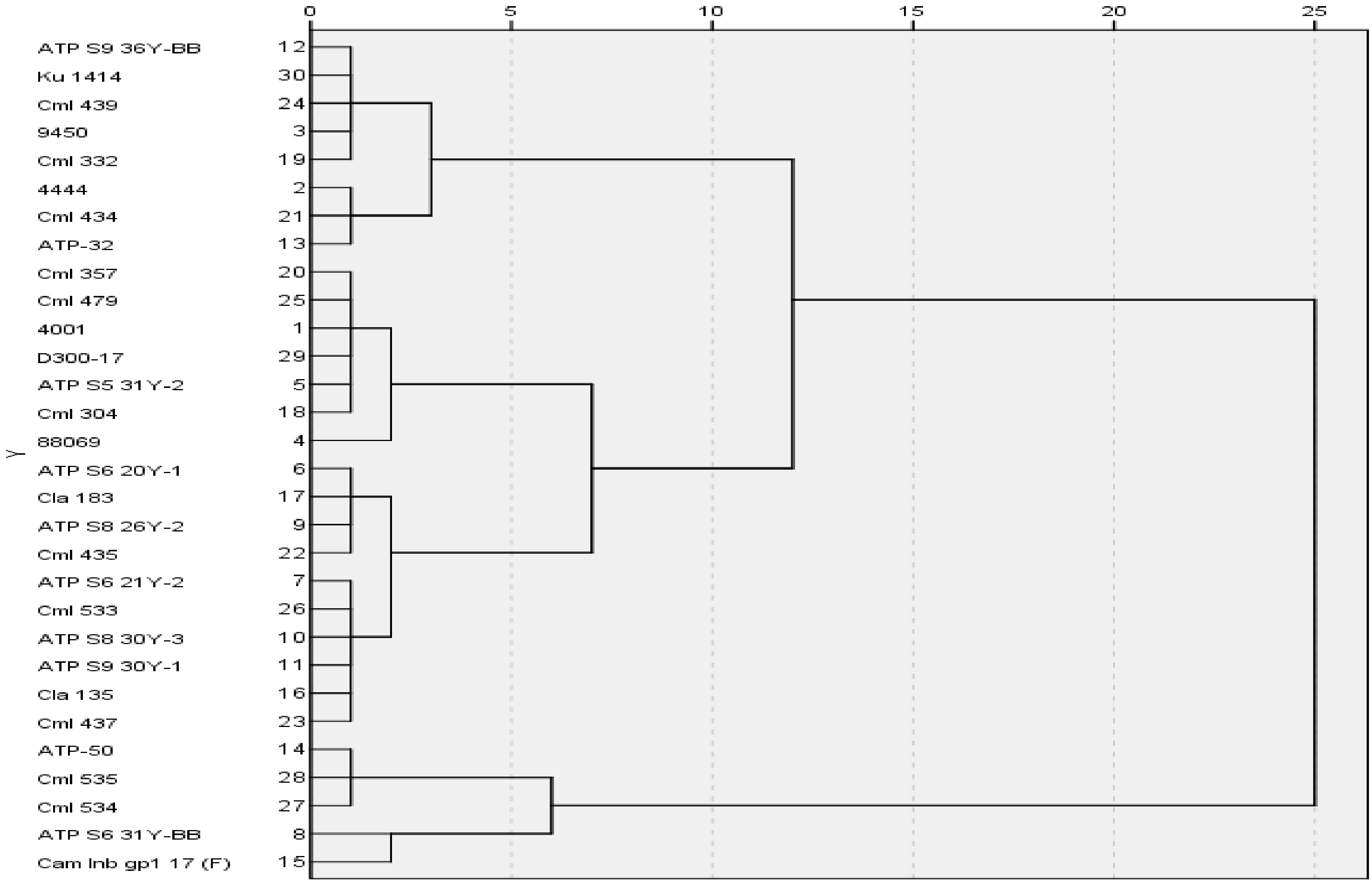


Figure 4.2: Dendrogram of 30 inbred lines based on the mean of the quantitative traits

Table 4.9: Clusters based on quantitative traits of maize lines

Cluster	**Lines**
Cluster 1: Sub-cluster I	4001, 88069, ATP S5 31Y-2, Cml 304, Cml 357, Cml 479, D300-17
Cluster 1: Sub-cluster II	Ku 14 14, Cml 439, Cml 434, Cml 332, ATP 32, ATP S9 36Y BB, 4444, 9450
Cluster 1: Sub-cluster III	ATP S6 20Y-1, ATP S6 21Y-2, ATP S8 26Y-2, ATP S8 30Y-3, ATP S9 30Y-1, Cla 135, Cla 183, Cml 435, Cml 437, Cml 533
Cluster 2	Cml 535, Cml 534, Cam Inb gp1 17 (F), ATP 50, ATP S6 31Y BB

4.3.4. Molecular characterization

4.3.4.1 Grouping of inbred lines based on SNP markers

Clusters were generated through DARwin by a simple matching dissimilarity index, a threshold equality of 0%, with 15 nodes (degree: minimum = 2, maximum = 3) (Figure 4.4). The edge length sum of the graph was 0.46. Different colors were applied to discriminate introduced inbred lines from the local (lines from IRAD were in black color). Two major clusters of lines were observed: group one include 28 inbred lines and the second group two lines (ATP S6 31Y-2 and ATP S6 20Y-1). The first group was divided into 16 sub-clusters: the first 10 sub-clusters each contained one line. The sub-cluster k had 2 lines, the sub-cluster l had 2 lines, m had 2 lines, n had 5 lines, o had 4 lines and p had 4 lines (Table 4.10). The introduced inbred lines were colored in blue while the inbred lines used as heterotic testers in the next chapter were colored in red (Figure 4.4).

Table 4.10: Clustering of maize inbred lines based on diversity in SNP markers

Cluster			Line
Cluster I	16 sub-clusters	a	4001
		b	88069
		c	ATP S9 36Y-1
		d	ATP S5 31Y-2
		e	CLA 135
		f	CLA 183
		g	CML 332
		h	CML 486
		i	CML 534
		j	Ku 1414
		k	CML 435, CML 434
		l	CML 304, CML 479
		m	ATP S8 30Y-2, ATP S8 26Y-2
		n	ATP 50, ATP S9 30Y-1, D300-17, 9450, CML 533
		o	CML 535, CML 439, CML 437, CML 533
		p	Cam Inb gp1 17, ATP 32, ATP S6 31Y-BB, Cam Inb gp1 17 (F)
Cluster II			ATP S6 31Y-1
			ATP S6 20Y-1

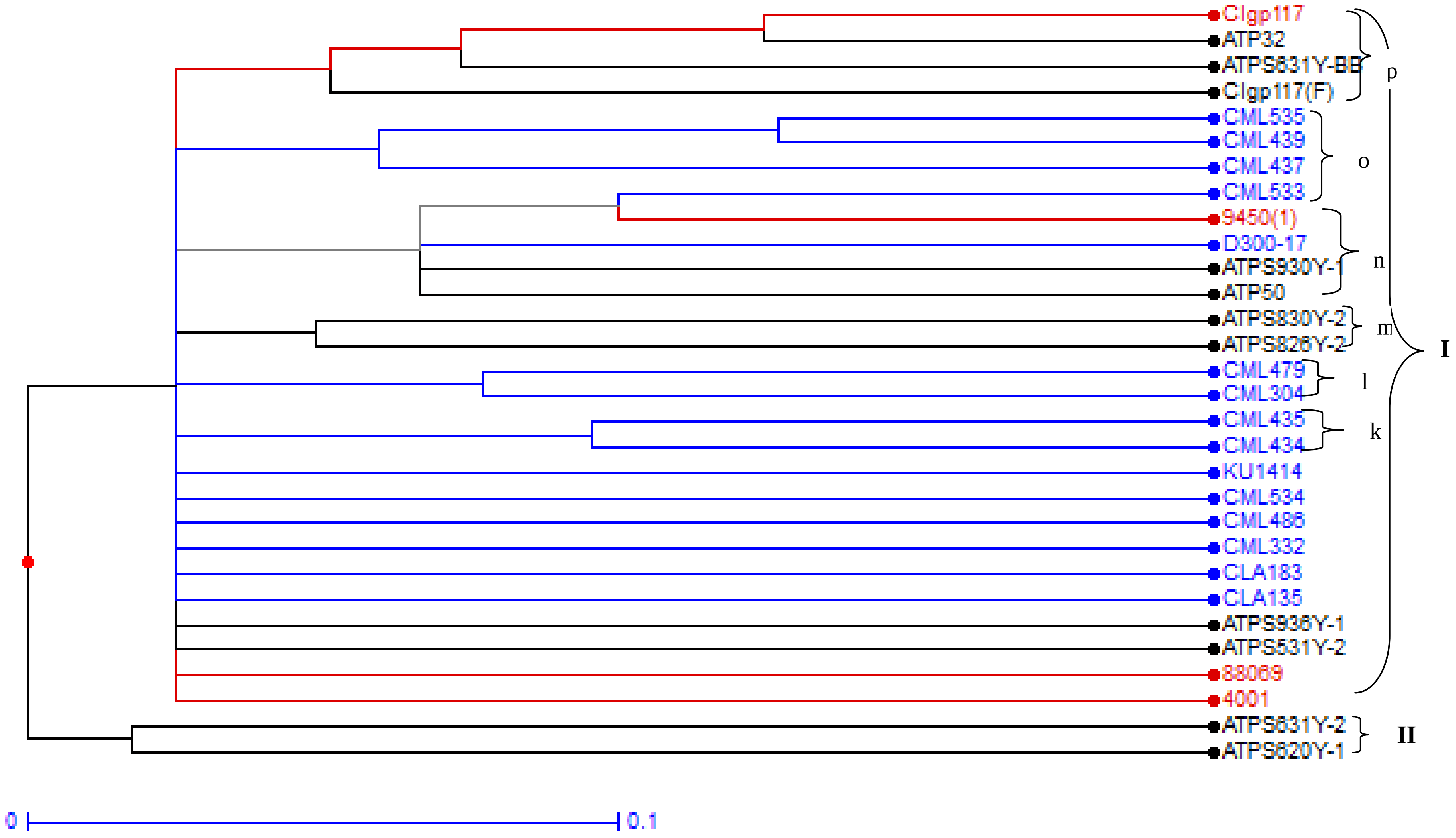


Figure 4.3: Dendrogram of maize inbred lines generated from the genotyping result of 200 SNP markers

4.3.4. 2 Genetic distance among inbred lines

The genetic distance among the inbred lines varied from 0.1 observed between CML 535 and CML 439 to 0.4 (Table 4.11). The genetic distance between inbred 88069 and most of the ATP lines (from number 4 to 13) was 0.4. The genetic distance between 4001, 88069, 9450 and Cam Inb gp1 17 varied from 0.3 to 0.4.

Table 4.11: Genetic distance among inbred lines using line codes

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
1																														
2	0.3																													
3	0.4	0.4																												
4	0.3	0.4	0.3																											
5	0.4	0.4	0.2	0.3																										
6	0.3	0.4	0.4	0.3	0.3																									
7	0.4	0.4	0.4	0.4	0.4	0.4																								
8	0.4	0.4	0.4	0.4	0.4	0.4	0.4																							
9	0.3	0.4	0.4	0.3	0.3	0.3	0.4	0.4																						
10	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.3	0.4																					
11	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.3																				
12	0.3	0.3	0.2	0.3	0.3	0.4	0.4	0.4	0.4	0.4	0.4																			
13	0.3	0.4	0.3	0.3	0.4	0.3	0.4	0.4	0.4	0.3	0.4	0.4																		
14	0.3	0.4	0.3	0.2	0.3	0.3	0.4	0.4	0.2	0.3	0.3	0.3	0.3																	
15	0.3	0.4	0.4	0.3	0.3	0.3	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.2																
16	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4															
17	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.3	0.3														
18	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.3	0.3	0.3	0.3													
19	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.4	0.3	0.3	0.3												
20	0.4	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.3											
21	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.4	0.3	0.3	0.4	0.4	0.3	0.3	0.4	0.3	0.3	0.3	0.3	0.2										
22	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.4	0.4	0.3	0.4	0.4	0.3	0.3	0.4	0.3	0.3	0.3	0.3	0.4	0.3									
23	0.3	0.4	0.4	0.4	0.3	0.3	0.4	0.4	0.3	0.4	0.4	0.4	0.3	0.3	0.3	0.3	0.4	0.3	0.3	0.3	0.2	0.3								
24	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.4	0.3	0.3	0.2	0.3	0.4	0.4	0.3	0.3							
25	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.4	0.4	0.4	0.4	0.3						
26	0.4	0.4	0.2	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4					
27	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.3	0.3	0.4	0.3	0.4	0.4	0.3	0.3	0.3	0.3	0.4				
28	0.3	0.4	0.4	0.4	0.3	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.3	0.3	0.3	0.3	0.4	0.3	0.3	0.4	0.3	0.3	**0.1**	0.3	0.3	0.4	0.3			
29	0.3	0.3	0.2	0.3	0.3	0.3	0.4	0.4	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.4	0.3	0.4	0.3	0.4	0.3	0.4	0.3	0.3	0.3	0.3	0.4	0.4		
30	0.3	0.4	0.4	0.4	0.4	0.3	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	0.4	

4.4 Discussion

The description of maize inbred lines based on quantitative traits is the first way for identify them. Results from this study indicated that all the local inbred lines (IRAD) had flint and indented, yellow kernels. Most of them had primary –secondary tassels with reddish color. The similarities found among inbred lines could be attributed to the fact that almost all of them were developed from the same acid tolerant population under similar stress conditions of soil acidity. The difference observed in some cases could be explained by the genetic factors of the lines and also by the environmental interaction based on where they were grown. The plants were grown in acid soil prone environments which could influence their phenotypic aspect. Similar research study was done by Law et al. (2011) who characterized 152 maize inbred lines based on morphological traits. The knowledge of the existing genetic variation and associations between various agro-morphological traits is vital for our breeding program.

Introduced inbred lines were incorporated into the evaluation and data on quantitative traits recorded. The mean yield of inbred lines in the environment under study was 1.4 t/ha. Eight inbred lines out-yielded the mean yield. Among those, two were introduced (Cml535 and Cml 534 (2.4 t/ha)). Also, yield was positively and highly correlated with plant height, ear height, and ears per plant and was negatively correlated with the anthesis-silking interval (Ngugi *et al.*, 2013). The high-yielding inbred lines produced one ears per plant, with an average of 2 days for anthesis-silking interval, a plant height of 161 cm with ear height of 78 cm. The weaknesses on traits characteristics observed among the lines were also due to several self pollination techniques they went through.

The principal component analysis shows that the first principal component resulted in 43.3% of the total variation among all the inbred lines under investigation while the second principal component explained 18.5% of the variation for all the traits recorded. Therefore, 61.8% of the variance was explained by the principal component analysis. The grouping of genotypes based on field data was done. The lines with similar traits were grouped together. Two major clusters were identified. The first major cluster was divided into three sub-clusters (groups). Group I was made of 7 seven inbred lines of which four were introduced. The mean yield of genotypes in this group was 1.6 t/ha. The second group was also made of 7 inbred lines with four being introduced lines. The mean yield in this group was 0.8 t/ha. The third group had 10 inbred lines out of which five were being introduced. The mean yield of lines in this group was 1.1 t/ha. The last group (second major cluster) was made up of five inbred lines out of which two introduced included were Cml 535, Cml 534, and three local (Cam Inb gp1 17 (F), ATP 50 and ATP S6 31Y-BB0. The introduced were spreaded all over the different groups. This result suggested that there were similarities among the local and the introduced inbred lines. Yadav and Singh (2010) reported in India that 30 maize inbred lines were divided into three groups using their morphological characters. In the present study, based on the average yield of each group compared to the mean yield, genotypes were classified as followed: The lines of group II (0.8 t/ha) and group III (1.1 t/ha) were considered as susceptible to acid soils; the lines of group I (1.6 t/ha) were considered as moderately tolerant and the lines of group IV (2.7 t/ha) considered as tolerant.

The minimum genetic distance of 0.00003 was observed between Ku 1414 and ATP S9 36Y BB indicating that the two lines were genetically closely related. Ku 1414 was introduced from IITA and ATP S9 36 BB is a local inbred line from IRAD. Yadav and Singh (2010) found that the minimum distance for closely related inbred lines was 0.35 while a distance of 1.92 was observed between inbred lines that differed from each other.

The molecular markers were used to get more information on the inbred lines of the study. The IRAD lines were interspersed between the introduced inbred lines on the dendogram. Two major groups were identified. ATP S9 36Y-1 and ATP S5 31Y-2 were the only lines in the main cluster II. They were local inbred lines from IRAD. The main group I was subdivided into 16 sub-clusters. The genotypes in red are the lines used in the next chapter as testers (Cam Inb gp1 17, 9450, 4001 and 88069). These were found to be in different sub-clusters in group I. The genetic distance among these testers varied from 0.3 to 0.4 indicating that they were closely related. The moderate and high-yielding inbred lines identified from the field data were all in the same main cluster meaning that their molecular structure was related. Genetic distance varied from 0.1 to 0.4 for the 30 inbred lines. The minimum distance (0.1), indicating closely related inbred lines, was between Cml 439 and Cml 535. Sserumaga *et al*., (2014) found that gene diversity ranged from 0. 18 to 0.92 between maize inbred lines with under adapted regimes of water.

Tester 9450 was genetically similar to several CIMMYT Cml lines and was closely related to Cam Inb gp1-17 but the hybrid between these two testers was the highest yielding in stressed plots in Chapter 6. Testers 88069 and 4001 were in adjacent sub-clusters suggesting that they are genetically very close but their hybrid was the highest yielding under control conditions in Chapter 6 indicating that they are in different heterotic groups. The results here again demonstrate that genetic distance as measured by molecular markers is not associated with heterosis. The prediction of the heterosis effect of the crosses between these inbred lines would have been in a negative way. According to Warburton *et al*.(2002) and Xia *et al*. (2004), heterosis has been predicted on the basis of genetic distance based on molecular markers. Goff

(2011) found that generally the greater the genetic diversity of the parents, the higher the level of heterosis achieved. This suggested that since the genetic distance among lines was not wide, it would have been impossible to get any good hybrid combination. The current results differed from the assumption used to establish the heterotic groups based on molecular maker data as stated by Reif *et al*. (2005). All these findings were different from the results got from the present study. Also Sserumaga *et al.*, (2014) realized that high overall genetic diversity (0.65) among the inbred line combinations indicates an opportunity to exploit the inbred lines for the development of varieties and start point of pedigree breeding population used to produce promising inbred lines (Sserumaga *et al.*, 2014). For a crop like maize, the strategy of developing good hybrids depends on genetic diversity present in the available inbred lines. In the present study, the molecular markers identified genetic diversity, and the sight appearance somehow evenly disperses the lines in the plot than the morphological method. However, there was little agreement on lines relationships between the morphological and the molecular methods. Lines that display high phenotypic dissimilarity might not be genetically dissimilar. Analysis of genetic diversity and of relationship among the elite breeding materials could significantly aid in crop improvement. Moreover, the lines find themselves close to clusters due to a decrease in variation between them.

4.5 Conclusions

Local inbred lines had flint and indented kernel, with a yellow color. Most of them had primary – secondary tassel type with reddish color. Based on the average yield of each group compared to the mean yield, genotypes were classified in four groups: The lines of group II and group III were considered as susceptible to acid soils; the lines of group I were considered as moderately tolerant and the lines of group IV were considered as highly tolerant. In general, the variability among morphology of the local ATP lines was not much. In the molecular grouping, two ATP lines were distinct from all the rest. The four inbred lines used as heterotic testers in the next chapter were found to be in different sub-clusters of the main cluster I. Tester 9450 was genetically similar to several CIMMYT Cml lines and was closely related to Cam Inb gp1-17. Testers 88069 and 4001 were in adjacent sub-clusters suggesting that they were genetically closed. In general, the genetic distance between the study lines was low. The prediction of the heterosis effect of the crosses between them would have been in the negative way. Cluster I contained all the introduced inbred lines and most of the locally adapted lines subdivided into 16 sub-clusters. All the four inbred lines used as heterotic testers in the next chapter were found to be in different sub-clusters based on molecular characterization but were all in the same main cluster I. The variability among these inbred lines was not very high.

CHAPTER V:

5.0 AGRONOMIC PERFORMANCE OF MAIZE HYBRIDS UNDER ACID AND CONTROL SOIL CONDITIONS

5.1 Introduction

Maize is the main actively produced cereal in the humid forest zone (HFZ) of Cameroon. The humid forest zone occupies about 16.5 million hectares of humid forest eco-zone (Robiglio *et al.*, 2010). The average maize yield production is very low and ranges from 0.8 to 1 t/ha (ACDIC, 2010). The acid soils have high Aluminium (Al) content which leads to grain yield losses up to 60% (The *et al.*, 2005). Higher yields of maize in the humid forest zone will require the reduction of soil acidity (The *et al.*, 2006; Pandey *et al.*, 2007).

Lime reduces exchangeable Al making plant nutrients, particularly phosphorus, available (Ngonkeu, 2009) and increases the level of exchangeable cations such as Ca^{2+} and Mg^{2+} (Horst *et al.*, 2000). However, the application of lime and mineral fertilizers had therefore lead to an increase in cost of maize production for poor farmers in that region (Rojas *et al.*, 2001). In addition to the cost of lime, its application may not be environmental threaten and has only a temporary beneficial effect (The *et al.*, 2001). Wood ash at 4 t/ha has been used and this has significantly increased the yield in acid soils (Mbah *et al.*, 2010). This method is however not always sustainable because of the non-availability of ash. Therefore, the use of acid soil-tolerant maize cultivars provides a less expensive and long term solution, contributing to sustainable crop production on acid soils (Granados *et al.*, 1993; Welcker *et al.*, 2005).

Several conventional breeding methods have been used to develop some acid tolerant germplasm of maize. Several yield-based stress indices have been used to identify stress tolerant genotypes. The stress indices which provide a measure of stress based on yield loss under stress conditions in comparison to normal conditions have been widely used (Talebi *et al.*, 2009; Moradi *et al.*, 2012; Dewi-Hayati *et al.*, 2014). Stress tolerance indices (STI) have been used for comparing genotypic performance across years or environments and identifying genotypes that perform well under both stress and non-stress conditions (Fernandez, 1992). While, stress susceptibility index (SSI) is the ratio of genotypic performance under stress and non-stress conditions (Fischer and Maurer, 1978).

The most acid-tolerant open-pollinated (OP) variety (ATP-SR-Y) so far released to date suffers from yield reduction due to soil acidity within the ranges of 57 to 60% (Tandzi, 2005; The *et al.*, 2006). Maize hybrids are higher yielding and more stress tolerant than populations or OP varieties. The development of high-yielding maize hybrids adapted to soil acidity will improve the sustainability of maize production in the acid prone areas.

The objectives of this study were to:

- Identify high-yielding hybrids in acid soil and in control conditions
- Evaluate yield loss, stress susceptibility and stress tolerance indices of the hybrids
- Estimate standard heterosis of hybrids under acid stress and corrected acid stress environments
- Estimate the correlations between agronomic traits, stress susceptibility and tolerance indices in acid soil and control conditions.

5.2 Materials and methods

5.2.1 Germplasm

- **Single crosses**

Twenty-five inbred lines from the Institute of Agricultural Research for Development (IRAD), CIMMYT and IITA) were crossed with 4 testers (Cam Inb gp1 17, 88069, 9450 and 4001) and 100 single hybrids were obtained. Crosses among the four testers were also made. These hybrids were used as hybrid check. A total of 106 single cross hybrids were evaluated.

- **Top crosses**

Three open-pollinated varieties, two commercial OPVs (ATP SR Y and CMS 8704) and one introduced OPV, were also crossed with the four testers and 12 top cross hybrids were obtained.

A total of 118 single cross and top cross hybrids plus the three OPVs used as checks (121 hybrids) were evaluated together under acid soil and control conditions. The list of the parental material used is shown in Table 5.1. The crosses were done at the nurse breeding field of IRAD Yaounde / Nkolbisson at the beginning of each agricultural campaign from 2011 to 2014.

Table 5.2: List of inbred lines and OPVs used and their origin

Genotype name	Origin	Type
ATP S5 31Y-2	IRAD	Line
ATP S6 20Y-1	IRAD	Line
ATP S6 21Y-2	IRAD	Line
ATP S6 31Y-BB	IRAD	Line
ATP S8 26Y-2	IRAD	Line
ATP S8 30Y-3	IRAD	Line
ATP S9 30Y-1	IRAD	Line
ATP S9 36Y-BB	IRAD	Line
ATP-32	IRAD	Line
ATP-50	IRAD	Line
Cml 304	CIMMYT	Line
Cml 357	CIMMYT	Line
Cml 435	CIMMYT	Line
Cml 437	CIMMYT	Line
Cml 439	CIMMYT	Line
Cml 533	CIMMYT	Line
Cml 534	CIMMYT	Line
Cml 535	CIMMYT	Line
Cml 332	CIMMYT	Line
Cml 479	CIMMYT	Line
Cla 183	CIMMYT	Line
Cml 434	CIMMYT	Line
Cla 135	CIMMYT	Line
D300-17	CIMMYT	Line
Cam Inb gp1 17 (F)	IRAD	Line
Testers		
Cam Inb gp1 17	IRAD	Tester
88069	IRAD	Tester
9450	IITA	Tester
4001	IITA	Tester
Checks		
C4RR SA4	CIMMYT	Introduced OPV
CMS 8704	IRAD	Commercial OPV
ATP SR Y	IRAD	Commercial OPV

OPV = open-pollinated variety

5.2.2 Experimental sites

Trials were carried out at two sites at the research fields of IRAD, Nkoemvone in Ebolowa, the Southern Region of Cameroon, from 2012 to 2014. Nkoemvone is found on altitude 615 m above the sea level and situated on 12° 24 E, 2° 40 N (The *et al*., 2006). The average temperature is 24° C and the annual rainfall is 1800 mm with bimodal distribution (The *et al.*, 2001). The soil is a highly weathered Kandiudox with high Al toxicity (FAO, 1992; The *et al.*, 2005) and is highly weathered (Yemefack *et al.*, 2005).

5.2.3 Experimental Design

The 121 hybrids were evaluated in a simple lattice design (11 x 11) with two replications in three years. Each site – treatment – year combination was considered as a test environment. The soil treatments were native acid soil and control conditions (4 t/ha of dolomite was applied). This produced two treatments on two sites each over three years giving 12 environments (Table 5.2).

Table 5.3: Acid soil and control environments

Environment	Component	
Environment 1	Site 1 * treatment 1 (acid) * year 1 (2012)	Acid soil environments (A)
Environment 2	Site 1 * treatment 1 (acid) * year 2 (2013)	
Environment 3	Site 1 * treatment 1 (acid) * year 3 (2014)	
Environment 4	Site 2 * treatment 1 (acid) * year 1 (2012)	
Environment 5	Site 2 * treatment 1 (acid) * year 2 (2013)	
Environment 6	Site 2 * treatment 1 (acid) * year 3 (2014)	
Environment 7	Site 1 * treatment 2 (control) * year 1 (2012)	Control environments (C)
Environment 8	Site 1 * treatment 2 (control) * year 2 (2013)	
Environment 9	Site 1 * treatment 2 (control) * year 3 (2014)	
Environment 10	Site 2 * treatment 2 (control) * year 1 (2012)	
Environment 11	Site 2 * treatment 2 (control) * year 2 (2013)	
Environment 12	Site 2 * treatment 2 (control) * year 3 (2014)	

5.2.4 Soil sampling and analysis

Soil was sampled from the field at the beginning of each experimental year for characterization to ascertain the inherent fertility of the soil which would serve as baseline information to measure the changes in soil characteristics due to the application of treatments. Due to the relative homogeneous of the soils at the experimental site, four composite soil samples were collected from the plough layer (0 - 20 cm) for characterization at IITA soil laboratory following their procedure.

5.2.5 Land preparation, planting and field management

The experimental sites were cleared from grasses manually and plowed. Each experimental site had two treatments of the soil with 2 m alley in between. One treatment was a native acid soil considered as the stress environment and the other was used as a control where the acidity was corrected with the incorporation of 4t/ha of dolomite lime. The dolomite was incorporated into the soil by plowing.

Each genotype was planted in a 4m long row, with two replications. The distance between the rows was 0.75 m and within row was 0.5 m. Three seeds per hill were hand-sowing and later thinned to two plants per hole, which corresponded to an expected plant density of approximately 53,333 plants/ha. Weeds were controlled manually and sometime by the application of herbicides (Plantomaïs, Roundup). The field trials received the recommended rate of fertilizer in split application, which was a basal dose of 37 N, 24 P_2O_5 and 14 K_2O kg/ha applied 10 days after sowing and top dressed with 46 kg N per hectare, applied 30 days after planting (The *et al.*, 2005).

5.2.6 Data collection

Data was collected on:

- Number of days to anthesis,
- Number of days to silking, anthesis to silking interval (ASI) using the formula:

ASI (days) = DS – DA

- Plant height (cm),

- Ear height (cm),
- Moisture content and grain yield were measured on a whole plot basis following standard CIMMYT procedure which was adjusted to 15% moisture using the formula below

  GY (t/ha) = [Grain Weight (kg/plot) x 10 x (100-MC) / (100-15) / (Plot Area)]

  Where MC = Grain Moisture Content (CIMMYT, 1985).
- Plant stand at harvest
- Number of ears at harvest were also recorded.

At harvest, all ears from each plot were counted and the number of ears per plant (EPP) was calculated using the formula: EPP = EC/PC, Where EC and PC = number of ears and number of plants per row, respectively.

5.2.7 Statistical analysis

The analysis of variance (ANOVA) was performed separately for acid soil and control environments using the PROC GLM in SAS. The blocks were nested within replication by environments and replications within environments were treated as random factors and the genotype as fixed. The statistical model used for the combined analysis is as follows:

$$Yijkg = \mu + Ei + Bk(ij) + Gg + EGig + \varepsilon ijkg$$

Where:

- Yijkg is the observed measurement for the gth genotype grown in the environment i, in the block k in replicate j;
- μ is the; grand mean;

- Ei is the main effect of environment;
- Bk (ij) is the effect of block nested within replicate j by environment i;
- Gg is the effect of the genotype;
- EGig is the interaction effect between genotype and environment,
- εijkg is the error term (Akinwale *et al.*, 2014).

Broad-sense heritability (H^2) was estimated as:

$H^2 = \sigma^2_g / (\sigma^2_{g\,+} (\sigma^2_{ge} / e) + (\sigma^2_e / re))$

σ^2_g is variance for genotype, σ^2_e is error variance, σ^2_{ge} is variance for genotype x environment interaction, *r* is number of replications, and *e* is number of environments (Fehr, 1991).

Standard heterosis

Standard heterosis defined as comparison of hybrids to the best performing check was estimated and tested according to the formula of Singh and Singh, (1994) using the formula below:

Standard heterosis (SH) = (F1 – check) / check x 100

Stress Susceptibility Index (SSI):

SSI = [1-(Ys) / (Yp)] / SI

Where: SI = Stress Intensity = $1 - \bar{Y}s / \bar{Y}p$,

With $\bar{Y}s$ = mean yield in stress environment,

$\bar{Y}p$ = mean yield in non-stressed environment (Fischer and Maurer, 1978).

Stress tolerance index (STI)

$\mathrm{STI} = (\mathrm{Ys} \times \mathrm{Yp}) / (\bar{\mathrm{Y}}\mathrm{p})^2$

Where Ys = yield under stress environment;

Yp = yield under control environment;

$(\bar{\mathrm{Y}}\mathrm{p})^2$ = mean yield under control environment (Fernandez, 1992).

Yield loss percentage:

YLP = (Yp-Ys)/Yp x 100

Where:

Yp = yield of hybrid under non-stressed environment;

Ys = yield of hybrid under stress environments.

5.3 Results

5.3.1 Soil characteristics of experimental environments

The soil analysis of the acid soil environments was strongly acid with pH in water of 4.3 and a very high Al saturation percentage of 73.2% (Table 5.3). The ECEC of the soil was also very low with a value of 3.27 cmol/kg. The soil however has a low C/N ratio of 10.5. Upon addition of dolomite, the pH increased by almost 0.7 pH units to 5 with an accompanying 54% decrease in Al saturation (33.8%). Liming increased also the ECEC to a value of 13.1 cmol/kg.

Table 5.4: Chemical properties of soil before and after liming

	Acid soil (Before liming)	Control (Limed soil)
pH H2O	**4.3**	**5.0**
Exchangeable Acidity (cmol(+).kg^{-1})	2.4	1.8
ECEC (cmol (+).kg^{-1})	3.3	5.4
Al saturation (%)	**73.2**	**33.8**
Mg (cmol (+).kg^{-1})	0.2	1.2
K (cmol (+).kg^{-1})	0.2	0.1
N total (%)	0.1	0.2
C/N	10.5	13.1

N = Nitrogen, Ca = Calcium, Mg = Magnesium, K = Potassium, Na = Sodium, Al = Aluminum, ECEC = Effective Cation Exchangeable Capacity, Al saturation (%) = Aluminum saturation percentage.

5.3.2 Mean square analysis of agronomic traits

The differences among crosses in acid soil environments were highly significant (P<0.001) for yield, plant height, ear height, ear and plant aspect while anthesis-silking interval was significant at P<0.01. Ears per plant effects were not significant (Table 5.4). The genotype by environment interaction was significant at P<0.05 for yield and ear aspect. Broad sense heritability varied from 8% for yield to 40% for ear height (Table 5.4). Anthesis-silking interval had the second low heritability of 9% under acid soil environments.

Table 5.5: Mean square for various traits recorded on hybrids evaluated under acid soil conditions in 2012-2014

Source A	DF	yield	asi	pltght	earght	epp	earasp	plasp
Environment	5	145.9***	264***	47194***	9362.9***	0.5***	55.4***	11.2***
Block(rep*enviro)	156	7***	14***	1284.8***	563.4***	0.05*	0.9***	0.6***
Genotype	120	6.1***	5.6**	1239.5***	569.3***	0.05 NS	0.8***	0.6***
Genotype*environment	600	3.2*	3.8 NS	609 NS	302.9 NS	0.04 NS	0.5**	0.3 NS
Error	570	2.7	4.5	544.5	279	0.04	0.4	0.3
H^2 (%)		8.0	9.0	27.0	40.0	14.0	28.0	17.0

***P<0.001; **P<0.01; *P<0.05; yield =grain yield; pltasp= plant aspect; earasp=ear aspect; epp= ear per plant; earght = ear height; pltght = plant height; asi =anthesis-silking interval; plstd = plant stand; DF=degrees of freedom; Rep=replication; H^2 (%) = Broad sense heritability in percentage, enviro = environment.

In control environments (pH of 5), significantly better performances were recorded among hybrids for anthesis-silking interval, ear height, ears per plant, and ear aspect (P<0.001) and yield and plant aspect were significant at P<0.05 and plant height at P<0.01 (Table 5.5). The genotype by environment interaction was highly significant (P<0.001) for yield, plant height, ear aspect and plant aspect. Broad sense heritability estimate varied from 20% for yield to 58% for ear height (Table 5.5). Anthesis-silking interval had the second high heritability (56%).

Table 5.6: Mean squares for various traits recorded on of hybrids grown in the control conditions

Source	DF	yield	asi	pltght	earght	epp	earasp	plasp
Environment	5	107.5***	389***	18322***	12099***	1.2***	4.3***	15.3***
Block(rep*enviro)	156	6.9***	6.2***	922***	506.8***	0.07***	0.7***	0.5***
Genotype	120	6.1*	4.3***	891**	580.9***	0.07***	0.7***	0.4*
Genotype*environment	600	6.02***	2.7 NS	625.5***	326.5 NS	0.05 NS	0.4***	0.3***
Error	570	4.6	2.8	622.1	292.8	0.05	0.3	0.2
H^2 (%)		20.0	56.0	41.0	58.0	33.0	51.0	34.0

***P<0.001; **P<0.01; *P<0.05; yield =grain yield; pltasp= plant aspect; earasp=ear aspect; epp= ear per plant; earght = ear height; pltght = plant height; asi =anthesis-silking interval; plstd = plant stand; DF=degrees of freedom; H^2 = broad sense heritability.

5.3.3 Mean agronomic performance of hybrids in acid soil environments

The overall mean yield was 3.3 t/ha in acid soil environments, with a minimum yield of 1.4 t/ha (ATP S6 31Y-BB x 88069) and maximum of 6.1 t/ha (Cla 183 x 88069) (Table 5.6 and Appendix 5.1). While the mean of plant aspect was 3.2, ear aspect was 2.7, ears per plant was 1.05, ear height was 71.5 cm, plant height was 158.5 cm and anthesis-silking interval was 2.6 (Table 5.6).

Twenty four hybrids were selected based on their high yield in acid soil environments (Table 5.6). The yield of the selected hybrids ranged from 3.91 t/ha (ATP SR Y x Cam Inb gp1 17) to 6.12 (Cla 183 x 9450). The plant aspects ranged from 2.63 (C4RR SA4 x 88069 and Cla 183 x 9450) to 3.53 (ATP S8 26Y-3 x Cam Inb gp1 17). The ear aspects varied from 1.92 (Cla 183 x 88069) to 2.82 (C4RR SA4 x 88069). One ear per plant was recorded among these genotypes. Moreover, the ear height of these hybrids ranged from 64.48 cm (ATP S8 26Y-3 x Cam Inb gp1 17) to 101.52 cm (Cla 183 x 9450). The plant height varied from 151.33 cm (ATP S8 26Y-3 x Cam Inb gp1 17) to 198.02 cm (Cla 183 x 9450). The anthesis-silking interval varied from 1.66 (Cml 437 x 9450) to 4.31 (C4RR SA4 x 88069).

Among these hybrids, four were top crosses ATP SR Y x Cam Inb gp1 17 (3.91 t/ha), C4RR SA4 x 88069 (4.06 t/ha), CMS 8704 x 88069 (4.23 t/ha), C4 RR SA4 x Cam Inb gp1 17 (4.26 t/ha). The best hybrid from crosses between testers was 9450 x Cam Inb gp1 17 which yielded 4.00 t/ha under this environment (Appendix 5.2). The best OPV check was CMS 8704 which yielded 3.17 t/ha under acid soil environments (Appendix 5.2).

Table 5.7: Performance of the top 24 high-yielding hybrids in acid soil conditions

Genotypes	Yield (t/ha)	pltasp	earasp	epp	Earght (cm)	plthgt (cm)	asi
Cla 183 x 9450	6.12	2.63	2.02	0.88	101.52	198.02	2.17
ATP S9 36Y-BB x 4001	5.37	3.02	2.77	1.06	76.60	171.20	3.21
Cla 183 x 88069	5.36	2.73	1.92	0.95	79.91	174.65	3.84
Cml 434 x Cam Inb gp1 17	5.11	2.72	2.38	0.99	79.57	176.11	2.97
ATP S5 31Y-2 x 4001	5.07	2.89	2.27	1.15	74.48	159.15	2.88
Cml 437 x Cam Inb gp1 17	4.84	3.11	2.20	0.93	70.68	167.90	3.01
ATP S8 26Y-3 x Cam Inb gp1 17	4.72	3.55	2.67	1.08	64.48	151.33	2.37
Cml 534 x 4001	4.42	3.12	2.37	0.99	78.05	165.09	2.42
Cla 183 x Cam Inb gp1 17	4.42	2.83	2.20	0.98	75.68	177.52	3.11
Cml 439 x 4001	4.39	3.22	2.24	0.93	75.83	155.14	1.69
ATP S5 31Y-2 x 9450	4.34	3.14	2.54	1.04	79.05	169.74	3.07
C4RR SA4 x Cam Inb gp1 17	4.26	3.01	2.75	1.04	75.82	165.57	2.53
ATP S8 30Y-3 x Cam Inb gp1 17	4.25	3.17	2.20	1.01	81.67	168.69	2.91
Cam Inb gp1 17 (F) x 9450	4.23	3.24	2.44	1.12	79.28	163.96	3.54
CMS 8704 x 88069	4.23	3.13	2.47	1.03	73.61	167.22	2.62
Cml 439 x 9450	4.23	3.09	2.52	1.00	66.48	159.15	2.14
ATP S6 31Y-BB x 9450	4.20	3.22	2.44	1.03	83.13	169.42	3.08
ATP S8 30Y-3 x 4001	4.14	3.06	2.41	1.05	73.99	157.52	2.43
Cml 437 x 9450	4.13	3.26	2.57	1.00	73.26	162.82	1.66
C4RR SA4 x 88069	4.06	2.63	2.82	1.26	71.24	159.92	4.31
CLA 135 x 9450	4.05	2.90	2.50	1.02	77.19	169.54	2.42
Cla 183 x 4001	3.97	2.68	2.50	0.96	88.74	171.35	2.62
D300-17 x Cam Inb gp1 17	3.97	2.96	2.56	1.08	73.99	161.13	1.68
ATP SR Y x Cam Inb gp1 17	3.91	3.12	2.75	1.10	75.83	165.67	2.44
Mean	3.3	3.2	2.7	1.05	71.5	158.5	2.6
Minimum	1.4	2.6	1.9	0.9	52	198	-0.9
Maximum	6.1	3.8	3.4	1.3	101.5	135.4	4.6
SED	0.75	0.3	0.1	0.1	8.25	11.5	1.05

Asi = anthesis-silking interval, pltght = plant height, earght = ear height, epp = ear per plant, earasp = ear aspect, pltasp = plant aspect, SED = standard error of difference.

5.3.4 Mean agronomic performance of hybrids in control environments

In control environments, the overall mean yield was 5.3 t/ha (Table 5.7). The minimum yield was 3.50 t/ha and the highest yield was 7.4 t/ha (Table 5.7 and Appendix 5.2). The overall mean was 2.5 for plant aspect, 2.1 for ear aspect, 1.1 for ear per plant, 93.2 for ear height, 194.4 for plant height and 1.9 for anthesis-silking interval.

Twenty four hybrids were selected in control environments (Table 5.7). The yield of hybrids ranged from 5.86 t/ha to 7.4 t/ha. The plant aspect ranged from 1.99 to 2.82 whilst ear aspect varied from 1.58 to 2.29. The ears per plant varied from 0.95 to 1.23. Ear height ranged from 82.43 cm to 110.11 cm while plant height ranged from 165.53 cm to 213.99. The anthesis-silking interval varied from 0.64 to 3.80.

Among the 24 hybrids selected in control environments, two were top crosses were represented ATP SR Y x 4001 (7.04 t/ha) and CMS 8704 x 9450 (7.40 t/ha). Two were hybrids between testers, 4001 x 9450 (6.13 t/ha) which was the best hybrid check across these environments and 4001 x 88069 (6.09 t/ha). The best OPV was CMS 8704, which yielded 5.29 t/ha in this environment (Appendix 5.1).

Table 5.8: Performance of the top 24 high-yielding hybrids in control environments

Genotype	yield (t/ha)	pltasp	earasp	epp	earght	plthgt	asi
CMS 8704 x 9450	7.40	1.99	1.95	1.07	103.96	213.99	1.20
Cml 439 x Cam Inb gp1 17	7.24	2.01	1.60	1.06	89.01	203.31	2.15
ATP SR Y x 4001	7.04	2.35	1.59	1.16	83.07	190.15	0.64
Cml 535 x Cam Inb gp1 17	6.91	2.30	2.16	1.23	88.25	196.53	3.80
ATP S6 31Y-BB x 9450	6.89	2.43	1.94	1.14	105.30	200.18	2.08
Cml 332 x Cam Inb gp1 17	6.60	2.61	2.23	1.16	94.30	203.01	2.60
D300-17 x Cam Inb gp1 17	6.53	2.36	2.02	1.08	105.41	205.09	1.69
Cml 434 x Cam Inb gp1 17	6.35	2.43	1.88	0.97	87.01	192.58	3.35
Cla 135 x 9450	6.31	2.36	2.03	1.09	99.89	206.49	1.05
Cla 135 x 88069	6.29	2.54	1.94	1.03	93.44	196.07	1.32
ATP S5 31Y-2 x 9450	6.29	2.17	1.89	1.32	99.53	211.82	1.30
ATP S8 30Y-3 x Cam Inb gp1 17	6.26	2.53	2.29	1.22	90.51	185.82	1.80
Cml 304 x 9450	6.20	2.33	1.58	1.15	109.35	211.49	1.35
Cml 437 x 88069	6.17	2.36	1.75	1.17	97.96	199.26	2.83
ATP S6 20Y-1 x 9450	6.13	2.54	2.07	1.07	88.92	191.52	2.06
4001 x 9450	6.13	2.82	2.26	1.04	95.48	198.70	2.30
ATP-50 x 9450	6.12	2.45	2.18	1.28	100.90	209.78	1.70
Cml 357 x Cam Inb gp1 17	6.11	2.11	1.67	1.10	110.11	203.89	2.42
4001 x 88069	6.09	2.67	2.10	1.27	95.18	203.05	1.67
Cml 439 x 4001	6.06	2.64	1.83	1.06	89.03	187.49	1.06
ATP S9 30Y-1 x 9450	6.06	2.35	1.97	0.95	87.06	199.72	1.78
ATP S8 26Y-3 x 88069	5.94	2.74	2.25	1.09	82.43	165.53	1.03
Cml 357 x 4001	5.88	2.30	1.76	1.05	93.46	199.38	2.26
ATP-32 x 4001	5.86	2.26	1.99	1.17	87.65	187.47	3.01
Mean	5.3	2.5	2.1	1.1	93.2	194.4	1.9
Minimum	3.50	1.77	1.58	0.95	122.86	222.19	3.80
Maximum	7.40	2.98	3.29	1.36	76.65	165.53	-1.37
SED	1.05	0.3	0.3	0.15	8.4	10.65	0.75

Asi = anthesis-silking interval, pltght = plant height, earght = ear height, epp = ear per plant, earasp = ear aspect, pltasp = plant aspect, SED = standard error of difference.

5.3.5 Correlation between yield and other agronomic traits in acid soil and control environments

In acid soil and control soil environments, the correlations between yield and anthesis-silking interval, ear aspect and plant aspect were negative and highly significant ($P<0.001$) while plant height, ear height, and ear per plant were positively and highly significantly correlated with yield (Table 5.8 and Table 5.9).

Table 5.9: Pearson correlation coefficients among agronomic traits in acid soil environments

	asi	plthght	earhgt	epp	earasp	pltasp	Yield
asi							
plthght	-0.19***						
earhgt	-0.24***	0.80***					
epp	-0.06*	0.05*	0.05NS				
earasp	-0.19***	-0.17***	-0.12***	-0.03 NS			
pltasp	0.34***	-0.5***	-0.47***	-0.04NS	0.22***		
Yield	-0.13***	0.36***	0.28***	0.09***	-0.47***	-0.4***	

Asi = anthesis-silking interval, pltght = plant height, earght = ear height, epp = ear per plant, earasp = ear aspect, pltasp = plant aspect

Table 5.10: Pearson Correlation Coefficients among agronomic traits in control environments

	asi	plthght	earhgt	epp	earasp	pltasp	Yield
asi							
plthght	-0.19***						
earhgt	-0.25***	0.80***					
epp	-0.06*	0.05*	0.05 NS				
earasp	-0.19***	-0.17***	-0.12***	-0.03 NS			
pltasp	0.34***	-0.54***	-0.47***	-0.04NS	0.21924		
Yield	-0.13***	0.36***	0.28***	0.09***	-0.47***	-0.40***	

Asi = anthesis-silking interval, pltght = plant height, earght = ear height, epp = ear per plant, earasp = ear aspect, pltasp = plant aspect

5.3.6 Grain yield reduction, stress susceptibility index and stress tolerance index of hybrids under acid soil and control environments

The overall mean yield reduction of the hybrids was 38% while stress susceptibility index was 1.0 and stress tolerance index was 17.5 (Table 5.10). Yield loss ranged from -10% to 69% (Table 5.10 and Appendix 5.3). The stress susceptibility index ranged from -0.26 to 1.8 and the stress tolerance index varied from 5.9 to 35.

The best 24 high-yielding hybrids selected under acid soil expressed yield reduction from -10% to 33% (Table 5.10). Their stress susceptibility index varied from -0.3 to 1.0 and the stress tolerance index varied from 18.3 to 36.7. Four hybrids had good yields in both conditions. They were Cla 183 x 9450, ATP S9 36Y-BB x 4001, Cla 183 x 88069 and ATP S5 31Y-2 x 4001. Their stress susceptibility indices were lower compare to the rest and the stress tolerance indices were acceptable.

Table 5.11: Yield reduction percentage, stress susceptibility index and stress tolerance index of the top 24 high-yielding hybrids selected in acid soil environments

Genotype	yield Control	yield Acid soil	Yield reduction (%)	SSI	STI
Cla 183 x 9450	6.0	6.1	-2	-0.1	36.7
ATP S9 36Y-BB x 4001	5.5	5.4	2	0.1	29.4
Cla 183 x 88069	5.8	5.4	7	0.2	30.9
Cml 434 x Cam Inb gp1 17	6.4	5.1	20	0.5	32.5
ATP S5 31Y-2 x 4001	5.1	5.1	0	0.0	25.8
Cml 437 x Cam Inb gp1 17	5.8	4.8	17	0.5	28.2
ATP S8 26Y-3 x Cam Inb gp1 17	5.3	4.7	11	0.3	25.0
Cml 534 x 4001	4.9	4.4	9	0.2	21.5
Cla 183 x Cam Inb gp1 17	5.5	4.4	20	0.5	24.3
Cml 439 x 4001	6.1	4.4	28	0.7	26.6
ATP S5 31Y-2 x 9450	6.3	4.3	31	0.8	27.3
C4RR SA4 x Cam Inb gp1 17	5.8	4.3	26	0.7	24.7
ATP S8 30Y-3 x Cam Inb gp1 17	6.3	4.3	32	0.9	26.6
Cam Inb gp1 17 (F) x 9450	4.3	4.2	2	0.1	18.4
CMS 8704 x 88069	5.6	4.2	25	0.7	23.9
Cml 439 x 9450	4.7	4.2	9	0.2	19.7
ATP S6 31Y-BB x 9450	6.9	4.2	39	1.0	28.9
ATP S8 30Y-3 x 4001	4.4	4.1	6	0.2	18.3
Cml 437 x 9450	5.4	4.1	23	0.6	22.2
C4RR SA4 x 88069	5.0	4.1	18	0.5	20.1
CLA 135 x 9450	6.3	4.1	36	1.0	25.5
Cla 183 x 4001	3.6	4.0	-10	-0.3	14.4
D300-17 x Cam Inb gp1 17	6.5	4.0	39	1.0	25.9
ATP SR Y x Cam Inb gp1 17	5.8	3.9	33	0.9	22.7
Overall mean	5.3	3.3	38	-0.7	17.5
Minimum	3.5	3.3	-10	-0.3	5.9
Maximum	7.4	6.1	69	1.8	35.0

SSI = stress susceptibility index, STI = stress tolerance index.

Under improved soil pH condition of 5, yield reduction of the best 24 hybrids ranged from 20% to 55% while stress susceptibility index varied from 0.5 to 1.8 and stress tolerance index varied from 11.9 to 32.4 (Table 5.11). Four hybrids had good yields in both conditions. They were ATP

S6 31Y-BB x 9450, Cml 434 x Cam Inb gp1 17, ATP S5 31Y-2 x 9450 and Cml 439 x 4001. These hybrids had SSI between 0.5 to 1 and STI ranged from 19.5 to 32.4.

Table 5.12: Yield reduction percentage, stress susceptibility index and stress tolerance index of the best 24 high-yielding hybrids selected in control soil environments

Genotype	yield Control	yield Acid soil	Yield reduction (%)	SSI	STI
CMS 8704 x 9450	7.4	3.9	47	1.3	28.8
Cml 439 x Cam Inb gp1 17	7.2	3.8	47	1.3	27.6
ATP SR Y x 4001	7.0	3.7	48	1.3	25.8
Cml 535 x Cam Inb gp1 17	6.9	3.5	49	1.3	24.3
ATP S6 31Y-BB x 9450	6.9	4.2	39	1.0	28.9
Cml 332 x Cam Inb gp1 17	6.6	3.0	55	1.4	19.8
D300-17 x Cam Inb gp1 17	6.5	4.0	39	1.0	25.9
Cml 434 x Cam Inb gp1 17	6.4	5.1	20	0.5	32.4
Cla 135 x 9450	6.3	4.1	36	0.9	25.6
Cla 135 x 88069	6.3	3.5	44	1.2	22.2
ATP S5 31Y-2 x 9450	6.3	4.3	31	0.8	27.3
ATP S8 30Y-3 x Cam Inb gp1 17	6.3	4.3	32	0.9	26.6
Cml 304 x 9450	6.2	3.7	41	1.1	22.7
Cml 437 x 88069	6.2	3.4	45	1.2	21.1
ATP S6 20Y-1 x 9450	6.1	3.2	47	1.3	19.8
4001 x 9450	6.1	3.1	49	1.3	19.1
ATP-50 x 9450	6.1	2.8	54	1.4	17.3
Cml 357 x Cam Inb gp1 17	6.1	2.8	54	1.4	17.1
4001 x 88069	6.1	2.0	68	1.8	11.9
Cml 439 x 4001	6.1	4.4	28	0.7	26.6
ATP S9 30Y-1 x 9450	6.1	3.6	40	1.1	21.9
ATP S8 26Y-3 x 88069	5.9	2.9	51	1.3	17.4
Cml 357 x 4001	5.9	3.7	38	1.0	21.6
ATP-32 x 4001	5.9	2.6	56	1.5	15.2
Overall mean	5.3	3.3	38	-0.7	17.5
Minimum	3.5	3.3	-10	-0.3	5.9
Maximum	7.4	6.1	69	1.8	35.0

SSI = stress susceptibility index, STI = stress tolerance index.

5.3.7 Pearson correlation coefficients of different indices with yield in acid soil and control environments

In acid soil conditions, yield loss and stress susceptibility indices were highly significantly (P<0.001) and negatively correlated with yield (Table 5.12). Also, stress tolerance index was highly significantly and positively correlated with yield. In control conditions, only stress tolerance index was significant and positively correlated with yield.

Table 5.13: Correlation coefficients with yield and some indices

	Yield C	Yield A	Yield loss	SSI	STI
Yield A	0.27 NS				
Yield loss	0.12 NS	-0.92***			
SSI	0.16 NS	-0.90***	0.99***		
STI	0.58**	0.94***	-0.73***	-0.70***	

** = P<0.01, *** = P<0.001, Yield C = yield under control or control environments, Yield A = yield under acid soil environments.

5.3.8 Standard heterosis of the best 24 hybrids in acid soil conditions

The standard heterosis over the best OPV check (3.17 t/ha in acid soil environments) and over the best hybrid check (4 t/ha in acid soil environments) was estimated for the best 24 high-yielding hybrids selected in acid soil environments (Table 5.13). The standard heterosis ranged from 23% to 93%. All the best 24 hybrids out-yielded the best OPV check by more than 20%.

Moreover, the standard heterosis of the best hybrid check ranged from -2 to 53%. Ten hybrids out-yielded the best hybrid check by at least 10%.

Table 5.14: Standard heterosis of the top 24 high-yielding hybrids in acid soil environments

			Standard heterosis (%)	
			CMS 8704	9450 x Cam Inb gp1 17
Hybrids	yield C	yield A	Acid soil	Acid soil
Cla 183 x 9450	6	6.12	93	53
ATP S9 36Y-BB x 4001	5.48	5.37	70	34
Cla 183 x 88069	5.77	5.36	69	34
Cml 434 x Cam Inb gp1 17	6.35	5.11	61	28
ATP S5 31Y-2 x 4001	5.09	5.07	60	27
Cml 437 x Cam Inb gp1 17	5.83	4.84	53	21
ATP S8 26Y-3 x Cam Inb gp1 17	5.29	4.72	49	18
Cml 534 x 4001	4.86	4.42	39	11
Cla 183 x Cam Inb gp1 17	5.51	4.42	39	11
Cml 439 x 4001	6.06	4.39	39	10
ATP S5 31Y-2 x 9450	6.29	4.34	37	9
C4RR SA4 x Cam Inb gp1 17	5.79	4.26	34	6
ATP S8 30Y-3 x Cam Inb gp1 17	6.26	4.25	34	6
Cam Inb gp1 17 (F) x 9450	4.33	4.23	34	6
CMS 8704 x 88069	5.64	4.23	34	6
Cml 439 x 9450	4.66	4.23	34	6
ATP S6 31Y-BB x 9450	6.89	4.2	32	5
ATP S8 30Y-3 x 4001	4.42	4.14	31	3
Cml 437 x 9450	5.38	4.13	30	3
C4RR SA4 x 88069	4.95	4.06	28	1
CLA 135 x 9450	6.31	4.05	28	1
Cla 183 x 4001	3.62	3.97	25	-1
D300-17 x Cam Inb gp1 17	6.53	3.97	25	-1
ATP SR Y x Cam Inb gp1 17	5.81	3.91	23	-2
Mean	5.3	3.3	4	-18
Checks				
CMS 8704	5.29	3.17	0	-21
Best single hybrid check				
9450 x Cam Inb gp1 17	4.70	4.00	26	0

Yield C = yield under control environments, Yield A = grain yield under acid soil environments.

5.3.9 Standard heterosis of the best 24 hybrids in control soil environments

The standard heterosis over the best OPV check (CMS 8704 yielded 5.3 t/ha in control condition) ranged from 11% to 40% (Table 5.14). All the top 24 hybrids out-yielded the best OPV check. The standard heterosis over the best hybrid check under improved pH of 5 (yielded 6.1 t/ha) ranged from -4% to 21%. Five hybrids out-yielded the best hybrid check by more than 10%. They were ATP S6 31Y-BB x 9450, Cml 535 x Cam Inb gp1 17, ATP SR Y x 4001, Cml 439 x Cam Inb gp1 17, and CMS 8704 x 9450.

Table 5.15: Standard heterosis of the best 24 high-yielding hybrids in control soil environment

			Standard heterosis (%)	
			CMS 8704	4001 x 88069
Genotype	yield C	yield A	Control	Control
CMS 8704 x 9450	7.4	3.89	40	21
Cml 439 x Cam Inb gp1 17	7.24	3.81	37	19
ATP SR Y x 4001	7.04	3.67	33	15
Cml 535 x Cam Inb gp1 17	6.91	3.51	31	13
ATP S6 31Y-BB x 9450	6.89	4.2	30	13
Cml 332 x Cam Inb gp1 17	6.6	3	25	8
D300-17 x Cam Inb gp1 17	6.53	3.97	23	7
Cml 434 x Cam Inb gp1 17	6.35	5.11	20	4
CLA 135 x 9450	6.31	4.05	19	3
CLA 135 x 88069	6.29	3.53	19	3
ATP S5 31Y-2 x 9450	6.29	4.34	19	3
ATP S8 30Y-3 x Cam Inb gp1 17	6.26	4.25	18	3
Cml 304 x 9450	6.2	3.66	17	2
Cml 437 x 88069	6.17	3.42	17	1
ATP S6 20Y-1 x 9450	6.13	3.23	16	0
4001 x 9450	6.13	3.11	16	0
ATP-50 x 9450	6.12	2.82	16	0
Cml 357 x Cam Inb gp1 17	6.11	2.8	16	0
4001 x 88069	6.09	1.96	15	0
Cml 439 x 4001	6.06	4.39	15	-1
ATP S9 30Y-1 x 9450	6.06	3.62	15	-1
ATP S8 26Y-3 x 88069	5.94	2.93	12	-3
Cml 357 x 4001	5.88	3.67	11	-4
Overall mean	5.30	3.30	0	-13
Best OPV check				
CMS 8704	5.29	3.17	0	-13
Best hybrid check				
4001 x 88069	6.10	2.00	15	0

Yield C = grain yield in control environments; Yield A = grain yield in acid soil environments.

5.4 Discussion

The native soil with low soil pH of 4.3 and high Al concentration of 73.2% in the soil solution make the soil ideal for use as a medium for breeding of acid tolerant maize variety. The low ECEC of 3.3 cmol/kg also confirms the soil status as an Oxisol and shows that the soil's ability to hold cations in exchangeable form for plant uptake is very low. It also shows that despite the high biomass from litter fall, the exchange capacity of the soil is largely influenced by the clay type. The 6.2 times increment in the Mg content from 0.2 cmol/kg to 1.2 mol/kg upon addition of the dolomite may have replaced the Al at the exchange complex with a resultant increase in ECEC from 3.3 cmol/kg to 5.4 cmol/kg. The released Al from the exchange site into solution may have then been precipitated leading to decrease in the Al saturation and exchangeable acidity with a concomitant an increase in soil solution pH.

The significant differences recorded between genotypes and between genotype by environments interactions suggest that all the genotypes were different from each other and responded differently in various environments. Therefore, significant progress could be made by selecting these genotypes in acid soil and control environments (The *et al.*, 2006; Ifie, 2013).

In control environments, the heritability of yield (20%) was 2.5 times greater than the heritability under acid soil conditions (8%). All the traits recorded in acid soil environments had low broad sense heritability estimates compared to heritability under control soil conditions. Meaning that yield trait is not highly heritable. Therefore, selection of viable maize genotype should be done in a wide range of environments. According to Navas *et al.* (2008), the average heritability estimate of grain yield was 2.2 times greater for the normal fertile soil environments compared with the acid soil environments and the differences in heritability estimates were similar for all the traits. According to Badu-Apraku *et al.* (2013), grain yield is a complex trait controlled by polygene and has low heritability especially under stress environments.

The overall mean yield of the hybrids on limed soils was 5.3 t/ha and was consistently higher than the overall mean yield of hybrids (3.3 t/ha) on acidic soils. This suggests that Al toxicity significantly reduced grain yield of maize genotypes (Tandzi, 2005); The *et al.*, 2005; The *et al.*, 2006; Navas *et al.*, 2008; Dewi-Hayati *et al.*, 2014). A higher yield under limed soils is an indication that liming is effective in improving yield of maize under Al toxicity. However, liming of soil is laborious, expensive and always affordable for small scale farmers. Therefore a more sustainable and cost effective strategy would be the utilization of Al tolerant genotypes. Although the yields of Al tolerant hybrids identified in this study were not very high, yields of the 24 hybrids selected under acid soil environments and the 24 other selected under control conditions out-yielded the best OPV check (CMS 8704 5.29 t/ha under control conditions and 3.17 t/ha under acid soil environments) in each environment and yielded more than the average yield of 1 t/ha reported in Cameroon (ACDIC, 2010).

The best yielding hybrid under acid soil environments was Cla 183 x 9450 (6.12 t/ha). The parents of this hybrid are from CIMMYT and IITA showing the importance of the introduced inbred lines. In control conditions, the highest yielding hybrid was a top cross hybrid, CMS 8704 x 9450 (7.40 t/ha). This hybrid was a cross between a commercial OPV (CMS 8704) and an introduced inbred line from IITA. Crosses between introduced and local varieties could increase the probability of getting high-yielding hybrid combinations. The importance of top crosses is based on the ability to easily produce seeds since one parent is an open-pollinated variety.

In general, hybrids respond positively to better growing conditions. This is particularly important to avoid genotypes that will perform well under Al toxicity and very poor in control conditions.

Plant height, ear height, ears per plant, relatively short anthesis-silking interval, better plant aspect and ear aspect could be used to make indirect selections for high yield in stress and non-stress environments. Similar studies have shown that short anthesis-to-silking interval in maize hybrids subsequently led to better pollination (Bolanos and Edmeades, 1996; Araus *et al.*, 2012).

The percentage of yield reduction is an indication of Al toxicity effects. Dewi-Hayati *et al.* (2014) reported grain yield reduction in acid soil varied from 2.8 to 71% among their maize genotypes. In the current study, yield reduction ranged from -10% to 69%. The percentage yield reduction observed for Cla 183 x 4001 was negative, an indication that yield of the hybrid was higher under Al toxicity (3.97 t/ha under acid soil and 3.62 t/ha in control environments). This hybrid is not desirable because genotypes that perform well under poor conditions and optimal conditions are required. The hybrid ATP A9 36 Y-BB x 4001 had the lowest yield reduction (2%) under Al toxicity and had grain yield of 5.37t/ha in acid soil and 5.48 t/ha in control conditions. This hybrid is one of the well performed genotype needed. Cml 304 x 4001 yielded 5.3 t/ha in control soil environments and had very poor yield (1.41 t/ha) under acid soil conditions. This genotype could not be selected. The stress tolerance index ranged from 5.9 (ATP S6 31Y-BB x 88069) to 35 (Cla 183 x 9450). ATP S6 31Y-BB yielded 4.21t/ha in control conditions and 1.41 t/ha in acid soil environments whilst Cla 183 x 9450 yielded 6.00 t/ha under control conditions and 6.12 t/ha under acid soil. Therefore, Cla 183 x 9450 performed well under acid soil conditions and control environments and had high stress tolerance index. Cml 304 x 4001 and ATP S6 31Y-BB x 88069 were the most susceptible hybrids while Cla 183 x 4001 and Cla 183 x 9450 were the most tolerant. Cla 183 x 4001 was not among the best 24 high-yielding hybrids selected either in acid soil or in control environments. This result shows that the selection of high-yielding hybrids tolerant to Al toxicity should take into account a relatively low yield reduction, a high stress tolerance index and a good stress susceptibility index. Also, five hybrids performed well in control conditions but had high yield reduction percentage due to Al toxicity. These varieties were CMS 8704 x 9450 (yield reduction of 47%), Cml 439 x Cam Inb gp1 17 (47%), ATP SR Y x 4001 (48%), Cml 535 x Cam Inb gp1 17 (49%) and ATP S6 31Y-BB x 9450 (39%). Even though these hybrids were high-yielding, they were not tolerant to Al toxicity. These varieties could be advanced and released for environments where acidity is not a constraint for production. Similar results were obtained by The *et al*. (2005) who found thad five hybrids had relatively high grain yield on acid soil but were not necessarily tolerant because of the high yield reduction percentage presented due to soil acidity.

The correlation was highly significant suggesting that relatively low yield reduction, low stress susceptibility index and high stress tolerance index could be used to select high-yielding hybrids in acid soil environments. Dewi-Hayati *et al*. (2014) reported similar negative relationship between yield stress indices in acid soil conditions.

According to Hallaeur *et al*. (2010), heterosis is the increased vigor manifested in hybrids and represents the superiority in performance of hybrid individuals compared with their parents. In the present study, standard heterosis was used. It is the superiority of the hybrids over the best OPV and hybrid checks. Ten hybrids out-yielded the best hybrid check by at least 10% in acid soil conditions. Five hybrids out-yielded the best hybrid check by more than 10% in control environments. Cam Inb gp1 17 and 4001 were parents of 6 and 5 hybrids each in the best 15 hybrids selected. Therefore, they could be considered as best testers in this study. In control environments, the best testers were Cam Inb gp1 17 and 9450. These 15 hybrids could be considered for released after multi-locational and on farm trials. Among the 15 best hybrids, two were top crosses and 14 had at least one introduced parents. This means that the introduction of inbred lines was very efficient in the development of high-yielding hybrids in stress and control environments.

5.5 Conclusions

Variability exists among the inbred lines and OPVs which should allow for progress in selection for acid tolerant genotypes. Fifteen high-yielding hybrids were identified under acid soil and control soil environments. These high-yielding hybrids could be released for commercial purpose after multi-locational on-farm trials. Cam Inb gp1 17 and 4001 were parents of 6 and 5 hybrids each in the best 15 hybrids selected. Therefore, they were considered as best testers in this study. In control environments, the best testers were Cam Inb gp1 17 and 9450. Some traits such as plant height, ear height, ears per plant, anthesis-silking interval, plant aspect and ear aspect and indices (yield loss percentage, stress tolerance index and stress susceptibility index) were highly correlated with yield. These traits and indices could be used in the indirect selection of high yield in acid soil environments. All the traits recorded in acid soil environments had low broad sense heritability estimates compared to heritability under control soil conditions. Therefore, selection of maize genotypes should be done in a wide range of environments. Yield loss reduction due to acid soil was very high for some genotypes (varied from 2 to 69%). Therefore, significant progress could be made by selecting genotypes under acid soil and control environments and by classifying inbred lines into heterotic groups.

CHAPTER SIX

6.0 ANALYSIS OF COMBINING ABILITY AND HETEROTIC GROUPING OF MAIZE INBRED LINES UNDER ACID SOIL CONDITIONS

6.1 Introduction

The yield of maize has reduced and ranged from 0.8 to 1 t/ha (ACDIC, 2010). Maize production in Cameroon has been increasing steadily from an estimated 966,000 metric tonnes in 2004 (USDA, 2013), to 1,380 000 metric tons in 2009 (ACDIC, 2012) and 1,647 036 tons in 2013 (FAOSTAT, 2013). These increases have been mainly due to increases in area harvested rather than yield increase per unit area. Maize suffers from a wide range of production constraints, the most important being infertile soils (Meseka *et al.*, 2008).

Maize hybrids produce superior yields under stress and non-stress conditions. The development of hybrids is a major objective of this research. Predicting the performance of hybrids from visual assessment or measuring the performance of the component inbred lines is difficult because of very low correlations between traits in inbred lines and the same traits in the hybrids, especially traits controlled by polygenes (Hallauer and Miranda, 1988). Inbred lines need to be evaluated on the contributions they make to hybrid combinations. Combining ability is the ability of an inbred line to transmit desirable performance to a hybrid (Allard, 1960). It is important for not only selecting desirable parents but also generating information regarding the nature of and magnitude of gene effects controlling quantitative traits (Basbag *et al.*, 2007).

General combining ability (GCA) and specific combining ability (SCA) which identify lines or hybrids with high yield are the most important criteria used to select parental materials in a breeding program (Ceyhan, 2003). Sprague and Tatum (1942) defined general combining ability as the average contribution an inbred line makes to hybrid performance in a series of hybrid combinations in comparison to other inbreds in the same series of hybrid combinations. Specific combining ability is the contribution of an inbred to hybrid performance in a cross with a specific other inbred in relation to its contribution in crosses with an array of other inbreds. GCA is a characteristic of an inbred while SCA is a characteristic of a specific hybrid. Falconer (1981) observed that GCA is directly related to the breeding value of the parent and is associated with additive genetic effects while SCA is associated with non-additive effects such as dominance, over dominance and epistasis.

The line x tester design was used for breeding both self and cross pollinated plants to select favorable parents and crosses, and estimate their GCA and SCA Combining ability analysis is one of the useful tools in identifying the better combiners which may be hybridized to exploit heterosis and to select better crosses for direct use or further breeding work (Nigussie and Zelleke, 2001). Combining ability analyses of Cameroonian inbred lines have been conducted in previous studies but few single cross hybrids have been developed and released and none have been released for acid soil tolerance.

The objectives of this study were to:

- Estimate the combining abilities for agronomic traits in acid soil conditions;
- Identify heterotic groups of maize inbred lines in acid soil conditions, in control and across environments.

6.2 Materials and methods

6.2.1 Germplasm

Twenty-five inbred lines (11 from IRAD) and 14 from CIMMYT) and three open-pollinated varieties (C4RR SA4, CMS 8704, ATP SRY) were crossed to four testers (Cam Inb gp1 17, 88069, 9450 and 4001) (Table 6 1). The resultant 112, testcross hybrids and hybrid parents were used in this study. The lines had different levels of tolerance to acid soil toxicity. The crosses were done at the breeding nursery of IRAD Yaounde / Nkolbisson.

Table 6.1: Names and codes of maize genotype used in this study

Genotype name	Code	Origin	Type	Genotype name	Code	Origin	Type
ATP S5 31Y-2	1	IRAD	Line	Cml 534	17	CIMMYT	line
ATP S6 20Y-1	2	IRAD	Line	Cml 535	18	CIMMYT	line
ATP S6 21Y-2	3	IRAD	Line	Cml 332	19	CIMMYT	line
ATP S6 31Y-BB	4	IRAD	Line	Cml 479	20	CIMMYT	line
ATP S8 26Y-2	5	IRAD	Line	Cla 183	21	CIMMYT	line
ATP S8 30Y-3	6	IRAD	Line	Cml 434	22	CIMMYT	line
ATP S9 30Y-1	7	IRAD	Line	Cla 135	23	CIMMYT	line
ATP S9 36Y-BB	8	IRAD	Line	D300-17	24	CIMMYT	line
ATP-32	9	IRAD	Line	Cam Inb gp1 17 (F)	25	IRAD	line
ATP-50	10	IRAD	Line	Cam Inb gp1 17	26	IRAD	tester
Cml 304	11	CIMMYT	Line	88069	27	IRAD	tester
Cml 357	12	CIMMYT	Line	9450	28	IITA	tester
Cml 435	13	CIMMYT	Line	4001	29	IRAD	tester
Cml 437	14	CIMMYT	Line	C4RR SA4	30	CIMMYT	OPV
Cml 439	15	CIMMYT	Line	CMS 8704	31	IRAD	OPV
Cml 533	16	CIMMYT	Line	ATP SR Y	32	IRAD	OPV

6.2.2 Experimental sites

Trials were conducted at IRAD - Nkoemvone station located in the Southern Region of the country. The characteristics of the experimental sites were as described in Chapter 5 section 5.1.2.

6.2.3 Experimental Design

The experimental site was made of 2 treatments of the soil. The first treatment was a native acid soil (A) and the second treatment was the control or control soil environments. On the control (C), acidity level of the soil was reduced by the use of 4t/ha of dolomite. The genotypes were planted in simple lattice design 12 x 12 (12 incomplete blocks x 12 genotypes) using two replications during three years.

6.2.4 Land preparation, planting and field management

The land preparation and seed planting were conducted as explained in Chapter 5, section 5.1.5. Two different planting dates (three weeks interval) were used to create additional environments as stated by Singh and Chaudhary (Singh and Chaudhary, 1979). The different environments are presented in Table 6.2.

Table 6.2: List of acid soil and control environments

Environment	Component	
Environment 1	Site 1 * treatment 1 (acid) * year 1 (2012)	Acid soil environments (A)
Environment 2	Site 1 * treatment 1 (acid) * year 2 (2013)	
Environment 3	Site 1 * treatment 1 (acid) * year 3 (2014)	
Environment 4	Site 2 * treatment 1 (acid) * year 1 (2012)	
Environment 5	Site 2 * treatment 1 (acid) * year 2 (2013)	
Environment 6	Site 2 * treatment 1 (acid) * year 3 (2014)	
Environment 7	Site 1 * treatment 2 (control) * year 1 (2012)	Control environments (C)
Environment 8	Site 1 * treatment 2 (control) * year 2 (2013)	
Environment 9	Site 1 * treatment 2 (control) * year 3 (2014)	
Environment 10	Site 2 * treatment 2 (control) * year 1 (2012)	
Environment 11	Site 2 * treatment 2 (control) * year 2 (2013)	
Environment 12	Site 2 * treatment 2 (control) * year 3 (2014)	

6.2.5 Data collection

Data were recorded on: plant stand after thinning, number of days to anthesis (DA), number of days to silking (DS), anthesis to silking interval (ASI) calculated using the formula ASI (days) = DS – DA, plant height (cm), ear height (cm), moisture content, and grain yield (GY) measured on a whole plot basis following standard CIMMYT procedure (CIMMYT, 1985) adjusted to 15% moisture using the formula below

GY (t/ha) = [Grain Weight (kg/plot) x 10 x (100-MC) / (100-15) / (Plot Area)]

Where MC = Grain Moisture Content.

The number of ears at harvest was also recorded and ears per plant (EPP) was calculated using the formula EPP = EC/PC, Where EC and PC = number of ears and number of plants per plot, respectively. Also, ear aspect and plant aspect were recorded using the scale 1 to 5 (5 being the worst and 1 the best).

6.2.6 Data analysis

- **Analysis of variance**

Analyses of variance were computed for each environment (E) and combined acid soil environments, control soil environments and across environments for all the traits recorded. The environment effects were treated as ramdom and cross effects as fixed. The line by tester analyses were performed for each environment using the method described by Kempthorne (1957). The statistical model used to obtain the different effects was as follows:

$$Y_{ijk} = \mu + l_i + t_j + (l \text{ x } t)_{ij} + Bk_{ke} + e_{ijk}$$

Where: Y_{ijk} is the kth observation on ijth progeny, μ is the general mean, l_i is the effect of the ith line, t_j is the effect of the jth tester, $(l \text{ x } t)_{ij}$ is the interaction effect of the cross between ith line and jth tester, Bk_{ke} is the effect of block nested within replicate k by environment e and e_{ijk} is the error term associated with each observation.

General combining ability (GCA) and specific combining ability (SCA) were generated for each of the traits according to the procedure described by Kempthorne (1957). The statistical model for the analysis study was as followed:

$$Yijke = \mu + E_e + l_i + t_j + (l \text{ x } t)_{ij} + Bk_{ke} + gE_{eg} + sS_{es} + \varepsilon_{ijke}$$

Where Yij is the observed measurement for the ijth cross grown in kth replication in the eth environment; μ is the grand mean; Ee is the main effect of Environment; g_i and g_j are the line and tester effects; s_{ij} is the line by tester effect; gE_{eg} is the interaction effect between line, tester and Environment; Bk_{ke} is the effect of block nested within replicate k by environment e, sEes is the interaction effect between line by tester and the Environment, and εijke is the error term associated with the ijth cross evaluated in the kth replication in eth environment.

Estimation of general (GCA) and specific combining ability (SCA) effects

The GCA and SCA effects for the lines, testers and line by tester were generated through SAS version 9.2 software.

Proportional contribution of line, tester and line x tester

The estimation of lines (l), testers (t) and lines x testers (lxt) was done using the formula below (Singh and Chaudhary, 1979):

Contribution of line = SS (l) * 100 / SS (crosses)

Contribution of tester = SS (t) * 100 / SS (crosses)

Contribution of line x tester = SS (lxt) * 100 / SS (crosses)

Where SS is sum of squares

6.2.7 Heterotic grouping of inbred lines

The inbred lines were assigned to heterotic groups by using the traditional method of specific combining ability (Vasal *et al.*, 1992). Lines in genetically different heterotic groups are usually identified by positive SCA effects between them while inbred lines in the same heterotic group have a tendency to exhibit negative SCA effects when crossed (Vasal *et al.*, 1992). The inbred line classified into heterotic groups had to perform well in crosses when compared to the best check (10% of superiority).

6.3 Results

6.3.1 Analysis of variance for all the traits

The analysis of variance across acid soil environments showed significant differences among the lines (GCA) for yield, plant aspect, ear aspect, ear height, plant height and anthesis-silking interval while, for the testers (GCA), significant differences were recorded for ear aspect, ears per plant, ear height and plant height. Lines x tester (SCA) effects were significant for all traits (Table 6 3). The interaction environment by lines was significant for yield, plant aspect, ear aspect, ear height and plant height. The interaction environment by tester and environment by (line x tester) was not significant for all the traits recorded.

In control environments, significant differences were recorded in lines (GCA) for plant aspect and anthesis-silking interval; in testers (GCA) for yield and anthesis-silking interval; in line x tester (SCA) for ear aspect, ears per plant, ear height and anthesis-silking interval and in environments for all the traits measured across environments (table 6 4). The interaction environment by lines was significant for all the traits recorded.

Across environments, line effect were significant for all traits except yield, tester effect were significant for all traits except plant aspect and anthesis-silking interval, and line x tester were significant for all the traits (Table 6 5). The environment x line interaction effects was highly significant for all traits. The environment by tester interaction was not significant for all the traits. The line x tester interaction with environment was significant for yield, plant and ear aspect.

Table 6.3: Mean squares for various traits recorded on lines, tester and lines by testers in acid soil environments

Source	DF	Yield (t/ha)	Pltasp	Earasp	Epp	Earght (cm)	Pltght (cm)	Asi (day)
Block (rep*env)	120	7.4***	0.7***	1.1**	0.06***	612.3***	1403.3***	19.1***
Line (GCA)	27	7.2*	0.98**	1.2*	0.06 NS	961.9**	1801**	10.09**
Tester (GCA)	3	3.1 NS	0.7 NS	0.8*	0.1*	3786***	6649***	2.6 NS
Line x tester (SCA)	81	5.7***	0.5*	0.8**	0.05*	412.9**	989.6***	6.3**
Env x line	135	4.5**	0.4*	0.7*	0.04 NS	443.9***	447.5***	4.9 NS
Env x tester	15	1.4 NS	0.3 NS	0.2 NS	0.03 NS	359.7 NS	519.2 NS	6.3 NS
Env x line x tester	405	3.3 NS	0.3 NS	0.5*	0.04 NS	281.5 NS	511.2 NS	4NS
Error	652	3	0.3	0.4	0.04	284.2	567.1	4.2
Mean		3.4	3.2	2.7	1	71.8	158.9	10.6

*Significant at 5% level; **Significant at 1% level;*** Significant at 0.1% level; NS = non-significant; pltasp = plant aspect; earasp = ear aspect; epp = ear per plant; earght = ear height; pltght = plant height; asi = anthesis-silking interval; GCA = general combining ability; SCA = specific combining ability, rep = replication, env = environment.

Table 6.4: Mean squares for various traits recorded on all lines, testers and lines by testers in control soil environments

Source	DF	Yield (t/ha)	pltasp	earasp	epp	Earght (cm)	Pltght (cm)	Asi (day)
Block (rep*env)	120	7.6***	0.5***	0.7***	0.05 NS	616.5***	1290***	8.5***
Line (GCA)	27	4 NS	0.6*	0.7 NS	0.1 NS	672 NS	1113.9 NS	6.3*
Tester (GCA)	3	22.9*	0.07 NS	0.5 NS	0.04 NS	791NS	197 NS	10.5*
Line x tester (SCA)	81	6.5 NS	0.35 NS	0.7***	0.06*	512.6**	637 NS	4.3***
Env x line	135	8.3***	0.4**	0.6**	0.07***	435**	748.8**	4***
Env x tester	15	4.4 NS	0.4 NS	0.3 NS	0.05 NS	305.4 NS	689 NS	2.4 NS
Env x line x tester	405	5.6*	0.3*	0.4***	0.04 NS	323.2 NS	587**	2.6 NS
Error	652	4.6	0.2	0.3	0.05	221	446.7	2.6
Mean		5.3	2.5	2.1	1.1	93.5	194.6	2

*Significant at 5% level; **Significant at 1% level;*** Significant at 0.1% level; NS = non-significant; pltasp = plant aspect; earasp = ear aspect; epp = ear per plant; earght = ear height; pltght = plant height; asi = anthesis-silking interval; GCA = general combining ability; SCA = specific combining ability, rep = replication, env = environment.

Table 6.5: Mean squares for various traits recorded on lines, testers, and lines x testers across environments

Source	DF	Yield	pltasp	earasp	epp	earght	pltght	asi
Block(rep*env)	231	7.4***	0.6***	0.9***	0.6**	614.3***	1349***	14***
Line (GCA)	27	5.5 NS	0.9**	1.3***	0.09*	1366.6***	2455.2***	14.5***
Tester (GCA)	3	17.4 **	0.45 NS	1.3***	1.13*	3927.7***	7907.6***	10 NS
Line*tester (SCA)	81	7.8***	0.5**	1***	0.07***	611***	945.5***	7.8***
Env*line	297	6.3***	0.4***	0.6***	0.05***	431***	808.8***	4.2***
Env*tester	33	3.4 NS	0.3 NS	0.2 NS	0.04 NS	356.5 NS	615.9 NS	4.3 NS
Env*line*tester	891	4.4*	0.3*	0.5***	0.04 NS	302.7 NS	561.1 NS	3.2 NS
Error	1323	3.8	0.3	0.4	0.04	287.6	506.4	3.4
Mean		4.4	2.8	2.4	1.1	82.6	176.7	2.3

*Significant at 5% level; **Significant at 1% level;*** Significant at 0.1% level; NS = non-significant; pltasp = plant aspect; earasp = ear aspect; epp = ears per plant; earght = ear height; pltght = plant height; asi = anthesis-silking interval; GCA = general combining ability; SCA = specific combining ability, rep = replication, env = environment.

6.3.2 Relative contribution of GCA lines, GCA testers and SCA of traits in acid soils, control and across environments

The relative contribution of GCA and SCA to the total sum of squares of crosses indicated that, for grain yield, GCA accounted for 28% for lines and 1% for testers to the variation among crosses and SCA accounted for 68% of the variation in acid soil conditions; GCA accounted for 17% of lines and 6% of testers whilst SCA accounted for 53% of the total variation across environments; and GCA accounted for 15% of lines and 10% for testers of the variation among crosses and SCA accounted for 73% of the variation in control environments (Table 6.6). In general, the contribution of SCA was higher than the contribution of GCA for all the traits recorded under acid soil, under control soil and across environments.

Table 6.6: Relative contribution (%) of GCA and SCA for yield, ears per plant, anthesis-silking interval and ear height in acid soil, control and across environments

	Yield (t/ha)			Ears per plant			Anthesis-silking interval (day)			Ear height (cm)		
Component	Acid soil	Control	Across	Acid soil	Control	Across	Acid soil	Control	Across	Acid soil	Control	Across
Line (GCA)	28	15	17	25	35	28	35	32	38	36	30	38
Tester (GCA)	1	10	6	6	1	4	1	6	3	16	4	12
Line x tester (SCA)	68	73	53	70	63	64	75	66	62	47	68	51

GCA = general combining ability; SCA = specific combining ability.

6.3.3 General combining ability for lines and testers in acid soil, control soil and across environments

Estimates of general combining ability for yield, ear aspect, plant aspect, ear height, plant height, ears per plant and anthesis-silking interval showed significant difference for yield of ten lines (ATP S8 26Y-2, ATP S8 30T-3, ATP S9 30Y-1, ATP S9 36Y-BB, ATP-32, ATP-50, Cml 533, Cml 479, Cla 183 and CMS 8704) in acid soil conditions (Table 6.7). Among those genotypes, five had positives value of GCA for yield. These were ATP S8 26Y-2 (0.87 t/ha), ATP S8 30Y-3, ATP S9 30Y-1, ATP S9 36Y-BB and Cla 183. The GCA of plant aspect was significant for six genotypes. Among the significant effects of GCA, two genotypes were positively significant ATP-32, and Cml 533. GCA of 6 genotypes was positively significant for ear aspect. Twelve genotypes had significant effect of GCA for ears per plant while four genotypes had positive and significant GCA effects for ear height. For plant height, 5 genotypes had positive significant effect of GCA. These genotypes were (Cml 301, Cml 479, Cla 135, C4RR SA4 and ATP SR Y) had positive significant effect. Anthesis-silking interval had significant effect of GCA throughout except for genotype Cml 534 which had positive and non-significant value. Fourteen of 29 genotypes had positive significant GCA effect for anthesis-silking interval (Table 6.7).

Table 6.7: General combining ability of ‘lines’ for all the traits in acid soil environments

Inbred lines	Yield (t/ha)	Pltasp	Earasp	Epp	Earght (cm)	Pltght (cm)	Asi
ATP S5 31Y-2	0.17	-0.08	-0.06	0.03	2.35	-3.28	0.00
ATP S6 20Y-1	0.33	0.05	-0.09	-0.04	0.69	-5.23	0.24
ATP S6 21Y-2	0.41	0.09	-0.10	-0.01	1.15	-3.03	0.40
ATP S6 31Y-BB	0.28	-0.07	-0.15	0.05	12.5*	8.64*	0.13
ATP S8 26Y-2	0.87*	-0.12	-0.24*	0.02	2.93	-0.13	-0.40
ATP S8 30Y-3	0.98*	-0.05	-0.28*	0.00	7.53*	10.27*	-0.30
ATP S9 30Y-1	0.69*	-0.2*	-0.39*	-0.02	6.88*	12.7*	0.70*
ATP S9 36Y-BB	0.64*	-0.21*	-0.08	0.02	2.03	3.03	0.80*
ATP-32	-0.68*	0.21*	0.40*	-0.04	-7.19*	-6.43	0.80*
ATP-50	-0.62*	0.13	0.33*	0.04	-0.08	5.42	0.00
Cml 304	-0.39	0.06	0.09	-0.04	1.56	-0.16	0.40
Cml 357	-0.21	0.08	0.04	-0.01	-3.44	-0.17	0.97*
Cml 435	0.13	0.09	0.04	0.04	-7.11*	-6.24	0.80*
Cml 437	0.11	0.05	-0.10	-0.06	-0.81	-1.77	0.97*
Cml 439	0.25	-0.01	-0.20*	-0.04	-7.23*	-6.76	-0.40
Cml 533	-0.57*	0.17*	0.20*	-0.01	-7.35*	-11.8*	-0.70*
Cml 534	-0.23	0.10	-0.04	-0.02	-4.83	-3.15	-0.30
Cml 535	-0.38	-0.3*	-0.02	0.04	1.44	-3.38	0.83*
Cml 332	-0.4	0.02	0.09	0.00	-3.38	-4.88	0.00
Cml 479	-0.67*	0.05	0.03	0.04	-4.00	2.85	-1.10*
Cla 183	0.73*	-0.3*	-0.29*	-0.03	10.8*	15.2*	-0.30
Cml 434	0.16	-0.14	-0.09	-0.01	0.03	7.48*	-0.70
Cla 135	-0.23	0.08	0.02	0.02	-2.81	-2.02	-0.50
D300-17	-0.23	0.06	0.04	0.04	2.77	1.94	-0.40
Cam Inb gp1 17 (F)	0.00	-0.02	0.06	0.06	-1.30	-6.17	-0.60
C4RR SA4	-0.09	0.07	0.28*	-0.02	0.89	-0.97	0.00
CMS 8704	-0.57*	0.10	0.20*	-0.03	-4.09	-5.07	-0.80*
ATP SR Y	-0.49	0.10	0.29*	-0.01	0.04	3.06	-0.70

Pltaspe =plant aspect, earasp = ear aspect, epp = ear per plant, earght = ear height, pltght = plant height, asi = anthesis-silking interval, * = significant at P<0.05.

The estimate of the general combining ability of all the quantitative traits in control environments gave only one negative significant difference for yield observed with C4RR SA4 (Table 6.8). Five lines had significant GCA for plant aspect, among them 3 had positive effects. For ear aspect, three genotypes gave positive significant effect of GCA. There were no significant effects of GCA for ears per plant whilst three lines (ATP S6 31Y-BB, Cml 304 and C4RR SA4) showed positive significant effect of GCA for ear height. Similarly, five genotypes (Cml 304, (Cml 479, Cla 135, C4RR SA4, ATP SR Y) had positive and significant GCA effects for plant height. For anthesis-silking interval, only Cml 534 gave a positive value of GCA in control environments.

The testers Cam Inb gp1 17 and 9450 showed positive GCA for yield while testers 88069 and 4001 gave negative GCA for yield in acid soil environments (Table 6 9). A significant and positive GCA was observed in tester 88069 for plant aspect, in tester 9450 and 4001 for ear aspect and with tester 88069 for plant height. In control environments, only the GCA of Cam Inb gp1 17 had positive and significant effect for yield and anthesis-silking interval (Table 6 10).

Table 6.8: General combining ability of ‘lines’ for all the traits in control environments

Inbred lines	yield (t/ha)	pltasp	earasp	epp	earght (cm)	pltght (cm)	asi
ATP S5 31Y-2	-0.42	-0.06	0.12	0.12	1.03	-0.93	-0.37*
ATP S6 20Y-1	0.46	-0.09	-0.27*	-0.04	-1.42	-6.18	-0.11*
ATP S6 21Y-2	0.24	0.10	-0.11	0.02	1.76	-2.46	-0.09*
ATP S6 31Y-BB	-0.09	0.01	-0.07	0.05	8.82*	1.84	-0.17*
ATP S8 26Y-2	0.12	0.10	-0.07	0.10	-1.08	-6.80*	-0.63*
ATP S8 30Y-3	0.36	0.06	-0.09	0.02	-0.59	0.78	-0.30*
ATP S9 30Y-1	-0.01	0.07	0.06	-0.08	2.88	4.60	0.53*
ATP S9 36Y-BB	0.08	0.01	0.03	-0.03	-3.40	-4.64	0.16*
ATP-32	-0.26	0.04	0.17	0.00	-3.22	-9.00*	0.27*
ATP-50	-0.09	0.11	0.23*	0.08	-1.46	3.10	0.53*
Cml 304	0.43	-0.17*	-0.20*	-0.03	6.70*	6.96*	0.46*
Cml 357	0.48	-0.14	-0.15	-0.01	2.08	4.34	0.82*
Cml 435	0.00	0.02	0.05	-0.05	-10.65*	-9.60*	0.59*
Cml 437	0.59	0.07	-0.19*	-0.01	1.24	-0.39	1.12*
Cml 439	0.41	0.02	-0.01	-0.04	-8.80*	-8.60*	-0.20*
Cml 533	-0.36	0.16*	0.18*	0.02	-2.55	-6.58	-0.65*
Cml 534	-0.36	0.08	0.06	0.04	-3.23	-2.78	0.00
Cml 535	-0.34	-0.12	0.09	0.08	0.11	-3.04	1.01*
Cml 332	-0.45	0.06	0.07	0.04	-3.90	-6.16	0.12*
Cml 479	-0.38	-0.02	-0.03	-0.04	2.83	8.53*	-0.38*
Cla 183	-0.22	-0.03	0.06	0.01	4.60	3.91	0.10*
Cml 434	0.49	-0.09	-0.20*	0.01	-4.55	2.36	-0.45*
Cla 135	0.46	-0.06	-0.19*	-0.04	0.95	6.98*	-0.59*
D300-17	-0.33	0.10	0.03	-0.03	4.12	1.86	-0.40*
Cam Inb gp1 17 (F)	-0.55	0.30*	0.00	-0.01	-3.11	-3.17	-0.20*
C4RR SA4	-0.66*	-0.15*	0.27*	-0.06	7.80*	13.99*	-0.13*
CMS 8704	0.49	0.26*	0.04	-0.08	2.41	3.39	-0.40*
ATP SR Y	-0.09	-0.10	0.16	-0.05	0.62	7.66*	0.26*

Pltaspe =plant aspect, earasp = ear aspect, epp = ear per plant, earght = ear height, pltght = plant height, asi = anthesis-silking interval, * = significant at P<0.05

Table 6.9: General combining ability of the testers in acid soil environments for all the traits

Tester	Yield (t/ha)	pltasp	earasp	epp	earhgt (cm)	pltght (cm)	asi
Cam Inb gp1 17	0.03	-0.05	-0.04	0.02	-1.1	1.79	0.04
88069	-0.07	0.07*	0.07	0.02	-4.28*	-6.13*	0.03
9450	0.11	-0.003	0.004	-0.01	2.96*	3.87*	-0.13
4001	-0.06	-0.01	-0.04	0.01	2.4*	0.47	0.07

pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, pltght = plant height, asi = anthesis-silking interval, * = significant at P<0.05.

Table 6.10: General combining ability of the testers in control soil environments for all the traits

Tester	yield (t/ha)	pltasp	earasp	epp	earght (cm)	pltght (cm)	asi
Cam Inb gp1 17	0.35*	-0.002	-0.02	0.02	-0.72	1.04	0.25*
88069	-0.14	-0.01	0.04	-0.01	-1.77	-3.4*	-0.1
9450	0.03	-0.01	0.03	-0.01	1.50	2.13	-0.08
4001	-0.25*	0.02	-0.04	0.00	0.99	0.27	-0.07

pltasp =plant aspect, earasp = ear aspect, epp = ear per plant, pltght = plant height, asi = anthesis-silking interval, * = significant at P<0.05.

Across environments, 20 out of 28 ‘lines’ gave positive GCA but only two were significant for yield: ATP S9 30Y-1 and Cml 479 (Table 6.11). The GCA’s of the testers were all negative and significant across environments.

Table 6.11: SCA and GCA of genotypes for grain yield across environments

	SCA for yield				
Genotypes	Cam Inb gp1 17	88069	9450	4001	**GCA**
ATP S5 31Y-2	-1.40*	-0.47	0.91*	1.08*	-0.06
ATP S6 20Y-1	-0.47	0.76	0.41	0.28	0.24
ATP S6 21Y-2	-0.09	0.7	0.09	0.27	0.18
ATP S6 31Y-BB	-0.83*	-0.8	1.34*	-0.22	0.32
ATP S8 26Y-2	0.64	0.62	0.19	-0.55	0.37
ATP S8 30Y-3	1.04*	-0.25	0.13	0.59	0.39
ATP S9 30Y-1	-0.02	-0.13	0.3	-0.15	0.43*
ATP S9 36Y-BB	0.34	0.15	-0.76	0.99*	0.27
ATP-32	0.43	-0.13	-0.5	0.12	-0.36
ATP-50	-0.88*	-0.16	0.32	-0.29	0
Cml 304	0.34	-0.54	0.94*	-0.35	0.02
Cml 357	-0.06	-0.31	-0.35	0.56	0.27
Cml 435	0.06	0.13	0.06	0.35	0.01
Cml 437	0.83*	0.16	0.15	-0.14	0.2
Cml 439	0.35	-0.01	-0.13	0.21	0.32
Cml 533	-0.31	-0.25	0.01	0.39	-0.33
Cml 534	-0.55	-0.4	-0.4	0.44	0.03
Cml 535	0.89*	0.24	-0.56	-0.33	-0.33
Cml 332	0.45	0.61	-0.58	-0.28	-0.38
Cml 479	0.11	-0.33	-0.4	0.5	-0.40*
Cla 183	-0.22	0.54	1.06*	-0.64	0.16
Cml 434	1.09*	0.23	-0.13	-0.26	0.19
Cla 135	0.39	0.36	0.34	-0.41	0.04
D300-17	0.73	-0.21	0.22	-1.03*	-0.11
Cam Inb gp1 17 (F)	-0.82	-0.05	-0.01	-0.01	0.04
C4RR SA4	-	-	-	-	-0.02
CMS 8704	-	-	-	-	0.28
ATP SR Y	-	-	-	-	0.01
GCA	-2.59*	-1.8*	-2.4*	-2.2*	

Pltaspe =plant aspect, earasp = ear aspect, epp = ear per plant, earght = ear height, pltght = plant height, asi = anthesis-silking interval, NS = non-significant, * = significant at P<0.05, Prob = probability.

6.3.4 Specific combining ability of the hybrids in acid soil, control soil and across environments

Significant and positive SCA effects for grain yield were obtained for ATP S5 31Y-2 with 4001 and a negative and significant SCA was obtained with the same line when crossed with Cam Inb gp1 17 in acid soil environments (Figure 6.1 and Appendix 6.1). More than ten lines had positive effect of SCA in stress environments when cross with all the testers. In control environments, Cml 535 had significant and positive SCA with Cam Inb gp1 17, and ATP S6 31Y-BB specifically combined with 9450 and 4001, respectively, for yield (Figure 6 2 and Appendix 6 2).

Across environments, 14 inbred lines had positive SCA values with Cam inb gp1 17, 11 gave positive values with 88069, 15 lines with 9450 and 12 lines with 4001 (Table 6.11). The SCA of 8 lines (ATP S5 31Y-2, ATP S6 31Y-BB, ATP S8 30Y-3, ATP-50, Cml 437, Cml 535 and Cml 434) were significant and four of them were positive with Cam Inb gp1 17; 4 inbred lines were positively significant with 9450 (ATP S5 31Y-2, ATP S6 31Y-BB, Cml 304and Cla 183). ATP S5 31Y-2 had positive and significant effect of SCA with 9450, ATP S9 36Y-BB had positive and significant SCA with 4001 and D300-17 had positive and significant SCA with Cam Inb gp1 17 (Table 6.11).

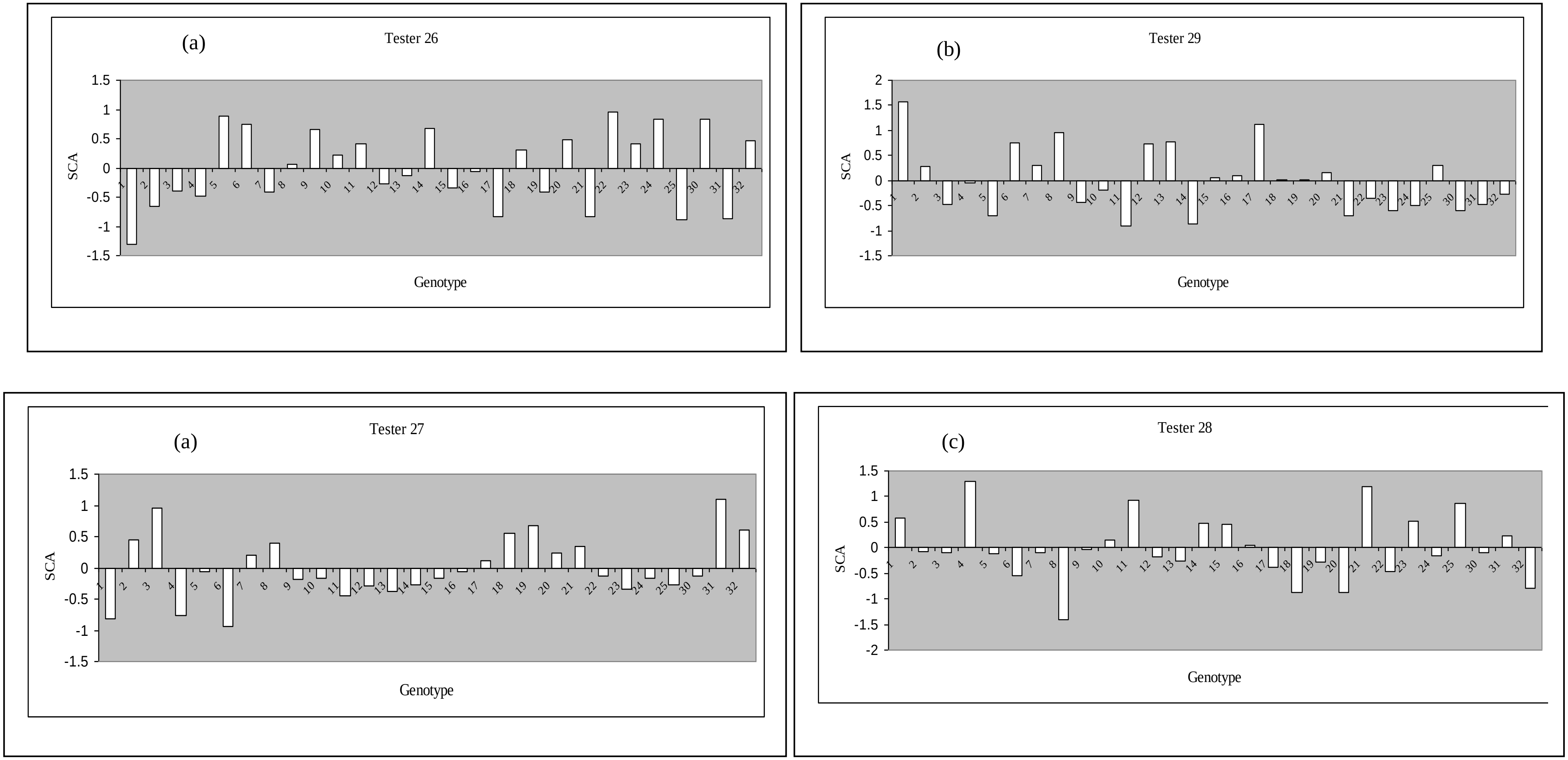


Figure 6.1: Specific combining ability of testers 26 (a), 27 (d), 28 (b) and 29 (b) with the 28 ‘lines’ for yield trait under acid soil environments.

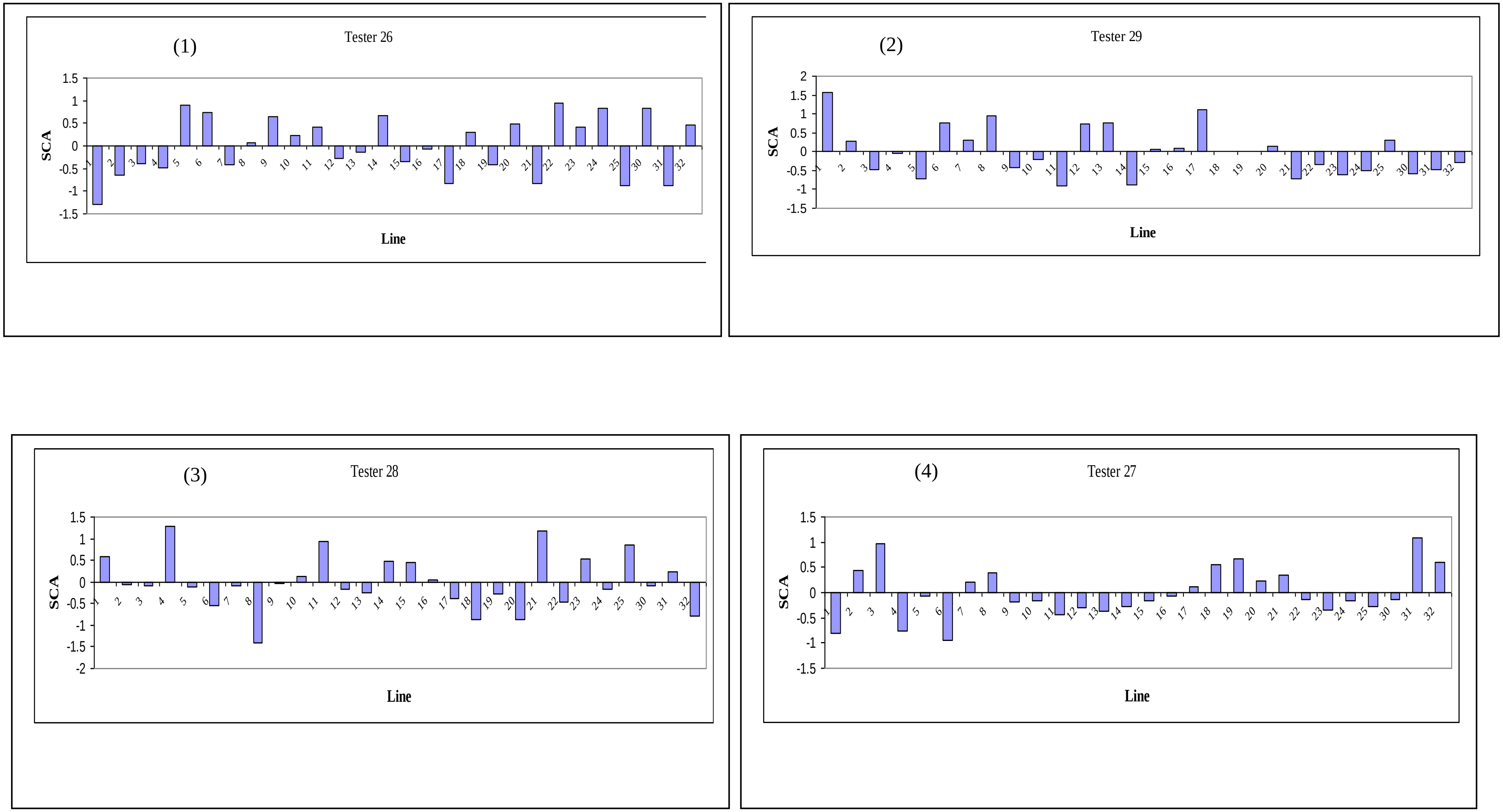


Figure 6.2: Specific combining ability of testers 26 (1), 27 (4), 28 (3) and 29 (2) with the 28 'lines' for yield trait under control environments.

6.3.5 Heterotic groups in acid soil, control soil and across environments

Inbred lines were classified into heterotic groups based on their specific combining ability with each of the four testers (Cam Inb gp1 17, 88069, 9450 and 4001) and also based on their yield compare to the yield of the best hybrid check in a given environment (Table 6.12). The best check under acid soil conditions was 9405 x Cam Inb gp1 17 which yielded 4.0 t/ha. Any testcross hybrids with a positive specific combining ability and expressing a yield of 10% greater than the best check when crossed with a tester was classified in the anti group of that tester. Ten out of 25 inbred lines were classified into four heterotic groups in acid soil environments. For instance, Heterotic group A had three inbred lines (ATP S8 26Y-2, ATP S8 30Y-3 and Cml 434) which were anti to Cam Inb gp1 17.

In control condition, the best hybrid check was 4001 x 88069 and yielded 6.1 t/ha. The inbred lines expressing yield 10% higher than the yield of the best check were classified into anti heterotic group of the tester. Heterotic group A had three introduced inbred lines (Cml 437, Cml 439 and Cml 434) and heterotic group C had one inbre line (ATP S6 31Y-BB). Group B and D were empty.

Across environments, 17 inbred lines out of 25 were classified into heterotic groups. Group A had the highest number of lines (10 inbred lines) which yielded at least 10% higher than the best check when crossed with Cam Inb gp1 17. Heterotic group C had 8 inbred lines; group B and D had four lines each. Four checks out of six yielded 4.3 t/ha across environments.

Table 6.12: Heterotic grouping of inbred lines in acid soil control soil and across environments

Group A/Anti Cam Inb gp1 17	**Group B/Anti 88069**	**Group C/Anti 9450**	**Group D/Anti 4001**
Under acid soil environments			
ATP S8 26Y-2	ATP S6 21Y-2	ATP S6 31Y-BB	ATP S5 31Y-2
ATP S8 30Y-3	ATP S9 36Y-BB	Cla 183	ATP S8 30Y-3
Cml 434	Cla 183	Cam Inb gp1 17 (F)	ATP S9 30Y-1
			ATP S9 36Y-BB
Best hybrid check			
9450 x Cam Inb gp1 17	4.0 t/ha		
Under control conditions			
Cml 437	/	ATP S6 31Y-BB	/
Cml 439	/		/
Cml 434	/		/
Best hybrid check			
4001 x 88069	6.1 t/ha		
Across environments			
ATP S8 26Y-2	ATP S6 20Y-1	ATP S5 31Y-2	ATP S5 31Y-2
ATP S8 30Y-3	ATP S6 21Y-2	ATP S6 20Y-1	ATP S8 30Y-3
ATP S9 36Y-BB	ATP S8 26Y-2	ATP S6 31Y-BB	ATP S9 36Y-BB
Cml 304	Cla 183	ATP S8 26Y-2	Cml 357
Cml 437		ATP S8 30Y-3	
Cml 439		ATP S9 30Y-1	
Cml 535		Cml 304	
Cml 434		Cla 183	
Cla 135			
D300-17			
Best hybrid checks			
4001 x 9450			
88069 x Cam Inb gp1 17			
9450 x 88069			
9450 x Cam Inb gp1 17	4.3 t/ha		

Anti A = opposite tester Cam Inb gp1 17, Anti B = apposite tester 88069, anti C = anti 9450 and anti D = anti 4001.

6.4 Discussion

The significant differences recorded among environment and line x tester interaction across environments indicated that genotypes were different from each other and responded differently in different environments (The *et al.* 2006, Badu-Apraku *et al*. 2013 and Ifie 2013). The presence of significant GCA and SCA mean squares for all the traits recorded under acid soil and across environments for anthesis-silking interval under control environments revealed that these traits were controlled by both additive and non-additive gene actions (The *et al.*, 2005; Badu-Apraku *et al.*, 2013; Ifie, 2013).

The comparison of GCA sum of squares to SCA sum of squares showed that the contribution of SCA was higher for almost all the traits (yield, anthesis-silking interval, ears per plant) recorded in acid soil, control and across environments except for ear height in acid soil environments. This result revealed that all these traits were predominantly controlled by non-additive gene actions in their expression. On average, SCA explained 68%, 73% and 53% of the total sum of squares among crosses in acid soil, control soil and across environments, respectively, for yield. Therefore yield was maintly controlled by the non-additive genes than the additive gene in the study environments. This confers the advantage of exploiting heterosis to improve grain yield of maize hybrids in acid soil control soil and across environments. This implied that appreciable breeding progress could be made using hybridization, backcrossing, and recurrent selection methods for the development of hybrids and synthetic varieties as well as in population improvement after classifying inbred lines into heterotic groups. These findings were also reported by Fan *et al.* (2008), Meseka *et al.* (2008), Worku *et al.* (2008), Badu-Apraku *et al.* (2011b) and Ifie (2013). The result obtained in the present study was different to that of The *et al.* (2005) who reported that tolerance to soil acidity was predominantly controlled by additive gene actions. The difference observed in the two studies could be due to the difference in plant materials utilized as well as the environments used for the evaluation. The larger proportion of GCA effects of inbred lines for ear height than the SCA effects in acid soil environments suggested that additive gene action played a dominant role in the inheritance of the measured traits. This result implied that additive gene action was more important than the non-additive for this trait and that GCA was the main component accounting for the differences among the hybrids for the study environment. Akinwale *et al.* (2014) and Badu-Apraku *et al*. (2013) made the same observations under different stress environments studied. The results of the current study were different from the findings of Tekeu *et al.* (2014) who found that tolerance to acid soils with aluminum toxicity was controlled by additive gene effects while on acid soil manganese toxicity, the contribution of non-additive gene effects was dominant. The difference observed might be due to the different genotypes and environments used.

In the present study, five inbred lines had positive and significant GCA effects under acid soils. They were ATP S8 26Y-2, ATP S8 30Y-3, ATP S9 30Y-1, ATP S9 36Y-BB and Cla 183. ATP S8 26Y-2 gave positive SCA with Cam Inb gp1 17; ATP S8 30Y-3 gave positive SCA with Cam Inb gp1 17 and 4001; ATP S9 30Y-1 gave positive SCA with 88069 and 4001; ATP S9 36Y-BB gave positive SCA with Cam Inb gp1 17, with 88069 and with 4001; and finally Cla 183 gave SCA with 88069 and with 9450. The five inbred lines stated above also gave positive SCA with Cam Inb gp1 17, 88069 or 9450 in control environments. These lines also gave good GCA and SCA values across environments. Moreover, genotypes ATP S5 31Y-2, ATP S6 31Y-BB, ATP S9 30Y-1, Cml 304, Cml 437 and Cml 434 had positive and significant SCA across environments when crossed with all the testers. They also gave positive GCA across environments except ATP S5 31Y-2 which had a negative GCA value with Cam Ing gp1 17 and

88069. These results suggested that the lines contributed to higher grain yield of their hybrids. These inbred lines could be of potential use in breeding new lines (Makumbi *et al.*, 2011; Badu-Apraku *et al.*, 2013; Ifie, 2013).

The specific combining abilities for lines with testers associated with high yield performance compare to the best check were used to develop heterotic groups. Four heterotic groups (A, B, C and D) of lines were identified in acid soil and across environments. In control environments, two heterotic groups (A and C) were formed with Cam Ing gp1 17 and 9450. The hybrids made of inbred lines in group A combined well with Cam Inb gp1 17 and yielded 10% higher than the yield of the best check. The inbred lines in group B combined well with the tester 88069 and yielded 10% more than the best hybrid check. The lines of group C combined well with 9450 and yielded 10% more than the best checks and the lines of group D combined well with 4001 and yielded 10% more than the best hybrid check in each environmental condition. The inbred lines ATP S5 31Y-2, ATP S6 31Y-BB, ATP S8 30Y-2, Cml 434, ATP S9 36Y-BB, ATP S6 21Y-2, ATP S8 26Y-2 and Cla 183 were in different heterotic groups under acid soil, in control soil and across environments. These inbred lines could be potential testers for further studies and also they could be used in new source population for development of new high-yielding hybrids. Among these inbred lines, Cml 434 and Cla 183 were introduced from CIMMYT. Therefore, the introduction of inbred lines was efficient in creating variability and developing high-yielding hybrids (Fan *et al.*, 2008). In the present study, Cml 434 x Cam Inb gp1 17 and ATP S6 31Y-BB x 9450 were the best heterotic pattern in all the test environments.

In the present study, 10 inbred lines out of 25 were classified into heterotic groups in acid soil environments, four out of 25 inbred lines were classified in control conditions and 17 out of 25 were classified across environments. All the lines could not be classified into to heterotic groups based on the criteria of classification used. Similar results have been reported in previous studies (Vasal *et al.*, 1992; Menkir *et al*, 2003; Akinwale *et al.*, 2014 and Rajendran *et al*, 2014). Additionally, under control environments, only Cam Inb gp1 17 and 9450 were able to assign four inbred lines into two heterotic groups. According to Tekeu *et al*. (2014), Cam Ing gp1 17 was a good progenitor in acid soil conditions. The testers 88069 and 4001 were not good testers in control environments. In the present study, the testers used were parents of high-yielding hybrids but they have not yet been released for commercial purpose.

6.5 Conclusions

Al tolerance is in both additive and non-additive genetic control with the predominance of the non -additive gene action. Faster progress could be made by selecting for traits that are largely controlled by additive gene effect than those controlled by non-additive gene effects but such selection will not identify heterosis that would significantly increase yields. Therefore, the classification of lines into heterotic groups is required. Four distinct heterotic groups (group A, group B, group C and group D) were identified in acid soil and across environments based on the positive specific combining ability and yield compared to the best hybrid check. Cml 434 x Cam Inb gp1 17 and ATP S6 31Y-BB x 9450 were the best heterotic pattern in all the test environments. The lines of group A gave high-yielding hybrids when cross with Cam Inb gp1 17 and out-yielded the best check by 10%, the lines of group B gave high-yielding hybrids when cross with 88069 and out-yielded the best hybrid check by 10%, the lines of group C out-yielded the best check by 10% when crossed with 9450 and the lines of group D out-yielded the best check by 10% when crossed with 4001. In control environments, only Cam Inb gp1 17 and 9450 were able to assign four inbred lines into two heterotic groups. These testers were the best under control and across environments while under acid soil conditions, 4001 was the best. The inbred lines ATP S5 31Y-2, ATP S6 31Y-BB, ATP S8 30Y-2, Cml 434, ATP S9 36Y-BB, ATP S6 21Y-2, ATP S8 26Y-2 and Cla 183 expressed good and positive SCA and GCA in acid soil and across environments. They were good combiner under acid soil conditions and could be used as testers for further studies. Among them, Cml 434 and Cla 183 were introduced from CIMMYT. This showed that the introduction of lines was efficient for the development of high-yielding hybrids since they raised the variability and increased the probability of identifying some high-yielding hybrids tolerant to Al toxicity.

CHAPTER SEVEN

7.0 GENOTYPE BY ENVIRONMENT INTERACTION AND YIELD STABILITY OF MAIZE HYBRIDS EVALUATED IN CAMEROON

7.1 Introduction

Maize (*Zea mays* L.) is produced in all the five agro-ecological zones of Cameroon and is an important source of income to the rural households. The average yield of maize is very low (1.8 t/ha) (Aroga *et al.*, 2001; Ngoko *et al.*, 2002). To date, the average yield has reduced and ranged from 0.8 to 1 t/ha (ACDIC, 2010). Low yields have been attributed to the use of low-yielding varieties, saved seeds, poor soil fertility, pests and diseases, limited use of fertilizers, low plant population, and inappropriate weed control. Significant potential improvements in yields could be achieved through the use of high-yielding hybrid maize varieties (Adu *et al.*, 2013).

Crop breeders need to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of environmental conditions. Prior to release of the new varieties, they are evaluated in yield trials at several locations for two or more seasons in multi-environmental trials which provides important information that enables selection and recommendation of crop cultivars (Yan and Tinker, 2006; Yang *et al.*, 2009). Genotype by environment interaction (GxE) makes it difficult to select the best performing and most stable genotypes because of the differential ranking of genotype across locations or years (Adu *et al.*, 2013). Badu-Apraku (2011a) reported that G x E influences the ranking of the genotypes in different environments with some locations being better for genotype evaluations than others

The statistical methods for analyzing GxE effect include analysis of variance, stability analyses and multivariate methods which are more often used to identify GxE interactions in multi-environmental experiments. However, the analysis of variance has limitations due to the assumption of homogeneity of variance (Adu *et al.*, 2013). The Additive Main effect and Multiplicative Interaction (AMMI) method is more useful (Kandus et al., 2010). It interprets the effect of the genotypes (G) and sites (E) as additive effects plus the GxE as a multiplicative component and submits it to principal component analysis (Kandus et al., 2010). According to Finlay and Wilkinson (1963), an appropriate stable cultivar is capable of utilizing resources that are available in high yielding environments, while maintaining above average yield performance in all other environments. The GGE biplot has also been recognized as an innovative methodology in biplot graph analysis in plant breeding. Fan *et al*. (2007)showed that the GGE biplot was a useful tool to identify locations that optimized hybrid performance and make better use of limited resources available for maize testing programs. The GGE biplot graphically displays genotype main effect plus G×E of multi-environment trials in a way that facilitates visual evaluation of cultivars and mega-environment identification (Yan *et al.*, 2007).

Currently, the stability for grain yield of the developed hybrids is unknown, yet this is crucial in cultivar recommendation in specific or general environments. The objectives of this study were to:

- Determine the genotype by environment effect on yield;
- Identify the most high-yielding and stable maize hybrids across nine environments and identify the mega-environments.

7.2 Materials and methods

7.2.1 Plant materials

One hundred and twenty-one maize genotypes made up of 106 single cross hybrids, 12 top cross hybrids and three released open-pollinated varieties as checks, were used in this study (Table 7.1).

Table 7.1: The codes and names of maize hybrids in this study

Hybrids	Code	Hybrids	Code	Hybrids	Code	Hybrids	Code
Cla 183 x 9450	1	Cml 439 x 4001	21	Cam Inb gp1 17 (F) x 4001	41	ATP S8 26Y-3 x 9450	61
Cml 434 x Cam Inb gp1 17	2	Cml 439 x Cam Inb gp1 17	22	Cml 332 x 88069	42	ATP S9 36Y-BB x 88069	62
CMS 8704 x 9450	3	ATP S6 20Y-1 x 88069	23	Cml 437 x 9450	43	Cml 439 x 9450	63
Cml 437 x Cam Inb gp1 17	4	ATP S5 31Y-2 x 4001	24	ATP S9 30Y-1 x Cam Inb gp1 17	44	Cml 357 x 9450	64
ATP S6 31Y-BB x 9450	5	ATP S8 26Y-3 x Cam Inb gp1 17	25	CMS 8704 x 4001	45	Cml 479 x Cam Inb gp1 17	65
Cla 183 x 88069	6	Cam Inb gp1 17 (F) x 9450	26	D300-17 x 9450	46	Cml 357 x 88069	66
D300-17 x Cam Inb gp1 17	7	ATP S9 36Y-BB x Cam Inb gp1 17	27	Cml 304 x Cam Inb gp1 17	47	ATP S6 21Y-2 x Cam Inb pg1 17	67
C4RR SA4 x Cam Inb gp1 17	8	ATP S8 30Y-3 x 9450	28	Cml 435 x 4001	48	Cml 435 x 9450	68
ATP S8 30Y-3 x Cam Inb gp1 17	9	ATP S8 30Y-3 x 4001	29	Cml 435 x Cam Inb gp1 17	49	Cml 439 x 88069	69
ATP S5 31Y-2 x 9450	10	Cla 135 x Cam Inb gp1 17	30	ATP SR Y x 88069	50	Cml 434 x 4001	70
ATP S9 36Y-BB x 4001	11	Cml 434 x 9450	31	ATP S9 30Y-1 x 88069	51	ATP S9 30Y-1 x 4001	71
CMS 8704 x 88069	12	Cla 183 x Cam Inb gp1 17	32	Cam Inb gp1 17 (F) x 88069	52	ATP S6 20Y-1 x 4001	72
ATP SR Y x 4001	13	ATP S6 21Y-2 x 88069	33	ATP S6 21Y-2 x 9450	53		
Cml 535 x Cam Inb gp1 17	14	Cml 479 x 4001	34	Cml 437 x 88069	54		
Cml 304 x 9450	15	Cml 357 x Cam Inb gp1 17	35	Cam Inb gp1 17 x 88069 (**check**)	55		
ATP S9 30Y-1 x 9450	16	ATP S6 20Y-1 x 9450	36	ATP S8 26Y-3 x 88069	56		
Cla 135 x 9450	17	Cml 534 x 4001	37	Cam Inb gp1 17 x 9450 (**check**)	57		
Cla 135 x 88069	18	Cml 332 x Cam Inb gp1 17	38	9450 x 4001 **(check)**	58		
Cml 357 x 4001	19	Cml 434 x 88069	39	9450 x 88069 **(check)**	59		
ATP SR Y x Cam Inb gp1 17	20	C4RR SA4 x 88069	40	ATP-50 x 9450	60		

Table 7.1 cont'd: The names and codes of maize hybrids used for the study

Hybrids	Code	Hybrids	Code	Hybrids	Code
ATP-32 x Cam Inb gp1 17	73	Cml 533 x 9450	90	Cml 304 x 4001	107
C4RR SA4 x 4001	74	Cml 533 x 88069	91	Cam Inb gp1 17 x 4001 (**Hybrid check**)	108
Cml 435 x 88069	75	ATP S9 36Y-BB x 9450	92	ATP S8 30Y-3 x 88069	109
Cml 437 x 4001	76	ATP-50 x 88069	93	ATP S6 21Y-2 x 4001	110
Cam Inb gp1 17 (F) x Cam Inb gp1 17	77	Cla 183 x 4001	94	C4RR SA4 **(Check, introduced OPV)**	111
Cml 535 x 9450	78	Cml 479 x 9450	95	D300-17 x 4001	112
Cml 535 x 88069	79	Cml 535 x 4001	96	ATP SR Y **(Check, commercial OPV)**	113
Cml 332 x 9450	80	CLA 135 x 4001	97	ATP S5 31Y-2 x 88069	114
CMS 8704 x Cam Inb gp1 17	81	Cml 332 x 4001	98	ATP-32 x 88069	115
CMS 8704 **(Check, commercial OPV)**	82	ATP-50 x Cam Inb gp1 17	99	ATP S6 31Y-BB x 4001	116
Cml 534 x Cam Inb gp1 17	83	ATP-32 x 4001	100	ATP S8 26Y-3 x 4001	117
Cml 533 x 4001	84	C4RR SA4 x 9450	101	ATP S5 31Y-2 x Cam Inb gp1 17	118
ATP S6 20Y-1 x Cam Inb gp1 17	85	Cml 534 x 88069	102	ATP-32 x 9450	119
Cml 479 x 88069	86	Cml 304 x 88069	103	ATP S6 31Y-BB x Cam Inb gp1 17	120
D300-17 x 88069	87	Cml 533 x Cam Inb gp1 17	104	ATP S6 31Y-BB x 88069	121
Cml 534 x 9450	88	ATP-50 x 4001	105		
88069 x 4001 (**Hybrid check**)	89	ATP SR Y x 9450	106		

7.2.2 Description of the environments

The study was conducted at two sites located in the humid forest zone of Cameroon in two different soil treatments (acid soil and acid soil corrected by the application of 4 t/ha of dolomite as 'control') over a three-year period (2012, 2013 and 2014). A total of nine environments were obtained (Table 7.2).

The trials were conducted in the same location at Nkoemvone in Ebolowa. Two planting dates that differed by three weeks were utilized each year for the two experimental trials to differentiate the environment as reported by Singh and Chaudhary (1979).

Table 7.2: Description of the environments

Environment	Correspondence
NKA1_2012	site1*treatment1 (acid)*year1 (2012)
NKA1_2013	site1*treatment1 (acid)*year2 (2013)
NKA1_2014	site1*treatment1 (acid)*year3 (2014)
EBA2_2013	site2*treatment1 (acid)*year2 (2013)
EBA2_2014	site2*treatment1 (acid)*year3 (2014)
EBC1_2012	site1*treatment2 (control)*year1 (2012)
EBC1_2014	site1*tretment2(control)*year 3 (2014)
EBC2_2013	site2*treatment2 (control)*year2 (2013)
EBC2_2014	site2*treatment2 (control)*year3 (2014)

7.2.3 Description of the experimental sites

The characteristics of the experimental sites were the same as described in Chapter Five, section 5.1.2.

7.2.4 Land preparation planting and field management

The land preparation and planting were conducted as presented in Chapter Five, section 5.15.

7.2.5 Experimental Design

The hybrids were arranged in 11 x 11 simple lattice design with two replications and the evaluations were done over three years in nine environments. The genotypes were assigned at random to the plots within each block.

7.2.6 Data collection

The grain yield was measured on a whole plot basis following standard CIMMYT procedure (CIMMYT, 1985) and was adjusted to 15% moisture using the formula below

GY (t/ha) = [Grain Weight (kg/plot) x 10 x (100-MC) / (100-15) / (Plot Area)]

Where MC = Grain Moisture Content.

7.2.7 Data analysis

The general linear model (GLM) of all the traits evaluated on the 121 genotypes was generated through SAS version 9.2 considering environment as random to estimate the means of the genotypes. The GGE biplot analysis was also done with Genstat software version 15. The mean yields of hybrids were arranged as recommended and analyzed using Breeding Management

System (BMS) software (Murray *et al.*, 2013). The means of genotypes per site were ranked to assess the importance of cross-over genotype x environment interactions based on the Finlay and Wilkinson (1963) regression model.

The MIXED MODEL procedure of Statistical Analysis System (SAS) version 9.2 was used for the combined analysis, with blocks nested within replication by environments and replications within environments were treated as random factors and the genotype as fixed. The statistical model used for the combined analysis is as follows:

$$Yijkg = \mu + Ei + Rj(i) + Bk(ij) + Gg + EGig + \varepsilon ijkg$$

Where Yijkg is the observed measurement for the gth genotype grown in the environment i, in the block k in replicate j; μ is the; grand mean; Ei is the main effect of environment; Rj(i) is the effect of replicate nested within environment effect; Bk(ij) is the effect of block nested within replicate j by environment i; Gg is the effect of the genotype; EGig is the interaction effect between genotype and environment, and εijkg is the error term (Akinwale *et al.*, 2014).

The yield data were subjected to AMMI and GGE biplot analyses using the Breeding Management System (BMS) software (Murray *et al.*, 2013). The AMMI model, which combines the standard analysis of variance with principal component analysis (Zobel *et al.*, 1988), was used to investigate the nature of GEI. The AMMI model first fits additive effects for the main effects of genotypes and environments, using the additive analysis of variance procedure. Subsequently the program fits multiplicative effects for GEI by principal component analysis (Zobel *et al.*, 1988; Gauch and Zobel, 1997). The GGE - biplot was used to illustrate the relationships among genotypes, environments and genotypes and environment interactions.

The AMMI model is:

$$Y_{ij} = \mu + g_i + e_j + \sum_{n=1}^{N} \lambda_k \gamma_{ik} \delta_{jk} + \rho_{ij} + \varepsilon_{ij},$$

where Y_{ij} is the yield of the ith variety in the jth environment, μ is the overall mean, g_i and e_j are the fixed varietal effects and environmental deviations, respectively, λ_k is a singular value of the K axis in the principal component analysis, γ_{ik} and δ_{jk} are genotype and environmental factors of the singular vectors associated with λ_k from the interaction matrix, N is the number of principal components retained in the model, ρ_{ij} is the residual G×E interaction, and ε_{ij} is the average independently assumed error $\varepsilon_{ij} \sim N(0, s^2)$ (Jorge de Oliveira *et al.*, 2014).

7.3 Results

7.3.1 Combined analysis of variance for yield

The combined Analyses of Variance (ANOVA) for yields of the 121 maize genotypes evaluated across nine environments according to the AMMI model are presented in Table 7.3. Highly significant difference ($P < 0.001$) for environments was observed. Genotypes were significantly different ($P < 0.05$). Genotype x environment interaction was also highly significant ($P < 0.001$). Two different IPCA (interaction principal component axis) were estimated and they were highly significant ($P < 0.001$). The IPCA 1 expressed 39.16% of the total variation while the IPCA2 expressed 15.30% giving a total variation due to G x E of 54.46%. The proportions of total sum of squares accounted for genotype, environment and their interaction were 3.77, 77.06 and 5.53% respectively. IPCA1 and IPCA2 accounted for 8.5 and 3.37% of the total variation of grain yield.

Table 7.3: Combined analysis of variance for grain yield of 121 genotypes across seven environments

Source	DF	% SS GxE	SS	%SS	MS
Genotype	120		452	3.77	3.77*
Environment	8		2692	77.06	336.55***
Genotype x environment	960		5306	5.53	5.50***
IPCA 1	127	39.16	1079	8.50	8.50***
IPCA 2	125	15.30	421	3.37	3.37***
Residual	708		1255	1.77	1.77 NS

DF = degrees of freedom; SS = Sum of square; MS = Mean square *, ** and *** denote significant differences at $P < 0.05$, $P < 0.01$, and $P < 0.001$ respectively. IPCA= Interaction principal component axis, NS = non-significant.

7.3.2 Grain yield performance of the hybrids across environments

The 121 maize genotypes had a mean yield range from 1.81 t/ha (NKA2_2013) to 6.66 t/ha (EBC1_2014) (Table 7.4). The variance ranged from 1.35 (NKA2_2013) to 9.16 (EBC1_2014). All the genotypes expressed negative effect of yield under NKA environments compared to the EBC environments. NKA2_2013 gave the highest negative effect with the highest coefficient of variation percentage. Moreover, that environment was ranked 9th from the Finlay and Wilkinson modified joint regression analysis while EBC1_2014 was ranked first. The top 5 environments were EBC1_2014, EBC2_2014, EBC2_2013, EBC1_2012 and NKA1_2012.

Table 7.4: Mean yield performance of 121 maize genotypes in the nine environments

Environment	Mean yield (t/ha)	Min	Max	SS	Variance	Effect	SE	% CV	Rank
EBC1_2014	6.66	0.51	16.66	1098.90	9.16	2.98	0.13	45.44	1
EBC2_2014	6.37	1.20	12.35	259.30	2.16	1.85	0.13	23.07	2
EBC2_2013	5.06	1.34	10.21	290.30	2.42	0.66	0.13	30.77	3
EBC1_2012	4.44	0.68	8.46	297.80	2.48	0.03	0.13	35.45	4
NKA1_2012	4.46	0.63	10.21	289.80	2.42	-0.04	0.13	34.83	5
NKA1_2014	3.91	0.37	8.90	413.70	3.45	-0.31	0.13	47.54	6
NKA2_2014	3.19	0.25	7.40	220.70	1.84	-1.01	0.13	42.55	7
NKA1_2013	2.25	0.01	6.58	174.20	1.45	-1.91	0.13	53.5	8
NKA2_2013	1.81	0.01	5.97	162.00	1.35	-2.25	0.13	64.37	9

SS= sum of square, SE= standard error, CV = coefficient of variation, Min = minimum and Max = maximum.

The best four hybrids in each of the nine environments were selected using the descending AMMI procedure (Table 7.5). Accordingly, Cla 183 x 9450 was selected as number one in the first grouping and also number one in 80% of the environments. In the second group, Cla 183 x 88069 represented 44% of the total hybrids selected. Whilst in the third group, Cml 437 x Cam Inb gp1 17 and Cla 183 x 88069 represented 33% of the total selections made. In the fourth group, CMS 8704 x 88069 represented 22% of the total hybrids.

Table 7.5: First four AMMI selections per environment

Number	Environment	Mean yield (t/ha)	1st	2nd	3rd	4th
1	EbA2_2013	1.81	G1	G6	G4	G12
2	EbA2_2014	3.19	G1	G6	G4	G12
3	EBC1_2012	4.44	G1	G3	G6	G5
4	EBC1_2014	6.66	G14	G44	G92	G3
5	EBC2_2013	5.06	G1	G32	G37	G34
6	EBC2_2014	6.37	G1	G32	G6	G37
7	NKA1_2012	4.46	G1	G6	G24	G5
8	NKA1_2013	2.25	G1	G6	G32	G4
9	NKA1_2014	3.91	G70	G34	G61	G63

7.3.3 Correlation among environments

The correlation of the nine environments used in the study was estimated (Table 7.6). NKA1_2012 showed highly significant and positive correlation (r = 0.56) with EBC1_2012. It was also positively and significantly correlated (r = 0.19) with NKA1_2013 and was significantly negatively correlated (r = -0.22) with EBC1_2014. EBC2_2014 was positively and significantly correlated with NKA1_2014 (r = 0.19) and was highly positively correlated with NKA2_2014(r=0.23).

Table 7.6: Pearson correlation coefficients among the nine environments

NKA1_2012	1								
NKA1_2013	0.19*	1							
NKA1_2014	-0.02	0.01	1						
NKA2_2013	-0.003	-0.10	0.08	1					
NKA2_2014	0.16	0.11	0.13	0.07	1				
EBC1_2012	0.56***	-0.07	-0.05	0.01	0.02	1			
EBC1_2014	-0.22*	-0.02	0.16	0.09	0.12	-0.12	1		
EBC2_2013	-0.04	0.00	0.02	0.02	-0.05	-0.11	-0.03	1	
EBC2_2014	0.12	0.05	0.19*	0.07	0.23**	0.08	-0.01	0.03	1
	NKA1_2012	NKA1_2013	NKA1_2014	NKA2_2013	NKA2_2014	EBC1_2012	EBC1_2014	EBC2_2013	EBC2_2014

*, ** and *** denote significant differences at $P < 0.05$, $P < 0.01$, and $P < 0.001$ respectively.

7.3.4 AMMI biplot and GGE biplot analysis for yield

The biplot of the hybrids and the environments showed the pattern of associations of G x E based on the PCA1 and PCA2 (Figure 7.1). The PCA1 and PCA2 expressed 39.16% and 15.30% of the variation respectively. The biplots were divided into four sectors whereby all the sectors had genotypes and environments distributed all over. The environment EBC1_2014 belonged to the sector at the lower left section of the biplot whilst NKA1_2014 belonged to the upper left sector. At the right of the biplot, the two environments were in the upper part (EBC2_2013 and EBC2_2014) and two others in the lower part (NKA1_2012 and EBC1_2012). Most of the hybrids were close to the axis except genotypes 3 (CMS 8704 x 9450), 92 (ATP S8 30Y-3 x 88069), 44 (ATP S9 30Y-1 x Cam Inb gp1 17), 91(4001 x Cam Inb gp1 17), 70 (Cml 434 x 4001) and 120 (ATP S6 31Y-BB x Cam Inb gp1 17).

The GGE biplot was computed based on principal components 1 and 2 which expressed 35.87% and 14.72% of total variation (Figure 7. 2). Three mega-environments (A, B and C) were identified from the biplot. The mega-environment A enclosed all the environments except EBC1_2014. These mega-environments overlapped at the origin of the biplot. The mega-environment B covered NKA2_2014, NKA2_2013, NKA1_2013, EBC2_2013 and EBC1_2014. The smallest mega-environment C had three environments which were EBC2_2013, NKA2_2013 and NKA1_2013.

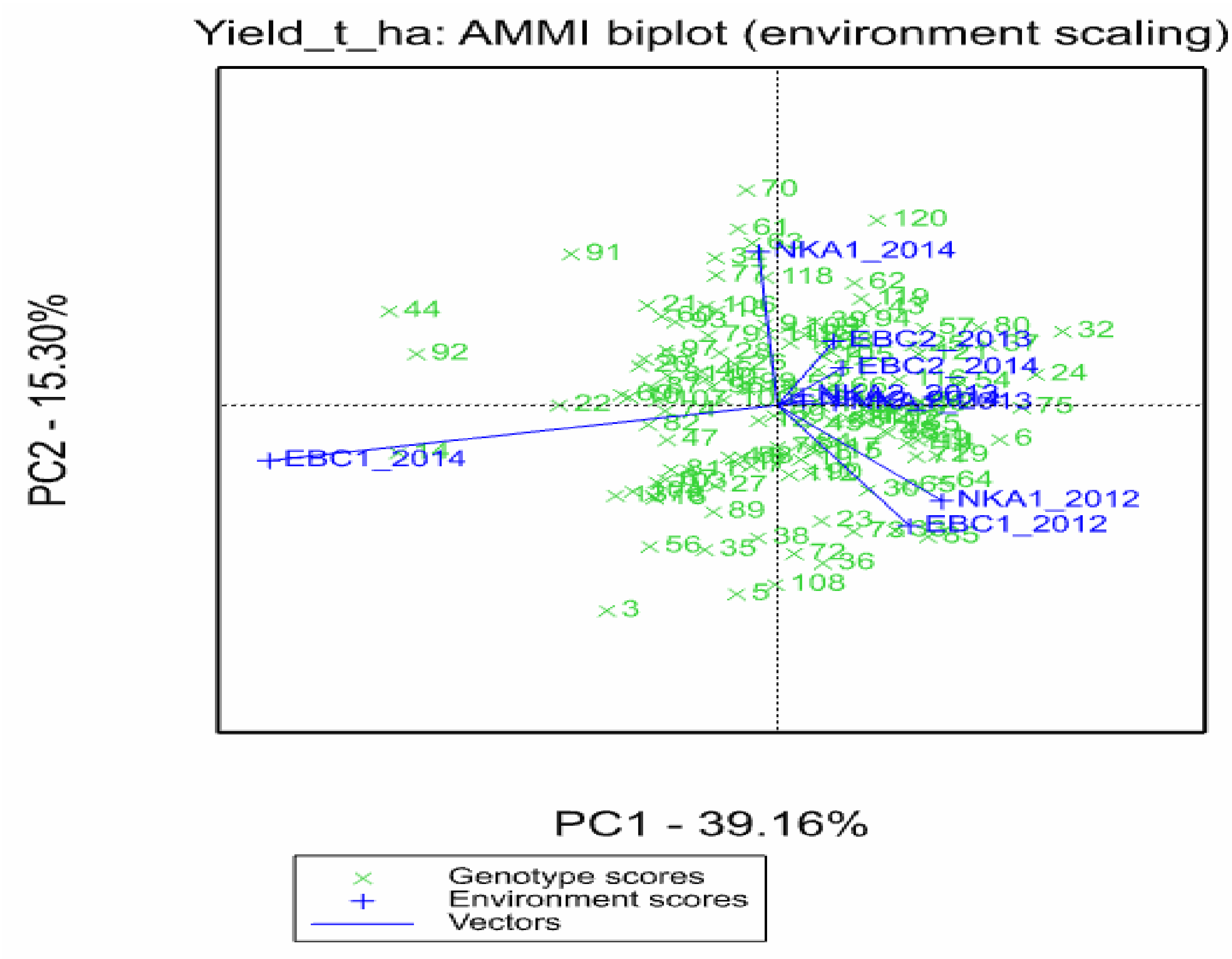


Figure 7.1: AMMI biplot for grain yield (t/ha) of maize hybrids showing hybrids across environments

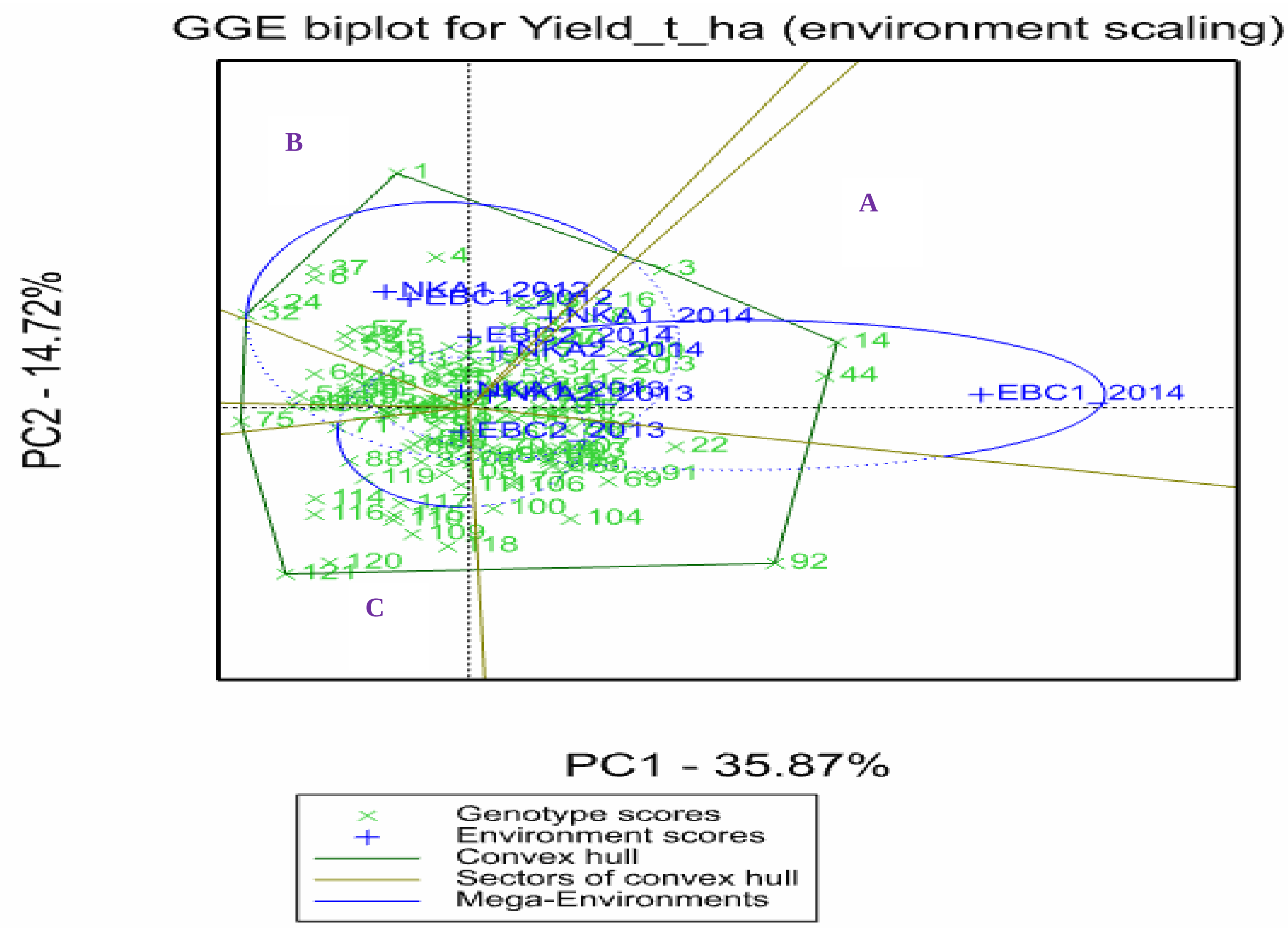


Figure 7.2: GGE biplot for yield of 121 maize hybrids under 9 environments

7.3.5 Most stable maize hybrids across environments

The most stable hybrids by environment were sorted based on their stability coefficient and the 20 best were selected and ranked (Table 7.7). The superiority coefficient of the 20 most stable hybrids ranged from 9.64 for CMS 8704 x 9450 to 13.45 for Cml 434 x Cam Inb gp1 17, with mean yields of between 4.84t/ha and 5.84 t/ha. The sensitivity coefficient varied from 0.53 for Cml 434 x Cam Inb gp1 17 to 1.45 for CMS 8704 x 9450. Cml 434 x Cam Inb gp1 17 had a high cultivar superiority coefficient (13.45) and was ranked 20, whilst CMS 8704 x 9450 had the lowest cultivar superiority coefficient (9.64) and was ranked first. The highest yielding hybrid was Cla 183 x 9450 with a yield of 5.84 t/ha across environments. This high-yielding hybrid had cultivar superiority coefficient of 12.62 with the lowest sensitivity coefficient (0.4) and was ranked 13. Ten hybrids yielded 20% more than the best hybrid check. They were CMS 8704 x 9450 (5.56 t/ha), Cml 437 x Cam Inb gp1 17 (5.28 t/ha), C4RR SA4 x 88069 (5.84 t/ha), ATP SR Y x 4001 (5.35 t/ha), ATP S5 31Y-2 x 9450 (5.33 t/ha), Cml 439 x 4001 (5.27 t/ha), CMS 8704 x 88069 (5.33 t/ha), C4RR SA4 x Cam Inb gp1 17 (5.21 t/ha), ATP SR Y x Cam Inb gp1 17 (5.13 t/ha) and Cml 535 x Cam Inb gp1 17 (5.58 t/ha).

Table 7.7: The best 20 most stable maize hybrid by environment

Rank	Genotype	Code	Superiority coefficient	Mean yield (t/ha)	S.E.	Sensitivity coefficient	S.E.	MSD
1	CMS 8704 x 9450	**3**	9.64	**5.56**	0.54	**1.45**	0.2	2.89
2	ATP SR Y x 4001	13	9.95	5.35	0.54	1.24	0.2	1.57
3	ATP S5 31Y-2 x 9450	10	10.32	5.33	0.54	0.93	0.2	1.03
4	Cml 439 x 4001	21	10.47	5.27	0.54	1.14	0.2	1.47
5	CMS 8704 x 88069	12	10.53	5.33	0.54	0.83	0.2	0.89
6	C4RR SA4 x Cam Inb gp1 17	8	10.6	5.21	0.54	1.17	0.2	1.45
7	ATP SR Y x Cam Inb gp1 17	20	10.7	5.13	0.54	1.33	0.2	1.96
8	Cml 535 x Cam Inb gp1 17	**14**	10.76	**5.58**	0.54	**1.83**	0.2	5.36
9	Cml 439 x Cam Inb gp1 17	22	11.6	5.00	0.54	1.29	0.2	2.89
10	Cml 304 x 9450	15	11.98	5.05	0.54	1.02	0.2	1.78
11	ATP S9 30Y-1 x 9450	16	12.00	4.97	0.54	1.16	0.2	2.01
12	Cml 437 x Cam Inb gp1 17	4	12.56	5.28	0.54	0.70	0.2	3.67
13	Cla 183 x 9450	**1**	12.62	**5.84**	0.54	**0.40**	0.2	6.86
14	C4RR SA4 x 88069	40	12.91	4.84	0.54	0.94	0.2	1.26
15	ATP S9 36Y-BB x Cam Inb gp1 17	27	12.91	4.91	0.54	0.85	0.2	1.35
16	ATP S8 30Y-3 x Cam Inb gp1 17	9	13.00	5.11	0.54	0.55	0.2	2.44
17	ATP S8 30Y-3 x 9450	28	13.06	4.83	0.54	0.74	0.2	1.2
18	Cla 135 x 88069	18	13.25	4.99	0.54	0.93	0.2	5.23
19	D300-17 x Cam Inb gp1 17	7	13.32	4.87	0.54	0.78	0.2	1.68
20	Cml 434 x Cam Inb gp1 17	2	13.45	5.01	0.54	0.53	0.2	1.96

Best hybrid check: Cam Inb gp1 17 x 9450 4.4 t/ha

Overall mean yield of hybrids: 4.2 t/ha

MSD = mean square deviation, S.E. = standard error

7.3.6 Additive main effect and multiplicative interaction (AMMI) analysis of the top 20 hybrids across environments

The biplot of the top 20 hybrids and the environments clearly shows the pattern of associations between hybrids and environments (Figure 7.3). The code of hybrids in this figure is explained in Table 7.8. The IPCA scores of a hybrid in the AMMI analysis are an indication of the stability of a genotype over environments.

Environments were distributed from lower yielding in quadrant I (top left) and IV (bottom left) to the higher yielding in quadrants II (top right) and III (bottom right) (Figure 7.3). The higher yielding environments classified according to the AMMI model were EBC1_2014, EBC2_2014, EBC2_2013, EBC1_2012, NKA1_2014 and NKA1_2012. The lower yielding environments were EbA2_2013, EbA2_2014 and NKA1_2013.

The hybrids categorized under favorable environments had average mean yields ranging from 5.28 to 5.84 t/ha. The hybrids grouped under low yielding environments as ATP S8 30Y-3 x 9450 were shown at the lower left quadrant of the biplot (Figure 7.3). Generally Cla 183 x 9450 and Cml 535 x Cam Inb gp1 17 were the most unstable hybrids identified by the AMMI model (Figure 7.3). Hybrids that were closer to each other tend to have similar performance and those that were closer to an environment were better adaptated to that particular environment. Hence hybrid Cml 437 x Cam Inb gp1 17 was better adapted to NKA1_2012 and NKA1_2014 than Cla 183 x 9450.

The greater the IPCA score, either positive or negative, the more specifically adapted a genotype is to certain environments. The more IPCA scores approximate to zero, the more stable the genotype is over all environments sampled. Accordingly, CMS 8704 x 9450, ATP S9 30Y-1 x 9450, ATP SR Y x 4001, ATP S5 31Y-2 x 9450 and C4RR SA4 x 88069 were close to zero.

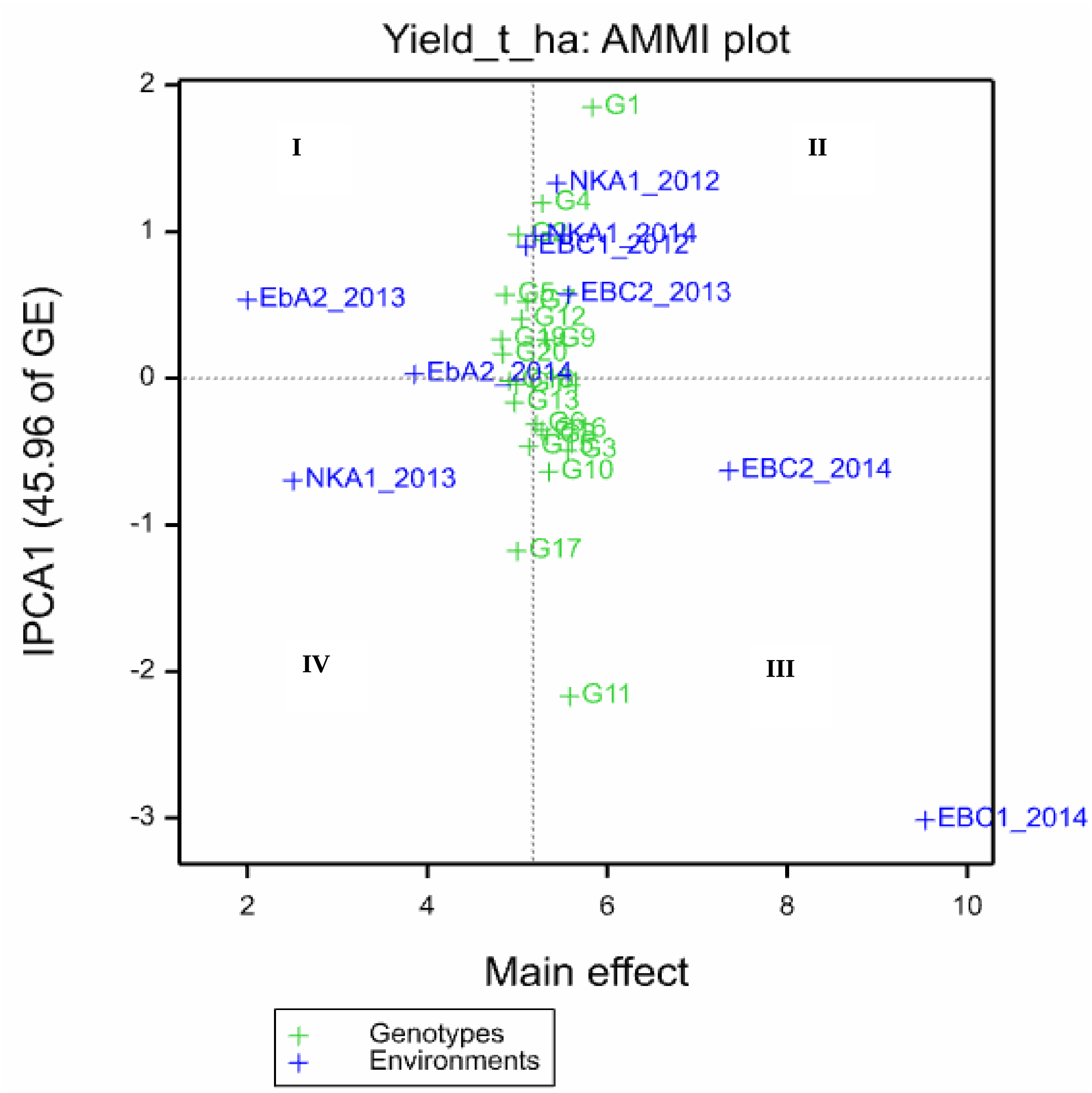


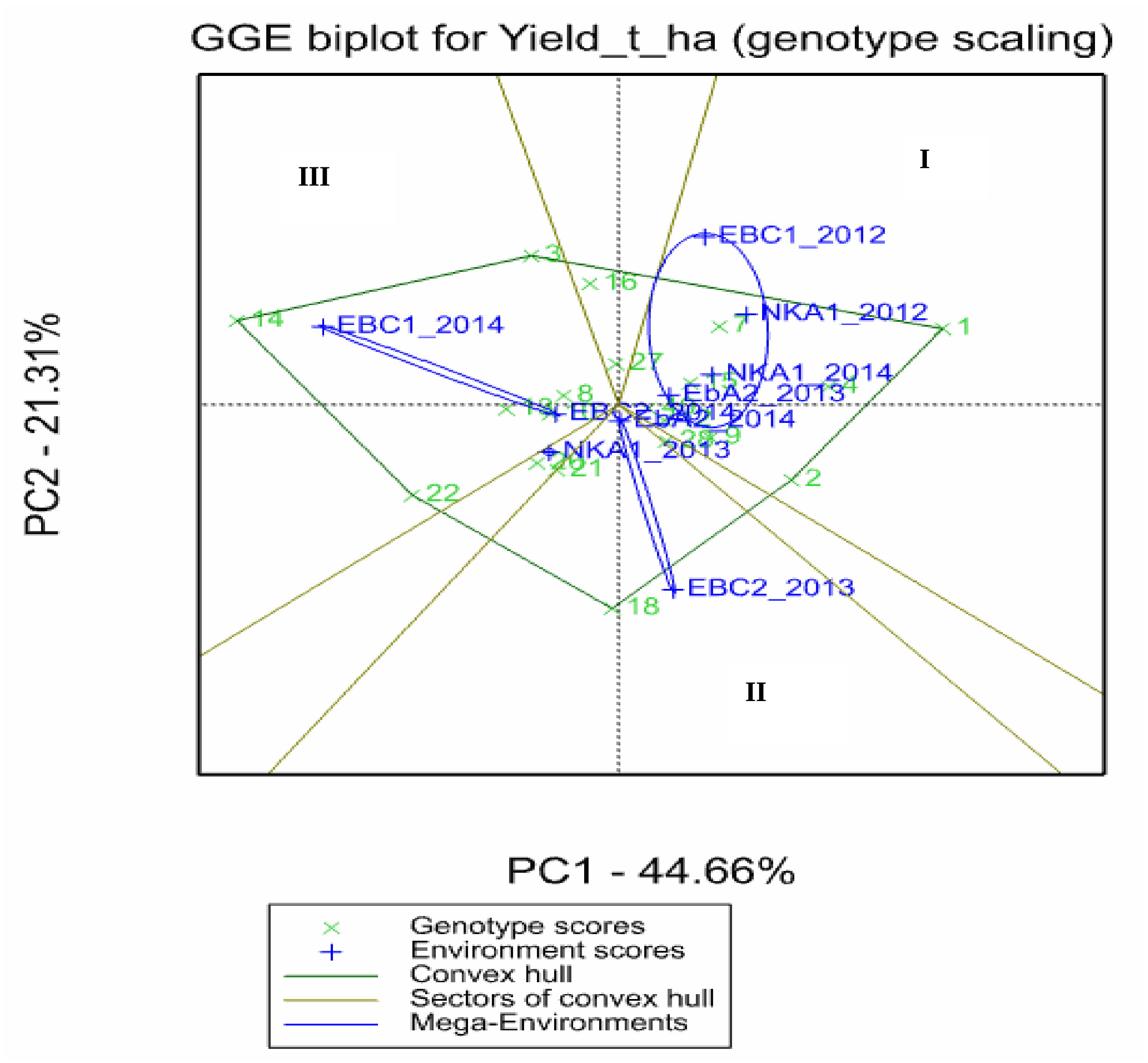
Figure 7.3: AMMI biplot for grain yield of the top 20 maize hybrids showing genotypes and environments plotted against their IPCA1 score

Table 7.8: Code and name of hybrids used in AMMI biplot showing genotypes and environments plotted against their IPCA1 score

Code 2	Code	Name of hybrids	Code 2	Code	Name of hybrids
G1	1	Cla 183 x 9450	G11	14	Cml 535 x Cam Inb gp1 17
G2	2	Cml 434 x Cam Inb gp1 17	G12	15	Cml 304 x 9450
G3	3	CMS 8704 x 9450	G13	16	ATP S9 30Y-1 x 9450
G4	4	Cml 437 x Cam Inb gp1 17	G14	18	Cla 135 x 88069
G5	7	D300-17 x Cam Inb gp1 17	G15	20	ATP SR Y x Cam Inb gp1 17
G6	8	C4RR SA4 x Cam Inb gp1 17	G16	21	Cml 439 x 4001
G7	9	ATP S8 30Y-3 x Cam Inb gp1 17	G17	22	Cml 439 x Cam Inb gp1 17
G8	10	ATP S5 31Y-2 x 9450	G18	27	ATP S9 36Y-BB x Cam Inb gp1 17
G9	12	CMS 8704 x 88069	G19	28	ATP S8 30Y-3 x 9450
G10	13	ATP SR Y x 4001	G20	40	C4RR SA4 x 88069

7.3.7 Genotype and genotype by environment interaction biplot analysis (GGE) for 20 best performing hybrids across all environments

The GGE biplot of the 20 most stable and high-yielding maize hybrids selected was constructed and the PCA1 and PCA 2 were shown to contribute to 65.97% of variation in grain yield across the environments (Figure 7.4). Similar biplot was constructed for the distribution of the hybrids in the target environments for yield (Figure 7.5). Under the nine environments, the 20 hybrids were distributed into six sectors of the biplot with 3 mega-environments (I, II and III). Mega-environment I was made up of 4 environments (EBC1_2012, NKA1_2012, NKA1_2014 and EbA2_2013). It covered 2 sectors of the biplot containing nine hybrids. The hybrids Cla 183 x 9450, Cml 434 x Cam Inb gp1 17, Cml 437 x Cam Inb gp1 17 and D300-17 x Cam Inb gp1 17 were the best in this mega-environment. Mega-environment II had 2 environments (EBC2_2013 and EbA2_2014) covered by two sectors and containing two hybrids. Cla 135 x 88069 was the best hybrid or the most adapted hybrid. Mega-environment III had two environments (EBC1_2014 and EBC2_2014), covered by 2 sectors and containing six hybrids. The most adapted hybrids in this mega-environment were CMS 8704 x 9450, Cml 535 x Cam Inb gp1 17 and Cml 439 x Cam Inb gp1 17.



Note: EbA2_2013 and EbA2_2014 = EBA2_2013 and EBA2_2014 respectively.

Figure 7.4: GGE biplot of the top 20 hybrids across environments

GGE biplot based on genotype-focused scaling was also constructed in order to detect the best locations of hybrids (Figure 7.5). CMS 8704 x 9450 was the ideal genotype based on the orientation of the environment coordinates AEC (close to the center of concentric circles) and genotypes closer to the ideal genotypes are more desirable than the others. The hybrids ATP S9 30Y-1 x 9450, D300-17 x Cam Inb gp1 17, ATP S9 36Y-BB x Cam Inb gp1 17, Cml 304 x 9450, Cml 437 x Cam Inb gp1 17 and Cla 183 x 9450 were the most stable. However, hybrids ATP S9 30Y-1 x 9450, D300-17 x Cam Inb gp1 17 and ATP S9 36Y-BB x Cam Inb gp1 17 were undesirable because of their low yield performance (Figure 7.5 and Table 7.7). Cml 535 x Cam Inb gp1 17 was very unstable but was high-yielding and was specifically adapted to EBC1_2014 environment.

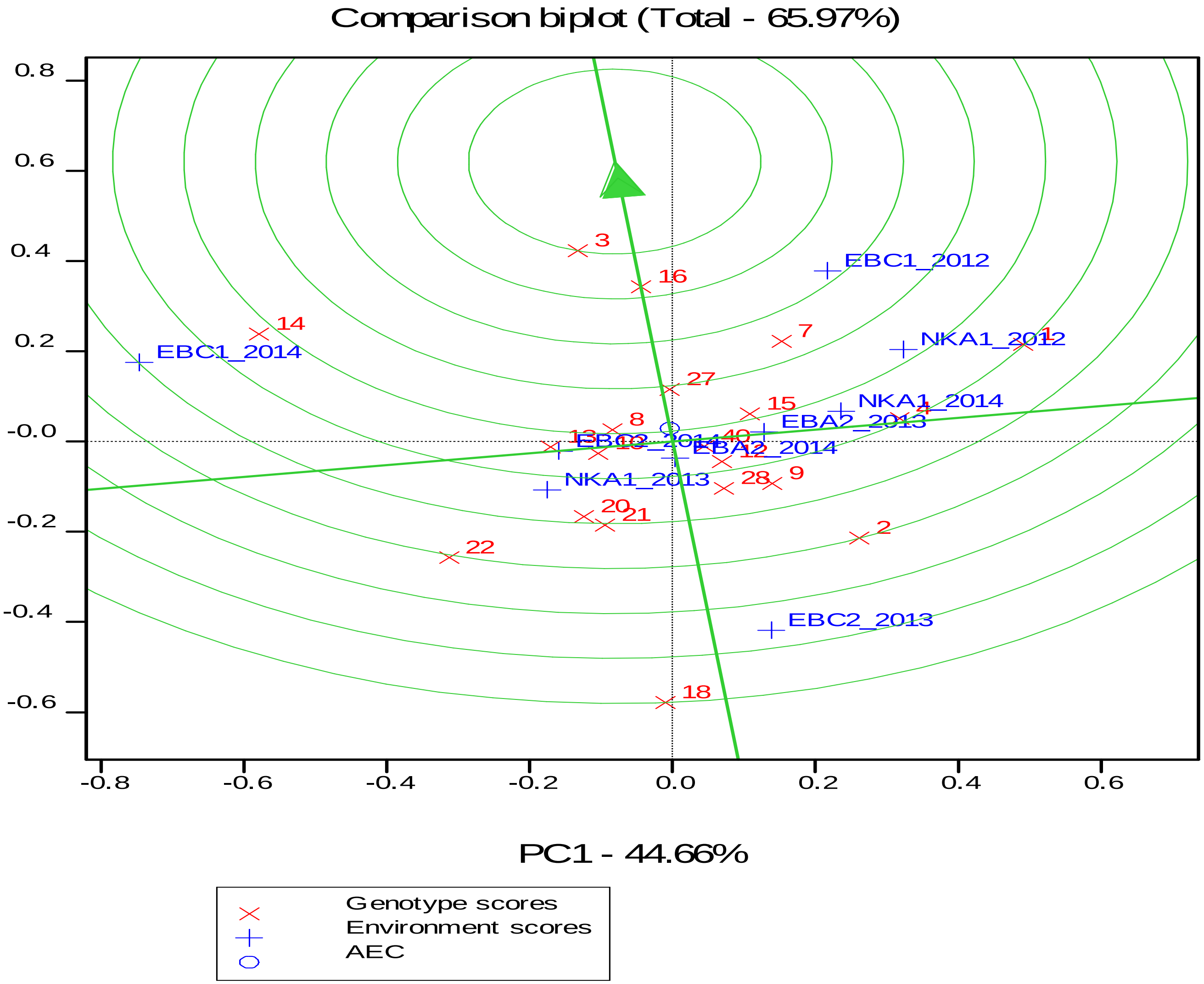


Figure 7.5: Genotype and genotype by environment interaction biplot based on genotype-focused scaling for the top 20 yielding maize genotypes.

7.4 Discussion

The yields recorded among hybrids were significantly different meaning that they responded differently to each other. The significant effect of environments showed the differences were between environments used for the study. The result also suggests that the ranking of genotypes was different between environments and this may complicate selection because of the different responses of the genotypes in the environment and therefore there was a need to identify high-yielding and stable genotypes across the test environments (Badu-Apraku *et al.*, 2012; Ndhlela, 2012; Mengesha, 2013).

Genotypes contributed 4.03% to the variance partition from the total sum of square of AMMI while the combination of the IPCA 1 and 2 explained 69.76% of the G x E interactions. This result implies that the variation observed among mean yields of hybrids was mainly due to the environment as well as G x E interaction to the genotype by the environment interaction. Also, G×E was much greater than genotype effect, including the existence of mega-environments (Choukam, 2010; Mohanmed *et al*., 2013).

According to Gauch and Zobel (1997) in the normal multi-location yield experiments, location accounted for about 80% of the total variation whilst genotype and G x E interaction each accounted for about 10%. The percentage and the contribution of the G x E interaction accounted for 5.53% of total variation in maize yield. This suggests that the mean yield of genotype varied from one environment to another. These results were different from those of Ndhlela (2010) who partitioned the total sum of square into 40.7% for the environment, 3.6% for genotype and 6.7% for the G x E interaction. The difference in the G x E interaction percentage of variation observed between these two studies could be due to the different environments used.

The phenotype of an individual is a combination of its genotype (G) and the environment (E) where the genotype is grown and the genotype × environment interaction (G × E). The G × E usually complicates the process of selecting superior genotypes. According to Crossa (1990), a number of genotypes respond to certain environments in a systematic, significant, and interpretable manner whereas noise suggests that the responses are unpredictable and uninterruptable. In the current study, the incomplete block design was used to reduce the GXE effect with the genotypes assigned at randomly to the plots within each block as reported by Bos and Caligari (2008).

An ideal environment should highly differentiate between genotypes and at the same time be representative of the target environment (Dehghani *et al.*, 2006; Tonk, 2010). In this study, some environments were positively correlated to each other whereas others were negatively correlated. The positive correlations suggests that the genotypes that performed well in one environment could also perform well in the others, whilst the negative correlation indicates that the varieties that performed well in one environment will not do well in the other. For instance, NKA1_2012 showed highly significant and positive correlation (r = 0.56) with EBC1_2012. This means that a genotype which performed well in environment NKA1_2012 may also perform well in EBC1_2012. Therefore, the two environments could belong to the same mega-environment. Ndebeh (2013), found a positive correlation between Fumesua (in the Forest ecology) and Kpeve in the (Coastal -Savannah Transition) of Ghana implying that hybrids which performed well in one location also performed well in the other location.

The different environments were ranked based on their variance associated with the mean of genotypes obtained within. The environment EBC1_2014 was the best with the overall mean of 6.66 t/ha and was followed by EBC1_2012. This shows that the most adapted high-yielding hybrids identified in these environments (EBC1_2014 and EBC1_2012) could also do well in other environments where the conditions are the same. For instance, among the top four hybrids selected by the AMMI analysis, Cla 183 x 9450 and CMS 8704 x 9450 were among the four best hybrids adapted to EBC1_2012. These hybrids did well at NKA2_2014, NKA1_2013, NKA1_2012, EBC2_2014 and would do well in any other environments similar to EBC1_2012 or belonging to the same mega-environment. Badu-Apraku *et al*. (2011a) in another study involving the locations Ejura, Sotouboua, Bagou, and Katibougou made the same observations.

The PCA score values of genotypes in the AMMI analysis are an indication of the stability or adaptation over environments (Steyn *et al.*, 1993). The greater the PCA scores, the more specifically adapted a genotype is to a certain environment. The closer the PCA scores are to zero, the more stable or adapted a genotype is across environments (Gauch and Zobel, 1996a). In the present study, although the most stable genotypes were much closer to the origin of the AMMI biplot, all of them were not high-yielding. Therefore there was a need to identify some hybrids showing a combination of high yielding and high stability across environments. Genotypes that were similar to each other were closer in the biplot than genotypes that were different. Similarly, environments that were more alike tend to group together. As a result, twenty most stable hybrids were selected based on their cultivar superiority coefficient. CMS 8704 x 9450 was the first most stable hybrid, followed by Cml 304 x 9450, Cml 437 x Cam Inb gp1 17 and Cla 183 x 9450. Cml 535 x Cam Inb gp1 17 had low stability but was high-yielding and was specifically adapted to EBC1_2014 environment. The mean yield of the selected hybrids across environments was 5.14 t/ha. Eight of these hybrids out-yielded the best hybrid check (Cam Inb gp1 17 x 9450, 4.4 t/ha) by 20%. They were Cla 183 x 9450 with 5.84 t/ha, Cml 535 x Cam Inb gp1 17 with 5.58 t/ha, CMS 8704 x 9450 with 5.56 t/ha, ATP SR Y x 4001 with 5.35

t/ha, ATP S5 31Y-2 x 9450 with 5.33 t/ha, CMS 8704 x 88069 with 5.33 t/ha, Cml 437 x Cam Inb gp1 17 with 5.28 t/ha and Cml 439 x 4001 with 5.27 t/ha. Among them were three top crosses (CMS 8704 x 9450, ATP SR Y x 4001, CMS 8704 x 88069). All these hybrids had at least one introduced parent except CMS 8704 x 88069. These results suggest that the introduction of inbred lines is nesessary for the development and the identification of the high-yielding and stable maize hybrids under acid soils of the humid forest zone of Cameroon. These varieties could be released after on-farm trials. The importance of top crosses is based on the ability to produce more seed when needed since one parent is an open-pollinated variety. The best hybrids were able to tolerate Al toxicity in the acid soil stress environments. These hybrids might contain the Al tolerant genes which must have enabled them and survive and yielded well under the stress conditions.

The sensitivities of the most stable maize varieties were estimated by Finlay and Wilkinson (1963) regression modified analysis method. The sensitivity of the genotypes varied from 1.45 to 0.53. The genotype with the highest sensitivity coefficient was assumed to be the most stable meaning that from one environment to another, the mean of that variety did not vary much. CMS 8704 x 9450 was ranked first based on the sensibility coefficient.

In the GGE biplot analysis, Principal Components 1 and 2 (PC1 and PC2) together explained 50.59% of variation in grain yield. This shows that 50.59% of the variation in yield was due to genotype and genotype by environment effects. Result from the GGE biplot also called “which won where, grouped the nine test environments into three mega-environments. Mega-environment A had all the study environments except EBC1_2014. The mega-environment B had NKA2_2014, NKA2_2013, NKA1_2013, EBC2_2013 and EBC1_2014. The mega-environment C contained EBC2_2013, NKA2_2013 and NKA1_2013. This result indicated that some of the study environments were similar and were grouped together (Badu-Apraku *et al.*, 2011a; Badu-Apraku *et al.*, 2012; Ndhlela, 2012; Ifie, 2013).

The GGE biplot of the 20 high-yielding and most stable maize hybrids selected were constructed and the PCA1 and PCA 2 contributed to 65.97% of variation in grain yield across all environments. These hybrids were also grouped in three mega-environments (I, II and III). The mega-environment I had EBC1_2012, NKA1_2012, NKA1_2014and EbA2_2013. Three study environments were acidic soils. The most adapted and high-yielding hybrid identified in this mega-environment was Cla 183 x 9450. Therefore this hybrid (Cla 183 x 9450) was the highest-yielding and most stable under acid soil environments. The mega-environment III had only control environments (EBC1_2014 and EBC2_2014). The most adapted hybrid identified under these conditions was Cml 535 x Cam Inb gp1 17. This hybrid could perform well where acid soils are not a limiting factor to plant growth. When all environments fall into a single sector, this indicates that, a single cultivar had the highest yield in those environments. When the environments fall into different sectors, this indicates that different cultivars won in different sectors. The ideal genotype was a genotype to be on average environment coordinate (AEC) on positive direction and had vector length equal to the longest vectors of the genotypes on the positive side the AEC with the longest vector length of high-yielding genotypes (Kaya *et al.*, 2006; Yan and Tinker, 2006). In this regard, Cla 183 x 9450 was an ideal genotype suitable to all the environments and EBC1_2012 was the most discriminating environment.

7.5 Conclusions

This study has confirmed the year-to-year fluctuation and variability among sites and level of treatments (acid soil and control) as the important contributors for the G x E interactions. The study environments were grouped into three mega-environments. Eight most stable hybrids out-yielded the best hybrid check by 20%. They were Cla 183 x 9450, Cml 535 x Cam Inb gp1 17, CMS 8704 x 9450, ATP SR Y x 4001, ATP S5 31Y-2 x 9450, CMS 8704 x 88069, Cml 437 x Cam Inb gp1 17 and Cml 439 x 4001. Among them were three top cross hybrids (CMS 8704 x 9450, ATP SR Y x 4001, CMS 8704 x 88069). The most adapted hybrid under acid soil conditions was Cla 183 x 9450 while under control environments, Cml 535 x Cam Inb gp1 17 was the most adapted. All these hybrids had at least one introduced parent except CMS 8704 x 88069. The introduction of inbred lines was necessary and efficient for development and identification of high-yielding and stable maize hybrids under acid soils of the humid forest zone of Cameroon. These varieties are proposed for potential released after on farm trials involving farmers.

CHAPTER EIGHT

8.0 GENERAL CONCLUSION

8.1 Introduction

Maize yields in the Bimodal Humid Forest Zone of Cameroon are low mainly due to high soil acidity caused by Aluminum toxicity as a result of the high intensity of rainfall in the zone. Consequently a breeding program for tolerance to soil acidity seen as the most feasible and cost effective means, was carried out with a view of increasing the yield of the crop in the region. This chapter summarizes the research objectives and highlights the core findings, the implications and recommendations of the study. The objectives of the study were to:

- Identify constraints to maize production and preferred farmers' traits on maize cultivars
- Determine morphological and molecular trait variation among inbred lines under acid stress environments
- Determine performance of hybrids under acid soil and control conditions and determine the correlation between yield and other related traits.
- Estimate the combining abilities, the gene action and classify inbred lines into heterotic groups
- Evaluate yield stability of hybrids across environments.

8.2 Findings and implications of the study

A participatory rural appraisal (PRA) was conducted in five villages in the Bimodal Humid Forest zone of Cameroon using focus group discussions and structured questionnaire revealed that maize was the cereal of choice produced in the study area with about 96% of farmers growing open-pollinated varieties, 73% growing local varieties and only 9.3% of the farmers using maize hybrids seeds as planting material. The main land management practice in the area is slash and burn with a fallow system. The study showed that the youth of the area under 31 to 45 years of age) are engaged in farming activities.

The major constraints to maize production was inadequacy of improved varieties, post-harvest handling challenges, weeds infestation, poor soil fertility and high cost of fertilizers.

The pieces of information needed by farmers to enhance their production include awareness on the availability of improved seeds, knowledge on appropriate soil management practices to raise the level of fertility, knowledge on pest and disease management strategies, means of accessing credit facilities, and improved marketing system.

The farmers in the BHFZ have no specific preference for grain color but are willing to adopt improved maize hybrids that will be readily available and high yielding, with good grain quality such as sweet taste and soft endosperm, early maturity, pests and diseases resistant.

An assessed for tolerance to soil acidity using morphological characterization and molecular markers for the genetic diversity of 30 inbred lines from CIMMYT, IITA and IRAD revealed that inbred lines were grouped into two main clusters.

Characterization based on plant morphology of locally IRAD inbred lines showed that all the lines had primary to secondary tassel type, reddish color with yellow flint and indented kernels. Most of the leaves were pendant and the silks were reddish or whitish green. This information is useful for the gene bank database of the maize program of IRAD.

The inbred lines (local and introduced) were grouped in two main clusters under acid soils environments. Cluster one was sub-divided in three groups (I, II and III) while the second major cluster was group IV.

- Group I contained 4001, 88069, ATP S5 31Y-2, Cml 304, Cml 357, Cml 479, and D300 17. These inbred lines were moderately tolerant to acid soils. Two heterotic testers (4001 and 88069) were in this group.
- Group II contained K4 1414, Cml 439, Cml 434, Cml 332, ATP 32, ATP S9 36Y BB, 9450 and 4444 (Cam Inb gp117) and group III contained ATP S6 20Y-1, ATP S6 21Y-2, ATP S8 26Y-2, ATP S8 30Y-3, ATP S9 30Y-1, Cal 135, Cla 183, Cml 435, Cml 437, and Cml 533. All these lines were susceptible to acid soils and two known heterotic testers (Cam Inb gp1 17 and 9450) were found in this group. Also, the parents of the best high-yielding hybrid identified under acid soil environments (Cla 183 x 9450) were in this group, implying that crosses among inbred lines of this group could express very good heterosis.
- Group IV contained Cml 535, Cml 534, Cam Inb gp1 17 (F), ATP 50 and ATP S6 31Y-BB. These lines were tolerant to acid soils. In general, low variability was seen among ATP lines developed in Cameroon. These result revealed that the inbred lines clustered predominantly based on their responses to acid soil conditions.

Molecular characterization grouped lines into two major clusters. Cluster I contained all the introduced inbred lines and most of the locally developed lines. This cluster was subdivided into 16 sub-clusters. All the four inbred lines used as heterotic testers were in this main cluster but in different sub-clusters. The genetic distance among these inbred lines were low to moderate (0.3 to 0.4) implying that the prediction of the heterosis effect of the crosses among these lines would not yield materials with good traits. These results revealed that genetic distance as measured by molecular markers is not always associated with heterosis. Variability exists among the inbred lines which could be exploited in the development of acid tolerant hybrids.

In order to estimate the performance of the inbred lines in hybrid combinations, twenty-five inbred lines and three open-pollinated varieties were crossed with 4 testers (Cam Inb gp1 17, 88069, 4001 and 9450) and were evaluated under six acid soil environments and six control environments. Three OPVs (two commercial (ATP SR Y and CMS 8704)) and one introduced (C4RR SA4) were used. The following were the major findings:

Fifteen hybrids out-yielded the best hybrid check by 10% under acid soil and control environments. These hybrids were Cla 183 x 9450, ATP S9 36Y-BB x 4001, Cla 183 x 88069, Cml 434 x Cam Inb gp1 17, ATP S5 31Y-2 x 4001, Cml 437 x Cam Inb gp1 17, ATP S8 26Y-3 x Cam Inb gp1 17, Cml 534 x 4001, Cla 183 x Cam Inb gp1 17, Cml 439 x 4001, ATP S6 31Y-BB x 9450, Cml 535 x Cam Inb gp1 17, ATP SR Y x 4001, Cml 439 x Cam Inb gp1 17, and CMS 8704 x 9450. Almost all of these hybrids contained at least one introduced parent from IITA or CIMMYT showing the importance of the introduction of inbred lines in the development of new high-yielding hybrids.

Some related traits (such as plant height, ear height, ears per plant, anthesis-silking interval, plant aspect and ear aspect) and selection indices (yield reduction percentage, stress tolerance index and stress susceptibility index) highly correlated with yield. These traits could be incorporated into a base index for the identification of high yielding hybrids under acid soil environments. Heritability estimates of all the traits recorded under acid soil environments was low compared to the control soil conditions.

The results of combining ability studies revealed that both additive and non-additive effects were important in controlling grain yield with the predominance of non-additive gene effects under acid soil and across environments, suggesting that breeding gain can be realized through exploitation of heterosis in the program.

Four distinct heterotic groups (A, B, C and D) were identified under acid soil and across environments based on the specific combining ability and yield superiority over the best hybrid check. Two heterotic groups made of group A (Cml 437, Cml 439 and Cml 434) and group C (ATP S6 31Y-BB) were identified under control environments using Cam Inb gp1 17 and 9450 as testers. These testers were the best under control conditions and across environments while 4001 was the best under acid soil environments. Cml 434 x Cam Inb gp1 17 and ATP S6 31Y-BB x 9450 were good heterotic pattern under all the environments.

Some inbred lines viz., ATP S5 31Y-2, ATP S6 31Y-BB, ATP S8 30Y-2, Cml 434, ATP S9 36Y-BB, ATP S6 21Y-2, ATP S8 26Y-2 and Cla 183 expressed good general combining ability with superior specific combinations with other inbreds. These lines could be of potential use in breeding new lines for tolerance to acid soils.

The yield stability analysis of the hybrids across nine environments revealed that the main problem in selecting superior varieties in Cameroon was the unpredictable environmental conditions. The year-to-year fluctuation and variability among sites and level of treatments (acid soil and control) were important contributors to the G x E interactions. The nine study environments used in the study were grouped into three mega-environments.

The hybrids Cla 183 x 9450, Cml 535 x Cam Inb gp1 17, CMS 8704 x 9450 (top cross), ATP SR Y x 4001 (top cross), ATP S5 31Y-2 x 9450, CMS 8704 x 88069 (top cross), Cml 437 x Cam

Inb gp1 17 and Cml 439 x 4001 out-yielded the best hybrid check by more than 20%. The most adapted hybrid under acid soil conditions was Cla 183 x 9450. All the selected hybrids had at least one introduced parent except CMS 8704 x 88069. These results suggest that the introduction of inbred lines was efficient in the development and the identification of the high-yielding and stable maize hybrids under acid soils of the humid forest zone of Cameroon.

In conclusion, eight high-yielding and stable maize hybrids were developed and could be considered to be released to the farmers of the humid forest zone of Cameroon. They were Cla 183 x 9450, Cml 535 x Cam Inb gp1 17, CMS 8704 x 9450, ATP SR Y x 4001, ATP S5 31Y-2 x 9450, CMS 8704 x 88069, Cml 437 x Cam Inb gp1 17 and Cml 439 x 4001. Among them were three top crosses (CMS 8704 x 9450, ATP SR Y x 4001, CMS 8704 x 88069). These hybrids had at least one introduced parent from CIMMYT and / or IITA. This suggests that the introduction of the inbred lines increases the variability among the parental material used and was effective in the development and the identification of high-yielding, stable and tolerant maize hybrids under acid soil environments. Even though the genetic distance from molecular study among the parental hybrids used was low, some high-yielding crosses were identified. This indicated that genetic distances from molecular markers are not always associated with heterosis. The expression of heterosis in crosses was consistent confirming that genetic distance measured by molecular markers would have not been efficient to identify heterotic patterns in the present study. Also, the best tester were 9450, Cam Inb gp1 17 and 4001 which were involved in three crosses (9450) and two crosses each (Cam Inb gp1 17 and 4001) of the top eight hybrids selected.

8.3 Recommendations

- ✓ The participatory Rural Appraisal could be conducted in other regions within the Bimodal Humid forest Zone of Cameroon to elicit farmers' constraints to maize production and preference for maize varieties, which may be different from those in the study area of the present work. This when done will present a holistic view of farmers' maize varietal preferences in the Bimodal Humid Forest Zone which would be incorporated in the national breeding program.
- ✓ Further study should be done to check the existence of the genes for Al tolerance in the tolerant inbred lines of group IV (Cml 535, Cml 534, Cam Inb gp1 17 (F), ATP 50 and ATP S6 31Y-BB). This would be useful for introgression of Al tolerance genes into farmers preferred varieties that are susceptible.

The high-yielding and most stable hybrids identified could be considered for release after multi-locational and on-farm trials. The early maturity and the sweetness of these hybrids need to be tested.

The inbred lines that exhibited positive GCA effects for grain yield under acid soil environments could be used to form synthetics and other open-pollinated varieties.

Further selection should be done under acid and control environments to increase the number of high-yielding tolerant hybrids in Cameroon. Evaluation of crosses between inbred lines in different heterotic groups should also be done for identification of better high-yielding acid tolerant hybrids.

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APPENDICES

Appendix 3.1: Questionnaire for individual interview of a randomly selected farmer

GENERAL INFORMATION

a) Name of interviewee (Optional)	
b) Name of Region	
c) Name of the district	
d) Name of village	

DEMOGRAPHIC INFORMATION OF HOUSEHOLD

Gender of household head	Male	1						
	Female	2						
Age of household head	<30yrs	**1**	31-45	**2**	51-65	**3**	>65yrs	**4**

Household Composition		**Male**	**Female**	
	Elderly >60 Yrs			**1**
	Adults > 18 – 60 Yrs			**2**
	Youth 12 – 18 Yrs			**3**
	Child < 12 Yrs			**4**
	Total			**5**

Level of education	None	**1**
	Adult literacy	**2**
	Primary	**3**
	Secondary	**4**
	Post secondary	**5**

ENTERPRISES

Main source of livelihood	Crop production	**1**
	Livestock production	**2**
	Business/trading	**3**
	Casual labour	**4**
Specify	Other	**5**
Crops grown	Cereal (Maize/Rice/sorghum)	**1**
	Legumes (beans/groundnut/ green leaves)	**2**
	Tuber/root crops (sweet potatoes/Cassava)	**3**
	Cocoa	**4**
	Fruits	**5**
Specify	Other	**6**

Average land holding size	<5ha	**1**	6 - 10ha	**2**	11-20ha	**3**	>20	**4**
Size of land under maize	<1ha	**1**	1-2ha	**2**	3-5ha	**3**	>5ha	**4**
Type of farming system	Pure maize	**1**	Intercropping	**2**	Relay cropping	**3**	Other (specify)	**4**
When do you plant maize	Short rain season	**1**	Long rain season	**2**	Both seasons	**3**	Other (specify)	**4**

Type of maize production system	Rainfed	**1**
	Irrigation	**2**
	Rainfed supplemented with irrigation	**3**
Specify	Other	**4**
Type of maize varieties		**1**
Composites	ATPSRY, CMS 8704, CMS 8501…	**2**
Hybrids	CHC 101…	**3**
Specify	Other	**4**
Sources of maize varieties	Seed companies	**1**
	Research institutes (IRAD)	**2**
	Own seeds/neighbors	**3**
Specify	Other	**4**

What are the reasons for the preferred varieties (Scale : **1= Highly rated; 2= Low rate**)	
1. Color of seeds	
2. Poor yield performance	
3. Susceptibility to poor soil fertility (soil acidity)	
4. Susceptibility to pests and diseases	
5. Size of seeds	
6. Long duration cycle	
7. Inaccessible varieties	
8. Other (Specify)……………………………………………………………	
Reasons for the non preferred varieties (Scale : **1= Highly rated; 2= Low rate**)	
9. Color of seeds	
10. Poor yield performance	
11. Susceptibility to poor soil fertility (soil acidity)	
12. Susceptibility to pests and diseases	
13. Size of seeds	
14. Long duration cycle	

15. Inaccessible varieties	
16. Other (Specify)………………………………………………………	

How long have you planted maize	<1yr	**1**
	1-2yrs	**2**
	3-5yrs	**3**
	6-10yrs	**4**
	>10yrs	**5**
a) Do you change the varieties you grow	Yes	**1**
	No	**2**

b) If yes after how long	1-2yrs	**1**	2-4yrs	**2**	**4-8yrs**	**3**	**>10yrs**	**4**

c) Reasons for changing the varieties	Availability of released varieties	**1**
	Accessibility of new varieties	**2**
	Awareness of new varieties	**3**
Specify	Other	**4**
d) Reasons for not changing the varieties	Unavailability of released varieties	**1**
	Inaccessibility of new varieties	**2**
	Lack of awareness of new varieties	**3**
Specify	Other	**4**

MAIZE YIELD, USE AND MARKETING

On average what is your yield of maize (per 50kgs)	< 2bags	**1**
	2-4bags	**2**
	5-7bags	**3**
	8-10bags	**4**
	>10bags	**5**
What do you use your maize for?	Consumption	**1**
	Local market	**2**
Specify	Other	**3**

Are there inputs and output markets available within your area?	Yes	**1**	No	**2**

Where do you sell your maize	Local market	**1**
	Export to neighboring countries	**2**
Specify	Other	**3**
What type of transport network is available	Tarmac road	**1**
	Weathered road	**2**
How far is the market from your farm	<5km	**1**
	5-10km	**2**

	>10km	**3**
What period of the year do you sell maize	Immediately after harvest	**1**
	During planting season	**2**
	When there is availability of market	**3**
Specify	Other	**4**
What is the average price per kg of maize	<100 FCFA	**1**
	100 – 120 KES	**2**
	120 – 150 KES	**3**
	>150 KES	**4**

EXTENSION SERVICES

Who amongst the following provides you with farming advice?			
Public extension workers			**1**
Private extension workers/research institutes/universities			**2**
Development agencies			**3**
Friends (Other farmers)			**4**
Other (Specify)			**5**
How far is it to get to Extension service?	<5km		**1**
	5-10km		**2**
	=>11km		**3**
Have you ever received any technical assistance from extension Workers/researchers		Yes	**1**
		No	**2**
How often do extension officers/researchers visit you?	Once per year		**1**
	Twice per year		**2**
	Three times per year		**3**
	Four times per year		**4**
	Never		**5**
How do you receive technical assistance?	Visits to extension officers		**1**
	Visits from extension officers/researchers		**2**
	Farmer field schools (FFS)		**3**
	Field days		**4**
	Demonstrations		**5**
Specify	Other		**2**
In your opinion how do you view the quality of the extension by	Excellent		**1**

officers/researchers from institutes/universities who visit you?	Very good	**2**
	Satisfactory	**3**
	Poor	**4**

AGRICULTURAL INFORMATION

Do you need agricultural information to deal with farming activities?	Yes	**1**	No	**2**

If **yes** what type of information?	Crop management (poor soil fertility, acidity,	**1**
	Livestock management	**2**
	Marketing	**3**
	Credit and finance	**4**
Specify	Other	**5**
If **NO** how do you cope without agricultural information?		

How do you rate the information you get?	Always relevant	**1**
	Sometimes relevant	**2**
	Never relevant	**3**

Which of the following sources provides agricultural information that you use?	
Mass media (Radio, Television)	
Electronic Media (internet, web, Telephone)	
Print media (newspapers, pamphlet, posters, bronchures)	
Face – to – face (Extension agents, researchers, friends/relatives, FFS//groups)	
Other (Specify)	
1=Not at all **2=Not frequently** **2= Frequently** **3=Most Frequently**	

What are some of the challenges you encounter during maize production?

1) 2) 3)

What can you comment about maize production in your area?

1) 2) 3)

Appendix 5.1: Mean performance of hybrids under control environments

Genotype	yield C	pltasp	earasp	epp	earght	plthgt	asi
ATP S5 31Y-2 x Cam Inb gp1 17	4.05	2.90	3.29	1.16	80.32	178.77	2.53
ATP S5 31Y-2 x 88069	4.59	2.41	2.28	1.33	96.12	197.60	1.74
ATP S5 31Y-2 x 9450	6.29	2.17	1.89	1.32	99.53	211.82	1.30
ATP S5 31Y-2 x 4001	5.09	2.43	1.94	1.23	93.87	191.02	2.02
ATP S6 20Y-1 x Cam Inb gp1 17	4.90	2.53	1.92	1.12	90.10	184.72	2.58
ATP S6 20Y-1 x 88069	5.63	2.45	2.22	0.99	87.93	180.15	2.56
ATP S6 20Y-1 x 9450	6.13	2.54	2.07	1.07	88.92	191.52	2.06
ATP S6 20Y-1 x 4001	5.22	2.68	2.14	1.14	84.69	182.54	1.87
ATP S6 21Y-2 x Cam Inb pg1 17	5.84	2.72	2.30	1.24	88.26	191.48	2.48
ATP S6 21Y-2 x 88069	5.09	2.75	2.20	1.12	91.31	187.24	2.47
ATP S6 21Y-2 x 9450	5.30	2.53	1.95	1.08	85.38	185.69	1.75
ATP S6 21Y-2 x 4001	5.30	2.42	1.96	1.00	94.64	191.45	1.67
ATP S6 31Y-BB x Cam Inb gp1 17	4.07	2.50	2.11	1.12	93.37	187.21	1.46
ATP S6 31Y-BB x 88069	4.21	2.54	2.50	1.17	89.37	185.65	1.71
ATP S6 31Y-BB x 9450	6.89	2.43	1.94	1.14	105.30	200.18	2.08
ATP S6 31Y-BB x 4001	4.51	2.86	2.11	1.11	97.20	188.31	1.63
ATP S8 26Y-3 x Cam Inb gp1 17	5.29	2.58	2.23	1.26	86.31	186.84	1.22
ATP S8 26Y-3 x 88069	5.94	2.74	2.25	1.09	82.43	165.53	1.03
ATP S8 26Y-3 x 9450	4.82	2.71	2.07	1.14	90.66	182.27	1.32
ATP S8 26Y-3 x 4001	4.02	2.88	2.52	1.30	90.93	187.81	0.99
ATP S8 30Y-3 x Cam Inb gp1 17	6.26	2.53	2.29	1.22	90.51	185.82	1.80
ATP S8 30Y-3 x 88069	4.71	2.64	2.44	1.23	85.49	187.43	1.34
ATP S8 30Y-3 x 9450	5.62	2.44	1.89	1.04	93.23	204.69	1.38
ATP S8 30Y-3 x 4001	4.42	2.64	2.03	1.03	86.59	186.89	1.28
ATP S9 30Y-1 x Cam Inb gp1 17	5.02	2.70	2.45	0.96	96.37	197.96	2.91
ATP S9 30Y-1 x 88069	4.32	2.65	2.48	0.95	89.87	184.62	2.29
ATP S9 30Y-1 x 9450	6.06	2.35	1.97	0.95	87.06	199.72	1.78
ATP S9 30Y-1 x 4001	3.88	2.47	2.23	1.23	97.47	195.29	1.92
ATP S9 36Y-BB x Cam Inb gp1 17	5.75	2.55	2.04	1.17	82.11	189.46	1.84
ATP S9 36Y-BB x 88069	4.05	2.41	2.13	1.05	89.01	175.55	1.49
ATP S9 36Y-BB x 9450	5.24	2.47	2.06	1.14	89.02	193.17	1.71
ATP S9 36Y-BB x 4001	5.48	2.47	2.57	1.03	93.50	195.14	1.90
ATP-32 x Cam Inb gp1 17	5.68	2.37	2.36	1.23	89.45	181.85	1.64
ATP-32 x 88069	4.76	2.65	2.56	1.09	87.04	185.12	1.33
ATP-32 x 9450	4.13	2.61	2.44	1.08	90.28	185.99	1.25
ATP-32 x 4001	5.86	2.26	1.99	1.17	87.65	187.47	3.01
ATP-50 x Cam Inb gp1 17	4.32	2.67	2.60	1.21	85.47	194.50	1.57
ATP-50 x 88069	5.58	2.46	2.63	1.12	83.43	190.74	2.46
ATP-50 x 9450	6.12	2.45	2.18	1.28	100.90	209.78	1.70
ATP-50 x 4001	5.06	2.45	2.03	1.19	97.81	208.11	1.57
Cml 304 x Cam Inb gp1 17	5.81	2.33	2.06	1.07	101.82	203.37	1.74
Cml 304 x 88069	4.78	2.31	2.01	1.01	95.28	196.60	2.03
Cml 304 x 9450	6.20	2.33	1.58	1.15	109.35	211.49	1.35

Genotype	**yield C**	**pltasp**	**earasp**	**epp**	**earght**	**plthgt**	**asi**
Cml 304 x 4001	5.30	2.10	1.77	1.14	98.74	200.69	1.60
Cml 357 x Cam Inb gp1 17	6.11	2.11	1.67	1.10	110.11	203.89	2.42
Cml 357 x 88069	5.44	2.34	2.28	1.02	84.14	197.47	1.74
Cml 357 x 9450	4.90	2.50	2.15	1.18	89.66	196.51	1.79
Cml 357 x 4001	5.88	2.30	1.76	1.05	93.46	199.38	2.26
Cml 435 x Cam Inb gp1 17	5.21	2.45	1.95	0.98	84.29	189.63	1.55
Cml 435 x 88069	5.59	2.47	1.77	1.14	79.94	183.01	1.99
Cml 435 x 9450	5.14	2.51	2.27	1.12	88.34	187.93	2.11
Cml 435 x 4001	5.08	2.52	2.19	1.05	87.62	195.33	1.82
Cml 437 x Cam Inb gp1 17	5.83	2.59	1.96	1.06	91.29	188.96	1.96
Cml 437 x 88069	6.17	2.36	1.75	1.17	97.96	199.26	2.83
Cml 437 x 9450	5.38	2.53	2.00	1.15	98.53	199.08	1.66
Cml 437 x 4001	5.65	2.60	1.78	1.07	99.74	205.59	2.82
Cml 439 x Cam Inb gp1 17	7.24	2.01	1.60	1.06	89.01	203.31	2.15
Cml 439 x 88069	5.27	2.57	2.22	1.07	87.17	186.69	2.35
Cml 439 x 9450	4.66	2.71	2.55	1.11	89.39	186.35	1.15
Cml 439 x 4001	6.06	2.64	1.83	1.06	89.03	187.49	1.06
Cml 533 x Cam Inb gp1 17	4.88	2.75	2.23	1.29	83.90	185.20	2.56
Cml 533 x 88069	5.07	2.71	2.85	1.12	81.04	182.35	-1.37
Cml 533 x 9450	5.20	2.61	2.24	1.15	98.84	196.80	2.17
Cml 533 x 4001	5.37	2.42	2.36	1.10	101.16	195.44	3.10
Cml 534 x Cam Inb gp1 17	5.74	2.37	2.15	1.36	92.63	203.38	2.52
Cml 534 x 88069	4.24	2.45	2.38	1.13	88.60	184.47	1.98
Cml 534 x 9450	5.04	2.74	2.39	1.10	86.45	188.50	1.96
Cml 534 x 4001	4.86	2.57	2.24	1.04	91.90	189.99	2.29
Cml 535 x Cam Inb gp1 17	6.91	2.30	2.16	1.23	88.25	196.53	3.80
Cml 535 x 88069	4.70	2.38	2.73	1.02	105.78	200.67	2.52
Cml 535 x 9450	5.15	2.26	2.08	1.26	96.34	202.85	3.15
Cml 535 x 4001	4.29	2.43	2.28	1.32	89.26	187.90	2.81
Cml 332 x Cam Inb gp1 17	6.60	2.61	2.23	1.16	94.30	203.01	2.60
Cml 332 x 88069	5.16	2.49	2.23	1.14	89.79	194.70	2.18
Cml 332 x 9450	4.44	2.47	2.56	1.17	84.26	188.76	2.01
Cml 332 x 4001	4.26	2.72	2.23	1.16	87.10	190.28	1.48
Cml 479 x Cam Inb gp1 17	4.52	2.75	2.46	1.07	93.75	203.54	2.00
Cml 479 x 88069	4.46	2.56	1.99	1.10	87.23	195.09	2.65
Cml 479 x 9450	5.16	2.56	2.45	1.00	100.70	207.63	1.81
Cml 479 x 4001	5.84	2.07	1.77	1.05	107.91	222.19	1.33
Cla 183 x Cam Inb gp1 17	5.51	2.27	2.15	1.11	88.93	202.29	2.24
Cla 183 x 88069	5.77	2.36	1.83	1.02	89.40	185.97	2.51
Cla 183 x 9450	6.00	2.40	2.10	1.10	122.86	217.39	2.48
Cla 183 x 4001	3.62	2.87	2.55	1.00	103.81	198.09	2.71
Cml 434 x Cam Inb gp1 17	6.35	2.43	1.88	0.97	87.01	192.58	3.35
Cml 434 x 88069	5.70	2.47	1.87	1.05	99.68	207.84	2.91
Cml 434 x 9450	5.64	2.40	1.86	1.05	88.36	193.52	0.98
Cml 434 x 4001	4.44	2.64	2.10	1.18	96.49	196.88	0.72
CLA 135 x Cam Inb gp1 17	5.84	2.49	1.95	1.01	94.39	202.63	2.08

Genotype	**yield C**	**pltasp**	**earasp**	**epp**	**earght**	**plthgt**	**asi**
CLA 135 x 88069	6.29	2.54	1.94	1.03	93.44	196.07	1.32
CLA 135 x 9450	6.31	2.36	2.03	1.09	99.89	206.49	1.05
CLA 135 x 4001	4.98	2.49	2.02	1.09	92.84	200.75	1.92
D300-17 x Cam Inb gp1 17	6.53	2.36	2.02	1.08	105.41	205.09	1.69
D300-17 x 88069	4.93	2.45	2.09	1.16	101.18	201.83	1.53
D300-17 x 9450	5.85	2.64	2.22	1.19	92.56	184.69	2.16
D300-17 x 4001	3.71	2.79	2.49	1.02	83.27	185.91	0.57
4001 x Cam Inb gp1 17	4.85	2.89	1.93	1.15	91.52	188.42	2.43
4001 x 88069	6.09	2.67	2.10	1.27	95.18	203.05	1.67
4001 x 9450	6.13	2.82	2.26	1.04	95.48	198.70	2.30
9450 x Cam Inb gp1 17	4.91	2.72	2.10	1.19	79.32	183.49	1.59
9450 x 88069	5.15	2.77	2.32	1.12	95.60	203.87	2.27
88069 x Cam Inb gp1 17	5.42	2.54	2.02	1.02	96.53	196.72	2.17
ATP SR Y x Cam Inb gp1 17	5.81	2.41	2.29	1.04	99.94	211.97	2.44
ATP SR Y x 88069	4.67	2.48	2.28	1.06	94.90	203.16	1.49
ATP SR Y x 9450	4.50	2.48	2.40	1.08	96.45	203.26	1.58
ATP SR Y x 4001	7.04	2.35	1.59	1.16	83.07	190.15	0.64
CMS 8704 x Cam Inb gp1 17	5.21	2.33	2.09	1.00	101.89	205.45	1.91
CMS 8704 x 88069	5.64	2.47	1.94	1.06	91.65	194.51	1.67
CMS 8704 x 9450	7.40	1.99	1.95	1.07	103.96	213.99	1.20
CMS 8704 x 4001	5.75	2.43	2.32	1.04	93.38	188.52	3.19
C4RR SA4 x Cam Inb gp1 17	5.79	2.79	2.11	0.97	91.17	195.46	1.53
C4RR SA4 x 88069	4.95	2.52	2.24	1.02	113.35	205.40	1.48
C4RR SA4 x 9450	3.50	1.77	2.50	1.07	102.95	213.57	1.98
C4RR SA4 x 4001	5.23	2.14	2.04	1.06	106.97	220.77	2.03
Cam Inb gp1 17 (F) x Cam Inb gp1 17	5.24	2.56	1.69	1.29	94.01	195.53	1.70
Cam Inb gp1 17 (F) x 88069	5.48	2.84	1.88	1.11	93.55	189.92	1.97
Cam Inb gp1 17 (F) x 9450	4.33	2.84	2.16	1.08	76.65	180.96	1.87
Cam Inb gp1 17 (F) x 4001	4.72	2.81	2.14	1.11	92.65	196.15	1.35
C4RR SA4	4.84	2.54	1.97	1.11	88.98	179.37	1.81
CMS 8704	5.29	2.67	2.06	1.25	79.00	185.19	1.21
ATP SR Y	3.99	2.98	2.20	1.23	88.40	204.38	2.29

Appendix 5.2: Mean performance of 121 hybrids evaluated under acid soil environments

Genotypes	**yield**	**pltasp**	**earasp**	**epp**	**earght**	**plthgt**	**asi**
ATP S5 31Y-2 x Cam Inb gp1 17	2.52	3.36	3.28	1.00	78.44	166.44	3.10
ATP S5 31Y-2 x 88069	2.43	3.51	2.95	1.15	61.72	138.86	2.34
ATP S5 31Y-2 x 9450	4.34	3.14	2.54	1.04	79.05	169.74	3.07
ATP S5 31Y-2 x 4001	5.07	2.89	2.27	1.15	74.48	159.15	2.88
ATP S6 20Y-1 x Cam Inb gp1 17	2.47	3.41	2.92	0.98	72.83	147.08	3.47
ATP S6 20Y-1 x 88069	3.79	3.32	2.85	0.96	69.63	152.76	3.71
ATP S6 20Y-1 x 9450	3.23	3.73	2.83	0.99	64.82	142.06	2.46
ATP S6 20Y-1 x 4001	3.03	3.41	2.81	1.01	67.44	150.09	2.16
ATP S6 21Y-2 x Cam Inb pg1 17	3.15	3.27	2.59	0.90	60.48	142.00	2.00
ATP S6 21Y-2 x 88069	3.75	3.54	2.55	1.06	61.67	137.61	2.98
ATP S6 21Y-2 x 9450	2.41	3.65	3.34	1.06	62.87	135.41	2.36
ATP S6 21Y-2 x 4001	1.97	3.35	2.81	1.10	70.52	157.55	2.88
ATP S6 31Y-BB x Cam Inb gp1 17	2.00	3.39	3.07	1.08	74.92	154.82	2.49
ATP S6 31Y-BB x 88069	1.41	3.57	3.36	1.19	69.00	142.35	2.21
ATP S6 31Y-BB x 9450	4.20	3.22	2.44	1.03	83.13	169.42	3.08
ATP S6 31Y-BB x 4001	2.14	3.39	2.66	1.07	70.60	147.23	1.34
ATP S8 26Y-3 x Cam Inb gp1 17	4.72	3.55	2.67	1.08	64.48	151.33	2.37
ATP S8 26Y-3 x 88069	2.93	3.22	2.77	0.93	67.93	142.86	1.60
ATP S8 26Y-3 x 9450	2.91	3.61	2.88	1.04	67.27	142.79	1.93
ATP S8 26Y-3 x 4001	2.24	3.58	3.22	1.07	66.38	140.82	2.50
ATP S8 30Y-3 x Cam Inb gp1 17	4.25	3.17	2.20	1.01	81.67	168.69	2.91
ATP S8 30Y-3 x 88069	2.27	3.67	3.26	1.02	64.17	137.68	2.07
ATP S8 30Y-3 x 9450	3.00	3.49	2.85	1.01	70.63	157.56	0.84
ATP S8 30Y-3 x 4001	4.14	3.06	2.41	1.05	73.99	157.52	2.43
ATP S9 30Y-1 x Cam Inb gp1 17	2.98	2.97	2.46	1.03	79.12	172.53	2.41
ATP S9 30Y-1 x 88069	3.64	3.26	2.63	1.03	68.44	150.55	3.20
ATP S9 30Y-1 x 9450	3.62	2.90	2.43	0.98	70.39	167.62	2.16
ATP S9 30Y-1 x 4001	3.53	3.18	2.30	1.04	73.22	159.89	3.57
ATP S9 36Y-BB x Cam Inb gp1 17	3.71	2.94	2.68	1.09	62.81	158.78	1.60
ATP S9 36Y-BB x 88069	3.87	3.19	2.67	1.03	66.56	137.10	3.73
ATP S9 36Y-BB x 9450	3.06	2.97	2.55	1.21	80.52	171.42	2.93
ATP S9 36Y-BB x 4001	5.37	3.02	2.77	1.06	76.60	171.20	3.21
ATP-32 x Cam Inb gp1 17	3.12	3.16	2.63	1.00	64.18	150.00	3.63
ATP-32 x 88069	2.68	3.66	3.23	1.02	52.42	139.95	2.51
ATP-32 x 9450	2.83	3.43	3.14	1.03	71.50	167.59	2.36
ATP-32 x 4001	2.59	3.48	3.38	1.10	64.39	142.89	2.77
ATP-50 x Cam Inb gp1 17	3.34	3.09	3.01	1.21	75.75	167.38	1.72
ATP-50 x 88069	2.60	3.69	3.31	0.96	51.98	135.74	2.07

Genotypes	yield	pltasp	earasp	epp	earght	plthgt	asi
ATP-50 x 9450	2.82	3.13	2.72	1.11	80.10	174.35	1.79
ATP-50 x 4001	2.06	3.39	3.20	1.11	72.89	162.47	1.22
Cml 304 x Cam Inb gp1 17	3.23	3.15	2.72	0.93	74.86	163.31	1.91
Cml 304 x 88069	2.52	3.40	3.02	0.99	63.50	144.74	1.83
Cml 304 x 9450	3.66	3.08	2.54	0.96	84.70	177.98	2.20
Cml 304 x 4001	1.64	3.42	3.17	1.08	66.71	139.70	2.57
Cml 357 x Cam Inb gp1 17	2.80	3.31	2.75	0.95	66.36	162.23	2.86
Cml 357 x 88069	2.46	3.46	3.27	0.99	61.41	152.95	2.97
Cml 357 x 9450	2.74	3.01	2.65	1.10	71.75	160.97	1.89
Cml 357 x 4001	3.67	3.13	2.49	1.00	68.01	152.44	1.74
Cml 435 x Cam Inb gp1 17	3.78	2.99	2.37	1.20	63.25	159.27	2.36
Cml 435 x 88069	2.57	3.59	2.80	1.13	64.07	147.60	2.93
Cml 435 x 9450	3.32	3.25	2.69	0.99	63.53	157.52	2.93
Cml 435 x 4001	2.62	3.33	3.00	1.05	65.58	150.68	2.02
Cml 437 x Cam Inb gp1 17	4.84	3.11	2.20	0.93	70.68	167.90	3.01
Cml 437 x 88069	3.42	3.05	2.54	1.05	70.81	160.54	3.49
Cml 437 x 9450	4.13	3.26	2.57	1.00	73.26	162.82	1.66
Cml 437 x 4001	2.09	3.49	2.59	0.98	74.48	156.95	2.53
Cml 439 x Cam Inb gp1 17	3.81	2.75	2.32	1.10	70.01	163.45	3.17
Cml 439 x 88069	3.67	3.36	2.74	0.94	68.37	152.27	2.82
Cml 439 x 9450	4.23	3.09	2.52	1.00	66.48	159.15	2.14
Cml 439 x 4001	4.39	3.22	2.24	0.93	75.83	155.14	1.69
Cml 533 x Cam Inb gp1 17	3.00	3.55	2.60	1.07	71.31	161.70	4.61
Cml 533 x 88069	3.21	3.50	3.08	1.04	59.38	137.44	-0.89
Cml 533 x 9450	2.96	3.23	2.99	0.95	75.57	157.89	1.43
Cml 533 x 4001	2.78	3.34	3.13	1.00	72.56	146.44	3.44
Cml 534 x Cam Inb gp1 17	2.37	3.39	2.79	1.07	63.61	158.82	2.44
Cml 534 x 88069	3.24	3.11	2.73	0.97	72.09	156.44	2.53
Cml 534 x 9450	2.89	3.65	2.91	1.07	68.06	147.32	1.61
Cml 534 x 4001	4.42	3.12	2.37	0.99	78.05	165.09	2.42
Cml 535 x Cam Inb gp1 17	3.51	2.80	2.37	1.11	75.05	161.81	2.78
Cml 535 x 88069	3.51	2.91	2.91	0.98	73.74	157.09	2.81
Cml 535 x 9450	3.16	2.94	2.99	1.14	75.53	160.29	3.84
Cml 535 x 4001	3.25	3.02	2.88	1.17	78.06	159.39	3.62
Cml 332 x Cam Inb gp1 17	3.00	3.24	3.19	1.12	75.90	167.71	1.84
Cml 332 x 88069	3.79	2.99	2.73	1.07	72.08	172.67	3.17
Cml 332 x 9450	3.74	3.10	2.92	1.06	67.35	150.94	2.47
Cml 332 x 4001	3.17	3.69	3.04	0.99	63.07	141.23	2.12
Cml 479 x Cam Inb gp1 17	3.53	3.22	2.65	1.10	62.51	161.35	1.79
Cml 479 x 88069	3.67	3.09	2.57	0.97	68.98	159.81	2.60
Cml 479 x 9450	2.67	3.26	2.85	1.09	76.90	173.62	1.04

Genotypes	**yield**	**pltasp**	**earasp**	**epp**	**earght**	**plthgt**	**asi**
Cml 479 x 4001	3.27	3.09	2.53	0.99	70.76	168.94	2.97
Cla 183 x Cam Inb gp1 17	4.42	2.83	2.20	0.98	75.68	177.52	3.11
Cla 183 x 88069	5.36	2.73	1.92	0.95	79.91	174.65	3.84
Cla 183 x 9450	6.12	2.63	2.02	0.88	101.52	198.02	2.17
Cla 183 x 4001	3.97	2.68	2.50	0.96	88.74	171.35	2.62
Cml 434 x Cam Inb gp1 17	5.11	2.72	2.38	0.99	79.57	176.11	2.97
Cml 434 x 88069	3.81	3.15	2.47	1.04	68.78	162.63	3.21
Cml 434 x 9450	3.49	3.16	2.69	0.95	69.21	164.04	1.14
Cml 434 x 4001	2.93	3.20	2.52	1.01	80.85	170.03	1.96
CLA 135 x Cam Inb gp1 17	3.68	3.40	2.71	1.11	60.45	147.64	2.39
CLA 135 x 88069	3.53	3.39	2.77	1.05	72.45	160.68	2.03
CLA 135 x 9450	4.05	2.90	2.50	1.02	77.19	169.54	2.42
CLA 135 x 4001	2.05	3.43	2.73	1.11	67.27	150.98	1.47
D300-17 x Cam Inb gp1 17	3.97	2.96	2.56	1.08	73.99	161.13	1.68
D300-17 x 88069	2.65	3.48	2.82	1.15	68.80	146.98	1.91
D300-17 x 9450	3.15	3.01	2.72	1.12	82.09	173.20	2.73
D300-17 x 4001	2.47	3.21	2.83	0.98	70.93	161.87	1.74
4001 x Cam Inb gp1 17	2.65	3.44	2.69	1.04	57.79	135.43	2.02
4001 x 88069	1.96	3.55	3.14	1.04	59.04	147.72	2.52
4001 x 9450	3.11	3.41	2.40	1.00	74.71	158.60	2.21
9450 x Cam Inb gp1 17	4.00	3.33	2.81	1.05	70.55	155.25	2.18
9450 x 88069	3.13	3.23	2.81	1.07	61.79	140.50	3.09
88069 x Cam Inb gp1 17	3.43	3.77	2.82	1.12	62.99	149.02	2.11
ATP SR Y x Cam Inb gp1 17	3.91	3.12	2.75	1.10	75.83	165.67	2.44
ATP SR Y x 88069	3.87	2.86	2.67	1.00	70.17	162.52	1.77
ATP SR Y x 9450	2.64	3.54	3.00	1.08	72.92	156.53	2.26
ATP SR Y x 4001	3.67	2.91	2.83	1.10	65.38	160.44	2.19
CMS 8704 x Cam Inb gp1 17	2.13	3.23	3.21	1.12	52.89	143.06	2.61
CMS 8704 x 88069	4.23	3.13	2.47	1.03	73.61	167.22	2.62
CMS 8704 x 9450	3.89	2.96	2.65	1.03	73.73	171.46	2.75
CMS 8704 x 4001	3.62	3.07	2.52	1.03	79.75	167.70	2.05
C4RR SA4 x Cam Inb gp1 17	4.26	3.01	2.75	1.04	75.82	165.57	2.53
C4RR SA4 x 88069	4.06	2.63	2.82	1.26	71.24	159.92	4.31
C4RR SA4 x 9450	3.42	3.45	2.92	1.00	77.70	168.29	2.97
C4RR SA4 x 4001	3.55	3.64	2.65	0.96	79.50	166.60	3.23
Cam Inb gp1 17 (F) x Cam Inb gp1 17	2.84	3.69	3.29	1.21	61.74	146.00	2.08
Cam Inb gp1 17 (F) x 88069	3.26	3.42	3.14	1.02	66.49	151.50	3.86
Cam Inb gp1 17 (F) x 9450	4.23	3.24	2.44	1.12	79.28	163.96	3.54
Cam Inb gp1 17 (F) x 4001	2.61	3.04	2.69	1.14	69.37	144.27	1.36
C4RR SA4	2.77	3.52	2.95	1.03	67.99	160.87	2.31
CMS 8704	3.17	3.61	2.97	1.19	78.31	168.44	2.39

ATP SR Y	2.98	3.50	2.91	0.92	85.11	177.03	2.78

Appendix 5.3: Yield loss, stress susceptibility index and stress tolerant index of all the hybrids evaluated under stress (A) and control (C) environments.

Genotype	**yield C**	**yield A**	**Yield reduction**	**SSI**	**STI**
Cla 183 x 9450	6.00	6.12	-2	-0.1	36.70
Cml 434 x Cam Inb gp1 17	6.35	5.11	20	0.52	32.45
Cla 183 x 88069	5.77	5.36	7	0.19	30.90
ATP S9 36Y-BB x 4001	5.48	5.37	2	0.05	29.45
ATP S6 31Y-BB x 9450	6.89	4.20	39	1.04	28.93
CMS 8704 x 9450	7.40	3.89	47	1.26	28.78
Cml 437 x Cam Inb gp1 17	5.83	4.84	17	0.45	28.25
Cml 439 x Cam Inb gp1 17	7.24	3.81	47	1.26	27.58
ATP S5 31Y-2 x 9450	6.29	4.34	31	0.82	27.31
Cml 439 x 4001	6.06	4.39	28	0.73	26.64
ATP S8 30Y-3 x Cam Inb gp1 17	6.26	4.25	32	0.85	26.60
D300-17 x Cam Inb gp1 17	6.53	3.97	39	1.04	25.90
ATP SR Y x 4001	7.04	3.67	48	1.27	25.81
ATP S5 31Y-2 x 4001	5.09	5.07	0	0.01	25.80
CLA 135 x 9450	6.31	4.05	36	0.95	25.54
ATP S8 26Y-3 x Cam Inb gp1 17	5.29	4.72	11	0.29	24.96
C4RR SA4 x Cam Inb gp1 17	5.79	4.26	26	0.70	24.69
Cla 183 x Cam Inb gp1 17	5.51	4.42	20	0.52	24.34
Cml 535 x Cam Inb gp1 17	6.91	3.51	49	1.30	24.25
CMS 8704 x 88069	5.64	4.23	25	0.66	23.88
ATP SR Y x Cam Inb gp1 17	5.81	3.91	33	0.87	22.69
Cml 304 x 9450	6.20	3.66	41	1.08	22.67
CLA 135 x 88069	6.29	3.53	44	1.16	22.21
Cml 437 x 9450	5.38	4.13	23	0.62	22.19
ATP S9 30Y-1 x 9450	6.06	3.62	40	1.07	21.97
Cml 434 x 88069	5.70	3.81	33	0.88	21.70
Cml 357 x 4001	5.88	3.67	38	0.99	21.61
CLA 135 x Cam Inb gp1 17	5.84	3.68	37	0.98	21.49
Cml 534 x 4001	4.86	4.42	9	0.24	21.47
ATP S6 20Y-1 x 88069	5.63	3.79	33	0.87	21.33
ATP S9 36Y-BB x Cam Inb gp1 17	5.75	3.71	36	0.94	21.31
Cml 437 x 88069	6.17	3.42	45	1.18	21.10

Genotype	**yield C**	**yield A**	**Yield reduction**	**SSI**	**STI**
CMS 8704 x 4001	5.75	3.62	37	0.98	20.78
C4RR SA4 x 88069	4.95	4.06	18	0.48	20.11
ATP S6 20Y-1 x 9450	6.13	3.23	47	1.26	19.79
Cml 332 x Cam Inb gp1 17	6.60	3.00	55	1.45	19.78
Cml 439 x 9450	4.66	4.23	9	0.24	19.71
Cml 434 x 9450	5.64	3.49	38	1.01	19.69
Cml 435 x Cam Inb gp1 17	5.21	3.78	27	0.73	19.68
Cml 332 x 88069	5.16	3.79	26	0.70	19.57
Cml 439 x 88069	5.27	3.67	30	0.80	19.33
ATP S6 21Y-2 x 88069	5.09	3.75	26	0.70	19.09
4001 x 9450	6.13	3.11	49	1.30	19.09
Cml 479 x 4001	5.84	3.27	44	1.17	19.08
9450 x Cam Inb gp1 17	4.91	3.85	22	0.58	18.90
Cml 304 x Cam Inb gp1 17	5.81	3.23	44	1.18	18.76
88069 x Cam Inb gp1 17	5.42	3.43	37	0.97	18.58
C4RR SA4 x 4001	5.23	3.55	32	0.85	18.57
D300-17 x 9450	5.85	3.15	46	1.22	18.44
ATP S6 21Y-2 x Cam Inb pg1 17	5.84	3.15	46	1.22	18.38
Cam Inb gp1 17 (F) x 9450	4.33	4.23	2	0.06	18.35
ATP S8 30Y-3 x 4001	4.42	4.14	6	0.17	18.28
ATP SR Y x 88069	4.67	3.87	17	0.45	18.09
Cam Inb gp1 17 (F) x 88069	5.48	3.26	41	1.07	17.88
ATP-32 x Cam Inb gp1 17	5.68	3.12	45	1.19	17.72
ATP S8 26Y-3 x 88069	5.94	2.93	51	1.35	17.38
ATP-50 x 9450	6.12	2.82	54	1.43	17.23
Cml 357 x Cam Inb gp1 17	6.11	2.80	54	1.44	17.09
Cml 435 x 9450	5.14	3.32	35	0.94	17.07
ATP S8 30Y-3 x 9450	5.62	3.00	47	1.23	16.85
CMS 8704	5.29	3.17	40	1.06	16.79
Cml 332 x 9450	4.44	3.74	16	0.42	16.61
Cml 535 x 88069	4.70	3.51	25	0.67	16.48
Cml 479 x 88069	4.46	3.67	18	0.47	16.35
Cml 535 x 9450	5.15	3.16	39	1.02	16.28
Cml 533 x 88069	5.07	3.21	37	0.97	16.24
9450 x 88069	5.15	3.13	39	1.04	16.12
ATP S9 36Y-BB x 9450	5.24	3.06	42	1.10	16.01
Cml 479 x Cam Inb gp1 17	4.52	3.53	22	0.58	15.94
ATP S6 20Y-1 x 4001	5.22	3.03	42	1.11	15.80
ATP S9 30Y-1 x 88069	4.32	3.64	16	0.42	15.74
ATP S9 36Y-BB x 88069	4.05	3.87	4	0.12	15.66
Cml 533 x 9450	5.20	2.96	43	1.14	15.43

Genotype	**yield C**	**yield A**	**Yield reduction**	**SSI**	**STI**
ATP-32 x 4001	5.86	2.59	56	1.48	15.16
ATP S9 30Y-1 x Cam Inb gp1 17	5.02	2.98	41	1.07	14.97
Cml 533 x 4001	5.37	2.78	48	1.28	14.91
Cam Inb gp1 17 (F) x Cam Inb gp1 17	5.24	2.84	46	1.21	14.87
Cml 533 x Cam Inb gp1 17	4.88	3.00	39	1.02	14.67
Cml 534 x 9450	5.04	2.89	43	1.13	14.58
ATP-50 x 88069	5.58	2.60	53	1.42	14.52
ATP-50 x Cam Inb gp1 17	4.32	3.34	23	0.60	14.44
Cla 183 x 4001	3.62	3.97	-10	-0.26	14.38
Cml 435 x 88069	5.59	2.57	54	1.43	14.38
ATP S8 26Y-3 x 9450	4.82	2.91	40	1.05	13.99
Cml 535 x 4001	4.29	3.25	24	0.65	13.93
Cml 479 x 9450	5.16	2.67	48	1.28	13.78
Cml 534 x 88069	4.24	3.24	23	0.62	13.74
ATP S9 30Y-1 x 4001	3.88	3.53	9	0.24	13.71
Cml 534 x Cam Inb gp1 17	5.74	2.37	59	1.56	13.59
Cml 332 x 4001	4.26	3.17	26	0.68	13.49
Cml 357 x 9450	4.90	2.74	44	1.17	13.44
C4RR SA4	4.84	2.77	43	1.13	13.41
Cml 357 x 88069	5.44	2.46	55	1.45	13.36
Cml 435 x 4001	5.08	2.62	48	1.28	13.33
D300-17 x 88069	4.93	2.65	46	1.22	13.09
Cml 434 x 4001	4.44	2.93	34	0.90	13.00
4001 x Cam Inb gp1 17	4.85	2.65	45	1.20	12.86
ATP S6 21Y-2 x 9450	5.30	2.41	55	1.45	12.77
ATP-32 x 88069	4.76	2.68	44	1.16	12.75
Cam Inb gp1 17 (F) x 4001	4.72	2.61	45	1.18	12.33
ATP S6 20Y-1 x Cam Inb gp1 17	4.90	2.47	50	1.31	12.13
Cml 304 x 88069	4.78	2.52	47	1.25	12.03
C4RR SA4 x 9450	3.50	3.42	2	0.06	11.99
4001 x 88069	6.09	1.96	68	1.80	11.94
ATP SR Y	3.99	2.98	25	0.67	11.90
ATP SR Y x 9450	4.50	2.64	41	1.09	11.90
Cml 437 x 4001	5.65	2.09	63	1.67	11.78
ATP-32 x 9450	4.13	2.83	32	0.84	11.69
ATP S5 31Y-2 x 88069	4.59	2.43	47	1.24	11.16
CMS 8704 x Cam Inb gp1 17	5.21	2.13	59	1.56	11.13
ATP S8 30Y-3 x 88069	4.71	2.27	52	1.37	10.70
ATP S6 21Y-2 x 4001	5.30	1.97	63	1.66	10.47
ATP-50 x 4001	5.06	2.06	59	1.57	10.42
ATP S5 31Y-2 x Cam Inb gp1 17	4.05	2.52	38	1.00	10.19

Genotype	**yield C**	**yield A**	**Yield reduction**	**SSI**	**STI**
CLA 135 x 4001	4.98	2.05	59	1.56	10.18
ATP S6 31Y-BB x 4001	4.51	2.14	53	1.39	9.65
D300-17 x 4001	3.71	2.47	34	0.89	9.17
ATP S8 26Y-3 x 4001	4.02	2.24	44	1.17	9.00
Cml 304 x 4001	5.30	1.64	69	1.83	8.71
ATP S6 31Y-BB x Cam Inb gp1 17	4.07	2.00	51	1.35	8.13
ATP S6 31Y-BB x 88069	4.21	1.41	66	1.76	5.94

Appendix 6.1: Specific combining ability of genotypes for yield under acid soil environments

Inbred lines	**Cam Inb gp1 17**	**88069**	**9450**	**4001**
ATP S5 31Y-2	-1.3*	-0.81	0.58	1.58*
ATP S6 20Y-1	-0.65	0.44	-0.07	0.28
ATP S6 21Y-2	-0.4	0.96	-0.09	-0.47
ATP S6 31Y-BB	-0.49	-0.76	1.29	-0.05
ATP S8 26Y-2	0.89	-0.07	-0.11	-0.71
ATP S8 30Y-3	0.74	-0.94	-0.55	0.75
ATP S9 30Y-1	-0.42	0.21	-0.1	0.31
ATP S9 36Y-BB	0.07	0.39	-1.4	0.95
ATP-32	0.65	-0.19	-0.03	-0.43
ATP-50	0.22	-0.16	0.14	-0.2
Cml 304	0.42	-0.44	0.93	-0.91
Cml 357	-0.27	-0.29	-0.17	0.73
Cml 435	-0.13	-0.38	-0.26	0.77
Cml 437	0.68	-0.28	0.47	-0.87
Cml 439	-0.35	-0.16	0.45	0.06
Cml 533	-0.07	-0.07	0.04	0.09
Cml 534	-0.84	0.12	-0.38	1.11
Cml 535	0.31	0.56	-0.88	0.01
Cml 332	-0.41	0.67	-0.29	0.02
Cml 479	0.48	0.24	-0.87	0.15
Cla 183	-0.84	0.35	1.19	-0.71
Cml 434	0.95	-0.14	-0.46	-0.35
Cla 135	0.42	-0.35	0.52	-0.6
D300-17	0.83	-0.17	-0.16	-0.5
Cam Inb gp1 17 (F)	-0.88	-0.28	0.86	0.3

Pltaspe =plant aspect, earasp = ear aspect, epp = ear per plant, earght = ear height, pltght = plant height, asi = anthesis-silking interval, NS = non-significant, * = significant at P<0.05, Prob = probability.

Appendix 6.2: Specific combining ability of genotypes for yield under control environments

Genotypes	**Cam Inb gp1 17**	**88069**	**9450**	**4001**
ATP S5 31Y-2	-1.55*	-0.14	1.15	0.53
ATP S6 20Y-1	-0.82	0.63	0.38	-0.19
ATP S6 21Y-2	-0.31	0	-0.23	0.54
ATP S6 31Y-BB	-0.96	-0.54	1.62*	-0.13
ATP S8 26Y-2	-0.09	0.89	0.03	-0.83
ATP S8 30Y-3	0.55	-0.27	0.03	-0.3
ATP S9 30Y-1	0.34	-0.42	0.68	-0.6
ATP S9 36Y-BB	0.21	-0.14	-0.49	0.69
ATP-32	0.22	0.02	-0.96	0.73
ATP-50	-1.51*	0.39	0.98	0.15
Cml 304	0.01	-0.79	0.74	0.04
Cml 357	0.2	-0.22	-0.46	0.48
Cml 435	-0.08	0.39	0.05	-0.36
Cml 437	0.44	0.14	-0.69	0.11
Cml 439	0.8	-0.03	-0.93	0.16
Cml 533	-0.52	-0.31	0.04	0.79
Cml 534	0.17	-0.42	0.02	0.23
Cml 535	1.32*	-0.17	-0.39	-0.77
Cml 332	1.16	0.49	-0.99	-0.67
Cml 479	-0.23	-0.8	0.11	0.93
Cla 183	-0.02	0.4	0.54	-0.93
Cml 434	0.72	0.18	-0.28	-0.61
Cla 135	-0.03	0.76	-0.19	-0.54
D300-17	0.74	-0.06	0.72	-1.40*
Cam Inb gp1 17 (F)	-0.36	0.67	-0.46	0.15

Pltaspe =plant aspect, earasp = ear aspect, epp = ear per plant, earght = ear height, pltght = plant height, asi = anthesis-silking interval, NS = non-significant, * = significant at P<0.05, Prob = probability.