COMBINING ABILITY AND HETEROSIS OF MAIZE (*Zea mays* L.) INBRED LINES UNDER LOW AND OPTIMUM SOIL NITROGEN

By

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DECLARATION

I hereby declare that except, for references used in this work which have been duly acknowledged, this is my original research and has neither in whole or part been submitted anywhere for a degree.

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ABSTRACT

Maize is the most relevant food crop in Ghana, and it accounts for the majority of millions of people's diets. Despite this, smallholder farmers still obtain low grain yields in maize as a result of low soil fertility. Low soil nitrogen (low N) threatens maize production in Ghana. Therefore, maize cultivars tolerant to low nitrogen will lessen the use of nitrogen inputs and expand maize production. Combining ability can be used to select parental lines with desirable genes and identify superior hybrid combinations. The objectives of this study were to (1) determine the general combining ability (GCA) effects of the parental maize inbreds, (2) identify the best performing hybrids based on their specific combining ability (SCA) effects, and (3) identify the gene action controlling the inheritance of grain yield under low N soil. Nine inbred lines were crossed in a half-diallel cross fashion to generate thirty-six (36) hybrids. The 36 hybrids plus four local (4) checks (GH110, Tintim, Afriyie, and Apraku) making a total of 40 genotypes were planted using 8 x 5 alpha lattice design in three replications on the low nitrogen soil (30 kg N ha^{-1}) and optimum N soil condition (90 kg N ha^{-1}). The hybrids were planted in the 2021 major season in Fumesua and Ejura. Significant GCA and SCA effects for grain yield and agronomic traits displayed the preponderance of GCA effects over SCA effects, showing that additive gene action controlled the inheritance of grain yield and other related traits. CRIZEQ-25 was the best general combiner under low N conditions. The single-cross hybrids, CRIZEQ-44 X CRIZEQ-14, CRIZEQ-25 X CRIZEQ-24, CRIZEQ-45 X CRIZEQ-25, CRIZEQ-46 X CRIZEQ-25, CRIZEQ-46 X CRIZEQ-42, and CRIZEQ-46 X CRIZEQ-45 were the best hybrid combinations but CRIZEQ-25 X CRIZEQ-24 and CRIZEQ-46 X CRIZEQ-45 were high yielding and tolerant to low N. These cultivars should be further tested in several locations for possible release and commercialization.

DEDICATION

I dedicate this work to my parents, Mr. and Mrs. Darko who have both worked tirelessly for me to get this education.

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LIST OF ABBREVIATIONS

GCA: General Combining ability

SCA: Specific Combining ability

N: Nitrogen

P: Phosphorus

K: Potassium

IITA: International Institute of Tropical Agriculture

SSA: Sub-Saharan Africa

OPVs: Open Pollinated Varieties

GEI: Genotype by Environment Interaction

MET: Multi-Environment Trials

AMMI: Additive Main Effects and Multiplicative Interaction

CIMMYT: International Maize and Wheat Improvement Center

MoFA: Ministry of Food and Agriculture

VAR: Variance

BPH: Better Parent Heterosis

MPH: Mid-Parent Heterosis

EH: Economic Heterosis

FAOSTAT: Food and Agriculture Organization Corporate Statistical Database

CHAPTER ONE

1.0 INTRODUCTION

In sub-Saharan Africa (SSA), maize (*Zea mays* L.) is a staple food for an estimated 50% of the population (Badu-Apraku and Fakorede, 2017) and accounts for about 15% of the calorific intake of the population (Badu-Apraku and Akinwale, 2011). Maize is a vital source of carbohydrates, vitamins A and B, proteins, and minerals. About 30 million hectares of arable land in SSA is devoted to maize production (Annor *et al.,* 2019). It is the main ingredient in a variety of popular dishes throughout Ghana, particularly in the Volta, Northern, Upper East, Upper West, Central, and Greater Accra regions (Tweneboah, 2000), but its production and productivity are limited by a number of abiotic stresses, the most important of which is low N stress. Prasanna *et al.* (2018) also mentioned that annual yield losses of maize in SSA fall within 21 to 53%. The soils in Ghana's key maize-growing regions have low levels of total N (< 0.2%), exchangeable K (100 mg/kg) and accessible P (Nyalemegbe and Osakpa, 2012 and Atakora *et al*., 2014). The annual yield loss of maize grain as a result of low nitrogen (N) stress alone varies from 10 to 50% (Wolfe *et al*., 1988; Logroño and Lothrop, 1997 and Meseka *et al.,* 2006). Some causes of low soil fertility are the continuous cropping of fields and the poor nature of soils. Organic manure and inorganic fertilizer, compost, and nitrogen-fixing legumes can all help to mitigate the negative effects of low nitrogen levels in Ghana. Developing maize genotypes with a high nitrogen use efficiency and high yield potential is an alternate technique for lowering fertilizer costs. Genotypes with high yield potential are also required to support the world's fast rising population, which is expected to reach 9.7 billion by 2050 (Ehrlich and Ehrlich, 2013), as well as to provide incentives to farmers who make an effort to enhance nitrogen application in their maize fields. It is therefore critical to create maize genotypes that are tolerant to low N stress in order to boost maize yield and productivity in Ghana as a whole. Inbred lines with high yield potential, good combining abilities, and abiotic stress tolerance would be valuable breeding materials for generating high yielding, low N tolerant hybrids. Analysis of general combining ability (GCA) and specific combining ability (SCA) in maize breeding programs is critical for identifying the best-inbred lines for hybrid production and hybrid combinations (Abrha *et al*., 2013 and Girma *et al*., 2015). Combining ability is an effective tool that gives useful genetic information for the choice of parents in terms of their performance in series of crosses (Sprague and Tatum, 1942). Maize hybrid adoption in Western Africa has been limited in recent years due to insufficient seed supply and marketing by present and emerging seed enterprises, as well as stringent seed legislation in most countries. However, in Ghana, Mali, and Nigeria, seed firms have developed in recent years, paving the way for large-scale hybrid production in these countries (Badu-Apraku *et al*., 2011). Open-pollinated varieties (OPVs) and hybrids have been developed, disseminated, and widely adopted in Ghana after several years of maize development, resulting in increased maize production and productivity (Morris *et al*., 1999). The exploitation of hybrid vigor in maize has gained high acceptance because of the potential of hybrids to provide substantial yield increases. Breeding maize hybrids that are tolerant to low soil N would increase maize production since one low N tolerant maize hybrids have been released in Ghana.

The main objective of this study was to identify high yielding, low N tolerant maize hybrids.

The specific objectives were to:

- determine the general combining abilities of the parental maize inbred lines,
- identify the best performing hybrids on the basis of their specific combining abilities, and
- identify the gene action controlling the inheritance of grain yield under low nitrogen soil.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Taxonomy, origin and botany

Maize is one of the most important cultivated crop species in the Western Hemisphere, with several theories claiming that it originated in the Guatemalan highlands and southern Mexico between 7,000 and 10,000 years ago (Hallauer and Carena, 2008). Wilkes (2004) claimed that teosinte (*Zea mays* L.: spp. mexicana) is an undomesticated weedy species native to Guatemala and southern Mexico, and is thought to be the progenitor of modern-day maize, based on information accumulated over the past six decades. Maize was first carried into West Africa in the 16th century by Portuguese traders traveling to the Gold Coast (now Ghana) via the West Indies, Central America, and South America (Fajemisin and Shoyinka, 1976). Maize is a grass that belongs to the Poaceae family's Andropogoneae tribe. *Zea nicaraguensis* (Iltis and Bruce), *Zea perennis* (Hitchcock), *Zea luxurians* (Durieu and Ascherson), *Zea diploperennis* (Iltis, Doebley, and Guzman), and *Zea mays* (Linnaeus) are the five species in the genus Zea, with *Zea mays* being the most economically important. It is a monoecious annual plant that can reach a height of 4.5 meters (Acquaah, 2007). Male flowers (staminate) are commonly found as tassels at the stalk's apex, but female flowers (pistillate) arise from the leaf axils with a multitude of enlarged styles (silks) protruding out its top as silky threads (Hitchcock and Chase, 1971). The staminate inflorescence produces pollen, and the pollen receptors, the silks, must be pollinated individually to generate a seed or kernel. It is protandrous because the anthers mature before the pistillate. A stalk can also produce one to three cobs. Eight or more rows of kernels can be found in a fertilized cob, commonly known as an ear (Acquaah, 2007). Cross-pollination occurs spontaneously, and self-pollination is frequently feasible.

2.2 Importance of Maize

Africans consume maize as a starchy base in a wide variety of porridges, pastes, grits, and beer. In both irrigated and rainfed agricultural systems in the semi-arid and arid tropics (Hassan *et al*., 2014), *Zea mays* is the most significant cereal fodder and grain crop, as well as animal feed, starch, and biofuel in the developed world (Hassan *et al*., 2014). Between 2007 and 2017, the area under maize cultivation in Sub-Saharan Africa expanded by over 60%. (FAOSTAT, 2019). Carbohydrates, vitamin A and B, protein, iron, and minerals are all abundant in it. Maize consumption per capita in Eastern and Southern Africa is estimated to be 100 kilograms per year, providing around 40% of calorie needs but 43.8 kg/head in 2005 in Ghana (MoFA, 2011). The crop provides both grains and silage for feed production, making it a great source of food for the animal production business. Grain is used to generate high quality starch, and more recently, the focus has shifted to the development of biofuel, particularly in the United States. As a significant crop for improving food security on the continent, the crop is extremely important in Africa.

2.3 Production Constraints

Maize is Ghana's second most significant staple crop, after cassava, and it is grown in all of the country's regions, which have similar climatic conditions that influence the country's ability to support rain-fed agriculture, with the transition zone producing the most (MoFA, 2011 and Adu *et al*., 2014). The most significant abiotic factors are drought and low soil nitrogen which limits maize production in SSA (Badu-Apraku *et al*., 2011). According to Adu *et al*. (2018), the soils in Guinea and Sudan Savanna zones of Ghana are generally poor in fertility as a result of bad cultural practices such as continuous cropping with little or no fertilizer input, bush burning and removal of crop residues have caused soils in maize production to become inherently low in N. Nitrogen (N) stress has been reported to reduce final grain number by increasing kernel abortion resulting in about 85 % of the abortion during the first twenty (20) days after flowering (Amegbor *et al*., 2017; Monneveux *et al*., 2005). Maize yield losses due to drought depend on the stage of the crop during which the drought occurs. The crop is most susceptible to drought from a few days before tassel emergence to the beginning of grain filling; drought at this stage may reduce grain yield by as much as 90% (NeSmith and Ritchie, 1992). Drought has been projected to cause a 15% annual yield loss in the savannahs of West and Central Africa. According to Edmeades *et al*. (1995), annual maize yields are reduced by 15% on average due to consistent drought caused by erratic rainfall patterns. According to Gasura *et al.* (2019), the parasitic weed *Striga hermonthica* causes cereal losses of up to $7 billion dollars. As land use escalates, a slew of other issues, such as soil erosion, reduced water retention capacity, and an increase in persistent weeds and Striga infestation, could emerge. The varied stresses frequently occur in tandem, causing serious damage and yield losses to the maize crop. Low nitrogen and drought, for example, aggravate the negative impacts of Striga infection (Badu-Apraku *et al*., 2019).

De Groote *et al*. (2008) also reported that Striga has severely impacted about six million hectares of agricultural land in Western, Eastern, and Southern Africa. Under severe infestation and unfavorable climatic conditions like low soil fertility, unpredictable rainfall patterns, and low-input conditions, the reduction in grain yield caused by *Striga hermonthica* parasitism could be as high as 100 percent (Samejima *et al*.,2016 and Badu-Apraku *et al*., 2019).

2.4 Physiological influence of Low N on maize

Plant dry matter production is closely related to leaf area and photosynthetic rate. As the kernel fills with grain, the amount of photosynthesis has a significant impact on maize grain yield (Muchow, 1988). The size of maize leaves responds to nitrogen levels, and there is a link between N concentration and photosynthetic capacity (Vos *et al*., 2005). Many factors, including maize variety, climatic conditions, CO_2 level, and temperature, can influence photosynthesis during grain filling. The amount of available nitrogen in the soil is another major factor that influences photosynthesis (Jaaffar and Gardner, 1988). N shortage has a crippling effect on plants due to the many roles that nitrogen plays in plant physiology and development. N deficit affects a plant's photosynthetic capability by reducing the rates of leaf photosynthesis and new leaf area development (Boussadia *et al*., 2010), which is consistent with the findings of Aderiran and Banyoko (1995) and Shanti *et al* (1997). Uhart and Andrade (1995) stated emphatically that deficiency in N delays both vegetative and reproductive development of the plant, reduced leaf emergence rate, and leaf expansion rate. Bertin and Gallais (2000) reported that the biochemical properties of maize leaves are generally affected under low N conditions. Nitrate reductase and glutamate synthase are enzymes that are highly related to leaf senescence are also affected under low N (Bertin and Gallais, 2000). Furthermore, N shortage causes and accelerates leaf senescence (Massignam *et al*., 2012), which is accompanied by transcriptional activation of several genes implicated in senescence-related biochemical and cellular changes, either directly or indirectly (Makhumbila, 2018). Furthermore, N deficiency leads to the degradation of photosynthetic pigments and proteins, and reduced enzyme synthesis in plants (Polesskaya *et al*., 2004), and this ultimately causes the maize leaf blade to change to yellow due to chlorophyll degradation according to Buchanan-Wollaston *et al*. (2003). In the synthesis of plant proteins, nitrogen is essential. As a result, a lack of nitrogen causes changes in protein expression and enzyme activity, which in turn causes alterations in plant metabolism (Wei *et al*., 2015). The post-translational modification of phosphoenolpyruvate carboxylase (PEPCase), for example, is influenced by nitrogen levels (Prinsi *et al*., 2009). N shortage has also been shown to reduce ribulose bisphosphate carboxylase/oxygenase (Rubisco) activity in various different crops (Heitholt *et al*., 1991), as well as the amount of Rubisco generated by the plant. Furthermore, a lack of nitrogen affects overall plant metabolism by reprogramming primary and secondary metabolic pathways (Scheible *et al*., 2004). The nitrogen status of soils affects countless plant processes and during the flowering stage and vegetative stage, nitrogen is significant for the good development of the plant (Ciampitti and Vyn, 2011). Notwithstanding these numerous symptoms aforementioned, there are maize lines that can withstand these conditions and such genotypes are of tremendous interest to plant breeders (Makhumbila, 2018).

2.5 Concerns of low soil nitrogen in maize

Nitrogen is of utmost importance to maize production in terms of increasing leaf area index through the interception of light and subsequently leading to higher grain yield. Dwyer and Ma (1998) also mentioned that fertilizer N is the energy-consuming component of maize production. Despite this credible information, smallholder farmers are aware of the benefits of utilizing nitrogen fertilizers, but the exorbitant prices and unavailability affect the quantities applied to their maize crops and this has tremendously affected maize production as reported by FAOSTAT (2019). Most farmers in developing countries like Ghana, however, usually rely on natural soil fertility for crop production. The inherently low nutrient status of most of the soils, however, renders them unsuitable for crop production (Bationo *et al*., 2018), necessitating the addition of external nutrients to meet the crop's nutrient demand (McLaughlin *et al*., 2011). Appiah *et al*. (2020) mentioned that where nutrient applications are done, successive fertilization with sole nitrogen has been noted to improve crop performance substantially. For instance, the application of a mixture of urea, triple superphosphate fertilizer, and farmyard manure excrement was found to improve the crop use of nitrogen and P_2O_5 fertilizer (McLaughlin *et al*., 2011). Thereafter, subsequent cropping with sole nitrogen was performed comparably to compound mixtures of fertilizers. Many studies, such as Gul *et al*. (2015) reported that starter nitrogen can improve early development and yield. Nitrogen thus remains the most important nutrient that is required for maize growth in most nutrient-poor soils of Africa (Van der Velde *et al*., 2014).

Improvement in soil N through the application of inorganic fertilizer during maize production in Sub-Saharan Africa is rarely done, and when carried out, the application is at rates considerably lower than recommended rates due to prohibitive prices of fertilizer to smallholder farmers (Amegbor *et al*., 2017). In effect, maize is usually grown under N stress resulting in a low yield of the crop. Chevalier and Schrader (1977), Pollmer *et al*. (1979), Pan *et al*. (1985), Pace and McClure (1986) reported that different maize hybrids exhibit different responses to nitrogen-use capacity. Variation in nitrogen supply has a significant impact on maize plant growth and development, according to McCullough *et al*. (1994). For example, some maize hybrids elicit adaptive mechanisms such as reducing their rate of leaf appearance, while others try to maintain their development in order to survive varying amounts of nitrogen fertilizers. For South African cultivars, low N yielded 0.65 - 3.85 t ha^{-1}, while optimal N yielded 4.17 - 6.93 t ha^{-1}, according to Smalberger and du Toit (2004). They discovered that the cultivar that yielded the most (6.93 t ha^{-1}) at optimal N yielded as little as 0.98 t ha^{-1} when grown in low N. Betrán *et al*. (2003) investigated maize hybrid yield in low and high nitrogen settings, finding that hybrid grain yield in the low N environment was 33% of hybrid grain yield in the high N environment. This highlights the need of breeding cultivars that produce high yields under both optimal and low N regimes. Diallo *et al*. (2004) tested 63 single crosses and seven local checks under low and high nitrogen circumstances, finding grain yields ranging from 1.2 - 3.5 t ha^{-1} under low nitrogen and 3.1 - 7.4 t ha^{-1} under high nitrogen. Banziger *et al*. (1997) found a 37 to 78 percent reduction in relative grain yield in tropical maize grown with low nitrogen. In their investigations, Banziger and Lafitte (1997) and Bänziger *et al*. (1999) found that relative grain yields were reduced by 37 to 89 percent and 20 to 50 percent, respectively. In comparison to optimum management, Monneveux *et al*. (2005) found a 67.4 percent yield drop for maize hybrids under low N conditions. Experiments with low nitrogen generating 25–35 percent (1.5–3.5 t ha^{-1}) of the yields generated under recommended agronomic management/high rainfall conditions (6.0–9.0 t ha^{-1}) are regarded to be the most effective for proving N stress tolerance in tropical maize (Banziger *et al*., 1997). According to Banziger and Lafitte (1997), low nitrogen resulted in significant reductions in plant height (27.1%), ear height (42.2%), ears per plant (11.2%), grains per ear (47.8%), and grain weight (30.7%). Each plant had a mean of less than one ear, indicating bareness rather than prolificacy, according to researchers. ASI increased from 0.33 days under optimal conditions to 2.42 days under low N conditions, which is more than seven times the best conditions, according to Monneveux *et al*. (2005). When N levels were low, ear rot was also more common (Banziger *et al*., 2006).

2.6 Breeding and selection for tolerance to low soil nitrogen

2.6.1 Conventional breeding strategies

Badu-Apraku *et al*. (2009, 2010, 2011) reported that selection for Striga resistance and drought tolerance in early-maturing maize populations enhanced low N tolerance in the maize varieties derived from the populations. Similarly, improvement for drought tolerance has resulted in specific adaptation and improved performance under low N conditions, suggesting that tolerance to either stress involves a common adaptive mechanism (Badu-Apraku *et al*., 2011; Bänziger *et al*., 1999). Selection for yield, or tolerance to low nitrogen soils in low nitrogen environments, can be increased by choosing secondary traits with high correlations to grain yield in low nitrogen conditions (Bänziger and Lafitte, 1997; Badu-Apraku 2011, 2012). Due to the low heritability of yield under stress conditions (Badu-Apraku *et al*., 2004, 2005), the use of secondary traits has been proposed for yield improvement. Secondary traits such as ears per plant (EPP), rate of leaf senescence (LS), and anthesis-silking interval (ASI) have strong associations with yield under low N and drought conditions and have been used to select for higher levels of tolerance to the drought and low N stresses in maize (Lafitte and Edmeades, 1995; Bänziger and Lafitte, 1997). Under low N in maize, phenotypic and genotypic relationships between grain production, kernel number, and kernel weight were highly significant, according to Bertin and Gallais (2000). Gallais and Coque (2005) further said that genotypes with a short anthesis-silking interval and a high number of ears per plant are effective at remobilizing nitrogen from the stover to the grain, especially during the early stages of embryo development, reducing embryo or ear abortion. Bänziger and Lafitte (1997) constructed selection indices based on these attributes, which considerably enhanced selection efficiency under stress conditions. However, the difficulty of quickly and precisely evaluating secondary traits has limited their usage in breeding programs (Monneveux and Ribaut, 2006). According to Zhao *et al*. (2019), plant breeders utilize some screening indices, based on grain yield under two contrasting nitrogen (N) conditions, the stress susceptibility index (SSI), yield stability index (YSI), mean productivity (MP), geometric mean productivity (GMP), stress tolerance index (STI), harmonic mean (HM), and low nitrogen tolerance index (LNTI) to select low nitrogen tolerant maize genotypes. Some plant breeders, such as Badu Apraku *et al*. (2020), postulated a base index (BI) that incorporates GY, EPP, ASI, PASP, EASP, and SG to select the best and worst performing genotypes under various stress conditions, such as drought, low N, Striga resistance, and others. A positive BI designates tolerance to the applied stress while a negative base index indicates susceptibility to the stress.

2.6.2 Genetic basis of maize tolerance to low nitrogen stress

To expedite and increase selection efficiency for low N environments, a better understanding of the genetic basis for maize development and production under low N conditions is essential (Bänziger and Lafitte, 1997). The value of inbred lines for hybrid maize breeding is determined by their capacity to combine. Sprague and Tatum (1942) proposed the concepts of general and specialized combining ability. General combining ability (GCA) was defined by Hallauer and Miranda (1988) as the mean performance of a line in all of its crosses, given as a deviation from the mean of all crosses. Specific combining ability (SCA) is the relative performance of a cross that is coupled with non-additive gene action, predominantly contributed by dominance, epistasis, or genotype by environment interaction effects, in comparison to other inbreds in the same series of hybrid combinations (Rojas and Sprague, 1952; Falconer and Mackay, 1996). GCA effects suggest largely additive gene action in statistical terms. Specific combining ability is linked to non-additive genetic effects that are unpredictable and temporary, making statistical models difficult to determine (Gardner and Eberhart, 1996). When a parent has a strong GCA effect for a particular trait, it means that that parent has additive gene effects for that trait. When parents with strong GCA effects are crossed, a large percentage of progenies are likely to have high values for the trait in question, supporting selection for that trait (Rigatti *et al*., 2018). Under low N environments, the results of GCA can be utilized to select superior genotypes. Tamilarasi *et al*., (2010) mentioned that combining ability analysis is critical for determining the ideal parents or parental combinations for a hybridization or population improvement effort. A number of biometrical approaches are available to assess the breeding value of the parents and the genetics of the traits under transfer. GCA and SCA effects, as well as their consequences in breeding, are estimated using diallel analysis, line x tester analysis, North Carolina 1 and etc. (Griffing, 1956 and Gardner and Eberhart, 1996). Griffing (1956) also mentioned that diallel crosses change depending on whether or not the parentals or reciprocal F1's is included or both. There are four diallel classification systems namely; Method 1 which includes F1's, Reciprocals, and Parents, the total number of entries to be evaluated is equal to p^2, where p is the number of parents included in a diallel. This is used when parents do not have selfincompatibility or male sterility. The inclusion of parents permits the estimation of heterosis. Method 2 encompasses parents and F1's but reciprocal F1's is not included. The total number of entries to be evaluated is equal to p (p + 1)/2. Method 3 is a full diallel without parents. The number of entries to be evaluated is equal to p (p - 1) combinations. Lastly, method 4 is a half diallel without parents. The number of entries to be evaluated is equivalent to p (p − 1)/2 combinations. There are some models which are employed in the diallel analysis. One classical model is where the population about which inferences are to be made is treated as the experimental material that is in model 1 (fixed-effect model). The goals are to compare parents' combining abilities when they are used as testers, as well as to uncover high yielding combinations. As a result, plant breeders are concerned with finding appropriate standard errors for differences between effects.

Random samples from the parent population are dealt with in model 2 (random effect model), and inferences are drawn about the parent population parameters rather than the individual lines in the sample. Breeders are especially interested in determining the genetic and environmental components of the complex population.

2.7 Developing hybrids and heterosis

The vigour shown in hybrids is referred known as heterosis, and it relates to the hybrids' superior performance above their parents (Hallauer *et al*., 2010). Hybrid vigour in maize is found in hybrids of inbred lines with high specific combining ability (Hallauer *et al*., 2010). Heterosis is essential in maize breeding and is dependent on epistasis expression and over dominance (Hallauer *et al*., 2010). The heterotic patterns produced in a series of varied crosses are used to determine genetic divergence between the two parental varieties (Hallauer *et al*., 2010). Heterosis can be classified in three ways. Hallauer *et al*. (2010) presented various approaches for determining a hybrid's high-parent heterosis (heterobeltiosis), economic heterosis, and mid-parent heterosis in relation to its parents: High-parent heterosis is a hybrid's performance in percentages compared to that of its best parent, while mid-parent heterosis is a hybrid's performance in percentages compared to the average performance of its parents, and economic/standard heterosis is the F1 hybrid's advantage over the best check. As a result, for maize hybrids to be commercialized, heterosis must be determined in comparison to a standard check (standard heterosis). Standard heterosis in maize has been thoroughly investigated so far for a variety of distinct inbred lines that have been developed/introduced and adapted at various times (Shushay, 2014; Reddy *et al*., 2015; Ziggiju *et al*., 2016; Natol *et al*., 2017 and Abiy *et al*., 2019). Heterosis in maize can be increased by crossing inbred lines from distinct heterotic groups (Makumbi *et al*., 2011). Maize breeders have created several heterotic groups, and inbred lines that are complementary to other inbred lines might be labelled opposite heterotic groups. Heterotic groups A and B, for example, are large classes of maize with a heterogeneous genetic foundation that complement each other and result in the manifestation of heterosis after crossing (Abrha, 2013). Heterosis will be expressed when maize cultivars from these complimentary groups are crossed. Synthetic varieties are created from inbred lines from the same heterotic group. Before inbred lines may be employed for cultivar development, it's crucial to understand their heterotic groupings (Makumbi *et al*., 2011 and Abrha, 2013).

2.8 Combining ability under low nitrogen stress

In maize breeding programmes, analysis of general combining ability (GCA) and specific combining ability (SCA) is essential for identifying outstanding crosses with good specific combining ability. The analysis also provides information on the type of gene action controlling quantitative traits, thereby assisting breeders in selecting suitable parental lines (Abrha *et al*., 2013; Girma *et al*., 2015).

Combining ability is a prerequisite for the development of good economically reliable hybrids in maize. It is useful in assessing the potential of inbred lines and identifying the gene action involved in the inheritance of various quantitative characters. Information on combining ability among maize germplasm is essential in maximizing the effectiveness of hybrid development. The GCA variances provide estimation for additive gene actions while the SCA variances provide estimates of non-additive gene action. Therefore, it is necessary to evaluate the combining abilities of the inbred lines that are used as parents in breeding programmes to develop high yielding cultivars that are tolerant to abiotic and biotic stress (Le Gouis *et al*., 2002; Machikowa *et al*., 2011 and Chigeza *et al*., 2014). The combining ability approach has been used successfully in maize (Colbert *et al*., 1987; Aliu *et al*., 2008; Izhar and Charkraborty, 2013; Akinwale *et al*., 2014; Bertoia and Aulicino, 2014), sorghum (Makanda *et al*., 2010) and sunflower (Machikowa *et al*., 2011) among other crops where SCA and GCA are significant for desired traits. SCA and GCA estimates are statistically robust and can aid the breeder to improve genotypes.

Makumbi *et al.* (2011) proposed that gene action controlling grain yield varied with the type of stress, with additive gene action appearing to be more important than non-additive gene action under drought stress while non-additive gene action was more important under low N stress, consistent with findings in previous studies. Under low N stress, hybrid performance was significantly correlated with inbred line performance, but not under drought stress, highlighting the importance of evaluating hybrids under stress to discover superior hybrids for stress conditions (Makumbi *et al*., 2011). Predicted hybrid performance using the additive model was strongly correlated with observed hybrid performance across stresses and environments. Makumbi *et al.* (2011) concluded that GCA accounts for a large proportion of the differences between crosses compared to SCA in this germplasm.

Benjamin Annor and Badu-Apraku (2016) and Ribeiro *et al.* (2020) also mentioned that GCA effects contributed more to the total variation among the hybrids for grain yield and most measured traits under each and across low N and optimum soil conditions suggesting that additive gene effects were more important in the inheritance of the traits. Moreover, Tesfaye *et al.* (2019) reported that the general combining ability sum of squares component was greater than SCA sum of squares for all of the studied traits, suggesting that variations among crosses were mainly due to additive rather than non-additive gene effects; and hence, selection would be effective in improving grain yield and other agronomic traits. According to Menkir *et al.* (2006), the percent sum of squares due to SCA effects for grain yield under low N was larger than the sum of squares due to GCA effects, indicating that non-additive genetic effect was important in the inheritance of grain yield under low N. This confers the advantage of exploiting heterosis to improve grain yield of maize hybrids in low N production environments. Their results agreed with those obtained by Betrán *et al.* (2003) and Meseka *et al.* (2006) but contradict the findings of other workers (Makumbi *et al.*, 2010; Annor and Badu-Apraku 2016 and Tesfaye *et al.*, 2019) who found additive gene action being more important for grain yield under low N. Inbred lines with consistently positive GCA and SCA effects in their crosses across low and high N conditions could have broad utility in maize breeding programmes targeted for low N as well as optimal growing environments.

2.9 Genotype x Environment Interaction

Baker (1988) defined genotype by environment interaction (GxE) as the inability of genotypes to achieve the same relative performance in contrasting environments. GxE occurs when two or more genotypes are compared across varied environments and their comparative achievements are found to differ. That is, one genotype may have the highest performance in one environment but perform poorly in others. This is as a result of the differential response of the cultivar, to various edaphic, climatic, and biotic factors. Genotype by environment interaction (G×E) in several crops has been reviewed widely (Alberts, 2004; Annicchiarico *et al.,* 2005; De La Vega and Chapman, 2006).

The term environment portrays the setting, circumstances, habitat, or atmosphere under which plants grow and this includes locations, years, and management practices adopted. Two environmental variables challenge plant breeders during genotype evaluation, namely; predictable and unpredictable factors. The predictable environmental factors are those that can be controlled and manipulated by the breeder whereas the unpredictable environmental factors are those that vary erratically like the weather which the breeder has no control over (Xu, 2010). Genotype on the other hand is the biological or genetic make-up of an individual. The observable characteristics and performance of a cultivar of plant is its phenotype, which is the result of the cultivar's genotype, as influenced by the environment (Comstock and Robinson, 1948; Falconer, 1989). When different genotypes (cultivars) are ranked in different environments, Genotype by environment interaction is a universal phenomenon (Brancourt-Hulmel and Lecomte, 2003; Yan and Kang, 2003). A major objective in many advanced plant breeding programs is to assess the suitability of individual crop genotypes for agricultural purposes across a range of agro-ecological conditions. To this purpose, breeders perform multi-environment trials. A group of genotypes is tested across many environments in a multi-environment experiment, with the goal of determining the environmental range in which the genotypes should perform well, either partially (specific adaptation) or entirely (broad adaptation) (Ceccarelli *et al.*, 2006). The selection of superior genotypes in many environments is being aggravated by GxE because a breeder's selection in one environment of superior performers may not hold true in another environment. Meaning one genotype may be the best in environment "A" but may not be the best performing genotype in environment "B" due to genotype by environment interaction. This interaction is very important to pay attention to because one factor depends heavily on the other. GxE obscures the relationship between phenotypic and genotypic values, slowing selection process (Ebdon and Gauch, 2002; Comstock and Moll, 1963; Magari and Kang, 1993). Improvement in yield and quality performance of genotypes across environments is accompanied by selection strategies.

Although the absence of uniformity and consistency in performance across environments makes cultivar selection more difficult, it can offer researchers with significant information (Busey, 1983; Kang, 1998). It gives researchers a notion of how cultivars are performing, which helps them justify the necessity for further broad-based testing in different environments and predict farm variability (Busey, 1983). Most quantitative agronomical and economic traits, such as grain yield, are affected by GxE. In the advanced stages of selection, this involves genotype testing across many environments (referred to as multi-environment trials [MET]) (Kang *et al*., 2004). Lu‟quez *et al.* (2002) reported that identifying the highest and stable cultivars can be achieved by growing cultivars in different environments. Plant breeders search for non-crossover GxE or, better yet, the lack of GxE when choosing genotypes for wide adaptability (Matus-Cadiz *et al*., 2003). As a result, estimating consistency in performance is critical for identifying genotypes with stable performance and high yields (Kang, 1998). Distinct concepts of stability are meticulously elaborated (Beck, 1981; Betrán *et al.,* 2003). To establish whether cultivars tested in MET are stable, a series of stability statistics have been used (Flores *et al*., 1998; Hussein *et al*., 2000; Robert, 2002; Sabaghnia *et al*., 2006). The fluctuations from both predictable and unpredictable environments regulate genes. That is, there is an interaction between the genotype and the environment that produces the phenotype. This interaction is not always the same for genotypes in different environments. For instance, in an environment "A", the conditions available during a particular time may be preferable for the genotype to produce at maximum potential. This instance might not be true for the same genotype in an environment "B" principally due to genotype by environment interaction. The GxE leads to a change in the relative ranking of genotypes in different environments. Genotype by environment interactions is of reasonable interest in plant breeding because they affect the genotypes to be selected in a given environment (Allard and Bradshow, 1964). As often realized, additional effects occur when more than one genotype is grown in more than one environment because of interaction between two or more treatments. These treatments cannot interact at all, interact positively, or interact negatively (Allard and Bradshow, 1964). These different kinds of interactions are depicted below with three genotypes evaluated in three environments (**Figure 2.1**).

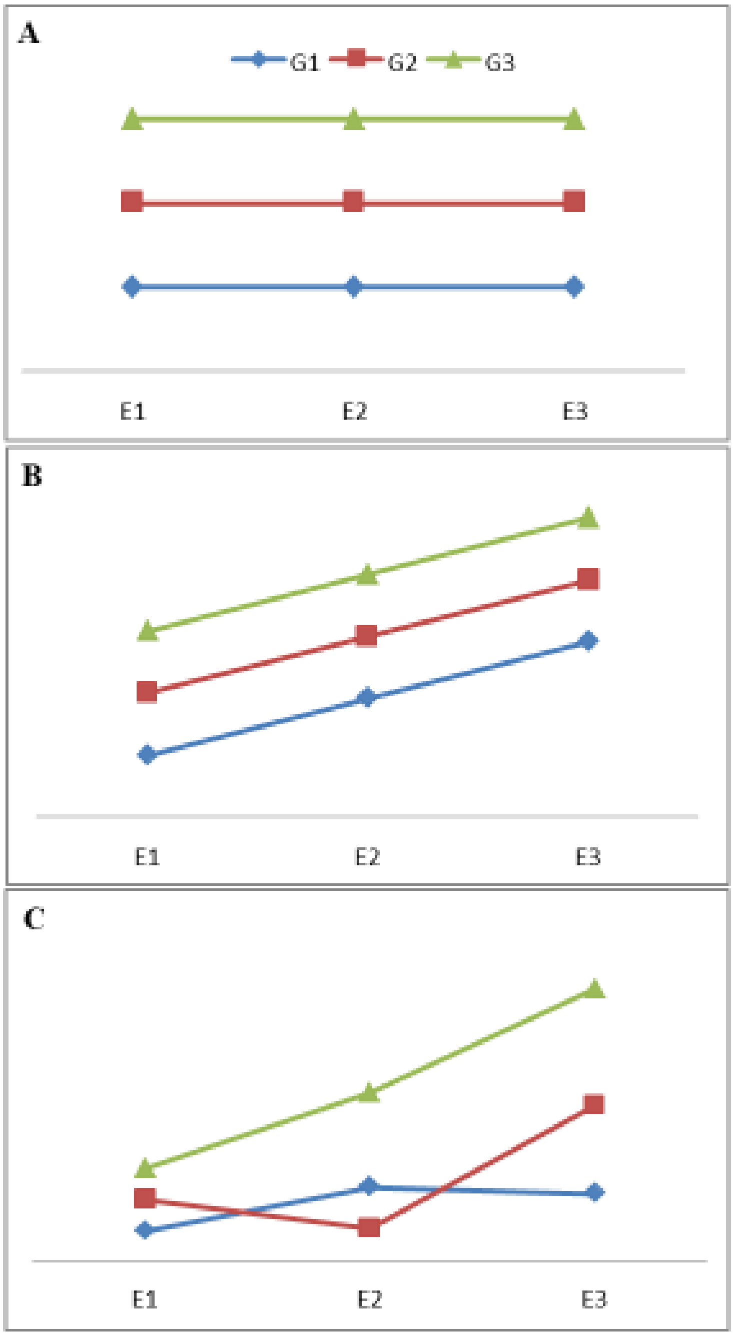

Figure 2.1 Different types of G×E interaction shown by three genotypes grown in three environments (A) No interaction between genotypes in different environments (B) Change in magnitude of response of genotypes in different environments (C) Cross-over interaction between genotypes in different environments

Figure 2.1A shows the performance of the genotype over different environments. This occurs when there is no interaction between genotypes and the environment. Notice that the lines are parallel meaning the effects of the genotypes are constant across all environments. For figure 2.1B, the effect of the three genotypes differs but G3 yields higher than G1 and G2. This response is dependent on the conditions of the environment. The type of this interaction is sometimes referred to as a change in the magnitude of the response interaction (Emodules: ELearning). On the contrary, figure 2.1C depicts a crossover interaction that shows the differential response of the genotypes in the environments resulting in changes in ranks for G1 and G2 across environments. This can be directly translated that G1 and G2 have their favored environments. When this occurs, results should be looked at carefully because failure to assess the interaction carefully can result in poor recommendation (Emodules: E-Learning).

First and foremost, assessment trials are set up in multi-locations to ascertain the occurrence of GxE. Data from the trials are generated and analyzed to reveal significance or no significance of Genotype by Environment Interactions in the assessment. If GxE is present, then it is convincing to justify if the crossover interactions are significant. Three ways have been suggested in dealing with GxE. These are (1) Avoid (2) Ignore (3) Exploit. Genotypes performing consistently high across varied environments without change in rank symbolizes no GxE interaction and hence can be avoided and ignored. However, GxE should not be ignored and avoided if genotypes performances are entirely different beyond contrasting locations but should rather be fully exploited (Yan and Tinker, 2006). Thus, exploitation of GxE is often advocated when GxE is significant while it becomes ideal to ignore and avoid when the interaction is of non-crossover in nature (Cooper and Hammer, 1996).

2.10 Concept of Stability and Adaptability

One of the relevant objectives in a breeding programme is to detect genotypes with distinguished production prospects, broad adaptability, and steadiness. This is why, before releasing hybrids and recommending them to farmers; hybrids are evaluated under many locations. However, cultivars evaluated in different environments may routinely exhibit dissimilar behavior due to environmental variations, which would characterize the interaction between genotype and environment (Haldane, 1946). Cruz *et al.* (2014) elaborated on adaptability and stability as an alternative for reducing the effects of this interaction. These authors testified the possibility to identify cultivars with predictable behavior, and those which are responsive to environmental improvements following their studies on adaptability and stability.

The term stability refers to the capability of the genotypes to be invariable, or persistent, or steady or unfluctuating in terms of having high or low yields in various environments (Eberhart and Russell, 1966). It is then on the account of the inherent ability of the genotype to produce excellent production under a perfect environment and it ought to give out satisfactory or appreciable achievement under a lesser environment. Having in-depth knowledge and understanding in genotype-stability over different production environments is remarkably a prerequisite for variety proposals (Cruz *et al.,* 2014).

Most often, breeders overlook the concepts of stability when the variety has excellent performance throughout different environments and years. This instance presents the best opportunity to recognize the excellent genotype (Fekadu *et al.,* 2009) but for as much as there is an interaction between the genotype and the environment, this situation becomes unattainable. This is because; the excellent genotype may have a high yield in some environments and very poor yield in some other environments. Therefore, knowledge of Genotype by Environment Interactions and stability studies becomes very vital and imperative to be able to comprehend and appreciate the performance of the genotype.

From the agricultural production perspective, two scenarios of stability evolve which can be desired or not desired. For instance, a genotype that has stable performance across environments is not desired if the genotype is not responsive to an increased or decreased level of inputs. However, a genotype that has stable performance, but gives response to the environment is desired thus, producing better yields at high performing environments and producing appreciable levels at low performing environments. In general, these stability scenarios can be categorized into the two stability concepts proposed by Betrán *et al.,* 2003: i.e., the static concept and the dynamic concept respectively. The static concept is viewed as biological stability whereas the dynamic concept is viewed as agronomic stability (Becker, 1981).

Different methods have been proposed to study both the adaptability and stability of maize cultivars. Among these is the method proposed by Eberhart and Russell (1966), based on linear regression analysis. According to Eberhart and Russell (1966) joint linear regression analysis, genotypes with high mean yield, low regression coefficients (b=1), and non-significant deviation from regression ($s^2d=0$) are the most stable. Advantages in using this method stem from its ease of application and interpretation of results. The recommendation of maize cultivars based on this method has been successfully employed by several authors (Rios *et al.,* 2009 and Scapim *et al.,* 2010). Another popular stability method used is Wricke‟s ecovalence (Wi) which is defined as a contribution of each genotype to the GEI sum of squares. According to this method, a genotype with a lower Wricke‟s ecovalence is stable (Fekadu *et al.,* 2009).

Among recent methods is AMMI analysis (Additive Main Effects and Multiplicative Interaction). It allows a more detailed evaluation of the genotype × environment interaction and enables easy graphical interpretation of the results (Gauch, 1992). The application of this analysis to evaluating maize cultivars can be found in the work of Balestre *et al.* (2009), Cargnelutti *et al.* (2009), and Miranda *et al.* (2009). According to Miranda *et al.* (2009), the AMMI method is relatively simple, making it possible to study the phenotypic stability and genotype behaviour of cultivars, as well as inferring the degree of divergence between the cultivars under evaluation.

In addition to the above methods, the method of mixed models has been used in recommending cultivars of various crops: coffee (Rocha *et al.,* 2015) and beans (Torres *et al.,* 2015). It displays some advantages over the traditional methods (Resende, 2007).

Adaptability, on the other hand, refers to the adjustment of an organism to its environment (Cooper and Byth, 1996). The adaptation concept can be viewed from two distinct levels; wide and specific adaptation. Widely adapted cultivars are those that manifest steady performances well in nearly all environments (Cooper and Byth, 1996). Consequently, plant breeders always expect non-crossover genotype-by-environment interaction in choosing steady cultivars (Matus *et al.,* 2003). Genotypes that reveal invariable performances well in a definite or unique set of environmental conditions are said to be specifically adapted. Specific adaptation can be exploited to maximize yield when genotype-by-environment interactions are large and repeatable (Ceccarelli, 1996; Cooper *et al.,* 1996).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental Site

The study was carried out at CSIR-Crop Research Institute (CRI), in Fumesua, semi-deciduous forest zone and Ejura CSIR-CRI Field, transitional zone in the Ashanti region. The experimental material was collected from the Maize Improvement Programme at CSIR-Crop Research Institute for the study.

3.2 Determination of the Soil Analysis of the Experimental sites

The nutrient status of the experimental field at CRI, Fumesua and Ejura was determined to give concrete evidence of the status of the field before the commencement of evaluations (Table 3.1). Soil samples were gathered at random from six different locations across each block prior to planting. Samples were bulked, air-dried, and sieved to pass through a 2-mm screen. Total nitrogen (N), accessible P, and exchangeable K were all measured independently in each composite sample.

3.2.1 Total nitrogen (N) of soil

Total nitrogen was determined using the micro-Kjeldahl technique, which entails the following steps: (i) Digestion: 10 g of soil was weighed and digested with concentrated sulphuric acid as a catalyst using a selenium combination. (ii) Distillation: an aliquot of 10 ml of the mixture was steam distilled by adding 40 percent sodium hydroxide (NaOH) and collected in boric acid/indicator solution. (iii) Volumetric analysis was performed on the obtained mixture, which was titrated with a known quantity of 0.1 M HCl and the percentage nitrogen was determined (Bremner *et al.,* 1982).

3.2.2 Available phosphorus

Bray-1 solution was used to extract this (Anderson and Ingram., 1989). The colour of a blue phospho-moly donate complex produced with a combination of molybdenum and a reducing agent was assessed using spectronic 20 at 520 nm wavelength (Bray and Kurtz, 1945)

3.2.3 Exchangeable potassium (K)

K was measured in a flame photometer after the soil was removed with neutral (pH 7.0) ammonium acetate.

Table 3.1 Soil analysis reports in Fumesua and Ejura

	Soil depth (cm)	
Locations	0-15	15-30
Fumesua		
% N	0.07	0.04
P (ppm)	571.68	510.57
K (cmol/kg)	0.495	0.295
Ejura		
% N	0.1296	0.1303
P (mg/kg)	15.27	14.72
K (me/100g)	0.2	0.12

3.3 Experimental Material

Nine (9) early maturing maize inbred lines (stress tolerant maize genotypes) were used for the study as shown in Table 3.2. The crossing block was at Crop Research Institute at Fumesua during the minor season in 2020.

Table 3.2 Inbred lines used and their source

INBRED LINES	SOURCE
CRIZEQ-14	CRI
CRIZEQ-24	CRI
CRIZEQ-25	CRI
CRIZEQ-40	CRI
CRIZEQ-42	CRI
CRIZEQ-44	CRI
CRIZEQ-45	CRI
CRIZEQ-46	CRI
CRIZEQ-49	CRI

3.4 Mating Design

The nine (9) maize inbred lines were crossed in a half-diallel: Griffing diallel method 4 (F1 individuals) was used in crossing the nine maize inbred lines to generate 36 different individuals containing F1s (Table 3.3). The Griffing diallel method follows this formula, $\frac{n\,(n-1)}{2}$ half-diallel containing F1s, where n stands for the nine (9) parents used. The abbreviations of the parents as well as hybrids are shown in table 3.4.

Table 3.3 Half-diallel cross of maize inbred lines for evaluation at Ejura and Fumesua

Males										
	Parental lines	**CRIZEQ-14 (P1)**	**CRIZEQ-24 (P2)**	**CRIZEQ-25 (P3)**	**CRIZEQ-40 (P4)**	**CRIZEQ-42 (P5)**	**CRIZEQ-44 (P6)**	**CRIZEQ-45 (P7)**	**CRIZEQ-46 (P8)**	**CRIZEQ-49 (P9)**
Females	**CRIZEQ-14 (P1)**									
	CRIZEQ-24 (P2)	CRIZEQ-24 x CRIZEQ-14								
	CRIZEQ-25 (P3)	CRIZEQ-25 x CRIZEQ-14	CRIZEQ-25 x CRIZEQ-24							
	CRIZEQ-40 (P4)	CRIZEQ-40 x CRIZEQ-14	CRIZEQ-40 x CRIZEQ-24	CRIZEQ-40 x CRIZEQ-25						
	CRIZEQ-42 (P5)	CRIZEQ-42 x CRIZEQ-14	CRIZEQ-42 x CRIZEQ-24	CRIZEQ-42 x CRIZEQ-25	CRIZEQ-42 x CRIZEQ-40					
	CRIZEQ-44 (P6)	CRIZEQ-44 x CRIZEQ-14	CRIZEQ-44 x CRIZEQ-24	CRIZEQ-44 x CRIZEQ-25	CRIZEQ-44 x CRIZEQ-40	CRIZEQ-44 x CRIZEQ-42				
	CRIZEQ-45 (P7)	CRIZEQ-45 x CRIZEQ-14	CRIZEQ-45 x CRIZEQ-24	CRIZEQ-45 x CRIZEQ-25	CRIZEQ-45 x CRIZEQ-40	CRIZEQ-45 x CRIZEQ-42	CRIZEQ-45 x CRIZEQ-44			
	CRIZEQ-46 (P8)	CRIZEQ-46 x CRIZEQ-14	CRIZEQ-46 x CRIZEQ-24	CRIZEQ-46 x CRIZEQ-25	CRIZEQ-46 x CRIZEQ-40	CRIZEQ-46 x CRIZEQ-42	CRIZEQ-46 x CRIZEQ-44	CRIZEQ-46 x CRIZEQ-45		
	CRIZEQ-49 (P9)	CRIZEQ-49 x CRIZEQ-14	CRIZEQ-49 x CRIZEQ-24	CRIZEQ-49 x CRIZEQ-25	CRIZEQ-49 x CRIZEQ-40	CRIZEQ-49 x CRIZEQ-42	CRIZEQ-49 x CRIZEQ-44	CRIZEQ-49 x CRIZEQ-45	CRIZEQ-49 x CRIZEQ-46	

Table 3.4 Single-cross hybrids and their corresponding abbreviations

HYBRIDS	ABBREVIATION
CRIZEQ-24 X CRIZEQ-14	G1
CRIZEQ-25 X CRIZEQ-14	G2
CRIZEQ-40 X CRIZEQ-14	G3
CRIZEQ-42 X CRIZEQ-14	G4
CRIZEQ-44 X CRIZEQ-14	G5
CRIZEQ-45 X CRIZEQ-14	G6
CRIZEQ-46 X CRIZEQ-14	G7
CRIZEQ-49 X CRIZEQ-14	G8
CRIZEQ-25 X CRIZEQ-24	G9
CRIZEQ-40 X CRIZEQ-24	G10
CRIZEQ-42 X CRIZEQ-24	G11
CRIZEQ-44 X CRIZEQ-24	G12
CRIZEQ-45 X CRIZEQ-24	G13
CRIZEQ-46 X CRIZEQ-24	G14
CRIZEQ-49 X CRIZEQ-24	G15
CRIZEQ-40 X CRIZEQ-25	G16
CRIZEQ-42 X CRIZEQ-25	G17
CRIZEQ-44 X CRIZEQ-25	G18
CRIZEQ-45 X CRIZEQ-25	G19
CRIZEQ-46 X CRIZEQ-25	G20
CRIZEQ-49 X CRIZEQ-25	G21
CRIZEQ-44 X CRIZEQ-42	G22
CRIZEQ-45 X CRIZEQ-42	G23
CRIZEQ-46 X CRIZEQ-42	G24
CRIZEQ-49 X CRIZEQ-42	G25
CRIZEQ-45 X CRIZEQ-44	G26
CRIZEQ-46 X CRIZEQ-44	G27
CRIZEQ-49 X CRIZEQ-44	G28
CRIZEQ-46 X CRIZEQ-45	G29
CRIZEQ-49 X CRIZEQ-45	G30
CRIZEQ-49 X CRIZEQ-46	G31
CRIZEQ-42 X CRIZEQ-40	G32
CRIZEQ-44 X CRIZEQ-40	G33
CRIZEQ-45 X CRIZEQ-40	G34
CRIZEQ-46 X CRIZEQ-40	G35
CRIZEQ-49 X CRIZEQ-40	G36

Continued

PARENTS	ABBREVIATION
CRIZEQ-14	P1
CRIZEQ-24	P2
CRIZEQ-25	P3
CRIZEQ-40	P4
CRIZEQ-42	P5
CRIZEQ-44	P6
CRIZEQ-45	P7
CRIZEQ-46	P8
CRIZEQ-49	P9

3.5 Establishment of Crossing block

Thirty-six (36) hybrids were generated from the nine (9) maize inbreds in the crossing block. Five (5) rows/maize inbred line with seven (7) hills per row and two seeds were planted per hill. A 3 m row length with a spacing of 75 cm x 45 cm was done. One row was used for maintenance of maize inbred line out of the five. The rest of each of the four (4) rows receive pollen from four different maize inbred lines.

Irrigation was provided in the minor season for the crossing blocks. This was applied twice a week after plants germinated. Pollen from specific male parents was collected and then crossed with specified female parents via artificial pollination. To gather enough pollen for the day, pollen bags were placed on the tassels of male plants very early in the morning (before 6:00 a.m.) and left on until mid-day. To prevent contamination from undesirable pollen, enough pollen was poured to completely cover the emergent silks of each female plant, which had previously been covered with transparent polythene (shoot bag).

3.6 Evaluation of hybrids for yield and heterosis on low nitrogen soil and optimum conditions.

The thirty-six (36) hybrids and four local checks to make a total of forty (40) lines was planted using an 8 x 5 alpha lattice design of five (5) blocks with each block containing eight (8) hybrids and three replications on the low nitrogen soil i.e., 30 kg N ha^{-1} (Ogunniyan *et al.,* 2019, Badu-Apraku *et al.,* 2010, Ribeiro *et al.,* 2020) and optimum N soil condition i.e., 90 kg N ha^{-1} (Ogunniyan *et al*., 2019, Badu-Apraku *et al.,* 2010, Ribeiro *et al.,* 2020 and Essel *et al.,* 2020). The spacing between the lines was 75 cm x 40 cm. The nine (9) parental lines were evaluated separately from the hybrids in a randomized complete block design (RCBD) with three replications to estimate heterosis.

Plate 3.1 Maize hybrids under optimum nitrogen soil condition

Plate 3.2 Maize hybrids under low nitrogen soil conditions

3.7 Data Collection

A total of five (5) plants/line was selected for data collection.

Data recorded include;

i. **Plant height (PH):** The length of a fully matured plant from the base of the plant to the height of the first tassel branch was measured in centimeters.

ii. **Ears per plant (EPP):** The number of ears per plant was recorded for each of the maize lines.

iii. **Days to 50 % silking (DFS):** Number of days from planting to the date when 50 % of the plants in a plot have emerged silks

iv. **Days to 50 % anthesis (DFA):** Number of days from planting to the date when 50 % of the plants in a plot have tassels shedding pollen.

v. **Anthesis-silking interval (ASI):** Difference between days to 50 % anthesis and days to 50 % silking.

vi. **Plant aspect (PASP)** was ranked on a scale of 1-5, with 1 representing excellent overall phenotypic appeal, 2 showing very good overall phenotypic appeal, 3 displaying good overall phenotypic appeal, 4 expressing poor overall phenotypic appeal, and 5 portraying very poor overall phenotypic appeal.

vii. **Ear aspect (EASP)** based on a scale of 1 to 9, where 1=clean, uniform, large, and well-filled ears and 9 ears with undesirable features), was recorded (Ribeiro *et al.*, 2018).

viii. **Husk Cover (HC)** based on a scale of 1 to 5, where 1=very tight husk cover, 2=tight husk cover, 3=slightly loosed husk cover, 4=loosed husk cover and 5=very loosed and opened tip of husk cover.

ix. **Chlorophyll concentration (CC)** was recorded based on the ear leaf of five plants that was randomly selected and measured approximately 2 weeks after anthesis with a portable SPAD meter.

x. **Stay green characteristic (SG)** was recorded on using a scale of 1 to 9, where 1 = 10% dead leaf area; 2 = 20% dead leaf area; 3 = 30% dead leaf area, 4 = 40% dead leaf area; 5 = 50% dead leaf area; 6 = 60% dead leaf area; 7 = 70% dead leaf area; 8 = 80% dead leaf area and 9 represented 90–100% dead leaf area.

xi. **Field weight (FW)**: The weights of cobs for each plot were taken in kilograms using an automatic digital weighing scale known as CAMRY.

xii. **Moisture content (MC):** Grain moisture was determined after each plot by means of a John Deere Moisture meter (Manufactured by AgraTronix^{TM}; Moisture Check Plus^{TM}; USA for Deere and Company; Batch SW08120).

xiii. **Root Lodging:** Data was recorded a week before harvest for the number of plants leaning more than 30 degrees from the vertical

xiv. **Stalk lodging:** The number of plants with broken stalks below the ear or stalks bending more than 45 degrees from the upright position was recorded a week before harvest.

xv. **Grain weight**: Weights of grains after shelling per plot in kilograms was recorded.

xvi. **Grain yield (GY) (t/ha);** Grain yield in t ha^{-1} was estimated from the shelled grain weight, adjusted to 15% moisture. Under optimal N, a shelling percentage of 80% was assumed for all cultivars and grain yield (obtained from ear weight and converted to t ha^{-1}) was adjusted to 15% moisture (Badu-Apraku *et al.,* 2015).

3.8 Statistical analysis

Independent analyses of variance (ANOVA) were done on data collected across the low N environments and optimum N environments from the locations with PROC GLM in SAS using a random statement with the SAS software version 9.3. Subsequently, an ANOVA was done across each N environments across locations which included environment, replicate within environment and block within replicate x environment as random factors whereas entries (36 hybrids and 4 checks) were treated as fixed effects (Appendix I). Same was also repeated for optimum N environments.

GCA effects of the parents and SCA effects of the crosses, as well as their mean squares in each N environments were estimated on the 36 diallel crosses excluding the checks, following the Griffing's method 4 model 1 (Fixed model) (Griffing, 1956) using AGD-R (Analysis of Genetic Designs in R) software, Version 5.0, Copyright @ 2015, CIMMYT.

3.9 Heritability estimates

To compute values of GCA variance as Vgca (additive variance) and SCA variance as Vsca (dominance) for each trait across research environments, the relative relevance of genetic components was assessed. The following equations were used to calculate variance components, heritability, and genetic ratios:

$$\text{Vgca} = \frac{\text{MSgca+MSscaenv}}{\text{MSsca+Msgcaenv}}$$

$$\mathrm{Vsca} = \frac{\mathrm{MSsca}}{\mathrm{MSscaenv}}$$

$$\mathrm{Vgcaenv} = \frac{\mathrm{MSgcaenv}}{\mathrm{MSscaenv}}$$

$$\mathrm{Vscaenv} = \frac{\mathrm{MSsca}}{\mathrm{MSe}}$$

$$\mathrm{H}^2 = \frac{2\mathrm{Vgca}+\mathrm{Vsca}}{2\mathrm{Vgca}+\mathrm{Vsca}+\frac{2\mathrm{Vgca}}{\mathrm{Env}}+\frac{\mathrm{Vsca}}{\mathrm{Env}}+\frac{\mathrm{Ve}}{\mathrm{REnv}}}$$

$$\mathrm{h}^2 = \frac{2\mathrm{Vgca}}{2\mathrm{Vgca}+\mathrm{Vsca}+\frac{2\mathrm{Vgca}}{\mathrm{Env}}+\frac{\mathrm{Vsca}}{\mathrm{Env}}+\frac{\mathrm{Ve}}{\mathrm{REnv}}}$$

$$\text{Baker's ratio} = \frac{2\mathrm{MSgca}}{2\mathrm{MSgca}+\mathrm{MSsca}}$$

where MSgca is the mean squares of GCA, MSsca is the mean squares of SCA, MSgcaenv is the mean squares of GCA x Environment interaction, MSscaenv is the mean squares of SCA x Environment interaction, MSe is the error mean squares, and REnv is the Number of replications x Environment, H^2 denotes broad-sense heritability, h^2 is the narrow sense heritability.

3.10 Estimation of heterosis

The Mid-Parent Heterosis (MPH), High/Better Parent Heterosis (BPH) and Economic Heterosis (EH) was according to the formulae is given as follows;

$$\mathrm{MPH}\ (\%) = \frac{\mathrm{F1}-\mathrm{MP}}{\mathrm{MP}} \times 100;\ \mathrm{MP} = \frac{\mathrm{P1}+\mathrm{P2}}{2}$$

BPH (%) = $\frac{\mathrm{F1-BP}}{\mathrm{BP}} \times 100$

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EH (%) = $\frac{\mathrm{F1-Best\ Check}}{\mathrm{Best\ Check}} \times 100$

F1= Mean of F1

Best Check = Mean of the best check

BP= Mean of a better parent

MP= Mean of mid-parent.

3.11 Correlation analysis for all the data collected

A correlation analysis was conducted for all response variables under data collection to find that which are highly correlated at a 5 % significant level. This was done using R software version 4.1.2. This was needed to find the traits which will be best in selecting individuals that are tolerant to low nitrogen soil.

3.12 Base Index for selection

A base index (BI) that incorporates grain yield, EPP, ASI, PASP, EASP, and SG was used to select the best and worst-performing genotypes under the low N soil. Each trait will be first standardized with a standard deviation of 1 and a mean of zero to minimize the effect of the different scales before putting it into the BI. The BI is shown by the equation:

BI = (2 * GY) + EPP- ASI - PASP - EASP - SG

where; GY is grain yield under low N, EPP is ears per plant, SG is stay-green characteristic and ASI is anthesis-silking interval, PASP is plant aspect, and EASP ear aspect.

A positive base index value shows tolerance to the low N soil while negative values will mean susceptibility to the low N soil (Badu-Apraku *et al*., 2020).

CHAPTER FOUR

4.0 RESULTS

4.1 Analysis of variance for grain yield and other related traits

The combined analysis of variance across low N soils from Fumesua and Ejura revealed that the mean squares for environments (Env) were significant ($P<0.05$) for all the agronomic traits with exception of SL, GY, and EPP but with optimum N soil environments, GY and other agronomic characters were significant ($P<0.05$) except PASP. Mean squares for hybrids (G) were significant ($P<0.001$) for GY, PASP, SG, DFS, and PH under low N soil and GY, PASP, CC, DFA, DFS, PH, and SL for optimum N environments (Table 4.1).

The mean square estimate of GCA for low N for GY, PASP, DFS and PH was significant ($P<0.01$) as well as EASP ($P<0.05$) when seperating G into GCA and SCA. CC, DFA, DFS, PH, SL, and on the other hand, had a significant mean square of GCA ($P<0.01$) in optimum N. RL and GY were also significant ($P<0.05$) GCA effect under optimum N. Mean square estimates of SCA for GY, ASI, PASP, SG, DFS, PH, and SL under low N were significant, unlike optimum N where GY, PASP, SG, DFA, DFS, PH, SL, and RL were significant. Significant ($P<0.05$) genotype (G) x environment (Env) interaction mean square estimate was observed for DFS in low N and EASP, SG, DFA, and DFS under optimum N. The GCA x environment interaction effect was significant ($P<0.05$) in DFS under low N and SG, DFA, DFS and RL under optimum N soil environments (Table 4.1). No significant differences were observed in SCA x environment interaction effect in all the traits under low N for EASP whereas, in optimum N, a significant SCA x environment interaction effect was revealed in EASP (Table 4.1).

Table 4.1 Mean Squares of ANOVA of grain yield and other agronomic traits of early maturing maize hybrids assessed under low N and Optimal N environments in Fumesua and Ejura.

Source of variation	DF	GY(t/ha)	EPP	ASI	PASP	EASP	SG	CC	DFA	DFS	PH	SL	RL
Low N soil environments													
Env	1	0.02	0.03	6.34*	24.67***	3.63*	7.78***	306.76***	1390.30	1208.89***	5766.00***	7.41	86.89***
Rep (Env)	4	0.63	0.53	1.94	0.80	0.96	0.76	90.92*	34.05	41.19***	845.90**	63.27***	12.21
Hybrids (G)	35	1.26***	0.27	2.40	1.24***	0.71	1.10*	23.95	17.03	17.87**	594.15***	14.00	6.71
GCA	8	1.31**	0.15	1.76	0.78***	1.58*	0.51	23.15	40.50	41.77***	1101.94***	5.90	5.76
SCA	27	1.25***	0.30	2.58*	1.38***	0.45	1.27***	24.18	10.07	10.79***	443.70***	16.40**	6.99
Hybrids (G) x Env	35	0.14	0.27	1.39	0.31	0.52	0.52	33.45	7.34	6.43*	174.15	8.34	6.06
GCA x Env	8	0.08	0.26	0.95	0.32	0.53	0.33	33.86	9.84	10.44*	257.93	2.10	7.70
SCA x Env	27	0.16	0.28	1.51	0.31	0.52	0.57	33.32	6.60	5.24	149.33	10.19	5.57
Error	140	0.40	0.26	1.47	0.37	0.67	0.43	31.27	4.83	4.97	219.26	8.26	7.19
Optimum N soil environments													
Env	1	5.97**	2.16***	13.50**	0.12	12.52***	18.96***	1924.91***	933.34***	722.34***	23437.50***	408.38***	58.07*
Rep (Env)	4	6.94***	0.29	8.61***	3.80***	2.12*	2.34***	484.76***	32.78***	72.03***	1930.18***	17.86	14.02
Hybrids (G)	35	1.73***	0.13	1.44	0.54**	0.92	0.91	79.70**	16.26*	16.13**	408.44**	17.90**	17.09
GCA	8	1.31*	0.08	2.32	0.31	1.03	0.54	180.86***	50.58***	50.32***	758.31***	28.91***	25.56*
SCA	27	1.86***	0.15	1.18	0.61*	0.89	1.02***	49.72	6.09*	5.99*	304.78*	14.64**	14.58
Hybrids (G) x Env	35	0.45	0.12	1.91	0.24	1.16*	0.62*	30.76	5.70*	7.03**	151.78	7.77	12.60
GCA x Env	8	0.12	0.17	2.38	0.19	0.83	1.41***	48.64	10.70**	12.22**	153.73	6.36	21.00*
SCA x Env	27	0.54	0.11	1.77	0.26	1.25*	0.39	25.47	4.22	5.49	151.20	8.18	10.11
Error	140	0.53	0.14	1.30	0.30	0.72	0.38	35.78	3.27	3.82	173.52	7.39	9.39

*, **, *** is the significance at 0.05, 0.01, 0.001 probability levels respectively, **GCA x Env:** General Combining ability x Environment interaction, **SCA x Env**: Specific Combining ability x Environment interaction, **Rep (Env)** is the Replication nested within Environment, **Env** is the environment, **SE**: Standard error **GY**: Grain yield in t/ha, **EPP**: Ears per plant, **ASI**: Anthesis Silking interval, **PASP**: Plant Aspect, **EASP**: Ear Aspect, **SG**: Stay-green characteristic, **CC**: Chlorophyll content, **DFA**: Days to 50 % anthesis, **DFS**: Days to 50 % Silking, **PH**: Plant Height, **SL**: Stem lodging, **RL**: Root lodging.

4.2 General combining ability effects of grain yield and other agronomic traits.

Significant ($P<0.001$) positive GCA for GY was seen in inbred P3 under low N environments and P5 and P6 under optimum N. On the other hand, P1 and P9 under low N as well as P8 and P9 in optimum N had significant negative GCA effects for GY (Table 4.2). ASI showed a significant ($P<0.05$) positive GCA in low N soil for inbred P1 and P5 in optimum N whereas P4 and P7 showed significant negative GCA effect still under optimum N. P1 and P6 had significant positive GCA effect while P2 and P3 expressed significant negative GCA effect under low N in PASP (Table 4.2). P1, P2, and P8 displayed a significant ($P<0.05$) positive GCA effect under low N soil conditions in Fumesua and Ejura not leaving P4 out which showed the same sign of GCA effect in optimum N soil environments in EASP. P2 and P7 under optimum N and low N respectively also had significant negative GCA effects in EASP. P5 was the only genotype under low N portraying a significant positive GCA effect in SG (Table 4.2). Significant positive GCA effect occurred in P1 and P8 and a significant negative GCA effect was observed in P5 and P7 under optimum N, all in CC. P5 and P7 expressed a significant positive GCA effect whereas P1, P4 and P6 depicted a significant negative GCA effect for DFF under low N. No significant differences for the GCA effect were seen in optimum N. Moreover, DFS had P5, P8, and P9 under low N and P2, P5, and P7 under optimum N express significant positive GCA effect with P3 and P6 under low N and P1, P4 and P5 under optimum N showing significant negative GCA effect (Table 4.2). Significant positive differences in the GCA effect were observed in PH for P2 and P5 in low N and P5 in optimum N. SL recorded significant positive GCA effects in genotype P4 and significant negative GCA effects in P7 and P9 under optimum N soil environments. RL had a significant positive GCA effect in P5 and P7 in optimum N soil environment whereas P1showed a significant negative GCA effect (Table 4.2).

Table 4.2 General combining ability effects of grain yield and other agronomic traits of early maturing maize inbreds under low N and Optimum N in Fumesua and Ejura.

PARENTS	GY(t/ha)	EPP	ASI	PASP	EASP	SG	CC	DFF	DFS	PH	SL	RL
Low N soil environments												
P1	-0.18*	-0.07	0.45**	0.17*	0.32**	0	1.13	-0.88*	-0.43	0.01	0.53	-0.76*
P2	0.01	0.04	-0.17	-0.16*	0.22*	-0.14	0.16	0.10	-0.07	4.79*	-0.35	0.38
P3	0.44***	-0.09	-0.24	-0.19*	-0.08	-0.14	-0.13	-0.40	-0.65*	1.37	0.22	0.05
P4	-0.02	0.06	-0.12	0.10	0.01	-0.07	-0.83	-1.38***	-1.50***	-7.33**	0.62	-0.31
P5	-0.06	-0.03	0.14	-0.07	0.03	0.19*	-0.23	1.36***	1.50***	10.06***	-0.12	0.36
P6	-0.00032	-0.04	0.04	0.15*	-0.08	0.07	-1.07	-0.81**	-0.76*	-3.40	0.00	0.31
P7	-0.08	0.08	-0.05	0.05	-0.25*	0	1.00	1.46***	1.40***	-3.47	-0.33	-0.09
P8	0.00673	0.03	0.04	0.07	0.08*	0.10	-0.33	0.50	0.54*	-2.54	-0.33	0.17
P9	-0.12*	0.02	-0.08	-0.12	-0.25	0	0.30	0.05	-0.03	0.51	-0.24	-0.12
SE	0.064	0.05	0.12	0.06	0.08	0.07	0.58	0.23	0.23	1.52	0.30	0.28
Optimum N soil environments												
P1	-0.00428*	-0.06	-0.03	0.03	0.12	-0.14	4.18***	-0.51	-0.54*	1.00	-0.26	-0.94*
P2	0.06	0.01	-0.06	-0.04	-0.29*	-0.14	-1.31	0.99	0.93**	1.41	-0.60	0.61
P3	0.0081	-0.01	0.13	-0.07	0.00	0.05	-0.60	-0.13	0.00	-0.95	0.48	-0.01
P4	0.125	-0.06	-0.27*	0.05	0.21*	-0.02	-0.03	-1.92	-2.19***	-3.09	1.74***	-0.96*
P5	0.214*	0.01	0.37*	-0.09	-0.12	0.10	-2.81**	0.47	0.84**	9.76***	0.57	0.78*
P6	0.177*	0.06	0.01	0.00	0.12	0.14	-1.80*	-0.63	-0.62*	-2.02	0.17	-0.22
P7	-0.05	0.04	-0.42*	-0.02	-0.14	-0.02	0.08	2.01	1.60***	-4.57**	-0.79*	1.21**
P8	-0.326**	0.03	0.13	0.19	0.02	0.14	0.37	-0.11	0.03	-2.95	-0.60	0.25
P9	-0.206*	-0.02	0.13	-0.04	0.07	-0.10	1.91*	-0.18	-0.04	1.41	-0.71*	-0.72
SE	0.07489	0.04	0.12	0.06	0.09	0.06	0.62	0.19	0.20	1.36	0.28	0.32

4.3 Specific combining ability effects of grain yield and its related traits

Specific combining ability (SCA) effects differed among all the hybrids across low N and optimum N soils in Fumesua and Ejura. The topmost genotype recording the most significant (P<0.001) positive SCA effect was G20 followed by G5 in low N in GY and optimum N soils found G6 being the prominent genotype expressing the same significant SCA effect in GY (Table 4.3 and 4.4). G2 and G13 expressed the most significant (P<0.01) negative SCA effect in low N and optimum N respectively in the same response variable. EPP recorded a significant (P<0.01) positive SCA effect for the most astounding genotype G7 followed by G14 across low N and G31 in optimum N. ASI displayed a significant positive (P<0.01) SCA effect in G6 under low N and G29 for optimum condition (Table 4.3 and 4.4). Also, in the PASP, G6 in optimum N and G11 in low N showed significant (P<0.05) negative SCA effect whereas the highest significant positive SCA effect was seen in G13 across the low and optimum conditions. Furthermore, with the EASP, only across optimum conditions experienced the best significant (P<0.05) positive SCA effect in G17. CC showed a significant (P<0.05) positive SCA effect in G2 and G23 across optimum conditions in Fumesua and Ejura. Most genotypes recorded a significant negative SCA effect in SG especially under low N with G12 being the highest (Table 4.3 and 4.4). The same result also happened for G36 under optimum conditions. G13 had the top significant positive SCA effect in both low and optimum N conditions in the SG. G12 in low N and G32 in optimum conditions received a significant (P<0.05) positive SCA effect for RL. Only G31 had a pronounced significant negative SCA effect in RL (Table 4.3 and 4.4). Significant positive SCA effect in SL occurred in several genotypes but the best among them in optimum and low conditions was G9 and G29 respectively. G2 in both low and optimum conditions showed the most significant negative SCA effects in SL. Moreover, PH displayed the most significant positive SCA effect for G20 and G12 in low and optimum conditions respectively. G13 in low and optimum conditions in both Fumesua and Ejura recorded the highest significant negative SCA effects. DFA was also found to show the most significant positive SCA effects for G16 in both low and optimum conditions whereas G9 was second to none in terms of significant negative SCA effects in the same response variable. Finally, G28 and G20 in low and optimum conditions correspondingly proved to show the highest significant negative SCA effect while G16 and G13 appeared to top all the rest of the genotypes for a significant positive SCA effect in DFS (Table 4.3 and 4.4).

Table 4.3 Specific combining ability effects of grain yield and other agronomic traits of early maturing maize hybrids evaluated under low N in Fumesua and Ejura

HYBRIDS	GY (t/ha)	EPP	ASI	PASP	EASP	SG	CC	DFA	DFS	PH	SL	RL
G1	-0.07	-0.06	-0.45	-0.23	-0.29	-0.15	2.19	1.10	0.65	6.98	1.31	-0.85
G2	-0.62**	0.08	-0.21	0.29	-0.31	0.18	-1.06	0.26	0.05	-7.43	-3.26**	-0.52
G3	0.16	-0.30	0.01	0.17	-0.05	-0.22	1.26	-0.76	-0.76	-1.57	0.17	-0.16
G4	-0.29	-0.05	-0.26	0.17	-0.07	0.18	-0.48	0.50	0.24	-5.79	-0.76	-0.66
G5	0.81***	-0.05	-0.16	-0.54*	0.02	-0.03	0.36	-0.33	-0.49	6.00	2.12*	0.39
G6	0.24	-0.07	1.27**	-0.28	0	-0.29	3.88	-0.10	1.17	5.57	-1.38	0.79
G7	-0.43	0.70***	0.01	0.20	0.24	0.28	-1.72	0.52	0.53	-1.86	-0.55	0.03
G8	0.21	-0.24	-0.21	0.22	-0.17	0.04	-4.44	-1.19	-1.40	-1.90	2.36*	0.98
G9	0.52*	-0.11	0.58	-0.04	0.31	-0.34	2.12	-2.21**	-1.64*	-0.38	2.45*	1.01
G10	-0.42	-0.20	-0.71	-0.16	-0.12	-0.24	-1.01	-0.40	-1.11	-0.02	0.38	-1.64
G11	0.14	0.19	-0.14	-0.66**	-0.31	-0.67**	1.51	0.19	0.05	0.26	-1.55	0.36
G12	0.38	-0.11	0.79	-0.71	-0.21	-0.72**	-1.83	-0.81	-0.02	7.71	-1.17	2.58*
G13	-0.66**	0.04	0.05	1.22**	0.43	1.02***	-3.34	0.76	0.82	-17.71**	-0.83	-0.18
G14	-0.28	-0.16	-0.71	0.53***	0	0.59*	-2.09	0.71	0.01	1.52	-0.50	-0.28
G15	0.39	0.41*	0.58	0.05*	0.14	0.52*	2.45	0.67	1.24	1.64	-0.10	-0.99
G16	-0.49*	-0.02	0.70	0.20	0.02	0.26	-1.06	2.76**	3.46***	-11.76*	-0.69	0.36
G17	-0.29	-0.05	-0.40	0.36	0.45	0.33	-0.90	2.19**	1.79*	-2.48	0.71	0.70
G18	-0.05	0.01	0.36	0.15	-0.07	0.45	-0.05	-1.31	-0.95	2.14	2.10*	-1.59
G19	0.24*	-0.04	0.29	-0.26	-0.17	-0.48*	0.18	-0.40	-0.11	-1.45	-0.07	0.48
G20	0.94***	-0.08	-1.14*	-0.95	-0.02	-0.58*	2.60	-0.62	-1.76*	19.29**	-0.57	-0.45
G21	-0.25	0.22	-0.18	0.24***	-0.07	0.18	-1.84	-0.67	-0.85	2.07	-0.67	0.01
G22	-0.04	0.05	-0.18	-0.09	0.52	-0.58*	0.54	-0.17	-0.35	1.38	-0.02	-0.78
G23	0.17	0.21	0.08	0.03	0.12	0.21	1.62	-0.50	-0.42	1.67	0.19	-0.23
G24	0.60*	0.11	-0.49	-0.38	-0.07	0.11	-0.43	-0.76	-1.26	13.07*	0.69	1.01
G25	0.02	-0.09	0.58	-0.07	-0.17	0.02	0.28	-1.98*	-1.40	2.14	1.69	1.58
G26	-0.01	0.24	0.03	0.29	-0.02	0.45	-1.20	1.81*	1.84*	-4.90	-2.40*	-0.14
G27	-0.01	0.15	-0.35	0.20	-0.24	0.28	-1.32	0.26	-0.09	4.79	-1.24	-0.23
G28	-0.04	-0.10	-0.59	0.12	0.10	0.35	0.38	-0.67	-1.26	4.86	1.60	0.67
G29	0.66**	-0.12	1.65***	-0.07	0.19	-0.08	0.38	-1.88*	-0.23	1.76	2.60*	0.41

G30	-0.13	-0.07	0.27	-0.04	0.12	0.18	-0.11	-0.43	-0.16	-4.79	-1.33	-0.47

Table 4.3 Continued

HYBRIDS	**GY (t/ha)**	**EPP**	**ASI**	**PASP**	**EASP**	**SG**	**CC**	**DFA**	**DFS**	**PH**	**SL**	**RL**
G31	-0.43	0.20	-0.83	0.41	-0.24	0.14	-1.00	0.17	-0.66	-8.86	-1.19	-1.45
G32	-0.55*	-0.14	-0.09	0.22	0.50	0.04	-0.45	2.12*	2.03*	-7.79	-1.02	-1.21
G33	-0.33	-0.28	0.20	0.24	-0.36	-0.36	2.66	0.40	0.60	-5.67	0.21	1.74
G34	-0.22	0.02	0.34	0.15	0.26	-0.05	-0.58	1.36	1.70*	-12.05*	-1.19	-0.14
G35	0.27	-0.15	-0.04	-0.99	-0.24	-0.79**	0.90	-0.36	-0.40	16.57**	2.38*	-1.18
G36	-0.15	-0.13	-0.64	-0.02***	-0.24	-0.22	1.57	-0.24	-0.88	-3.02	-0.45	0.05
SE	0.22	0.18	0.43	0.21	0.29	0.23	1.98	0.78	0.79	5.24	1.02	0.95

*****, ******, ******* is the significance at 0.05, 0.01, 0.001 probability levels respectively, **GY**: Grain yield in t/ha, **EPP**: Ears per plant, **ASI**: Anthesis Silking interval, **PASP**: Plant Aspect, **EASP**: Ear Aspect, **SG**: Stay-green characteristic, **CC**: Chlorophyll content, **DFA**: Days to 50 % anthesis, **DFS**: Days to 50 % Silking, **PH**: Plant Height, **SL**: Stem lodging, **RL**: Root lodging.

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Table 4.4 Specific combining ability effects of grain yield and other agronomic traits of early maturing maize hybrids evaluated under Optimum N in Fumesua and Ejura

HYBRIDS	GY(t/ha)	EPP	ASI	PASP	EASP	SG	CC	DFA	DFS	PH	SL	RL
G1	0.31	0.18	0.33	0.13	-0.42	0.04	-0.21	0.72	1.05	2.32	1.07	-1.54
G2	-1.05***	0.37**	-0.02	-0.35	-0.37	-0.32	4.87*	-1.33*	-1.35	-5.15	-3.67***	-2.25*
G3	-0.45	-0.04	0.05	0.03	0.25	0.25	-0.50	-0.04	0.01	3.15	0.23	2.20
G4	-0.21	-0.12	0.07	0.51*	0.08	0.30	-2.04	0.08	0.15	-2.37	2.07*	0.30
G5	-0.01	-0.05	-0.57	0.08	0.68*	-0.08	0.43	1.67*	1.10	-1.42	-0.20	-1.54
G6	0.88**	-0.05	0.19	-0.40*	-0.23	-0.08	-1.71	-0.64	-0.45	7.13	-0.08	2.54*
G7	0.28	-0.12	0.31	-0.28	-0.39	-0.25	-0.61	-0.52	-0.21	1.18	-1.27	0.49
G8	0.25	-0.17	-0.36	0.29	0.39	0.15	-0.24	0.05	-0.30	-4.85	1.85	-0.20
G9	0.35	-0.10	0.00	-0.11	0.04	-0.32	3.33	-1.49*	-1.49*	-7.56	0.83	1.04
G10	0.53	-0.03	-0.10	-0.07	-0.35	-0.42	-0.25	-0.21	-0.30	1.25	-0.27	-0.68
G11	-0.21	0.00	-0.90*	-0.26	-0.18	-0.37	1.97	0.08	-0.83	-1.77	-2.10*	1.25
G12	0.40	-0.16	0.62	-0.35	0.08	-0.08	-1.40	-1.16	-0.54	12.85*	1.64	2.25*
G13	-1.03***	-0.17	0.21	0.84***	0.35	1.08***	-2.50	1.70*	1.91*	-19.27**	-1.24	-1.68
G14	-0.33	0.16	-0.67	-0.04	0.51	-0.08	2.79	0.82	0.15	4.94	-0.27	-1.23
G15	-0.01	0.12	0.50	-0.14	-0.04	0.15	-3.73	-0.45	0.05	7.25	0.35	0.58
G16	-0.37	-0.06	-0.12	0.13	-0.30	0.56*	-3.40	1.74*	1.63*	0.44	1.16	-1.06
G17	-0.51	-0.02	0.07	0.43*	0.70*	0.44	-2.64	1.53*	1.60*	-4.25	0.49	-0.30
G18	0.48	-0.15	0.10	0.01	-0.20	-0.11	-0.43	-0.88	-0.78	1.87	0.73	-0.13
G19	0.37*	-0.11	-0.31	0.20	0.06	0.06	1.96	0.82	0.51	2.25	-0.15	0.61
G20	0.41	0.00	0.31	-0.18	0.39	-0.27	-4.11	-0.40	-0.09	7.13	0.33	1.39
G21	0.33	0.06	-0.02	-0.11	-0.32	-0.04	0.41	0.01	-0.02	5.27	0.28	0.70
G22	-0.29	0.10	0.31	-0.18	0.15	-0.32	3.50	0.32	0.63	-5.11	-2.43*	-0.68
G23	0.42	-0.05	-0.17	-0.11	-0.08	-0.04	4.80*	-0.76	-0.92	-1.15	0.47	-0.85
G24	0.17	0.14	0.43	0.08	0.01	-0.04	-3.85	-0.57	-0.14	-0.27	1.42	0.23
G25	0.51	0.05	-0.29	0.03	-0.32	0.13	-0.63	-0.11	-0.40	-1.23	0.90	0.85
G26	-0.51	-0.10	-0.12	0.10	0.63*	-0.13	0.32	-0.38	-0.49	2.92	-1.48	-0.01
G27	0.33	0.09	-0.31	-0.14	-0.25	-0.15	-2.75	0.03	-0.28	0.65	0.14	0.08
G28	0.72**	-0.09	-0.21	-0.45*	-0.32	-0.49*	-0.65	-2.11**	-2.33**	11.37*	1.09	1.49
G29	0.40	0.02	0.90*	0.01	-0.15	0.18	0.14	-0.66	0.24	0.08	2.23*	-1.06

G30	-0.22	0.02	0.07	0.08	-0.04	0.42	2.47	0.74	0.82	1.39	-1.48	-1.08

Table 4.4 Continued

HYBRIDS	GY(t/ha)	EPP	ASI	PASP	EASP	SG	CC	DFA	DFS	PH	SL	RL
G31	-0.78*	0.28*	-0.36	-0.21	-0.23	-0.54*	2.93	0.48	0.13	-8.18	-2.34*	-3.01*
G32	-0.72**	0.16	0.43	0.41*	-0.06	0.63**	0.71	0.43	0.86	-0.13	-1.36	2.44*
G33	-0.11	-0.13	0.26	0.32	0.06	0.37	-4.30	0.17	0.43	-4.49	0.92	0.75
G34	-0.58*	-0.24	-0.31	0.27	0.54	0.30	0.23	0.46	0.15	1.25	0.59	-1.15
G35	0.251	0.24	0.36	-0.33	-0.18	-0.30	3.60	-0.14	0.22	5.73	0.71	0.99
G36	0.03	-0.03	-0.69	-0.21	-0.51	-0.63***	1.47	-0.02	-0.71	-13.23**	-1.15	-1.73
SE	0.26	0.13	0.40	0.19	0.30	0.22	2.11	0.64	0.69	4.66	0.96	1.08

, **, ** is the significance at 0.05, 0.01, 0.001 probability levels respectively, **Rep** is the Replication, **Env** is the environment, **SE**: Standard error, **GY**: Grain yield in t/ha, **EPP**: Ears per plant, **ASI**: Anthesis Silking interval, **PASP**: Plant Aspect, **EASP**: Ear Aspect, **SG**: Stay-green characteristic, **CC**: Chlorophyll content, **DFA**: Days to 50 % anthesis, **DFS**: Days to 50 % Silking, **PH**: Plant Height, **SL**: Stem lodging, **RL**: Root lodging.

4.4 Mean performance of grain yield, base indices, and its agronomic characters of hybrids across low and optimum N across Fumesua and Ejura.

GY across optimal environments for both Fumesua and Ejura varied from 0.82 to 2.75 t/ha, with an average of 1.9 t/ha. The single-cross hybrids G23 (2.75 t/ha), G6 (2.70 t/ha), G10 (2.58 t/ha), G18 (2.54 t/ha), and G9 (2.12 t/ha) had the highest GY as compared to the checks except for G18 in which the GY was lower than that of Apraku (local check) (2.64 t/ha) and G2 showed the lowest GY (0.84 t/ha) (Table 4.5) under optimum N. In low N environments across Fumesua and Ejura, the mean GY was 1.19 t/ha with the genotype G20 revealing an outstanding GY (2.53 t/ha) over all the local checks followed by G9 with a GY of 2.12 t/ha. The hybrid with the least GY under low N was G13 (0.42 t/ha). The mean EPP under low and optimum N soil conditions were 1.38 and 1.17 respectively and it ranged from 0.43 to 1.38 under low N and 0.55 to 1.17 under optimum conditions. The mean ASI interval was 4.1 and 4.2 under low N and optimum N conditions (Table 4.5). This response variable ranged from 3.5 to 5.7 and 2.8 to 6.0 for optimum and low N conditions correspondingly. The PASP mean was 2.7 under optimum conditions and approximately 2.4 under low conditions (Table 4.5). The mean EASP was 2.1 and 1.9 under low and optimum conditions respectively. SG expressed a mean of 2.1 and 2.2 for low N and optimum N conditions. Out of the thirty-six hybrids evaluated across low N from Fumesua and Ejura, only fifteen (15) of them had positive base indices among which G18 indicated the highest base index under low N conditions across Fumesua and Ejura followed by G35 and G36 with G11 having the least base index (Table 4.5).

Table 4.5 Performance of the grain yield and other agronomic characters of early maturity maize hybrids under low and opimum nitrogen soils assessed in Fumesua and Ejura environments

	LOW	OPT	LOW	OPT	LOW	OPT	LOW	OPT	LOW	OPT	LOW	OPT	LOW
HYBRIDS	**GY(t/ha)**	**GY(t/ha)**	**EPP**	**EPP**	**ASI**	**ASI**	**PASP**	**PASP**	**EASP**	**EASP**	**SG**	**SG**	**BASE INDEX**
G1	0.91	2.24	0.66	0.91	4.00	4.50	2.17	2.83	2.17	1.50	1.83	2.00	-3.68
G2	0.78	0.82	0.67	1.09	4.17	4.33	2.67	2.33	1.83	1.83	2.17	1.83	-7.19
G3	1.11	1.54	0.43	0.61	4.50	4.00	2.83	2.83	2.17	2.67	1.83	2.33	1.66
G4	0.63	1.87	0.58	0.60	4.50	4.67	2.67	3.17	2.50	2.17	2.50	2.50	-3.01
G5	1.77	2.04	0.60	0.73	4.50	3.67	2.17	2.83	1.83	3.00	2.17	2.17	-5.49
G6	1.13	2.70	0.66	0.70	5.83	4.00	2.33	2.33	2.00	1.83	1.83	2.00	-3.98
G7	0.55	1.82	1.38	0.62	4.67	4.67	2.83	2.67	2.83	1.83	2.50	2.00	4.82
G8	1.06	1.91	0.44	0.55	4.33	4.00	2.67	3.00	2.17	2.67	2.17	2.17	-0.41
G9	2.12	2.29	0.59	0.67	4.33	4.33	2.00	2.50	2.00	1.83	1.50	1.83	4.25
G10	0.73	2.58	0.64	0.70	3.17	3.83	2.17	2.67	2.17	1.67	1.67	1.67	3.34
G11	1.25	1.94	0.94	0.82	4.00	3.67	1.50	2.33	2.00	1.50	1.50	1.83	-8.39
G12	1.55	2.51	0.63	0.69	4.83	4.83	1.67	2.33	1.83	2.00	1.33	2.17	-4.15
G13	0.42	0.85	0.90	0.66	4.00	4.00	3.50	3.50	2.33	2.00	3.00	3.17	1.68
G14	0.89	1.28	0.66	0.97	3.33	3.67	2.83	2.83	2.33	2.33	2.67	2.17	-1.63
G15	1.43	1.72	1.20	0.91	4.50	4.83	2.17	2.50	2.00	1.83	2.50	2.17	-1.79
G16	1.07	1.63	0.70	0.65	4.50	4.00	2.50	2.83	1.83	2.00	2.17	2.83	-1.44
G17	1.24	1.58	0.60	0.75	3.67	4.83	2.50	3.00	2.17	2.67	2.50	2.83	5.42
G18	1.54	2.54	0.62	0.70	4.33	4.50	2.50	2.67	2.17	2.00	2.50	2.33	11.03
G19	1.75	2.20	0.70	0.71	4.17	3.67	2.00	2.83	1.50	2.00	1.50	2.33	2.97
G20	2.53	1.96	0.62	0.80	2.83	4.83	1.33	2.67	1.83	2.50	1.50	2.17	-2.33
G21	1.22	2.00	0.89	0.82	3.67	4.50	2.33	2.50	1.33	1.83	2.17	2.17	-1.50
G22	1.08	2.59	0.82	0.94	4.00	4.33	2.67	2.50	2.00	1.83	2.67	2.33	-1.82
G23	0.97	2.75	0.69	0.76	3.67	4.00	2.50	2.17	1.67	1.50	2.67	1.83	-1.29
G24	1.75	2.15	0.63	0.82	6.00	5.67	2.33	2.83	2.00	1.83	2.33	2.67	-0.93

Continued

HYBRIDS	GY(t/ha)	GY(t/ha)	EPP	EPP	ASI	ASI	PASP	PASP	EASP	EASP	SG	SG	BASE INDEX
G25	0.84	1.66	0.69	0.78	4.50	4.83	2.17	2.67	1.33	2.00	2.50	2.67	-4.22
G26	0.65	1.22	0.98	1.17	3.33	3.50	3.00	2.50	1.50	1.83	2.33	1.83	-3.72
G27	0.61	1.00	0.61	1.03	4.17	4.83	2.83	3.33	1.67	2.17	2.33	3.17	-2.16
G28	0.70	1.73	0.46	0.67	4.33	4.67	2.67	3.00	1.83	2.33	1.83	2.67	6.13
G29	0.86	0.91	0.87	0.60	4.50	3.67	2.67	3.17	1.83	2.50	2.17	2.67	0.59
G30	1.22	1.87	0.68	1.05	4.00	4.33	1.33	2.33	1.17	1.83	1.33	1.83	1.09
G31	0.89	1.37	0.65	0.75	3.50	3.83	2.33	2.67	1.50	1.67	2.00	1.67	0.41
G32	1.03	1.92	0.84	0.84	4.00	4.67	2.33	2.50	1.83	2.33	1.67	2.00	5.43
G33	1.30	2.59	0.99	0.72	4.17	3.83	2.67	2.67	1.83	2.33	2.33	2.33	-1.23
G34	1.65	2.11	0.98	0.90	3.50	4.00	2.17	2.83	1.50	2.17	2.17	2.17	-1.59
G35	1.16	2.18	0.77	0.81	4.67	3.83	2.50	3.00	1.83	2.00	2.17	2.50	7.02
G36	1.00	1.28	1.08	0.59	4.00	4.00	2.67	2.83	2.17	3.00	2.50	2.00	7.10
Apraku	1.47	2.64	0.72	0.70	2.83	3.50	1.67	1.83	1.67	2.17	1.33	1.33	3.58
Tintim	1.85	2.26	1.24	0.86	4.17	3.50	2.33	2.50	1.67	1.67	1.50	1.67	-0.45
GH110	1.76	2.01	0.45	0.86	3.50	3.83	2.50	3.00	1.33	2.67	2.00	2.67	0.00
Afriyie	1.12	1.63	0.59	0.61	4.17	4.67	2.67	2.83	1.50	2.33	2.00	2.17	-1.56
Mean	1.19	1.90	0.75	0.78	4.12	4.22	2.38	2.71	1.87	2.10	2.08	2.22	0.06
Maximum	2.53	2.75	1.38	1.17	6.00	5.67	3.50	3.50	2.83	3.00	3.00	3.17	11.03
Minimum	0.42	0.82	0.43	0.55	2.83	3.50	1.33	1.83	1.17	1.50	1.33	1.33	-8.39
SE	0.07	0.08	0.03	0.02	0.10	0.08	0.07	0.05	0.05	0.06	0.07	0.07	0.66

OPT: Optimum, **GY**: Grain yield in t/ha, **EPP**: Ears per plant, **ASI**: Anthesis Silking interval, **PASP**: Plant Aspect, **EASP**: Ear Aspect, and **SG**: Stay-green characteristic.

4.5 Genetic variances and heritability

The variance components of GCA and SCA showed that variance of SCA (VARsca) was greater than the variance of GCA (VARgca) for all measured traits except EASP, DFA, CC and DFS across low N and optimum N environments (Table 4.6). The variance of SCA x E (VARscaenv) was relatively higher than GCA x E (VARgcaenv) for all measured traits except CC, EASP and RL under low N and EPP, ASI, SG, CC, DFA, DFS, and RL under optimum conditions (Table 4.6). It was deduced from the variance components that, VARgca + VARsca for all response variables contributed 59.1 % to the total phenotypic variance for grain yield, 46.9 % for EPP, 58.9 % for PASP, 46.9 % for the ASI, and 38.8 % for SL across low N soil condition. Additionally, under optimum conditions, the same variance components accounted for 54.2 % of the total phenotypic variance for grain yield, 51.3 % for EPP, 58.5 % for SG (Table 4.6). VARgcaenv + VARscaenv also considerably contributed 23.8 % to the total phenotypic variance (VARp) for GY under low N environments and 46.4 % under optimum N conditions. Broad sense heritability estimates were high that is recording 66 % for GY, EPP, PASP, and SG under low N and optimum N conditions (Table 4.6). The lowest broad sense estimate was seen in PH (14 %) under low N and 16 % for PH across optimum conditions. The narrow sense heritability estimates for GY under low N showed 15 % as compared to 23 % under optimum N conditions and 55 % for EASP and 53% for DFS for low and optimum conditions respectively. Baker's genetic ratios of GCA: SCA for grain yield were closer to unity under low N as compared to grain yield under optimum N conditions (Table 4.6).

Table 4.6 Genetic variance estimates and heritability for GY and related traits

	GY	EPP	ASI	PASP	EASP	SG	CC	DFA	DFS	PH	SL	RL
Low N soil environments												
VARgca	1.11	0.76	0.93	0.64	2.15	0.67	0.97	2.37	2.21	1.78	0.87	0.77
VARsca	7.85	1.10	1.71	4.50	0.86	2.23	0.73	1.53	2.06	2.97	1.61	1.25
VARgcaenv	0.48	0.93	0.63	1.05	1.01	0.58	1.02	1.49	1.99	1.73	0.21	1.38
VARscaenv	3.13	1.15	1.75	3.74	0.67	2.96	0.77	2.09	2.17	2.02	1.99	0.97
2VARgca	2.21	1.52	1.85	1.28	4.31	1.34	1.95	4.73	4.43	3.57	1.74	1.54
2VARgca/Env	1.11	0.76	0.93	0.64	2.15	0.67	0.97	2.37	2.21	1.78	0.87	0.77
VARe/REnv	0.07	0.04	0.25	0.06	0.11	0.07	5.21	0.80	0.83	36.54	1.38	1.20
VARsca/Env	3.93	0.55	0.85	2.25	0.43	1.12	0.36	0.76	1.03	1.49	0.80	0.63
VARp	15.16	3.97	5.58	8.72	7.86	5.43	9.22	10.19	10.56	46.35	6.40	5.40
Narrow Sense	0.15	0.38	0.33	0.15	0.55	0.25	0.21	0.46	0.42	0.08	0.27	0.29
Broad Sense	0.66	0.66	0.64	0.66	0.66	0.66	0.29	0.61	0.61	0.14	0.52	0.52
Baker's ratio	0.68	0.49	0.58	0.53	0.88	0.44	0.66	0.89	0.89	0.83	0.42	0.62
Optimum N soil environments												
VARgca	0.94	0.59	1.15	0.70	1.33	0.38	2.10	3.26	3.06	1.98	1.77	1.00
VARsca	3.41	1.40	0.67	2.41	0.71	2.64	1.95	1.44	1.09	2.02	1.79	1.44
VARgcaenv	0.22	1.53	1.35	0.73	0.67	3.65	1.91	2.54	2.22	1.02	0.78	2.08
VARscaenv	3.50	1.12	0.91	2.04	1.23	2.71	1.39	1.86	1.57	1.76	1.98	1.55
2VARgca	1.88	1.17	2.29	1.40	2.65	0.76	4.20	6.53	6.13	3.97	3.53	2.00
2VARgca/Env	0.94	0.59	1.15	0.70	1.33	0.38	2.10	3.26	3.06	1.98	1.77	1.00
VARe/REnv	0.09	0.02	0.22	0.05	0.12	0.06	5.96	0.54	0.64	28.92	1.23	1.56
VARsca/Env	1.71	0.70	0.33	1.21	0.35	1.32	0.98	0.72	0.55	1.01	0.89	0.72
VARp	8.02	3.88	4.66	5.77	5.16	5.16	15.19	12.50	11.47	37.90	9.21	6.74
Narrow Sense	0.23	0.30	0.49	0.24	0.51	0.15	0.28	0.52	0.53	0.10	0.38	0.30
Broad Sense	0.66	0.66	0.64	0.66	0.65	0.66	0.40	0.64	0.63	0.16	0.58	0.51
Baker's ratio	0.58	0.51	0.80	0.50	0.70	0.52	0.88	0.94	0.94	0.83	0.80	0.78

4.6 Heterosis estimates of grain yield and yield related traits

Mid-parent heterosis for GY under low N condition varied from 733 % to -43 % and under the optimum condition ranged from 1036 % to 10 % but in all cases G9 under low N and G7 under optimum N recorded the highest mid-parent heterosis (Table 4.7,4.8 and 4.9). For EPP, mid-parent heterosis ranges from 3 % to 463 % and 10 % to 361 % under low and optimum conditions respectively. G19 and G20 recorded the least ASI under low and optimum conditions correspondingly. G13 rather displayed highest value for PASP under both low and optimum environments (Table 4.7, 4.8, and 4.9). EASP ranged from 100% to -33 % and 140 % to -40 % under low and optimum conditions. Also, SG ranged from 33 % to -41 % for low N and 42 % to -27 % for optimum N. G9 and G18 recorded the highest value for better-parent heterosis for GY under low and optimum N environments respectively (Table 4.7, 4.8, and 4.9). G20 and G19 also recorded the least ASI for heterobeltiosis under both low and optimum. EPP also recorded 526 % to -39 % and 361 % to -81 % under low and optimum. 40 % to -56 % and 50 % to -22 % were found to be the range under low and optimum environs. Moreover, 89 % to -47 % and 100 % to -50 % in low and optimum N conditions respectively were found to be the ranges (Table 4.7, 4.8, and 4.9). SG also displayed 33 % to -47 % and 42 % to -27 % as the range for low and optimum N conditions correspondingly. Economic heterosis revealed G20 and G23 had the highest value under low and optimum N conditions respectively (Table 4.7, 4.8, and 4.9). EPP revealed a range of -66 % to 11 % and -36 % to 37 % whereas G20 and G25 showed the least ASI under low and optimum environs respectively. PASP ranges from 31 % to -50 % and 17 % to -28 % for low and optimum conditions respectively whereas 70 % to -30 % and 12 % to -44 % was the range for EASP under low and optimum environments respectively. Lastly, SG also recorded 50 % to -33 % and 19 % to -37 % for low and optimum conditions (Table 4.7, 4.8, and 4.90).

Table 4.7 Mid-parent heterosis of single-cross hybrids evaluated under low and optimum N environments

	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM
HYBRIDS	**GY**	**GY**	**EPP**	**EPP**	**ASI**	**ASI**	**PASP**	**PASP**	**EASP**	**EASP**	**SG**	**SG**
G1	0.46	2.59	1.40	2.31	-0.27	-0.18	-0.13	-0.13	-0.04	-0.33	-0.09	0.00
G2	0.33	0.40	1.25	2.65	-0.33	-0.31	0.07	-0.07	-0.19	-0.19	0.08	-0.08
G3	0.43	0.98	0.42	1.03	-0.05	-0.16	0.26	0.26	0.08	0.33	-0.08	0.17
G4	-0.32	1.05	0.06	0.10	-0.05	-0.02	0.19	0.41	1.00	0.73	0.25	0.25
G5	2.00	2.44	1.16	1.64	0.20	-0.02	-0.21	0.03	0.05	0.71	0.08	0.08
G6	0.63	2.89	0.55	0.66	0.01	-0.30	-0.07	-0.07	0.14	0.05	-0.19	-0.11
G7	-0.43	0.91	2.68	0.65	0.10	0.10	0.26	0.19	0.62	0.05	0.11	-0.11
G8	-0.16	0.52	0.03	0.29	-0.17	-0.24	0.19	0.33	0.73	1.13	0.08	0.08
G9	7.33	7.99	2.36	2.84	-0.31	-0.31	0.48	0.85	-0.27	-0.33	-0.25	-0.08
G10	0.65	4.86	2.67	2.99	-0.33	-0.19	0.60	0.98	0.08	-0.17	-0.17	-0.17
G11	1.15	2.35	1.21	0.92	-0.16	-0.23	-0.06	0.46	-0.20	-0.40	-0.25	-0.08
G12	5.03	8.76	3.20	3.61	0.29	0.29	0.26	0.76	-0.27	-0.20	-0.41	-0.04
G13	0.18	1.37	1.99	1.20	-0.30	-0.30	1.37	1.37	-0.07	-0.20	0.33	0.41
G14	0.45	1.08	1.63	2.87	-0.22	-0.14	0.99	0.99	0.17	0.17	0.33	0.08
G15	0.55	0.86	3.00	2.02	-0.14	-0.08	0.47	0.69	-0.11	-0.19	0.25	0.08
G16	1.64	3.01	2.52	2.27	-0.18	-0.27	0.11	0.26	0.05	0.14	0.08	0.42
G17	1.27	1.90	0.34	0.67	-0.33	-0.12	0.11	0.33	-0.04	0.19	0.25	0.42
G18	5.90	10.36	2.55	2.97	-0.04	0.00	-0.09	-0.03	-0.04	-0.11	0.11	0.04
G19	4.40	5.77	1.14	1.20	-0.36	-0.44	-0.20	0.13	-0.33	-0.11	-0.33	0.04
G20	3.35	2.37	1.24	1.91	-0.43	-0.03	-0.41	0.19	0.05	0.43	-0.25	0.08
G21	0.37	1.25	1.75	1.52	-0.39	-0.25	0.04	0.11	-0.33	-0.08	0.08	0.08
G22	0.97	3.73	0.92	1.22	0.33	0.44	0.07	0.00	0.00	-0.08	0.19	0.04
G23	0.50	3.24	0.20	0.32	-0.27	-0.20	0.11	-0.04	-0.17	-0.25	0.19	-0.19
G24	0.94	1.38	0.21	0.57	0.71	0.62	0.17	0.42	0.33	0.22	0.17	0.33
G25	-0.31	0.37	0.21	0.36	0.00	0.07	0.08	0.33	-0.24	0.14	0.25	0.33
G26	0.98	2.73	2.28	2.91	-0.17	-0.13	0.09	-0.09	-0.25	-0.08	-0.07	-0.27
G27	0.04	0.72	1.44	3.10	0.67	0.93	0.13	0.33	0.11	0.44	0.04	0.41
G28	-0.21	0.94	0.52	1.24	0.24	0.33	0.07	0.20	0.05	0.33	-0.19	0.19
G29	0.26	0.33	1.17	0.50	0.00	-0.19	0.19	0.41	0.22	0.67	-0.04	0.19
G30	0.23	0.88	0.52	1.32	-0.27	-0.21	-0.41	0.04	-0.33	0.05	-0.41	-0.19

Continued

HYBRIDS	GY	GY	EPP	EPP	ASI	ASI	PASP	PASP	EASP	EASP	SG	SG
G31	-0.29	0.10	0.62	0.89	-0.13	-0.04	0.17	0.33	0.20	0.33	0.00	-0.17
G32	0.41	1.63	0.86	0.87	0.00	0.17	0.17	0.25	0.22	0.56	-0.17	0.00
G33	2.18	5.32	4.63	3.13	0.39	0.28	0.07	0.07	0.22	0.56	0.04	0.04
G34	2.23	3.14	2.03	1.77	-0.30	-0.20	-0.04	0.26	0.00	0.44	-0.04	-0.04
G35	0.51	1.84	1.79	1.95	0.33	0.10	0.25	0.50	0.83	1.00	0.08	0.25
G36	-0.07	0.19	2.31	0.82	-0.11	-0.11	0.33	0.42	0.73	1.40	0.25	0.00

Table 4.8 Better-parent heterosis of single-cross hybrids evaluated under low and optimum N environments

	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM
HYBRIDS	**GY**	**GY**	**ASI**	**ASI**	**EPP**	**EPP**	**PASP**	**PASP**	**EASP**	**EASP**	**SG**	**SG**
G1	-0.05	1.33	0.65	1.28	-0.27	-0.18	-0.13	0.13	-0.28	-0.50	-0.09	0.00
G2	-0.18	-0.14	-0.40	-0.38	0.65	1.73	0.07	-0.07	-0.27	-0.39	0.08	-0.08
G3	0.16	0.61	-0.18	-0.27	0.68	0.52	0.13	0.13	0.44	0.78	-0.08	0.17
G4	-0.35	0.95	-0.18	0.17	-0.39	0.51	0.07	0.27	0.25	0.08	0.25	0.25
G5	0.85	1.12	-0.18	0.83	2.89	0.82	-0.13	-0.06	-0.08	0.50	-0.13	-0.13
G6	0.18	1.81	-0.03	-0.33	0.32	0.57	-0.07	-0.07	0.00	-0.08	-0.27	-0.20
G7	-0.43	0.89	-0.15	-0.15	0.64	0.55	0.13	0.07	0.89	0.22	0.25	0.00
G8	-0.32	0.99	-0.21	-0.27	2.07	0.21	0.07	0.20	0.44	0.78	0.08	0.08
G9	6.37	6.95	-0.38	-0.38	1.19	2.36	-0.20	0.00	-0.33	-0.39	-0.25	-0.08
G10	0.22	3.35	-0.42	-0.30	1.94	2.50	-0.13	0.07	-0.28	-0.44	-0.17	-0.17
G11	0.43	1.23	-0.27	-0.33	-0.08	0.17	-0.40	-0.07	-0.33	-0.50	-0.25	-0.08
G12	4.33	7.70	-0.12	-0.12	5.26	3.61	-0.33	-0.22	-0.39	-0.33	-0.47	-0.13
G13	-0.01	0.98	-0.33	-0.33	0.40	0.47	0.40	0.40	-0.22	-0.33	0.20	0.27
G14	-0.05	0.36	-0.39	-0.33	1.56	1.76	0.13	-0.06	-0.22	-0.22	0.33	0.08
G15	-0.08	0.11	-0.18	-0.12	0.46	1.01	-0.13	0.00	-0.33	-0.39	0.25	0.08
G16	0.81	1.75	-0.36	-0.43	5.01	2.27	0.00	0.13	-0.27	-0.20	0.08	0.42
G17	0.43	0.82	-0.48	-0.31	2.52	0.07	0.00	0.20	-0.13	0.33	0.25	0.42
G18	5.84	10.25	-0.38	-0.36	2.02	2.48	-0.17	0.07	-0.13	-0.20	0.25	-0.07
G19	3.09	4.13	-0.40	-0.48	0.38	0.59	-0.20	0.13	-0.40	-0.20	-0.40	-0.07
G20	1.69	1.08	-0.60	-0.31	0.99	1.28	-0.47	0.07	-0.27	0.00	-0.25	0.08
G21	-0.21	0.29	-0.48	-0.36	0.37	0.82	-0.07	0.00	-0.47	-0.27	0.08	0.08
G22	0.24	1.98	0.00	0.08	0.27	0.35	-0.11	-0.17	0.00	-0.08	0.07	-0.07
G23	0.12	2.16	-0.39	-0.33	0.17	0.09	0.00	-0.13	-0.17	-0.25	0.07	-0.27
G24	0.86	1.29	0.50	0.42	-0.01	0.18	0.17	0.42	0.00	-0.08	0.17	0.33
G25	-0.46	0.07	-0.10	-0.03	-0.09	0.11	0.08	0.33	-0.33	0.00	0.25	0.33
G26	0.51	1.71	-0.44	-0.42	0.54	1.61	0.00	-0.17	-0.25	-0.17	-0.07	-0.27
G27	-0.36	1.86	0.39	0.61	1.81	1.93	-0.06	0.11	-0.17	0.17	0.17	0.27
G28	-0.55	2.84	-0.13	-0.07	0.35	0.49	-0.11	0.00	-0.08	0.17	-0.08	0.07
G29	-0.08	1.03	-0.25	-0.39	0.01	0.33	-0.11	0.27	-0.08	0.25	-0.13	0.07
G30	-0.21	3.14	-0.33	-0.28	0.93	1.32	-0.56	-0.07	-0.42	-0.08	-0.47	-0.27

Continued

HYBRIDS	GY	GY	ASI	ASI	EPP	EPP	PASP	PASP	EASP	EASP	SG	SG
G31	-0.43	2.05	-0.30	-0.23	0.52	0.68	0.17	0.33	0.00	0.11	0.00	-0.17
G32	0.18	1.21	0.00	0.17	-0.07	0.20	0.17	0.25	-0.08	0.17	-0.17	0.00
G33	1.19	3.36	0.04	-0.04	3.19	2.62	-0.11	-0.11	-0.08	0.17	-0.07	-0.07
G34	1.78	2.56	-0.42	-0.33	1.19	1.00	-0.13	0.13	-0.25	0.08	-0.13	-0.13
G35	0.23	1.31	0.17	-0.04	1.81	1.32	0.25	0.50	0.83	1.00	0.08	0.25
G36	-0.36	-0.18	-0.20	-0.20	0.71	0.32	0.33	0.42	0.44	1.00	0.25	0.00

Table 4.9 Economic heterosis of single-cross hybrids evaluated under low and optimum N environments

	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM	LOW	OPTIMUM
HYBRIDS	GY	GY	EPP	EPP	ASI	ASI	PASP	PASP	EASP	EASP	SG	SG
G1	-0.51	-0.15	-0.47	0.06	-0.04	-0.04	-0.19	0.00	0.30	-0.44	-0.09	-0.25
G2	-0.58	-0.69	-0.46	0.28	0.00	-0.07	0.00	-0.22	0.10	-0.31	0.08	-0.31
G3	-0.40	-0.42	-0.66	-0.29	0.08	-0.14	0.06	-0.06	0.30	0.00	-0.08	-0.13
G4	-0.66	-0.29	-0.53	-0.30	0.08	0.00	0.00	0.06	0.50	-0.19	0.25	-0.06
G5	-0.04	-0.23	-0.52	-0.15	0.08	-0.21	-0.19	-0.06	0.10	0.12	0.08	-0.19
G6	-0.39	0.02	-0.47	-0.18	0.40	-0.14	-0.13	-0.22	0.20	-0.31	-0.08	-0.25
G7	-0.70	-0.31	0.11	-0.28	0.12	0.00	0.06	-0.11	0.70	-0.31	0.25	-0.25
G8	-0.43	-0.28	-0.65	-0.36	0.04	-0.14	0.00	0.00	0.30	0.00	0.08	-0.19
G9	0.15	-0.13	-0.53	-0.21	0.04	-0.07	-0.25	-0.17	0.20	-0.31	-0.25	-0.31
G10	-0.61	-0.02	-0.48	-0.18	-0.24	-0.18	-0.19	-0.11	0.30	-0.37	-0.17	-0.37
G11	-0.33	-0.27	-0.25	-0.05	-0.04	-0.21	-0.44	-0.22	0.20	-0.44	-0.25	-0.31
G12	-0.16	-0.05	-0.49	-0.19	0.16	0.04	-0.37	-0.22	0.10	-0.25	-0.33	-0.19
G13	-0.77	-0.68	-0.28	-0.23	-0.04	-0.14	0.31	0.17	0.40	-0.25	0.50	0.19
G14	-0.52	-0.52	-0.47	0.13	-0.20	-0.21	0.06	-0.06	0.40	-0.13	0.33	-0.19
G15	-0.23	-0.35	-0.03	0.06	0.08	0.04	-0.19	-0.17	0.20	-0.31	0.25	-0.19
G16	-0.42	-0.38	-0.43	-0.24	0.08	-0.14	-0.06	-0.06	0.10	-0.25	0.08	0.06
G17	-0.33	-0.40	-0.52	-0.12	-0.12	0.04	-0.06	0.00	0.30	0.00	0.25	0.06
G18	-0.17	-0.04	-0.50	-0.19	0.04	-0.04	-0.06	-0.11	0.30	-0.25	0.25	-0.13
G19	-0.05	-0.17	-0.44	-0.17	0.00	-0.21	-0.25	-0.06	-0.10	-0.25	-0.25	-0.13
G20	0.37	-0.26	-0.51	-0.07	-0.32	0.04	-0.50	-0.11	0.10	-0.06	-0.25	-0.19
G21	-0.34	-0.24	-0.28	-0.04	-0.12	-0.04	-0.13	-0.17	-0.20	-0.31	0.08	-0.19
G22	-0.42	-0.02	-0.34	0.10	-0.04	-0.07	0.00	-0.17	0.20	-0.31	0.33	-0.13
G23	-0.47	0.04	-0.45	-0.11	-0.12	-0.14	-0.06	-0.28	0.00	-0.44	0.33	-0.31
G24	-0.05	-0.18	-0.49	-0.04	0.44	0.21	-0.13	-0.06	0.20	-0.31	0.17	0.00
G25	-0.55	-0.37	-0.44	-0.09	0.08	0.04	-0.19	-0.11	-0.20	-0.25	0.25	0.00
G26	-0.65	-0.54	-0.21	0.37	-0.20	-0.25	0.12	-0.17	-0.10	-0.31	0.17	-0.31
G27	-0.67	-0.62	-0.51	0.20	0.00	0.04	0.06	0.11	0.00	-0.19	0.17	0.19
G28	-0.62	-0.35	-0.63	-0.22	0.04	0.00	0.00	0.00	0.10	-0.13	-0.08	0.00
G29	-0.53	-0.65	-0.30	-0.30	0.08	-0.21	0.00	0.06	0.10	-0.06	0.08	0.00
G30	-0.34	-0.29	-0.45	0.22	-0.04	-0.07	-0.50	-0.22	-0.30	-0.31	-0.33	-0.31

Continued

HYBRIDS	GY	GY	EPP	EPP	ASI	ASI	PASP	PASP	EASP	EASP	SG	SG
G31	-0.52	-0.48	-0.48	-0.12	-0.16	-0.18	-0.13	-0.11	-0.10	-0.37	0.00	-0.37
G32	-0.44	-0.27	-0.33	-0.02	-0.04	0.00	-0.13	-0.17	0.10	-0.13	-0.17	-0.25
G33	-0.30	-0.02	-0.21	-0.16	0.00	-0.18	0.00	-0.11	0.10	-0.13	0.17	-0.13
G34	-0.10	-0.20	-0.21	0.05	-0.16	-0.14	-0.19	-0.06	-0.10	-0.19	0.08	-0.19
G35	-0.37	-0.17	-0.38	-0.05	0.12	-0.18	-0.06	0.00	0.10	-0.25	0.08	-0.06
G36	-0.46	-0.52	-0.13	-0.31	-0.04	-0.14	0.00	-0.06	0.30	0.12	0.25	-0.25

Table 4.10 Pearson product correlation between grain yield and agronomic characters for Low and Optimum N environments

	GRAIN YIELD	
	LOW N	**OPTIMUM N**
PH	0.3258***	0.3506***
EH	0.285***	0.273***
PASP	-0.3137***	-0.4692***
DFA	-0.216**	-0.3653***
DFS	-0.1984**	-0.3881***
ASI	-0.0624**	-0.067
CC	0.16623	0.0599
SG	-0.216***	-0.29833***
SL	0.16715**	0.2365***
EPP	-0.122	-0.144
RL	0.1618*	0.22572**
HC	-0.1316*	0.07428
EASP	-0.1896**	-0.224***

Table 4.10 shows the phenotypic correlations (r) of GY with secondary variables in low and optimum N environments. Under low N, GY is positively correlated ($p < 0.01$) with plant height (r= 0.33) and ear height (r= -0.29), but negatively correlated (r=-0.21, -0.19, -0.31, -0.21, -0.12 respectively) with days to 50% anthesis, days to 50% silking, plant aspect, stay green characteristic, husk cover, and ears per plant. The value of a shorter ASI for greater grain yield is evidenced by the negative correlation between grain yield and ASI.

CHAPTER FIVE

5.0 DISCUSSIONS

5.1 Variance analysis of grain yield and other agronomic characters

The existence of genetic variability is of utmost importance for progeny from selection for improved grain yield under low and optimum N. The varying response of cultivars to different environmental conditions constitutes a major problem in the identification of superior maize genotypes (Wegary, 2014 and Owusu *et al.,* 2017) and this increases the chances of selection of certain crosses for further improvement. The significance of the hybrids and environment for the grain yield and related traits across all the environments suggests there is the presence of adequate variability among all the genotypes in the study (Badu-Apraku *et al.,* 2015). The lack of significance (P>0.05) of genotype (G) x environment (Env) interaction in both low N and optimum N conditions except EASP, SG, DFA, and DFS indicates the consistency in the performance of the single-cross hybrids in those environments (Table 4.1). These results are in correspondence with the results of Badu-Apraku *et al.* (2011 and 2013). The detected higher significant (P<0.01) mean squares of GCA over SCA effect for GY and agronomic traits under low N environments indicated the preponderance of additive gene action over non-additive gene action in the inheritance of grain yield (Table 4.1) and this confirms the results of Ribeiro *et al.* (2020) and Ige *et al*. (2020). The predominance of GCA over SCA for GY and agronomic traits further recommended that early generation testing could be feasible and that selection of potential single-cross hybrids through prediction from GCA effects alone could be plausible. This is in agreement with the findings of Badu-Apraku *et al.* (2015), Owusu *et al.* (2017), and Tesfaye *et al.* (2019). The combined analysis across low N environments in Fumesua and Ejura showed that additive gene action was responsible for the inheritance of GY, PASP, EASP, DFS, and PH, same gene action occurred in GY, CC, DFA, DFS, PH, SL, and RL under optimum N conditions. In the analysis under optimum N, significant ($P<0.05$) SCA mean square was observed for anthesis and silking date showed the importance of non-additive gene actions in governing this trait (Table 4.1). The finding of this study is in agreement with the findings of Melkamu (2013), Shushay *et al*. (2013), Tamirat *et al*. (2014), and Girma *et al*. (2015) who reported significant mean squares due to SCA for days to anthesis and silking.

Moreover, the higher mean square of SCA over GCA observed for GY and some agronomic under optimum N suggested that the non-additive gene action played a role in the inheritance of such traits (Table 4.1). The selection of these characters for further development could be feasible through hybridization, recurrent selection, and backcrossing methods. This is synonymous to Badu-Apraku *et al*. (2015) results who suggested that the significant mean squares of GCA and SCA for GY and agronomic traits could be associated with the action of both additive and non-additive genes and further argued that traits improvement could be achieved through backcrossing, hybridization and recurrent selection methods developing synthetics and hybrid varieties (Table 4.1). No significant ($P>0.05$) GCA x environment interaction observed for most characters under low and optimum N indicated that GCA effects of the parentals for these traits were not controlled by the environments. Musila *et al.* (2010) mentioned similar results for diallel crosses of quality protein maize inbred lines evaluated across stress and non-stress environments. Again, Musila *et al.* (2010) reiterated that the magnitudes of GCA x environment mean squares were consistently smaller than the corresponding GCA mean squares, suggesting the interaction effects may be of less importance as compared with the main effects that would not prevent detection of the best and the worst lines for GCA effects. Thus, there was consistency in the performance of the parentals across all N environments.

SCA x environment effects were not significant (P>0.05) for GY and all agronomic traits under both low and optimum N conditions, revealing the stability of SCA effects of the hybrids across the research environments (Table 4.1) and this is in correspondence with Ifie *et al*. (2015) reported findings who found stability of single-cross hybrids from CIMMYT early maturity maize inbred lines under low N environments.

5.2 Estimates of General and Specific Combining ability effects on grain yield and related traits.

P3 was the best general combiner for grain yield across both optimum and low N environments, indicating that the line contributed to increased grain yield in its crosses under all conditions and this is in agreement with Wegary *et al.* (2014) who reported that the GCA effect of a parent is a relevant indicator of producing superior genotypes like the hybrid G20 which was the best cross combination under low N (Table 4.2 and 4.3). On the other hand, inbred lines P1 and P9 showed consistently poor GCA effects under both N conditions (Table 4.2) and this supports the assertion made by Betrán *et al*. (2003) who reported that the existence of some inbred lines with consistent GCA effects across environments implied that the genetic systems controlling grain yield under different stress and non-stress conditions are at least partially the same. Similar findings were reported by Musila *et al*. (2010) for quality protein maize diallel entries evaluated under low-N, drought, and optimal environments. The parental lines P3 and P4 under both low and optimum N environments were the best general combiners for the anthesis-silking interval (Table 4.2 and 4.3). Murtadha *et al.* (2018) reported that short ASI is a good indicator of tolerance to induced stress. Reduced anthesis-silking interval is a sure indicator of low N tolerance; therefore, P3 and P4 could be the desirable genetic sources of low N tolerance (Table 4.2 and 4.3). The significant ($P<0.05$) positive GCA for GY seen in parental lines P3 under low N and P5 and P6 under optimum N condition and P3 across N environments (Table 4.2), indicates the possibility of introducing promising alleles from these parental lines to their progenies and could be beneficial for breeding to improve GY through hybridization. Akinwale *et al*. (2014) mentioned that cultivars with remarkable GCA and SCA for grain yield could be utilized for the development of heterotic populations for further improvement and for developing high yielding synthetic varieties and hybrids. The significant positive GCA for DFS observed for inbred lines P7 and P8 under low N and P2 and P7 under optimum N shows that these inbred lines could transmit favorable alleles to their progenies and be subsequently used to improve silking date (Table 4.2). Moreover, the significant positive GCA for GY, PASP, EASP, DFA, DFS, PH, and RL observed for some parental lines suggest that these lines could be useful for breeding to develop these traits. These are in agreement with the results of Badu-Apraku *et al*. (2013) and Owusu *et al*. (2017) who observed significant negative GCA for DFS, DFA, and PH and implied a possible selection of traits for improvement through hybridization. The significant negative GCA for RL for P1 under both low N and optimum N and P4 alone under optimum N suggests a likelihood of transmitting favorable alleles that could be useful for breeding to improve tolerance to root lodging. Significant negative GCA effect for P7 and P9 alone under optimum N environs for SL indicates the chance of introducing favorable alleles, which could be useful to plant breeders to breed for resistance to stem lodging. Significant and negative GCA effects were seen for the stay-green characteristic of inbred P2 across N environments (Table 4.2) indicating that the parental line will transmit the trait to its progenies or will slow down the rate of leaf senescence and this was seen in the results of Badu-Apraku *et al*. (2015).

The significant positive SCA for GY displayed for hybrid G20 under low N and G6 under optimum N was a sign of transmission of appropriate alleles from parents toward improved GY performance of these hybrids (Table 4.3 and 4.4). Annor and Badu-Apraku (2016) suggest that such hybrids should be evaluated in MET for yield stability before commercialization.

In most cases, however, cross combinations with favorable SCA estimates for grain yield contain parents with high GCA effects for the same trait, indicates the increased concentration of favorable alleles. Accordingly, the best combinations with favorable SCA estimates for grain yield were the crosses G20, G5, G29, G24 and G9, G6 and G28, under low-N and optimal environments. G20 was the most desirable cross combination under low N, as it showed desirable SCA effects for grain yield, days to 50 % anthesis, days to 50 % flowering, and anthesis-silking interval.

5.3 Heritability estimates and genetic variability of grain yield and agronomic traits

The variance estimates of GCA and SCA effects and heritability for grain yield and other agronomic traits varied due to the varying genetic composition of the set of inbred lines resulting from environmental effect and genotype x environment interactions. In Fumesua and Ejura, the changes were characterized by intermittent and uneven rainfall distribution, as well as an increase in air temperatures in relation to crop growth and development. The observed genetic ratios of GCA: SCA demonstrated stronger prediction of the performance of all traits of single-cross hybrids across locations based exclusively on GCA effects since the computed ratios were closer to unity (Baker, 1978). Under low and optimum N, GY and other agronomic characters had estimated ratios that were closer to unity, meaning that GCA impacts were more important than SCA, indicating the preponderance of additive gene effects and hence the prospect of genetic improvement of these traits. The results of this study revealed that the predictability ratios (PR) for EASP, DFA, DFS, and PH under low N and optimum N were high but GY (ratio ≤ 0.70) was moderately high (Table 4.6). Therefore, the possibility of determining progeny performance for grain yield from parent GCA alone is high under the environmental conditions used for the current study. Apart from the less environmental effect, the high H^2 expressed for GY, EPP, ASI, PASP, SG, DFA, and DFS under low N conditions, as well as the significant mean square estimate of the GCA effect (Table 4.1 and 4.6), highlight the fact that additive gene effect was the main factor accounting for variation in the inheritance of these traits and further suggest selection in early segregating generation. These results indicate that the phenotypic variance is larger than the genotypic variance, implying that selection based on phenotypic expression of these traits may be possible. This conclusion is consistent with the findings of Owusu *et al*. (2017), Akbar *et al*. (2008), and Kashiani *et al*. (2010), who found that GY and DFS traits have a higher share of broad-sense heritability. However, the low h^2 for GY under both low and optimum N conditions was not surprising since GY is a complex polygenic trait greatly influenced by the environment and this implies that selection of genotypes from early segregating generations for GY may be difficult due to the high influence of other genes in the expression of the total phenotypic variance. For this reason, selection based on individual plants for GY would be more effective when carried out on later generations instead of early ones. Kormsa-art *et al* (2002) indicated that selection for low heritability traits or those controlled by dominance is ineffective when carried out in early generations. This is in line with the observations of Mhike *et al*. (2011) and Bello *et al*. (2012), who found that GY is a product of many complex traits, and so direct selection of this trait may not be desired because it is influenced more by the environment. They suggested that indirect selection of other yield-related features could be used to boost yields further.

5.4 Heterosis and correlation estimates of grain yield and yield-related traits

Bisen *et al*. (2020) reported that though plant breeders have extensively explored and utilized heterosis in enhancing the yield of crops. The exploitation of hybrid vigor depends primarily on the magnitude of heterosis and feasibility of the hybrid seed production at commercial scale, the extent of heterosis depends generally on the wide genetic diversity among the parents and the magnitude of that superiority of hybrid over better parents which may be either due to dominance or overdominance or even combined effect of two (Bisen *et al.,* 2020). In a breeding program, the superiority of F1s over either mid-parent, a better parent, or standard check aids in determining the feasibility of commercial exploitation of heterosis. G9 had the highest value for better parent, mid-parent heterosis, and grain yield as compared to the local checks under both low and optimum N environments. G7 top economic heterosis as compared to all the hybrids for grain yield. Badu-Apraku *et al*. (2013) and Ribeiro *et al*. (2020) mentioned that improvement in grain yield is less reliable through direct selection under stressed environments and it is more effective in a selection program to use component traits that have a strong correlation with grain yield for indirect selection for improved yield. Badu-Apraku *et al*. (2012) mentioned that PASP, EASP, and SG could be used as selection criteria for identifying low N tolerant genotypes. Due to the negative correlation between grain yield and anthesis-silking interval, the grain yield of hybrids with low ASI is likely to be low N tolerant. A classic example is G20 (2.53 t/ha) which displayed a higher grain yield over all other hybrids and checks and a short ASI under low N environments across Fumesua and Ejura.

CHAPTER SIX

6.0 CONCLUSION

The greater proportion of mean squares of GCA over SCA effects for grain yield and agronomic traits suggested that additive gene action was the main contributor to the inheritance of grain yield in the single-crosses evaluated in all the low and optimum N environments. Additive gene action together with high heritability indicates that selection for greater grain yield would be effective and as such hybridization, backcrossing and recurrent selection in hybrid development will be successful. It should be stressed that grain yield is controlled by multiple genes and environment so the use of secondary characters that are highly correlated could be effective means of indirectly selecting genotypes for grain yield. P3 was the best general combiner under low nitrogen soil conditions (top significant positive GCA effect). Among all of the hybrids, G5, G20, G9, G19, G24, and G29 were the best combinations for grain yield under low N environments. G3, G7, G9, G10, G13, G17, G18, G19, G28, G29, G30, G31, G32, G35, and G36 were identified to be low N tolerant single-cross hybrids in the study whereas the remaining eleven (11) genotypes were susceptible to low N soils. G9 and G20 were the best performing hybrids over all the local checks under low N conditions in Fumesua and Ejura. G9 compared to all the other hybrids which had the highest mid-parent and better-parent heterosis value was second to G20 in economic heterosis, good SCA for grain yield, a better mean grain yield, and tolerant to low nitrogen soils.

7.0 RECOMMENDATIONS

The study's propitious hybrids should be thoroughly tested in several locations before being adopted since environmental conditions such as drought, erratic rainfall and high temperature affected the yields drastically. It is necessary to assess the consistency of the stability of the crosses across years. To enhance the number of high yielding tolerant hybrids in Ghana, further selection should be done in both low and optimum N conditions.

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APPENDIX I

Mean Squares of ANOVA of grain yield and related traits under N environments of the thirty-six (36) diallel crosses plus checks

Source of Variation	GY (t/ha)	HC	ASI	PASP	EASP	SG	EPP	DFA	DFS	PH	SL	RL
Low N environments												
Env	0.00012	6.34***	4.00	29.40***	4.00*	11.27***	0.07	1480.07***	1330.10***	6394.27***	21.00	114.82***
Entry	0.75*	0.59	2.39*	1.03***	0.54	1.03***	0.36*	18.87***	19.54***	453.26***	13.59**	9.27
Blk (Env*Rep)	0.78*	0.85*	1.13	0.25	0.69	0.52	0.40*	7.02	8.81**	371.85**	19.59***	9.59
Rep (Env)	0.51	1.13	1.84	0.55	1.13	1.03*	0.55*	27.34***	35.52***	759.13**	60.89***	14.53
Env*Entry	0.16	0.71	1.31	0.26	0.46	0.40	0.27	6.43	5.69	169.65	7.13	6.52
Error	0.36	0.50	1.40	0.38	0.62	0.41	0.21	4.45	4.28	182.79	7.20	6.29
Optimum N environments												
Env	3.98**	0.10	10.00**	0.15	10.84***	21.00***	2.81***	889.35***	710.70***	26729.48***	576.60***	63.04**
Entry	1.34***	0.59**	1.27	0.62***	0.93	1.07***	0.12	17.71***	16.19***	423.00***	16.86***	16.68**
Blk (Env*Rep)	1.08***	0.51*	0.66	0.67***	1.04	0.94***	0.14	5.19*	5.81*	312.03**	12.96**	12.94
Rep (Env)	8.15***	0.63	8.17***	4.33***	2.37**	2.89***	0.30	37.33***	77.22***	2120.28***	22.75**	22.13*
Env*Entry	0.69*	0.44	1.90	0.22	0.95	0.50*	0.11	5.92***	7.26***	165.92	5.23	13.18*
Error	0.42	0.31	1.35	0.28	0.67	0.29	0.13	2.80	3.34	154.73	5.94	8.41

*****, ******, ******* is the significance at 0.05, 0.01, 0.001 probability levels respectively, **Rep (Env):** Replicate within the environment, **Env**: Environment, **Blk (Env*Rep):** Block within replicate x environment **SE**: Standard error **GY**: Grain yield in t/ha, **ASI**: Anthesis Silking interval, **PASP**: Plant Aspect, **EASP**: Ear Aspect, **SG**: Stay-green characteristic, **CC**: Chlorophyll content, **DFA**: Days to 50 % anthesis, **DFS**: Days to 50 % Silking, **PH**: Plant Height, **SL**: Stem lodging, **RL**: Root lodging and **HC:** Husk cover