UNIVERSITY OF CAPE COAST

GENETIC DIVERSITY AND BREEDING VALUE OF OKRA (*Abelmoschus esculentus* (L.) GERMPLASM FOR TOLERANCE TO TWO OKRA VIRAL DISEASES UNDER LOW AND HIGH NITROGEN CONDITIONS

FELIX KUOR

2023

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BY

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Thesis submitted to the Department of Crop Science of the School of Agriculture, College of Agriculture and Natural Sciences, University of Cape Coast, in partial fulfillment of the requirement for the award of Doctor of Philosophy degree in Crop Science (Plant Breeding)

NOVEMBER, 2023

DECLARATION

Candidate's Declaration

I hereby declare that this thesis is the result of my own original research and that no part of it has been presented for another degree in this university or elsewhere.

Candidate's Signature …… Date …….

Name: Felix Kuor (AG/CSD/19/0008)

Supervisor's Declaration

We hereby declare that the preparation and presentation of the thesis were supervised in accordance with the guidelines on supervision of thesis laid down by the University of Cape Coast.

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ABSTRACT

Okra is a significant multipurpose vegetable crop cultivated extensively across the world. However, the productivity of the crop is constrained by abiotic (low N) and biotic (okra mosaic and leaf curl diseases) stresses. The excessive dependence on inorganic chemicals to combat viral diseases and low-N is harmful to the environment and unsustainable. Breeding for varieties tolerant to okra mosaic diseases (OMD) and leaf curl diseases (OLCD) with high N-use efficiency is the most practical and long-term strategy for reducing the losses caused by viruses and low-N. An assessment of genetic diversity and breeding value of okra germplasm for tolerance to okra mosaic and leaf curl virus diseases under low and high-N was carried out to identify hybrids and genotypes tolerant to low-N and the two viral diseases. Hundred okra germplasm were sourced, characterized and screened from Ghana's diverse agro-climatic and production regions. Twelve superior genotypes were selected based on tolerance to biotic and abiotic stresses and yield performance. Thirty-six (36) hybrids were generated from the twelve (12) germplasms using the North Carolina Design II mating scheme (NCD II). The 36 single cross hybrids together with four checks and the 12 parental genotypes were evaluated under low nitrogen (30 kg/ha) and high nitrogen (100 kg/ha) at two different locations, viz., Jacobu and Akumadan, during the major and minor growing seasons of 2021. The results of the diversity studies indicated wide genetic variability among the 100 okra germplasm studied, and 27 out of the 100 collected germplasms were duplicates. The parental genotype (Tamale 2E) was identified as the best low-N tolerant genotype with immunity against OLCD, OMD, and *Podagrica* spp. infestation under low-N environments. Similarly, Hilhaho × Paapa and Tamale 2E × G1 hybrids were identified as high-yielding, low-N tolerant hybrids and best-specific combiners. Also, single cross hybrid Paapa × Mampong had immunity against OMD, while hybrid cross Asontemtiatia × Paapa was the most resistant hybrid against OLCD under low-N conditions. Moreover, the study concluded that the additive gene effect was more significant than non-additive gene effects for the studied traits. Furthermore, maternal (cytoplasmic) effects influenced the inheritance of fruit yield and most yield components.

KEY WORDS

Characterization

Combining Ability

Genotypic coefficient of variation

Genetic Diversity

Germplasm

Simple Sequence Repeats

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DEDICATION

This work is entirely dedicated to my mother, Felicitas Kuor Tengan, my late father of blessed memory, Mr. Octavio Kuor and my late brothers and sister, who couldn't wait despite their insatiable quest to see me attain higher education. May their souls rest in eternal salvation.

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LIST OF ABBREVIATIONS

AFLPs	Amplified Fragment Length Polymorphisms
ANOVA	Analysis of Variance
CSIR-CRI	Council for Scientific and Industrial Research-Crops Research Institute
DNA	Deoxyribonucleic acid
FAO	Food and Agriculture Organization
FAOSTAT	Food and Agriculture Organization Statistics
GCA	General combining ability
GEI	Genotype by environment interaction
High-N	High soil nitrogen
IPGRRI	International Plant Genetic Resources Research Institute
Low-N	Low soil nitrogen
MOFA	Ministry of Food and agriculture NUE: Nitrogen Use Efficiency
NARP	National Agriculture Research Project
NCD II	North Carolina design II
NUE	Nitrogen Use Efficiency
OLCD	Okra leaf curl disease
OMD	Okra mosaic disease
PCR	Polymerase chain reaction
PIC	Polymorphic information content
RELPs	Restriction Fragment Length Polymorphisms
RNA	Ribonucleic acid
SCA	Specific Combining Ability SSA: Sub-Saharan Africa
SNPs	Single Nucleotide Polymorphisms
SSRs	Simple Sequence Repeats

CHAPTER ONE

1.0 GENERAL INTRODUCTION

Okra (*Abelmoschus spp,* (L) Moench) is one of the most important vegetable crops cultivated extensively across the tropical and subtropical regions of the world (Eshiet and Brisibe, 2015; Ali *et al.,* 2014; Bisht and Bhat, 2006). The crop belongs to the class dicotyledonae; order Malvales, and family Malvaceae (Schippers, 2000). In the Malvaceae family, it is the sole type of vegetable grown (Santos, 2012). The crop is called okra by the Americans and lady's finger by the British (Sinnadurai, 1992; Anwar *et al.,* 2011). The global estimation of the number of okra accessions is about 2,283, of which 2,029 originate from Africa, and 1,769 are from West Africa (Hamon and Van Slotten, 1989). The centre of origin of okra is still not yet known. Nonetheless, India, West Africa and Southern Asia have high genetic diversity (Hamon and Van Slotten, 1989). According to current statistics, global okra production as of 2020 was 9.96 million tons, with India leading the production with 6.18 million tons, followed by Nigeria (1,837,904 tons), Mali (659,809 tons), Sudan (315,812 tons), Cote d'Ivoire (188,736 tons) whiles Ghana recorded 67, 606 tons (FAOSTAT, 2020). Okra fresh pods are grown on an estimated 2 million hectares (ha) worldwide, with a yearly production of 9 million tons (FAO, 2018). The African continent produces 32.8 percent of all okra on the globe. Over 75% of overall okra output in Sub-Saharan Africa (SSA) comes from West and Central African countries (Kumar and Reddy, 2016). In terms of tonnage, the largest production regions in Ghana are Brong Ahafo, Ashanti, Northern, Volta, Greater Accra, and Central (NARP, 1993).

Okra holds a prominent position among vegetables because of its many and varied uses, including nutritional, therapeutic, and industrial value (Reddy *et al.*, 2013). The principal fatty acids found in okra seed oils are linoleic (49.54 percent), palmitic (28.60 percent), oleic (16.81 percent), stearic (3.57 percent), and linolenic (1.48 percent) (Mihretu *et al*. 2014). The seeds are a rich source of protein (22.14%), amino acids (i.e., lysine and tryptophan), fibre, vitamins (i.e., A, C and K), and mineral elements (i.e., calcium, potassium, sodium, and magnesium) (Sanjeet *et al*. 2010). The nutritional profile of okra makes it an essential source of nourishment to reduce malnutrition in Asian and Sub-Saharan African countries. Okra consumption provides several human health benefits, including lowering blood sugar levels and serum cholesterol (Gemede *et al*., 2015). Additionally, dried okra can be kept and utilized in soup. Okra is mainly used in our sub-region because of its high mucilage content and is employed to thicken soup (Schippers, 2000). Mucilage is found in most parts of the okra plant and is associated with other complex substances, such as tannins (Sengkhamparn *et al.*, 2009; Woolfe *et al.*, 1977).

Despite the potential of okra and the significant contribution by Sub-Saharan Africa (SSA) to worldwide okra production, the region's average yields are modest. In West Africa, okra productivity in farmers' fields is generally low, averaging 2.5 tons/ha, as opposed to over 6.2 tons/ha in East Africa and 8.8 tons/ha in North Africa (FAO, 2018). These low and variable yields in SSA are attributed to biotic and abiotic factors such as poor management practices (Alake, 2020), including soil fertility, incidence of viral diseases, pest infestation and drought. These considerably negatively impact

economic production due to poor fruit quality and a decreased market premium. Of these limiting factors, the incidence of viral disease infections, poor soil fertility, and deficient nitrogen are prominent.

The okra plant is susceptible to at least 19 viral diseases, with okra leaf curl disease (OLCD) and okra mosaic diseases (OMD) documented as the major diseases in Ghana (Bi-Kusi, 2013; Asare-Bediako *et al.*, 2014a, b). Okra leaf curl virus is transmitted by the whitefly (*Bemisia tabaci*), whereas okra mosaic virus is transmitted by insects belonging to *Podagrica* species (Brunt *et al.*, 1996). According to reports, these pests spread these infections through eating habits (Jose and Usha, 2003). Okra leaf curl virus infection can cause yield losses of up to 80% (Basu, 1995), whereas Okra mosaic virus infection has been reported to cause yield losses of up to 90% (Alegbejo *et al*., 2008). These viruses inflict significant economic losses through their interference with plant physiology and fruit growth, which result in distortions and smaller fruits. Symptoms of Okra leaf curl virus infection include the curling of leaves, yellowing of leaves, leaf distortion, stunted growth and reduced yield. The Okra mosaic virus also induces mosaic, vein chlorosis, banding and stunted growth (Krishnareddy *et al.*, 2003). Farmers are forced to employ synthetic chemicals like Attack, Consider, Golan, and many more pesticides to manage insect pests and viruses that affect okra. The excessive use of these synthetic compounds harms the environment, poses a risk to consumer health, and can result in the death of unintended animals. The most viable and long-lasting strategy for reducing the losses caused by these viruses is using resistant/tolerant cultivars.

Poor soil nutrition, particularly deficit soil N, is a significant abiotic stress affecting most vegetables, including okra productivity (Siemonsma & Kouame, 2004). Nitrogen and phosphorus are usually the most limiting nutrients in many African soils and are often simultaneously deficient. However, nitrogen is the first limiting nutrient in okra production that greatly influences crop growth and pod yield (Kumar *et al*., 2017). In SSA, continuous farming without proper fertilizer application has contributed to a decline in critical soil nutrients needed for plant growth (Sanchez, 2010). During periods of abundant rainfall, the leaching of soil nitrogen beyond the plant root zones causes nitrogen stress (Bello *et al.*, 2011). Poor weed control and crop residue removal for fuel and animal feeds also worsened the soil nitrogen deficiency (Noelle *et al*., 2017). Nitrogen deficiency interferes with protein synthesis, induces leaf senescence and therefore reduces the general growth of the plant (Bruns and Abel 2003), thereby limiting yield. Okra production in SSA is carried out under low-nitrogen conditions by small-scale farmers who cultivate okra with little or no nitrogen fertilizer application. Moreover, many farmers apply nitrogen fertilizer at sub-optimum regimes, which could be attributed to the high cost of chemical fertilizers (Bello et al., 2011) and the non-availability of fertilizer when it is needed most compared to fruit yield. This practice makes it uneconomical for farmers to apply fertilizer. In Ghana, the impact of low nitrogen on our soils can be reduced using compost, legumes that fix atmospheric nitrogen, and synthetic fertilizers. Farmers might use compost and green manure to boost nitrogen levels in the soil, but composting is time-consuming and may require adding a nitrogen source to ensure it is nitrogen-rich. Consequently, few farmers can afford to

prepare and spread enough good manure (Snapp *et al*., 2002; Rufino *et al*., 2006). As a result, it has become crucial to look into different options for increasing okra output under the current low soil N conditions.

One effective strategy to limit synthetic chemicals is the development of okra hybrids tolerant to okra leaf curl and mosaic virus with high nitrogen use efficiency and high yield potential. Okra varieties with high yield potential and resistance to OLCV and OMV are essential to support the rapidly growing population. They may provide incentives to farmers who are trying to make a modest increase in N application in their okra fields. The selection of hybrids with superior performance under low soil N supply may be vital for economic and environmental reasons. Currently, yield improvement and sustainability under unfavourable conditions through hybridization are significant objectives of okra breeding programs. Therefore, developing, deploying and producing hybrids resistant to disease stress with high N-use efficiency are highly relevant interventions to reduce food insecurity and environmental pollution.

Understanding genetic diversity is required to create breeding germplasms for all crops (Prakash *et al*., 2011). Crop improvement through breeding depends on the availability of genetic diversity and variability in the crop species and how easily this variability could be fixed in genotypes (Ariyo, 1990). The performance of plants can be permanently improved with proper crop diversity management, and breeders have a better chance of selecting directly for desired traits due to the high heritability of the traits. Furthermore, crop characterization is a critical first step in any crop development initiative (De Vicente *et al*., 2005). Characterization of okra is of great significance for both present and future genetic enhancement programs

of the crops (Shujaat *et al.*, 2014). Characterization of germplasm or genetic material refers to the technique by which these accessions or germplasms are distinguished, differentiated or identified based on their trait or feature (Merriam-Webster, 1991). In genetic terms, however, characterization refers to identifying variations due to differences in either DNA sequences or specific genes or modifying factors (IPGRI/CIP, 2003). Characterization provides information on diversity within and between crop collections. According to Sawadogo *et al.* (2006), characterization is established on peculiar features such as form, shape and colour of fruits and stems. Several diversity studies on okra use phenotypic or traditional tools (Sawadogo *et al.*, 2006; Prakash *et al.*, 2017; Singh *et al.*, 2017; Badiger *et al.*, 2017). Morphological characterization is affordable and accessible to initiate (Hoogendijk and Williams, 2001). However, morphological characterization is influenced by environmental or physiological factors or responses.

One of the most significant achievements in the field of molecular genetics is the discovery and use of molecular markers for the detection and exploitation of DNA polymorphism (Semagn *et al.*, 2006). Due to their extreme variety, superior genomic coverage, outstanding repeatability, automatability, and neutrality from environmental variations, molecular markers are essential for assessing genetic diversity (Bhandari *et al.*, 2017). To identify genetic diversity and DNA profiles of okra, several DNA or molecular marker systems such as random amplified polymorphic DNA (Nwangburuka *et al.*, 2011; Prakash *et al.*, 2011), simple sequence repeat or microsatellite (Sawadogo *et al.*, 2009; Schafleitner *et al.*, 2013), and amplified fragment length polymorphism (Kyriakopoulou *et al.*, 2014) have been employed. As a

result, selecting a specific molecular marker type is one of the most challenging tasks. Microsatellite or simple sequence repeats are ubiquitous and abundant in eukaryotic genomes and are one of several markers available. They combine desirable marker qualities as molecular markers, such as high-level polymorphism and information content, unambiguous allele designation, dispersal, selective neutrality, high repeatability, co-dominance, and rapid and easy genotyping procedures.

Combining ability of okra accessions depends on its ability to produce a superior hybrid combination distinguished from other accessions. Combining ability is one of the most effective strategies for identifying superior combiners that can be hybridized to exploit heterosis and identify better hybrids for direct usage or other breeding programs. The determination of combining abilities of parents seeks to provide enough data on the nature of gene action in the expression of quantitative traits (Falconer, 1989). However, no work has been done in Ghana and across the globe on combining ability studies for tolerance to okra leaf curls and mosaic virus diseases. Therefore, the study's main objective was to develop single-cross okra hybrids that are low N and viral disease tolerant. The specific objectives of the present study were to:

1. Determine the genetic diversity and relationship among 100 okra germplasm using morphological characters and SSR markers,
2. Determine the performance and heterosis of the okra hybrids and their parental genotypes for yield and fruit quality under low-N, high-N, and across the four research conditions,

3. Assess the breeding value and mode of gene action of selected okra genotypes for yield under low, high-N and across the four research conditions,
4. Determine the combining ability of the selected okra genotypes for resistance to OMD, OLCD and *Podagrica* spp. of hybrids in low N, high N and across the four research conditions.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 Origin and geographic distribution of okra

Okra (*Abelmoschus spp.* (L.) Moench) is the only vegetable crop in the Malvaceae family (Santos, 2012). There are two notable ideas concerning the geographical origin of *A. esculentus*. Some researchers suggest that one putative ancestor (*A. tuberculatus*) originated from northern India, suggesting the species is native to this geographic area (Ikram-ul *et al*., 2013). There is no definite evidence for its earliest cultivation in East Africa and the availability of other putative ancestors (A. ficulneus). Still, some scientists believe North Egypt or Ethiopia was the domestication site (Benchasri, 2012; Sorapong, 2012).

However, tropical Africa, notably West Africa, seems to be the proposed home of okra from where it was disseminated to America, Asia, and Southern Europe and is currently grown in many other countries (ECHO, 2003; Muhammad *et al.,* 2013). It has been cultivated for ages. The Nile Basin may have served as a conduit for the expansion of this crop across North Africa, the Eastern Mediterranean, Asia, and India. According to Bish *et al*. (1995) and Hamon *et al.* (1990), okra was introduced to North America by enslaved Africans via New Orleans. The crop can be cultivated in a garden or on a large commercial farm (Rubatzky and Yamaguchi 1997). Many countries, including India, Japan, Turkey, Iran, Western Africa, Yugoslavia, Bangladesh, Afghanistan, Pakistan, Myanmar, Malaysia, Thailand, India, Brazil, Ethiopia, Cyprus, and the Southern United States, grow okra on a commercial scale (Benjawan *et al*. 2007).

Okra accessions are estimated to number 2,283 worldwide, with 2,029 from Africa and 1,769 from West Africa (Hammon and Van Slotten, 1989). The crop is by far more heavily represented in West Africa than in other parts of the globe (Omonhinmin and Osawaru, 2005). West Africa, India, and Southern Asia are centres for okra genetic variation (Hamon and Van Slotten, 1989). Several accessions, both wild and domesticated species, are available. These include *A. esculentus*, *A. caillei*, *A. moschatus*, *A. manihot*, *A. ficulneus*, and *A. tetraphyllus*, to name a few. *Abelmoschus manihot* L, *Abelmoschus moschatus* L, and *Abelmoschus esculentus* L are the domesticated species in the genus (Stevels, 1988; Siemonsma, 1991). Some wild species are *A. ficuleus* L., *A. crinitus* L. and *A. Angulosus* L. The species *A. esculentus* is grown annually in most tropical and subtropical African nations, including Ghana, Guinea, Ivory Coast, Liberia, and Nigeria.

2.2 Taxonomy and Botany of okra

Okra is known by its Latin binomial names, *Abelmoschus esculentus* and *Hibiscus esculentus* (Kumar *et al.* 2010), and it also has a variety of local names in several areas across the globe. It is known as lady's finger in England (Anwar et al., 2011), gumbo in the United States, guino-gombo in Spanish, guibeiro in Portuguese, and bhindi in India (Ndunguru and Rajabu, 2004; Sorapong, 2012; Benchasri, 2012).

In Ghana, okra has several names depending on the language and region of the people. The Akan-speaking native call it *nkruma*, while the Ewes in the Volta region call it *fetiri* (National Research Council, 2006) *saalu* by the

Dagaabas in the Upper West region and is one of the most common and popular vegetables consumed locally in our sub-region.

There are about fifty (50) species of okra, of which only eight (8) are widely acknowledged (Borssum, 1966; IBPGR, 1990). In the genus *Abelmoschus*, there are considerable differences in the number of chromosomes and ploidy levels. *Abelmoschus angulosus* has the smallest number of chromosomes (2n = 56) (Ford, 1938), while *Abelmoschus caillei* has almost 200 chromosomes (Siemonsma, 1982). The chromosome numbers 2n=72, 108, 120, 132 and 144 among *Abelmoschus esculentus* are in regular patterns of polyploidy with n = 12 (Datta and Naug, 1968). This makes it abundantly evident that the crop is considered a polytypic complex (Singh *et al*., 1975) with considerable polyploidy and hybridity, of which the parents are unknown.

According to Nonnecke (1989), the plant has a fibrous, semi-woody, and herbaceous annual growth habit. The top 45 centimetres of the soil are covered by the plant's deep tap rooting system, composed of thick, shallow roots stretching out in all directions. Okra seeds have varying degrees of shape and roundness, being dicotyledonous with epigeal growth (Hamon *et al*., 1991; Ariyo, 1993).

The monoic flowers of okra are self-compatible (Hamon *et al*., 1990). The plant begins to flower when it attains the age of 30-60 days after planting, during which petals stay open for a day. Okra is usually a self-pollinated plant but can be cross-pollinated by insects such as bumble bees. The immature okra pods are ready for harvesting when they attain 4-5 days following anthesis. Harvesting can be done at least every two days for size and quality. The

growth of the plant declines if the pods are left to attain full maturity with few flower developments, but when harvesting is done continuously, the plant consistently produce fruit. The pods, which are harvested in an immature form have varying colours ranging from pale green, green, or purple and may be ridged depending on the accession or cultivar (Hamon *et al*., 1990). Matured pods have dark brown dehiscent or indehiscent capsules. Matured and ripe pods become fibrous and split longitudinally into five parts, exposing the seeds in five rows, with about 50 – 100 seeds per pod (Norman, 1992). The pod might be spherical or ridged, and it could be either short or long (Siemonsma, 1982). Spines on pods and plants of okra may cause allergies in some persons (Ariyo, 1993; Düzyaman, 1997).

2.3 Nutritional and health benefits of okra

Okra (*Abelmoschus* spp. (L.) Moench) contains a wealth of beneficial nutrients, and the majority of it is in the form of gums and pectins, which are soluble fibre (Candlish *et al*., 1987). According to Brown *et al*. (1999), soluble fibre helps lower serum cholesterol, which lowers the risk of heart disease. The remainder comprises the insoluble fibre, which protects the intestinal tract and reduces the risk of some cancers, particularly colorectal cancer (Schneeman, 1998). Okra is endowed with numerous vitamins, minerals, and dietary fibre, all essential for good health (Norman, 1992). It is suitable for expectant mothers since it is high in folic acid, which is crucial for developing the fetus' neural tube between the fourth and the twelfth weeks of pregnancy (Allen, 2007). Okra is particularly blessed with calcium and ascorbic acid

compared to other fruit vegetables such as eggplant and tomato (Siemonsma and Kouame, 2004).

The seed has an abundance of tryptophan and lysine amino acids, making it similar to but superior to soybeans in quality (Sanjeet *et al*., 2010; Adetuyi *et al*., 2012). The seed contains enough amino acids to augment diets riched in cereals (Ndangui *et al*., 2010). The pod contains digestible fibre, low calories, and fat-free contents (Reddy *et al.*, 2013) and is consumed as salads, boiled, and fried vegetables. The pods are rich in phenolic chemicals, and the seeds are a significant source of zinc (Cook *et al*., 2000). It is also rich in organic and inorganic nutrients like 86.1% water, 2.2 % protein, 0.2% fat, 9.7% carbohydrate, 1.0% fibre and 0.8% ash (Saifullah and Rabbani, 2009).

2.4 Pest and diseases of okra

Production of okra is hampered by vicious insects including disease infestations. Insect pests reported to infest okra in Ghana include flea beetles (*Podagrica* sp.), cotton stainer (*Dysdercus superstitus*), white fly (*Bemisia tabaci*), and green stink bug (*Nezera viridula*), among others (Obeng-Ofori and Sackey 2003; Bi-Kusi, 2013; Asare-Bediako *et al.*, 2014). Stem borers (*Earias* spp) and cutworms (*Agrotis* spp), which eat the leaves (Lamont, 1999), are sometimes found on okra fields. According to Echona and Offordile (2011), *Podagrica* spp. damage includes distinctive leaf perforations that limit the leaves' photosynthetic surface area and significantly lower okra yield. The late vegetative to reproductive stage of the okra plant is when diseases like powdery mildew and *Cercospora* leaf spot attack the plant. Fungal infection can spread rapidly in the field due to crowded and overlapping broad leaves of

the plants. Besides wind spreading the fungal spores to plants, people harvesting daily and passing along the okra rows are also responsible for the widespread infection in the field (Siemonsma, 1991).

Many plant viruses attack the plant, with okra leaf curl virus (OLCV) and okra mosaic virus (OMV) being the major diseases reported in Ghana (Bi-Kusi, 2013; Asare-Bediako *et al.*, 2014). The okra leaf curl disease (OLCD), which is suspected of being associated with a whitefly-transmitted geminivirus (Genus *Begomovirus*), and the okra Yellow vein mosaic virus (OYVMV), is spread by aphids, leafhoppers and whitefly consistently (Ghanem, 2003). The OLCV infection can cause yield losses of up to 80% (Basu, 1995) while yield losses of 75% as well as the typical chlorosis yellowing of the foliage, deformity, and small size of fruits were noted globally (Solankey *et al*., 2014). Symptoms of OLCV infection include the curling of leaves, yellowing of leaves, leaf distortion, stunted growth and reduced yield. Okra mosaic virus (OMV) has always been a severe problem in okra (Kucharek, 2004). About 20 - 50% of yield reductions have been documented (Kucharek, 2004). The situation may worsen to about 90% (Kucharek, 2004). The OMV also induces mosaic, vein chlorosis, banding, and stunted growth (Krishnareddy *et al*., 2003). The over reliance and continuous use of synthetic chemicals such as Golan, Attack, Consider, etc., to combat pests and diseases is detrimental to the atmosphere because contaminants from synthetic chemicals in fruits may endanger human health and kill unintended animals.

One effective strategy to limit synthetic chemicals is breeding okra hybrids that are tolerant to both okra leaf curl and mosaic virus with high yield potential. Okra varieties with high yield potential and resistance to OLCV and

OMV are essential to support the rapidly growing population. They may provide incentives to farmers who are trying to make a modest increase in okra yield. The selection of hybrids resistant to okra diseases may be critical for economic and environmental reasons. At present, yield improvement and sustainability under unfavourable conditions through hybridization should be an important focus of okra breeding programs in Ghana. Therefore, developing, deploying, and producing hybrids resistant to disease stress are highly relevant interventions to reduce food insecurity and environmental pollution.

2.5 Overview of plant germplasm

Collection, selection and evaluation of germplasm are fundamental requirements in every crop improvement programme (Doku *et al*., 2013). Germplasm involves a collection of genetic resources of an organism. Farmers, and scientists use this to conserve and manage crop genetic diversity for crop improvement programmes, among others. In Ghana, the Plant Genetic Resource Research Institute (PGRRI), located at Bunso, serves as a national germplasm conservation institute and has a germplasm collection primarily characterized by morphological markers. The main objective of assembling germplasm is to acquire, preserve, and make as much genetic variation available within a given gene pool to plant breeders and other users as possible (Ramanatha *et al*., 1998). The availability of well-characterized plant genetic resources is a prerequisite for crop improvement and genetic research (Roch *et al*., 2010). These resources form invaluable parental lines for developing improved cultivars (Aktas *et al*., 2009). To preserve the integrity and potency

of seed samples, it is required that the whole spectrum of genetic diversity is preserved on a long term basis while, at the same time, sufficient amounts of seeds for potential use is preserved.

2.6 The Concept of Genetic Diversity

Crop diversity could be explained as the degree of distinction and variation within or between species. Genetic diversity refers to variation in nucleotides, genes, chromosomes, or whole genomes of organisms within and among populations. Diversity is the lifeblood of the biological world. No two organisms (not even maternal twins) can be the same. The variation in the traits/characteristics of one or a few organisms is termed variability (Bhandari *et al.*, 2017). More often than not, genetic variability and diversity are sometimes considered to mean the same, which is wrong and inaccurate. Genetic variability is the difference expressed in alleles of genes or variation in DNA/RNA sequences in the gene resources of an organism in a population. This is manifested in terms of alternative pairs in phenotype. Genetic diversity, on the other hand, is extensive and contains all variations among different genotypes regarding the general genetic constitution, which is closely associated with a single species. Moreover, genetic diversity can be estimated by recording the number of genes in a gene bank. In contrast, genetic variation can only be expected to occur and cannot be measured. Therefore, genetic variability can be regarded as a basic unit or blocks of genetic diversity (Bhandari *et al.*, 2017).

Plant germplasm is an essential resource in the agriculture sector, food security and forestry because it supplies genetic diversity that farmers and breeders need to obtain new cultivars (Laurentin, 2009). Genetic diversity in the gene pool is the most critical genetic resource that contributes to plant breeding progress. Genetic diversity is essential when selecting parents in combination breeding of different autogamous crops to create transgressive segregants (Pradip *et al*., 2010). Shujaat *et al*. (2014) revealed that genetic variations are vital to achieving the diversified goals of plant breeding, which encompasses higher quality yield and resistance to diseases. Estimate of genetic diversity measures the variations and relationships within and among accessions and individuals based on some metric traits. It improves the accuracy of accession groupings and the recognition of subsets of core accessions that may be useful for specific breeding reasons (Mohammadi and Prasanna, 2003). Geleta (2003) reported that knowledge of genetic diversity and relationship in the gene pool as well as the prospective merit would be vital to all phases of crop improvement. The information about genetic diversity in available gene banks is essential for the optimal design of a breeding programme (Geleta, 2003), and the nature of genetic relationships among the population has been a critical tool for the effective management of diversity in a given gene bank (Manjarrez-Sandoval *et al.*, 1997).

There is a growing interest in the study of genetic diversity by both plant breeders and germplasm curators. This is where variation within or between individuals is analyzed using specific methods or combinations (Mohammadi & Prasana, 2003). Numerous factors affect the genetic diversity of plants. Among these are selection, mutation, evolutionary forces, migration

and changes in the frequency of an existing gene variant, which are fundamental to crop genetic diversity. These forces alter the genetic diversity of the crop plant by causing continual changes in allelic frequency in the population (Bhandari *et al*., 2017).

2.7 Measurement of Diversity

Four different techniques exist for estimating genetic diversity, namely, farmers view point and traditional classification, molecular characterization, morphological characterization and biochemical (Hoogendijk and Williams, 2001; Zannou, 2006). For this study, prominence will be given to morphological and molecular characterization. A thorough description of the unique characteristics of each sample must be made in order to characterize it. These characteristics must be inherited, straightforward to observe, and represented uniformly in all situations (Rubenstein and Heisey, 2003). Characterization of germplasm or genetic material could be defined as the process where germplasms are distinguished, differentiated or identified based on their characteristics (Merriam-Webster, 1991). Characterization, however, in the context of genetics refers to the recognition of variances brought on by differences in DNA sequences, particular genes, or modifying factors (IPGRI/CIP, 2003).

According to de Vicente *et al.* (2005), genetic characterization offers an enhanced power for detecting diversity (including genotypes and genes) that exceeds that of traditional methods. Genetic characterization is achieved by systematically recording data in an orderly manner to allow for the use of appropriate statistical tools to analyse and compare the data obtained from

different regions (CIAT, 2007). Historically, morphological characterization was the primary technique used for genetic diversity estimations and analysis (Obeng-Antwi *et al*., 2011; Farooq and Azam, 2002) and is still being used. Morphological diversity can be estimated by measuring phenotypic differences observed in plants. These traits or characters may be qualitative, such as the colour of the flower, leaf shape, growth habit, seed size, colour of seed coat, etc. and quantitative characters like growth and yield potential (Rao, 2004). It comprises morphological evaluation of various field-planted accessions, with morphological traits being the most important factor that determines the agronomic usefulness and taxonomy of plants (Cholastova and Knotova, 2012). The availability of published descriptor lists for most crop species, including okra, is one of the main benefits of conducting morphological characterisation, among other benefits (Hoogendijk and Williams 2001).

Morphological characterisation of genetic resources is also vital in establishing the description of each accession. It also shows duplicates within the same collection, detecting unique characters and the population structure for conservation purposes (Huamán, 1999). Phenotypic assessments do not require expensive technology and are inexpensive, straightforward, and simple. A morphological description allows exceptional identification for specific cultivated varieties. Therefore, it is strongly advised that it is carried out first in any diversity investigations before using more in-depth biochemical or molecular analyses. However, the disadvantages of morphological evaluation involve the non-reliability of its markers as they are susceptible to natural selection and their expression is partly influenced by

environmental factors (Hartings *et al*., 2008), depicting low level of polymorphism and low heritability (Beyene *et al*., 2005).

Researchers from all over the world have attempted to characterize the morphology of okra. Most of these researchers undertook these experiments on Asian soils. For example, in India, Singh *et al*. (2017), Prakash *et al*. (2017), Badiger *et al*. (2017), Prakash and Pitchaimuthu (2010), Akotkar *et al*. (2010), and Somashekahr *et al*. (2010) and in Nigeria, Bello and Aminu (2017), Olayiwola *et al*. (2015), Adekoya *et al*. (2014), Nwangburka *et al*. (2012) and Oppong-Sekyere *et al*. (2011) in Ghana. For most of the examined traits, all of the aforementioned authors found significant diversity among the various numbers of accessions. Muluken *et al*. (2016), Anteneh (2017) and Tesfa and Yosef (2016) investigated 25 to 58 okra accessions from various locations in Ethiopia. Numerous germplasm researchers have used morphological characteristics, isoenzymes, and protein markers. The method of choice for assessing genetic diversity is molecular markers due to their high variability, superior genome coverage, high reproducibility, automation, neutrality, and lack of environmental influence (Bhandari *et al*., 2017).

The discovery and application of molecular markers for assessing DNA polymorphism is essential in molecular genetics (Semagn *et al*., 2006; Gao *et al*., 2015). Molecular techniques have been proven to be powerful tools and have been primarily employed for genetic manipulation in many plants, mainly in the areas of germplasm characterization, variety identification, phylogenetic study and diversity analysis (Barker *et al*., 1999; Degani *et al*., 2001; Lefebvre *et al*., 2001). Molecular studies of cultivated plants and their wild relatives generate evidence for establishing breeding strategies (Gao *et*

al., 2015). The choice of molecular marker depends mainly on the research objectives, accessions to characterise, the cost involved and the inherent characteristics of the marker. A monomorphic marker is invariable in all organisms. Moreover, when a marker depicts variation in molecular weight, enzyme activity, structure or restriction site, it is said to be polymorphic and can be used as a basis for characterization (Semagn *et al.,* 2006; CIAT, 2007). Different markers have already been developed and employed on various plants, with new and straightforward systems being designed continually.

Among the different markers being employed over the years include Restriction Fragment Length Polymorphisms (RFLPs), Random Amplified Polymorphic DNAs (RAPDs), Sequence Tagged Sites (STS), Amplified Fragment Length Polymorphisms (AFLPs), Simple Sequence Repeats (SSRs) or microsatellites, Single Nucleotide Polymorphisms (SNPs) and others (Altpeter and Korzun, 2007; Gao, 2015).

2.8 Assessment of the breeding value of okra germplasm

According to Panhwar *et al*. (2008), combining ability (CA) is the capacity of parents to combine with each other during hybridization such that favourable characters are passed on to their offspring. Allard (1960), on the other hand, defined combining ability as an estimate of the value of genotypes based on the performance of their progenies produced in some definite mating system. Combining ability is one of the most effective strategies for identifying superior combiners that can be hybridized to exploit heterosis and identify better hybrids for direct usage or other breeding programs. Planning carefully for hybrids in a breeding program requires testing lines during

hybridization programs. The determination of combining abilities of parents seeks to provide enough data on the nature of gene action in the expression of quantitative traits (Falconer, 1989). Studying and contrasting genotype performance in hybridization programs is extremely important (Romanus *et al.*, 2007).

Rawlings and Thompson (1962) stated that CA is helpful in designing plant breeding programs, particularly in testing procedures for studying and comparing the performance of lines in hybrid combinations. Combining ability for yield, yield-related traits and other traits such as disease resistance, high N efficiency, drought tolerance and high protein concentration play a significant role in selecting appropriate parents for hybrid development. Combining ability studies is one of the powerful tools that can be exploited to estimate the effects of combining abilities and assist in selecting favourable parents and hybrids (Subhan *et al.*, 2003; Rashid *et al*., 2007). The combining ability of parents rests on their ability to produce superior cross-combinations with other parents. Combining ability cannot be predicted based on the phenotypic value of the parents but is assessed only by testing the progeny using a definite mating design. Parental genotypes that produce vigorous offspring in a hybrid combination are said to be good combiners.

Sprague and Tatum (1942) coined two types of CA that are exploited in quantitative genetics: general combining ability (GCA) and specific combining ability (SCA). According to Sprague and Tatum (1942), general combining ability (GCA) refers to a genotype's average performance in hybrid combinations. In contrast, specific combining ability (SCA) refers to cases where specific combinations perform better or worse than expected based on

the mean performance. GCA is defined by Allard (1960) as the average performance of genotypes in a series of hybrids. In contrast, SCA is defined as the departure from projected performance based on general combining ability (GCA). In his study of eight West African okra accessions, Adeniji (2003) identified accessions 3 and 6 as the highest general combiners. Ahmad *et al.* (2002) also identified accession B13 and B34 as the best general combiners out of the six types, citing their high positive GCA in all okra varieties studied.

General combining ability is connected to the breeding value or the additive aspect of genetic effects. In contrast, SCA is related to the non-additive genetic effects, which include dominance, over dominance, epistasis, and genotype-environment interaction effects (Falconer and Mackay, 1996). The additive genetic effect is crucial during selection, although the non-additive is helpful when making superior hybrids. GCA and SCA estimates accurately assess individual genotypes' relative merits in the hybridization process to guide selection and testing schemes. GCA estimate aids plant breeders to make use of existing variability in the germplasm to detect individual genotype(s) conferring favorable attributes and to differentiate relatedness among genotypes (Melania and Carena, 2005; Vacaro *et al.*, 2002). SCA estimate also aids breeders in establishing heterotic patterns among populations or genotypes, to determine promising single cross hybrids and to group them into heterotic groups (Parentoni *et al.*, 2001; Revilla *et al.*, 2002). Genotypes with high GCA effects are said to be good combiners and can be effectively deployed and used in synthetic variety development. Moreover, when high-yielding combinations are required in producing hybrids, SCA is a better option for parental selection. Combining ability studies of single cross

hybrids produced by crossing elite and diverse genotypes from the germplasm of okra has been made by several researchers (Pathak *et al*., 2001; Kumar and Thania, 2007).

In every successful breeding program, the effects of general combining ability (GCA) and specific combining ability (SCA) are critical. Several researchers have documented the importance of non-additive genetic components for fruit yield per plant, including Jayprakashnarayan *et al*. (2008), Singh *et al*. (2009) and Wammanda *et al*. (2010). Additive and non-additive genetic systems, controlling pod yield and yield-relating traits in okra, have also been documented by several authors, including (Kumar *et al*., 2006; Jaiprakashnarayan *et al*., 2008b; Jindal *et al*., 2009; Singh *et al*., 2009; Wammanda *et al*., 2010).

2.9 Importance of nitrogen in okra production

Nitrogen is essential for the growth and development of plants and is a critical component of all enzymes. Nitrogen is the second-most absorbed macro-nutrient by vegetables, which performs a fundamental function in their yield (Souza *et al*., 2017) and is an essential nutrient during the growth and development of a plant. It is an essential nutrient and a vital determinant in the growth and development of vegetables. It performs a necessary role in chlorophyll, protein, nucleic acid, hormone and vitamin synthesis and also aids in cell division and elongation (Bänziger *et al.*, 2000). In the production of okra, nitrogen provides a more significant response in fruit yield (Zubairu *et al*., 2017). In all plants, including vegetables, soil nitrogen (N) considerably influences the absorption of P and K and other plant nutrients. It plays a

significant part in flower opening, fruit setting and fruit development. Nitrogen is more abundant in plant leaves, where it is mainly found in photosynthetic enzymes and may make up as much as 4 percent dry matter (Bänziger *et al*., 2000). Nitrogen management results in efficient vegetative growth of crop plants and significant productivity improvement, and it thus serves as a structural component of various organic compounds that are important for plants, such as amino acids, proteins, and proline (Olaniyi *et al.*, 2010; Ferraz *et al*., 2017; Medeiros *et al*., 2017).

Singh (1995) documented a positive correlation in the green pod yield of okra with the application of N from 56 to 150 kg/ha. Nitrogen and phosphorus perform vital functions in the fruiting, seeding, and proper development of okra plants (NIHORT, 1985). It makes leafy vegetables and fodder crops more succulent. Nitrogen is responsible for an increase in the protein content of food and fodder crops. The response of okra to nitrogen, just like any other vegetable, should be high, and a higher dose of nitrogen is needed to keep the fruits soft and edible. The recommended N application rate for optimum fruit yield has been reported to be between 120 and 200 kg N/ha (Amjad *et al*., 2001; Rashid, 1999) and between 100 and 200 kg N/ha for seed production (Chattopadhyay and Sahana, 2000). Several recommendations for this nutrient, varying from 60 to 180 kg ha-1, have been suggested depending on the fertility of the soil and the growing region (Oliveira *et al*., 2014). Therefore, proper attention must be given to these nutrients while planning a project on plant nutrition (Khalil, 2006).

2.10 Low soil nitrogen effects on okra production

The most limiting macronutrient in okra production is nitrogen, which has a detrimental impact on crop development and fruit yield. Low soil nitrogen, which results from sparing fertilizer use and rapid mineralization of organic matter, is one of the most important abiotic factors limiting crop productivity in the tropics (Lafitte and Bänziger, 1996; Bänziger and Lafitte, 1997a; Abe *et al*., 2013). However, the reduction in yield due to the impact of low soil nitrogen for okra is not documented but noted to cause a significant amount of yield reduction. Nitrogen stress in okra is linked to reduced photosynthetic rate, decreased leaf area, and decreased number of buds per plant before flowering. In contrast, low-N stress during flowering may cause flower abortion. Nitrogen stress in the soil affects different yield-determining components. When N is limited, plants redistribute N to younger tissues from older tissues, which causes the lower leaf tissues to senesce early (Bänziger *et al*., 2000). The growth of plants tends to favour root growth over shoot growth under nitrogen stress conditions, and the root/shoot ratio increases even though there are typically fewer total roots for plants that develop under N stress compared to those that grow under optimum N environment (Bänziger *et al*., 2000).

2.11 Genetic studies on low N tolerance in okra

Understanding the actions of genes on how traits are passed on from parents to offspring in an N-depleted environment is essential to enhance okra productivity for future breeding programmes. Information on the action of genes under nitrogen-depleted soils is often scarce and inconsistent. Moreover,

there is very little research on the effects of genes in regulating the transmission of several agronomic traits under low soil N environment in okra. According to Ifie (2013), the non-additive gene effect has less impact than additive gene effects. However, Mafouasson (2014) and Betran *et al*. (2003) reported that the non-additive gene action was more significant than the additive.

Moreover, under low soil N conditions, the non-additive effect was more important than the additive gene effect (Messeka *et al*., 2006). According to Makumbi *et al.* (2011), the results of gene action conditioning yield varied depending on the kind of stress; under low N stress, non-additive gene action appeared to be more critical than additive gene action. The contradictory findings reported by several workers could be attributed to the low N level under which the lines were evaluated or variations in the genotypes used for the research (Mosiza, 2005). This contradiction, perhaps, calls for more thorough studies on the behavior of gene action, especially on okra, which is a studied crop with no research findings on tolerance to low soil N.

2.12 Heritability and Genetic Advance

Heritability is the ratio of phenotypic differences in a population attributed to genetic variation among individuals. In other words, heritability refers to the proportion of population differences attributed to genetic variables. However, Nyquist (1991) defined heritability as an estimate of the phenotypic difference in a population that is influenced by genetic factors and has a predictive role in plant breeding. Heritability is a reliable indicator of

how traits are passed from parents to young ones (Phani *et al*., 2015). In creating any suitable breeding programme, it is crucial to know the portion of phenotypic difference of the character that is heritable (Kearsey and Pooni, 1996) since the efficiency of a selection programme depends on the degree of genetic variation and heritability of the character (Falconer and Mackay, 1996).

According to Falconer (1989), heritability has been divided into broad and narrow senses, depending on whether it is genotypic or has breeding value. Broad-sense heritability refers to the proportion of genetic variance to phenotypic variance, designated as H^2= VG/VP. It estimates the ratio of phenotypic variation attributed to genetic values, which includes additive, dominant, and epistatic effects. A considerable percentage value for a trait is considered highly heritable. In contrast, smaller percentage values indicate that the environment is in charge of the phenotypic manifestations of the trait (Dabholkar, 1992). Broad sense heritability estimates provide data on the relative magnitude of genetics and environmental variation in genetic resources (Jindal *et al*., 2010; Pradip *et al*., 2010). On the other hand, heritability, in the narrow sense, refers to the proportion of additive variance to phenotypic variance, designated as h^2= VA/VP. This includes only the portion of genetic variation attributed to additive genetic values (Falconer and Mackay, 1995). High values for broad sense heritability for a trait make selection reasonably easy. In a trait with low heritability, selection may be substantially difficult or virtually impractical as a result of the masking effect of the environment on genotypic effects (Khanorkar and Kathiria, 2010).

Genetic advance is the variation between the mean genotypic value of the selected lines and the mean genotypic values of the parental population before selection. Estimates of heritability alone may be misleading and, when used with genetic advances, tend to increase the utility of heritability estimates. Ibrahim and Hussein (2006), therefore, concluded that when combined with the selection differential, the usefulness of heritability estimations is boosted. High heritability estimates combined with a high genotypic coefficient of variation and genetic advance are usually more helpful in predicting an individual's response to selection than heritability estimates alone (Das *et al*., 2012). High heritability in combination with low genetic advance for the traits implies that these characteristics are controlled by the environment rather than genotypes (Das *et al.*, 2012). According to Senapati *et al*. (2011), the incidence of yellow vein mosaic virus disease was highly heritable (98.02%), as were fruit yield (93.92%), edible maturity (90.98%), and days to 50% flowering (89.02%), indicating that these traits are more heritable and less influenced by the environment.

A trait with a high heritability and genetic advance indicates additive gene action. Traits with no such combination are influenced by non-additive gene effect (Mehta *et al.*, 2006). Mihretu *et al.* (2014b) revealed high estimations of heritability coupled with genetic advance for traits such as plant height, suggesting that additive gene action influences such traits and that selection based on these traits will be successful. Several authors, including Mihretu *et al*. (2014), Muluken *et al*. (2016), and Anteneh (2017), studied the heritability and genetic advance of okra germplasm. The study revealed high heritability and genetic advance for plant height, number of primary branches

per plant, weight of the fruit, and weight of the mature pod per plant. Anteneh (2017) also found high estimates of both heritability and genetic advance as a percentage of the mean for dry pod weight, the number of seeds per pod, and 100 seed weight. In contrast, Muluken *et al*. (2016) found average heritability with low genetic advance as a percent of the mean or vice versa for these characters.

Singh and Singh (2006) conducted a field experiment to determine heritability and genetic advance in 64 okra genotypes and found that heritability estimates for days to first flowering were high. The study also discovered that additive gene effects influenced genetic advancement and heritability of traits such as fruit yield and number of branches. Bello and Aminu (2017) noted high heritability for plant height, fruit length, diameter, and average fruit weight in a related study. In furtherance of this study, Bello and Aminu (2017) again observed that broad sense heritability greater than 60 % was obtained for pod yield and days to anthesis. According to Nagre *et al.* (2011), leaf area had the highest estimated heritability, followed by the number of leaves per plant, yield per plant, fruit length, number of nodes per plant, chlorophyll content, and number of fruits per plant.

2.13 Genotype x environment (GEI) interaction

Genotype-by-environment interactions are crucial for agricultural and animal breeding because environmental factors affect the genetic architecture of traits and, consequently, the processes of evolution (Ouborg *et al*., 2010). The existence of a genotype × environment interaction (GEI) is determined by how a genotype behaves differently depending on the environment. When GEI

is significant, the source of variance is broken down into constituent parts to pinpoint the genotypes with the best and most consistent yielding ability across environments.

Before promising genotypes are commercialized, their performance in diverse locations, including farmer's fields, is evaluated across numerous environments. This process is known as multi-environment trials (MET). Locations where crop cultivars are grown may have varying conditions, including edaphic, climatic and management practices. During production, all these cumulated conditions constitute the growing environment for the crop varieties (Abdulai *et al*., 2007). This poses a severe challenge to plant breeders in identifying and selecting appropriate genotypes to perform consistently in multiple environments (Ngaboyisonga, 2008). Environmental influences affect quantitative traits more so than qualitative traits. Seasonal variations, as well as soil properties, among others, influence G×E interactions. The environment (E), genotype (G) and genotype × environment interaction (GEI) components determine the phenotypic expression of an individual (Sharifi *et al*., 2017). An individual's genotype is its genetic composition, i.e., the transmissible DNA nucleotide sequence. The common types of G × E interaction include genotype × environment interaction, genotype × year interaction, and genotype × environment × year interaction effects (Crossa, 1990).

Studies on G × E interaction have been conducted elsewhere to determine the stability in yield performance of new genotypes bred for growing in broader or specific target growing environment(s) (Hooyer, 2012; Kamutando *et al*., 2013). The presence of G × E interaction frequently changes the genotype ranks in different environment making selection difficult

(Beyene *et al*., 2011; Abuali *et al.*, 2014). For instance, Troyer (1996) reported that genotype × year interaction was more significant than genotype × environment interaction due to different soil moisture present during flowering. G×E interaction that changes the order of rank of performance of a genotype is referred to as cross-over interaction. Sallah *et al.* (2004) reported that, the phenotype of a crop can be determined by G × E interactions other than its genotype, accounting for more yields attainable in improved varieties. Ewool (2004) reported a high G × E interaction effect on the yield of crops due to soil fertility status, season and location, and dates of sowing in Ghana. Significant GEI is advantageous for generating location-specific variants. As stated by Badu-Apraku and Fakorede (2017), it is not preferred when cultivars are to be suited to a variety of production environments. Each cultivar reacts specifically to changing climatic and soil conditions; some exhibit high G × E interaction, while others it is low. Quantitative and qualitative interactions may occur between cultivars and the environment (Dia *et al*., 2016; Larkan *et al.*, 2016; Parent *et al.*, 2017). Assessing the stability of cultivars' yield provides valuable information about their behaviour in specific environments (Bernardo *et al*., 2018). Analysis of G × E interaction becomes indispensable for breeders and varietal experimentation.

Data from multi-location trials (METs) can be analyzed and interpreted using several statistical programs. For instance, depending on the goals of the researcher, frequently used software includes the Additive Main Effects and Multiplicative Interaction (AMMI) package (Gauch and Zobel, 1997) and the Genotype and Genotype x Environment (GGE) biplot tool (Yan et al., 2000).

2.14 Correlation among Traits

The correlation coefficient is a statistical tool for determining the strength of association among variables. Without considering any other factors, it measures how closely two variables are related (Akinyele and Osekita, 2006). The correlation between two traits, moreover, refers to a situation where the two traits vary with each other, either positively or negatively, within a breeding population. The correlation coefficients among the quantitative traits in the accessions of okra selection for a single character may increase the trait's value, which are positively correlated characters, and decline the values for negatively correlated traits (Ahiakpa *et al.*, 2013). Correlation can be caused by the environment or genes. An environmental correlation is a consequence of the interaction of several environmental elements, which differ depending on the environment. The main contributors to correlations are the pleiotropic effects of genes and genetic linkage (a phenomenon in which genes are inherited together).

Pleiotropic is the property of a gene which affects two or more characters; as a result, it causes simultaneous variations in the two characters when the gene is segregant (Singh, 1993). The higher genotypic correlation coefficient over the phenotypic correlation coefficient observed in characters suggests very strong inherent association between various characters at a genetic level. It indicates the masking action of genes on the influence of environment in the expression of characters, implying the association is mainly due to genetic effect (Nwangburuka *et al.*, 2012).

The intensity of correlation between different variables is represented by correlation coefficient r. The correlation coefficient, r, ranges from -1 to 1. If r is -1, the two variables have a 100% correlation but vary in opposite directions (negative correlation). On the other hand, if r is +1, it implies a perfect correlation (100%) where both traits vary in the same direction (positive correlation). If r=0, there is no correlation between two variables; that is the two variables are independent of each other or no correlation indicates that genes concerned are located far apart on the same chromosome or different chromosomes. In plant genetics and breeding studies, correlated characters are of prime importance because of genetic causes of correlations through pleiotropic action or developmental interactions of genes and changes brought about by natural or artificial selection (Falconer and Mackay, 1996; Sharma, 1998). The genotypic correlation coefficient between several character pairings matched the corresponding phenotypic correlation coefficient (Rashwan, 2011; Somashekhar *et al*., 2011). Pal *et al.* (2010) observed genotypic correlations higher in magnitude than their phenotypic associations for most trait combinations. Edible fruit yield was positively and significantly correlated with plant height and number of fruits per plant in parents, F1 and F2 population levels. This indicated that any selection based on these characters would enhance the performance and improve the edible fruit yield in okra.

Chaukhande *et al.* (2011) revealed that the yield per plant exhibits a positive and significant correlation with plant height, number of flowering nodes on the main stem, number of fruits per plant and average weight of fruit. Senapati *et al.* (2011) reported that the correlation studies exhibited that the

genotypic estimates were higher than the phenotypic ones for most traits, indicating a strong inherited association between the characters. Fruit yield is the most important economic trait and showed positive and significant association with the number of nodes per plant, number of fruits per plant and fruit length. The correlation coefficient between the number of seeds and fruits per plant and its seed yield was positive and statistically significant at both the genotypic and phenotypic levels (Somashekhar *et al.*, 2011).

Reddy *et al.* (2013) examined 100 germplasm lines of okra during the kharif season. They found that plant height, fruit length, width, weight, total number of fruits per plant, number of marketable fruits per plant, and total yield per plant all had significant positive correlations at the phenotypic and genotypic levels. In 20 okra genotypes studied across four seasons, Adekoya *et al.* (2014) found positive and significant genotypic and phenotypic associations of seed yield per plant with plant height, number of pods per plant, mature pod width, mature pod weight, and 100-seed weight. Additionally, they reported that significant genotypic correlations with seed yield per plant across the seasons existed for the number of pods per plant, length of matured pods, weight of matured pods per plant, number of ridges per pod, number of seeds per pod, and 100 seed weight. These genotypic correlations varied according to the season and the days of flowering. According to Mihretu *et al*. (2014), correlation research between numerous quantitative characters revealed strong relationships between the characters. Saryam *et al.* (2015) reported that fruit yield per plants was significant and positively associated with number of fruits per plant (0.803), fruit diameter (0.376), fruit length (0.349), number of seeds per fruit (0.316), days to

maturity (0.301), fruit weight (0.274), 100 seed weight (0.219), petiole length (0.151), and stem diameter (0.150) at the phenotypic level. In furtherance of this, Abd-Allah (2015) found that seed yield was significant and positively correlated with the number of branches per plant, mature pods per plant, and seeds per pod. Ahamed *et al.* (2015) revealed that the highest range of variation was recorded in average fruit weight (18.25- 25.41g), followed by yield per plant (98.90 – 1650.00g).

2.15 Multivariate techniques for interpretation of genetic distance

Notwithstanding the size of the population, genetic distance among accessions is envisaged by applying various multivariate statistical tools that analyse genetic relatedness among accessions and characteristics and classify them based on their genetic distance from variant measurements on individual operative taxonomic units. The most usual multivariate techniques entail the following: cluster analysis, principal component analysis, principal coordinate analysis, and multidimensional scaling (Thompson *et al.,* 1998).

2.15.1 Clustering

Clustering, also known as class discovery, is an exploratory data analysis tool which classifies the same groups of samples across the variables into specific groups by optimizing the degree of homogeneity within a group and heterogeneity between the groups**.** Cluster analysis (Hair *et al*., 1995) classifies individual samples based on homogeneity in their characteristics such that accessions within clusters are similar and dissimilar among clusters. It is also known as segmentation or taxonomy analysis and is a group of

multivariate techniques used to classify objects (subjects, respondents, products, etc.) based on their peculiar characteristics. Each object in the cluster will be similar to other objects and groups based on their peculiar characteristics or relationships. Cluster analysis allows visualization of similarities among taxa by the levels at which they are grouped (Crawford, 1990).

Two methods of clustering based on i) genetic distance measurement by Johnson and Wichern (1992) and the more robust maximum likelihood estimation and Bayesian methods of Pritchard *et al*. (2000) established to curb the constraints of distance-based methods are commonly applied. Mohammadi and Prasanna (2003) compared the frequently used hierarchical clustering method to the less widely used non-hierarchical one. Some methods could be used to estimate the genetic distance among clusters, and these vary according to how "closest" is defined at each stage of merging groups. Some examples are single link (nearest neighbour), complete link (farthest neighbour), and average link (UPGMA) (Aldenderfer and Blashfield, 1984).

2.15.2 Hierarchical Clustering/ Hierarchical Cluster Analysis

Hierarchical clustering is based on the assessment of similarity and the distance among individuals such that nearby objects are more related than those far apart. Each cluster depicts the optimum distance which links members so that different clusters have different maximum distances. Hierarchical methods often give a graphical output called a dendrogram or tree, demonstrating this hierarchical clustering structure. Instead of consisting of a single set of clusters, the dendrogram is a multi-level hierarchy where

clusters at one level are linked to clusters at a higher level. An agglomerative hierarchical clustering algorithm was utilized to explore the relationships among different accessions (Dopazo, 2007). This algorithm initially considers all the accessions separately and then successively classifies accessions into larger clusters until only a single cluster is obtained (Podani, 2001).

2.15.3 Principal Component Analysis (PCA)

The Principal component analysis (PCA) is a multivariate statistical method that attempts to simplify and analyze the interrelationship among a large set of variables in terms of a relatively small set of variables or components without losing any vital information of the original data set (Arpita and Kumar, 2016). PCA is the most frequently used visualization technique in multivariate statistics. It estimates the variability of genotypes or accessions with minimum loss of information available in the dataset. Pearson correlations among variables were, first, noted to get an overview of the suitability of all the datasets for principal component analysis (PCA). The application of PCA has been essential in all spheres of agriculture, genetics, biology, chemistry, ecology and food research (Menozzi *et al*., 1978). The PCA remarkably lowers an extensive series of data into smaller components by looking for groups with robust inter-correlation in a set of variables, and each component explains the percent variation to the total variability. The objective of PCA is to decrease the dimensions of information set with vast numbers of variables while maintaining the variance of the original data. Per its linear nature, PCA transforms the original data into new data sets of linear variables' principal components (Johnson and Wichern, 2007; Wilks, 2006).

The statistical power of PCA in genetic diversity studies is evident with the use of a descriptor list, a common practice to evaluate many morpho-molecular characters.

CHAPTER THREE

3.0 Phenotypic and molecular characterization of okra (*Abelmoschus esculentus* (L.) Moench) germplasms in Ghana

3.1 Introduction

Okra (*Abelmoschus esculentus*, (L) Moench) productivity in Sub-Saharan Africa (SSA), including Ghana, is saddled with low yield, averaging 2.5 tons/ha in West Africa as compared to over 8.8 tons/ha in North Africa (FAO, 2018). This wide yield gap of okra in West Africa, is attributed to the use of genetically inferior and unimproved cultivars and poor management practices (Alake, 2020), including soil fertility and drought. In many locations of the country, landraces have been cultivated over time (Ahiakpa *et al*. 2013). However, these are sensitive to diseases, nematode infections, pests and worms (Sinnadurai, 1992). Being a crop in tropical areas where funding for research is inadequate compared to highly industrialized countries, little effort has been made to improve okra genetically (Werner *et al.* 2015) in Ghana. To meet the demand of the ever-growing human population in the country, it is thus imperative to find alternative means for increasing the yield potential of okra in a sustainable manner. Therefore, accessing the most appropriate genotype is fundamental to breeding.

The worth of germplasm collection depends on the number of accessions contained and their diversity, which are imperative for reasonably utilising plant genetic resources (AdeOluwa and Kehinde, 2011). Genetic diversity is the variability among different genotypes of a species (Bello *et al*., 2012b). Genetic diversity plays a significant role in crop improvement for identifying distinctive accessions vital for the curators of Gene banks (Bello *et*

al., 2011). In any diversity studies, morphological characterization is recommended as the first step before in-depth molecular and biochemical analyses are employed (Akash *et al*., 2013). Several researchers observed a high degree of morphological variation among the West African okra accessions (Akanbi *et al*., 2010; AdeOluwa and Kehinde, 2011). Earlier works done by Oppong-Sekyere *et al.* (2011) in Ghana focused mainly on using morphological traits to determine diversity among okra germplasms. Compared to phenotypic variability studies, few reports are available on the molecular characterization of okra in Ghana. Moreover, the morphological characterization of plants can be influenced by environmental or physiological factors.

Therefore, to enhance our understanding of genetic diversity and genetic relatedness among genotypes, the use of molecular markers is more feasible since they are minimally influenced by environmental conditions or plant development factors (Schafleitner *et al*., 2013). Molecular markers such as simple sequence repeats (SSRs) (Kumar *et al*., 2017), inter-simple sequence repeat (ISSR) (Yuan *et al*., 2014), amplified fragment length polymorphism (AFLP) (Salameh, 2014) and random amplified polymorphic DNA (RAPD) (Kaur *et al*., 2013) have been applied in okra genetic diversity analysis. Among several markers available, microsatellite or simple sequence repeats occur ubiquitously and abundantly in eukaryotic genomes. As molecular markers, they combine many desirable marker properties, including high-level polymorphism and information content, an unambiguous designation of alleles, even dispersal, selective neutrality, high reproducibility, co-dominance

and rapid and simple genotyping assays. The study was initiated with the following specific objectives;

1. To assess genetic diversity among 100 Ghanaian okra germplasms using morphological characters and SSR markers.
2. To identify and select promising okra accessions for yield and its component traits.
3. Identify distinct genotypes and eliminate obvious duplicates from the germplasm.

3.2 Materials and methods

3.2.1 Source of Genetic Materials

A total of hundred (100) okra genotypes [*Abelmoschus esculentus* (L.) originating from different agro-climatic zones of Ghana were collected and used for the experiment. Ten (10) were procured from the Plant Genetic Resources Research Institute (PGRRI) of the Council for Scientific and Industrial Research (CSIR), Bunso, Eastern Region; forty-seven were obtained from the Horticulture Division of CSIR-Crops Research Institute, Kwadaso, Kumasi and forty-three were collected across eleven production regions of Ghana (Upper West, Upper East, Northern, Bono East, Bono, Ahafo, Ashanti, Central, Western North, Oti and Volta Region) (Table 3.1.)

Table 3.1 Details of collected okra accessions and their sources

Ent.	Accessions	Community	Ent.	Accessions	Community
1	Hihaho	Gbogbame	51	OK11P13	CSIR, Kwadaso
2	AKD3	CSIR, Kwadaso	52	Asontem ASH	Nkwankwaa
3	Alama	Adabokrom	53	G7	CSIR, Kwadaso
4	Maanpeli	CSIR, Kwadaso	54	OK11P30	CSIR, Kwadaso
5	MR OFFEI	CSIR, Kwadaso	55	Nkruma Fitaa	Kutre No.2
6	5	CSIR, Kwadaso	56	Owni Maana	Zanlerigu
7	Bropo	Kwameseikrom	57	Kobonmani	Wa
8	Fabae 008	CSIR, Kwadaso	58	G	CSIR, Kwadaso
9	Mangbaa	Balungu	59	Tamale 2A	CSIR, Kwadaso
10	Wun mana	Tingoli	60	AFRIYIE	CSIR, Kwadaso
11	OK11PT25	CSIR, Kwadaso	61	Clemson	Kejetia (Shop)
12	Asontem tiatia	Akumadan	62	G12	CSIR, Kwadaso
13	G6	CSIR, Kwadaso	63	Asontem CR	Mankessim
14	BBN8	CSIR, Kwadaso	64	Bamo	PGRRI, Bunso
15	Ayigbe	Ntafrewaso	65	Bosikese 002	Bosikese
16	57	CSIR, Kwadaso	66	AKD1	CSIR, Kwadaso
17	Penkruma	Kobreso	67	Sepaale	Sepaale
18	14	CSIR, Kwadaso	68	K8PT14	CSIR, Kwadaso
19	EJS 1	Ejisu	69	Asontem 1	PGRRI, Bunso
20	FNBAC11	CSIR, Kwadaso	70	Kran fono	Kutre No.2
21	39	CSIR, Kwadaso	71	AMO/96/218	CSIR, Kwadaso
22	AKD8	CSIR, Kwadaso	72	Nkruma	PGRRI, Bunso
23	Paapa	Adamsu	73	47	CSIR, Kwadaso
24	BBN3	CSIR, Kwadaso	74	Lougoeoemama	PGRRI, Bunso
25	Sengevi	Agortime	75	Akorofu	Worawora

Table 3.1 cont'd

Ent.	Accessions	Community	Ent.	Accessions	Community
26	Tamale 2E	CSIR, Kwadaso	76	Ogye Abaatan	PGRRI, Bunso
27	SGKP3	CSIR, Kwadaso	77	OSOFO 003	CSIR, Kwadaso
28	Ejisu 001	Ejisu	78	Sepale Wuro	Guo
29	21	CSIR, Kwadaso	79	Asontem 2	PGRRI, Bunso
30	Bropo Asontem	Asare	80	Nyubalsi	Kpasolgu
31	Tamale 2H	CSIR, Kwadaso	81	Essoumtem	Ashanti
32	Zedulie kopiene	Dondometeng	82	Keta	CSIR, Kwadaso
33	AKD11	CSIR, Kwadaso	83	Ayisha Ash	Asuoso
34	GH3734	CSIR, Kwadaso	84	Fetri	PGRRI, Bunso
35	Ayisha BA	Tanoso	85	Abapa	Mankranso
36	51	CSIR, Kwadaso	86	AKD 9	CSIR, Kwadaso
37	Siengu Maana	Zanlerigu	87	Nkran Nkruma	Addisa
38	50	CSIR, Kwadaso	88	Fetri 2	PGRRI, Bunso
39	FUNAAB 2	CSIR, Kwadaso	89	Normiri	PGRRI, Bunso
40	Nyufulma	Kpasolgu	90	Asante Aba	Adugyama
41	G1	CSIR, Kwadaso	91	Atuogya	PGRRI, Bunso
42	3	CSIR, Kwadaso	92	Dagara Saalu	Guo
43	Sepale Were	Ko	93	EDUB 004	Ashanti
44	Adesheman	Kejetia market	94	BBN11	CSIR, Kwadaso
45	Baabo	Nyamebekyere	95	Wun mansala	Kpalung
46	33	CSIR, Kwadaso	96	G 11	CSIR, Kwadaso
47	24	CSIR, Kwadaso	97	25	CSIR, Kwadaso
48	YELEEN	CSIR, Kwadaso	98	Asante Nkruma	Ntafrewaso
49	55	CSIR, Kwadaso	99	CRI 1	CSIR, Kwadaso
50	Avata	Agorkpo	100	Mampong	Bosikese

3.2.2 Experimental Site

The experiment was conducted at the experimental field of CSIR-Crops Research Institute, Kwadaso-Kumasi, between April and October 2020. The area is located on latitude 06º40' North and longitude 01º39' West. With an elevation of 260 m above sea level, the region is distinguished by a semi-deciduous forest zone. The region has a bimodal annual rainfall distribution pattern. In the major season, rains start in late March and end in the middle of July. The agro-ecology is characterized by short dry spells in August. The minor rainy season starts from September to the latter part of November. The mean annual rainfall of the area is between 1200 mm and 1500 mm. Approximately 23°C and 31°C on average for minimum and maximum temperatures, respectively (Table 3.2). The soil is moderately drained sandy loam. The vegetative cover of the area was dominated by *Panicum maximum* and *Ageratum conyzoides*.

Table 3.2 Average monthly temperature (ºC), rainfall (mm) and relative humidity (%) during the 2020 season at Kwadaso

Location: Kwadaso					
Months	**Temperature (ºC)**		**Rainfall**	**Relative humidity (%)**	
	Minimum	**Maximum**	**(mm)**	**Minimum**	**Maximum**
April	24.8	33.8	3.6	59	88
May	24.3	31.1	6.1	61	92
June	23.9	31.3	3.7	65	91
July	23	29	1.7	71	91
August	22.9	29.9	0.3	62	88
September	22.7	30.4	6.7	65	93
October	23.5	32	5.4	61	93

3.2.3 Experimental design and treatments

The field experiment used two replications of a 10 × 10 alpha lattice design. Each accession was planted in a one-row plot of 4.05m long; hills were spaced at 0.45m while rows were spaced 0.75m apart, with one guard row on either side. Two seeds were sown per hill and later thinned to one plant two weeks after emergence to give a plant population of 3,091 with a total experimental area of 1,043.25 m^2. Each accession was represented by 10 individual plants. Data were randomly recorded on five tagged plants of each accession. The soil's physical and chemical properties at the experimental site are presented in Table 3.3.

Table 3.3 Soil physical and chemical properties at Kwadaso experimental sites in the 2020 cropping season

	Location
Soil Properties	**Kwadaso**
pH 1:2.5	6.23
Organic Carbon (%)	0.6
Organic Matter (%)	1.03
Total Nitrogen (%)	0.03
Exchangeable cations (me/100g)	
Ca	3.62
Na	0.01
Mg	0.64
K	0.01
Total Exchangeable bases	4.28
Exchangeable acidity (me/100g)	0.15
ECEC (me/100g)	4.43
Available P (mg/kg)	3.94
Particle size (%)	
Sand	76
Silt	15
Clay	9

3.2.4 Agronomic practices

The land was ploughed to a depth of about 30 cm with a tractor-mounted plough and harrowed to break down large clods of soil to a fine tilth during the 2020 major cropping seasons. The area was lined and well-demarcated/pegged. Golan SL TM and Sunpyrifos 48% EC insecticide were used to control grasshoppers and *Podagrica* spp., respectively which were the most notorious and predominant insect pests at the field. *Panicum maximum,* which was the dominant weed in the area, was controlled by manual weeding. Earthing up was also done to provide support for plants. The compound fertilizer, NPK (15-15-15), was applied as a basal dressing using the side placement method two weeks after planting (WAP), and this was followed by a top dressing with sulphate of ammonia at four WAP. The fertilizer applications were done immediately after irrigation to avoid scorching of plants and to ensure nutrient availability to plant roots.

3.2.5 Parameters measured

3.2.5.1 Qualitative Parameters;

Qualitative data were collected on fruit type (form), growth habit (general appearance), and stem. Pod pubescence, stem colour, leaf colour, leaf shape, petal colour, fruit colour, and fruit shape were all measured per the International Plant Genetic Resources Institute (IPGRI, 1991) descriptor list for okra species before harvesting (Table 3.4).

Table 3.4 Qualitative Morphological Characteristics Evaluated in the Study and their Codes

S/N	Keys	Characters measured	Character codes
1	SS	Seed size	1= Small, 2 = medium, 3 = large
2	SC	Seed colour	1= dark, 2 = black, 3 = whitish to dark, 4= purple to black
3	SSH	Seed shape	1 - round, 2 = kidney, 3 = oval
4	LRC	Leaf rib colour	1= green, 2 = green + red vein
5	PtC	Petiole colour	1= green, 2 = green + red vein. 3 = purple
6	PC	Petal colour	1= golden yellow, 2 = yellow
7	StC	Stem colour	1= green, 2 = green + purple tinge. 3 = purple
8	FC	Fruit colour	1= green, 2 = green + red spots. 3 = dark green to black 4 = green to yellow, 5 = purple
9	FP	Fruit pubescence	1= smooth, 2 = little rough. 3 = downy + hairs
10	LP	Leaf pubescence	1= smooth, 2 = little rough. 3 = downy + hairs
11	LSh	Leaf shape	From types 1 to 11
12	FSH	Fruit shape	From types 1 to 15
13	FO	Fruit orientation	1 = intermediate, 2 =slightly falling, 3 = horizontal 4 = erect, 5 = drooping
14	ShES	Shape of epicalyx segment	1 = linear, 2 = lanceolate, 3 = triangular

3.2.5.2 Quantitative traits

The following quantitative characters, viz. days to first flowering, were measured as the time from planting to the start of first flowering, and days to 50% flowering were computed as the time from planting to when 50% of the plants had emerged flowers. The height of the plant was measured from its base to the tip of its main stem while, stem diameter was also calculated by measuring the diameter of the stem with a standard graduated vernier caliper. The number of internodes was calculated per plant and counted at final picking. In contrast, internode length was determined as the length of the internodes between the fifth and sixth nodes at maturity. Dry pod length and width were measured as the length of pods and width from each harvest in each plot, and the average length and width were calculated and recorded, respectively. The number of dry pods per plant was calculated by dividing the

total number of dry pods per plot by the number of collected plants. The number of seeds per pod was counted as the number of seeds extracted from each dry pod after harvest. Hundred seed weight was determined by extracting seeds from five mature, dry pods; 100 seeds were counted, oven-dried and weighed.

3.2.6 Molecular characterization

The molecular analysis was conducted at the Kwame Nkrumah University of Science and Technology Biotechnology lab, KNUST-Kumasi, under the Department of Crops and Soil Sciences, between September 2021 and February 2022.

3.2.6.1 Genomic DNA isolation

Okra is highly mucilaginous, and its mucilage interferes with DNA isolation procedures as an impurity. To overcome this challenge during the extraction process, the yellow and etiolated fresh leaves were picked from a two-week-old seedlings raised in sachet plastic bags under dark conditions. This method was used alongside an SDS-based protocol developed by Demissie *et al.* (2020) for highly purified DNA isolation. Total genomic DNA was then extracted from the young seedlings and purified. Ninety (90) mg of fresh cleaned okra leaf tissue were ground to paste. Eight hundred (800) µl of cell lysis buffer (0.5% SDS (w/v) in 10X TE) was added to each tube, followed by vortexing at high speed for approximately 2 minutes until the paste was fully mixed with buffer. The samples were incubated for 10 minutes at room temperature (RT). This step was followed by precipitation of genomic

DNA with 200 µl 3 M sodium acetate (pH 5.2) and mixed by inversion of tubes. The mixture was then incubated on ice. The samples were centrifuged at 16,000Xg for 5 minutes at RT to pellet the leaf material. The supernatant was transferred carefully to an empty 1.5 ml centrifuge tube.

An equal volume of ice-cold isopropanol was added to the supernatant and completely suspended by vortexing and inverting the tube for approximately 20 seconds. The samples were again incubated for 15 minutes at RT by inverting tubes every three minutes by hand. Samples were centrifuged at 16,000Xg for 3 minutes at RT. Then, the supernatant was removed with a pipette. 500 µl of freshly prepared wash buffer (1ml of 5M NaCl in 100ml of 95% ethanol) was added to each tube and completely suspended by vortexing the tubes for approximately 20 seconds. The step was followed by centrifuging the samples at 16,000Xg for 3 minutes at RT to pellet the genomic DNA. The last step was the removal of the supernatant and washing the pellet with 75% cold ethanol (4°C). The pellet was allowed to dry at RT before diluting with 60 µl of 1XTE buffer. The DNA was stored temporarily at four °C before its quality and quantity were checked. The purity and concentration of extracted DNA were checked with nanodrop. DNA integrity was checked using gel electrophoresis at 1% agarose gel.

3.2.6.2 Screening for Polymorphism

All extracted DNA were bulked using 10 per sample. Thirteen SSR primer pairs were screened for polymorphism using the bulked DNA. The PCR reaction was carried out for each primer pair plus the bulked DNA in a 20 µl reaction mixture. Gel electrophoresis was used to detect the amplified

products on 2% agarose gel. Only primers showing multiple bands were selected for PCR for the DNA of the 100 okra genotypes (Table 3.5).

Table 3.5 Primer sequence of the 6 SSR primers used to analysis the Genetic diversity of 100 okra genotypes

No.	Primer Name	Primer sequence (5' - 3')	Length	Tm
1	AEKVR-117 F	TACGTTCCGTACCTTACTTCGG	22	60.07
	AEKVR-117 R	GTTACGACGAGGTTTACCAAGG	22	60.07
2	AEKVR-119 F	TAACTGAGCTATCCCGACCATTA	23	58.39
	AEKVR-119 R	CTCGTTCATCCTATCTTTTGCC	22	58.21
3	AEKVR-108 F	TAGCGAAGAAATCACAGTTCACA	23	56.60
	AEKVR-108 R	CGGGGAAATAAAGTAGAAAGGC	22	58.21
4	AEKVR-165 F	TAGCAAAAGCGATGATTGTCTG	22	56.35
	AEKVR-165 R	CCCCTAAACCCTAATCCTGACT	22	60.07
5	AEKVR-183 F	TGGTTTAGGGTTTACCGACTACG	23	60.17
	AEKVR-183 R	TAAGTTCGGGTTTAGGGTACGA	22	58.21
6	AEKVR-187 F	TCCGAGATTCAAGCGGATTATAG	23	58.39
	AEKVR-187 R	ACGACCACGCAACCGTAT	18	57.30

Source: SBS Gene Tech Company limited, Beijing-China

3.2.6.3 PCR amplification

The PCR reaction was performed on each DNA sample in a 20 µl reaction mixture containing 4 µl of 10 × Taq buffer (100 mM Tris- HCL, pH 8 with 50 mM EDTA, 500 mMNaCl, 10 mM 2- Merceptoethanol), 3 µl of 1 mM dNTPS, 0.2 µl of 5 unit of Taq DNA polymerase, 1.2 µl of 25 mM MgCl2, 2 µl of template genomic DNA and 2 µl each of SSR primers. The genomic DNA was subjected to PCR amplification using 20 random decamer primers. PCR amplification was performed in 96 microtiter plate wells in the Thermocycler of Applied Biosystems (Model EP Gradients). The reaction mixture was preheated at 94°C for 4 min followed by 45 cycles for 1 min denaturation at 94°C, 1 min annealing at 37°C and elongation or extension at 72°C for 2 min. Annealing temperature varied from primer to primer. After

the last cycle, a final step of 8 min at 72°C was added to allow complete extension of all amplified fragments of DNA.

3.2.6.4 DNA gel electrophoresis

Four µl of 6X loading dye was added to each amplified product and mixed thoroughly. This mixture loaded 10 µl of each sample in 1.5% agarose gel prepared in 1X TBE buffer. The PCR products were resolved by running gel at 5 V/cm for 3 h. The gels were visualized under UV light using a photo documentation system.

3.2.6.5 Statistical Analysis

Using SAS statistical software (9.2), the morphological data acquired for all variables examined were first subjected to ANOVA to assess the degree of genetic variability. Treatment means were separated by the Least Significant Difference at a 5% probability level. Principal component analysis was done using SAS statistical software (9.2). Cluster analysis and construction of the dendrogram were carried out for all morphological characters. With reference to yield parameters, Pearson's Correlation analysis was also carried out between pairs of quantitative parameters. The genotypic and phenotypic variance and their coefficient of variation were computed using the formula suggested by Burton and de Vane (1953) as follows;

$$Genotypic\ variance\ (\sigma^2 g) = \frac{GMS - EMS}{r} \quad \text{(1)}$$

Where,

GMS = Genotypic mean sum of square

EMS = Error mean sum of square

r = number of replications

$$Phenotypic\ variance\ (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where,

$\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Error variance

Phenotypic and genotypic co-efficient of variation

$$\text{Genotypic co-efficient of variation (GCV)} = \left(\frac{\sqrt{\sigma^2 g}}{\bar{x}}\right) \times 100 \quad \text{_____(2)}$$

Where,

$\sigma^2 g$ = Genotypic variance

$\bar{x}$= Population mean

$$\text{Phenotypic co-efficient variation (PCV)} = \left(\frac{\sqrt{\sigma^2 p}}{\bar{x}}\right) \times 100 \quad \text{_____ (3)}$$

Where,

$\sigma^2 p$ = Phenotypic variance

$\bar{x}$= Population mean

PCV and GCV values were categorized as low, moderate, and high values as indicated by Sivasubramaniah and Menon (1973) as follows:

0 - 10% = Low,

10 – 20 = Moderate,

> 20 = High

Using the formula employed by Falconer and Mackay (1996), broad sense heritability values were calculated as follows:

$$\text{Heritability, } h^2 b\% = \frac{\sigma^2 g}{\sigma^2 p} \times 100 \quad \text{_____ (4)}$$

Where,

h^2b = Heritability in the broad sense,

σ^2g = Genotypic variance,

σ^2p = Phenotypic variance

According to the procedures shown by Johnson *et al.* (1955), the genetic advance in an absolute unit (GA) and percent of the genetic advance as a percent of the mean (GAM), assuming the selection of superior 5% of the genotypes, were estimated as follows:

Genetic advance, $GA = K.\frac{\sigma^2 g}{\sigma^2 P}.\sigma p$ _____ (5)

Where,

K = Selection intensity, the value which is 2.06 at 5% selection intensity

σp = Phenotypic standard deviation,

h^2b = Heritability in the broad sense,

σ^2g = Genotypic variance,

σ^2p = Phenotypic variance

Genetic advance (of mean) = $\frac{Genetic\ Advance\ (GA)}{Population\ mean} \times 100$ _____ (6)

The GA as a percentage of the mean was categorized as low, moderate and high as suggested by Johnson *et al.* (1955) as follows.

0 - 10% = Low,

10 – 20 = Moderate,

> 20 = High

Phenotypic (rp) and genotypic (rg) correlations between two traits were calculated according to the formula suggested by Johnson *et al.* (1955)

$$rpxy = \frac{COVpxy}{\sqrt{\sigma^2 px.\sigma^2 py}} \quad \text{(7)}$$

Where,

$rpxy$ = phenotypic correlation coefficient between character x and y,

$COVpxy$ = phenotypic variance between character x and y,

$\sigma^2 px$ = phenotypic variance for character x

$\sigma^2 p$ y = phenotypic variance for character y

$$rgxy = \frac{COVgxy}{\sqrt{\sigma^2 gx.\sigma^2 gy}} \quad \text{(8)}$$

Where;

$rgxy$ = genotypic correlation coefficient between character x and y,

$COVgxy$ = genotypic variance between character x and y,

$\sigma^2 gx$ = genotypic variance for character x

$\sigma^2 g$ y = genotypic variance for character y

3.3 Results

3.3.1 Seed Characteristics

The ANOVA showed statistically highly significant ($p<0.001$) variations among the genotypes for seed colour (SC), seed size (SS) and seed shape (SSh). Seed size ranged from small to large according to the okra descriptor. Most germplasm in the population was predominantly medium-sized seed (60%), while 31% of the okra collections had large seed sizes and 9% were characterized by small seed sizes (Figure 3.1). Similarly, the colour of seeds varied from dark, black to whitish-to-dark. The population was dominated by black colour (56%) followed by whitish to dark colour (28%) and dark colour recording the least among the population (16%). Moreover,

the shape of the seed spanned from round to oval. Round seed shape controlled the population (44%) and was followed by kidney seed shape (30%) (Figure 3.2).

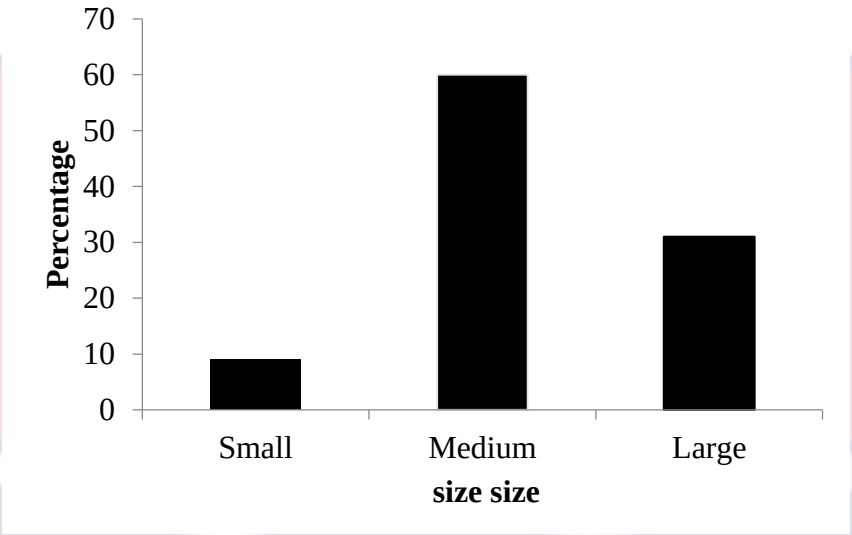


Figure 3.1 Variations in seed size

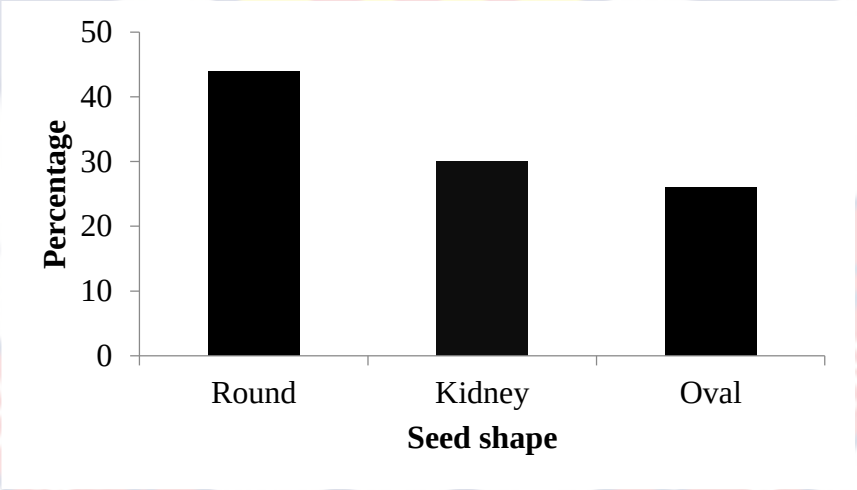


Figure 3.2 Variations in seed shape

3.3.2 Stem colour

Green, green + purple tinge and purple were the three distinct colours of the stem. About 83% of the okra accessions were predominantly green, while 16% of the plant population had green + purple tinge stems. However, Siengu maana (1%) was characterized by purple stem colouration (Figure 3.3).

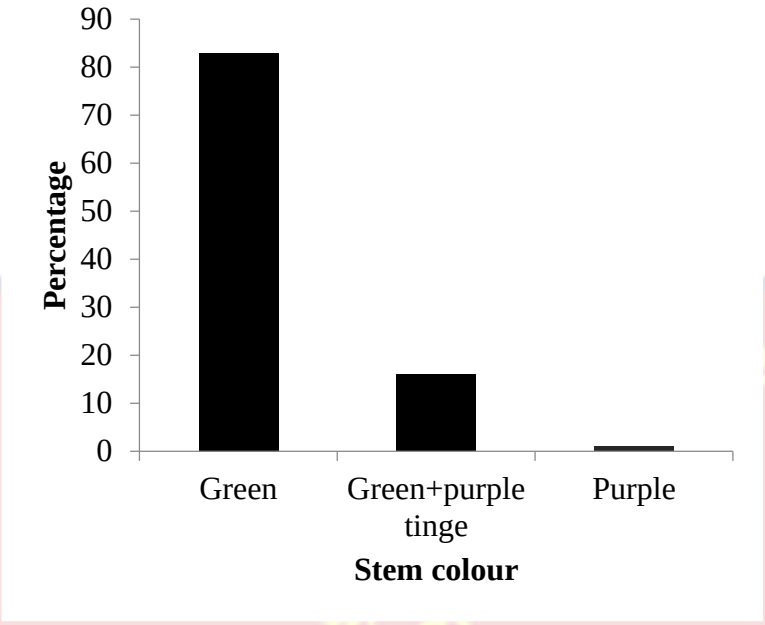


Figure 3.3 Variations in stem colour

3.3.3 Leaf pubescence

There were highly significant ($p<0.001$) differences among the genotypes for leaf pubescence. About 57% of the collected accessions produced conspicuous pubescence on the leaves, while 1% of the populations were smooth. Meanwhile, 42% of the germplasm had slight pubescence on the leaves (Figure 3.4).

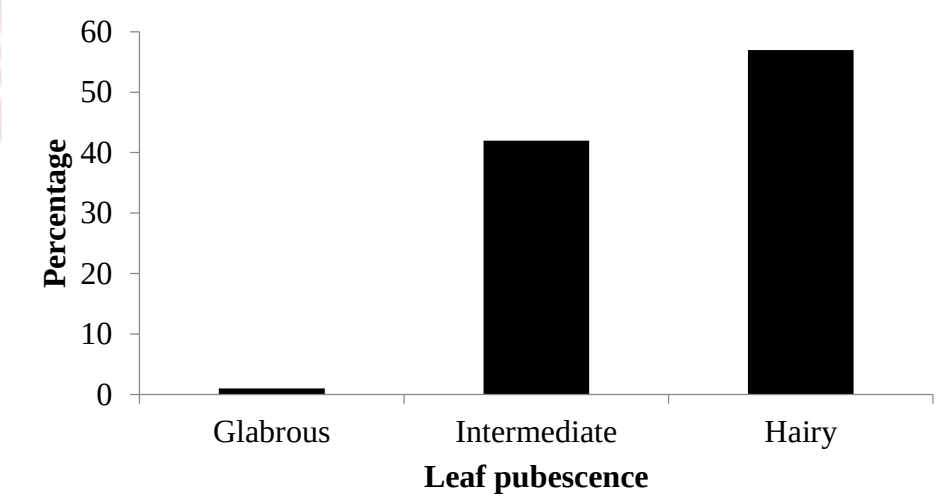


Figure 3.4 Variations in leaf pubescence

3.3.4 Leaf shape

There were significant ($p<0.001$) variations among the genotypes for leaf shape (Figure 3.5). Leaf shape ranged from distinct types, type 1 to type 9, according to the okra descriptor (IBPGR, 1991). Thirty-nine percent of the collected germplasm produced leaves with type 3 scores, while 35% of the germplasms produced type 4 leaf shapes. Meanwhile, 2% of the population produced type 6 and 7 leaf shapes. However, 1% of the genotypes had leaves scored as type 8 and type 9 (Figure 3.5).

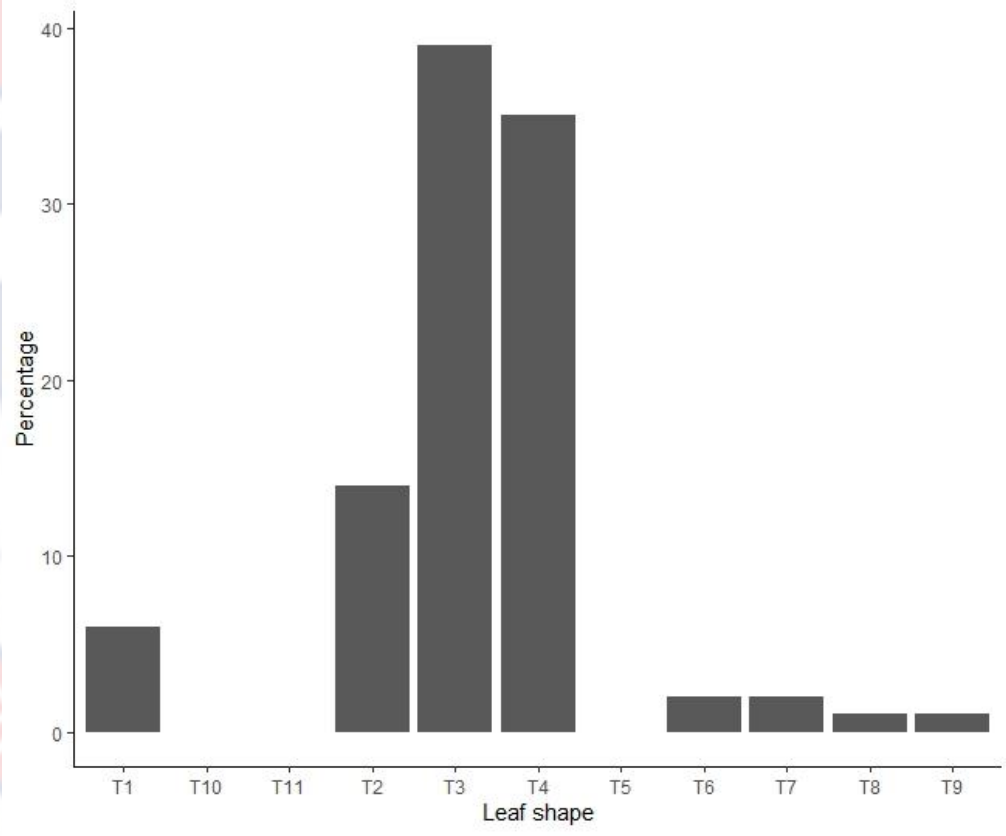


Figure 3.5 Variations in leaf shape

3.3.5 Leaf rib and petiole colour

The result showed highly significant ($p<0.001$) variations among the genotypes for leaf rib and petiole colour. The ANOVA displayed two varying colours: green + red vein and green. Fifty-nine percent of the germplasms

produced leaves with green + red veins, while 41% of the collected accessions had leaves entirely dominated by green colours (Figure 3.6).

Leaf petioles ranged from green to purple colourations. Large proportions (60%) of the genotypes produced petioles with green + plus red veins, while 39% of the plant population had leaves that produced green petioles. However, 1% of the genotypes produced purple leaf petioles (Figure 3.7).

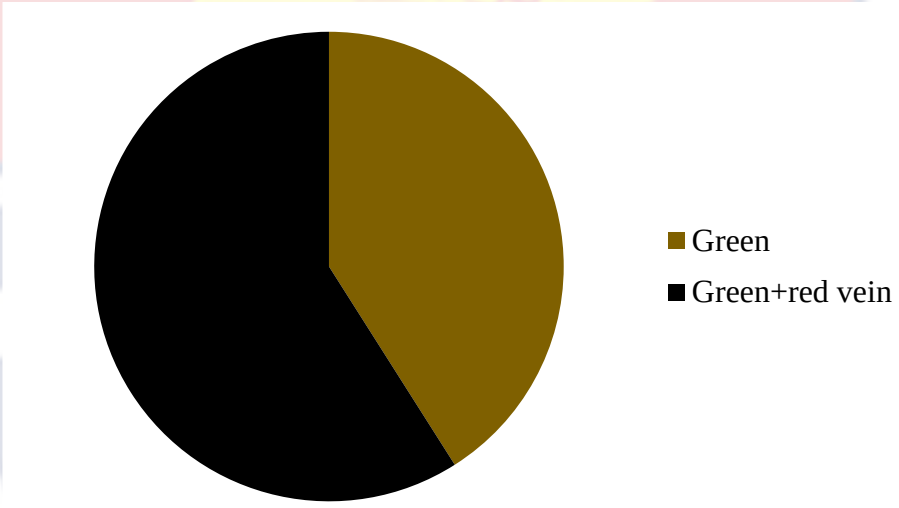


Figure 3.6 Variations in leaf rib colour

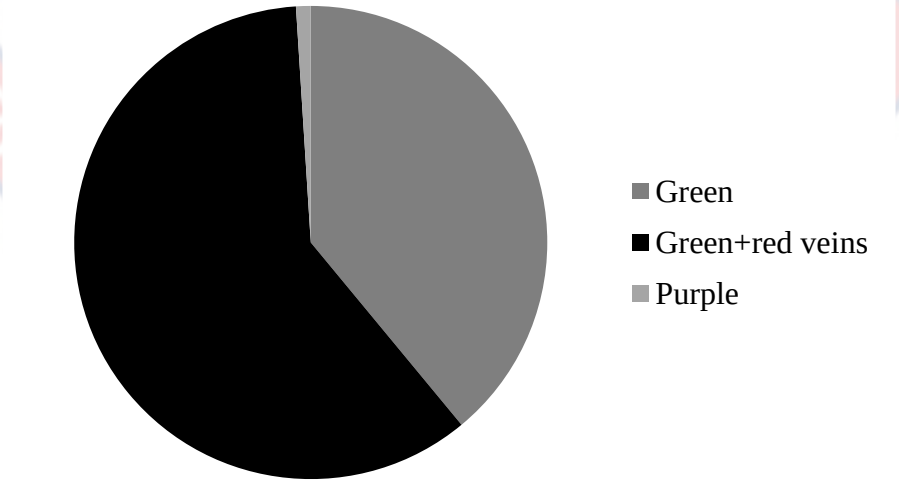


Figure 3.7 Variations in leaf petiole colour

3.3.6 Petal colour

The ANOVA showed significant ($p<0.001$) differences among the genotypes for petal colours. Petal colours ranged from golden yellow to yellow colours. Plants with yellow petal colourations characterized a large proportion of the plant's population (81%). Meanwhile, 19% of the plants produced petals with golden yellow colouration (Figure 3.8 and Figure 3.9).

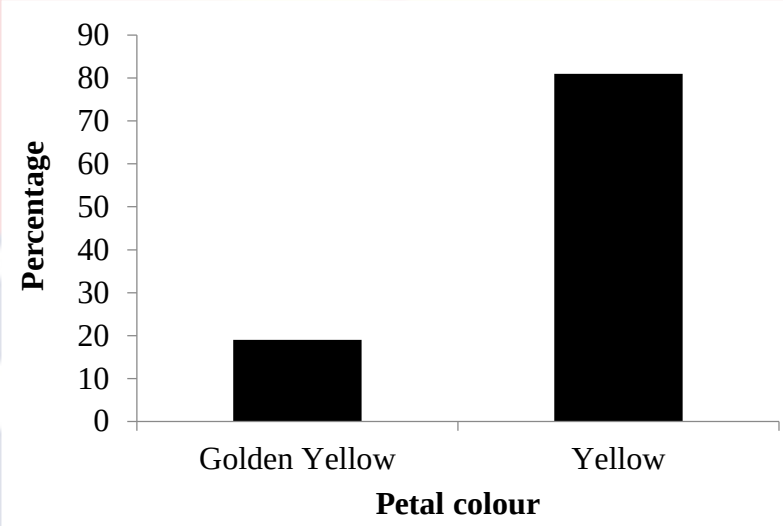


Figure 3.8 Variation in petal colour

Golden yellow petal **Yellow petal**

Figure 3.9 Variations in petal colour

3.3.7 Shape of epicalyx segment

There ANOVA revealed significant ($p<0.001$) differences among the genotypes for the shape of epicalyx segments of the okra flowers. 76% of the population produced a lanceolate shape of epicalyx segments, while 24% produced a triangular shape. However, none of the plants had a linear epicalyx segment shape (Figure 3.10 and Figure 3.11).

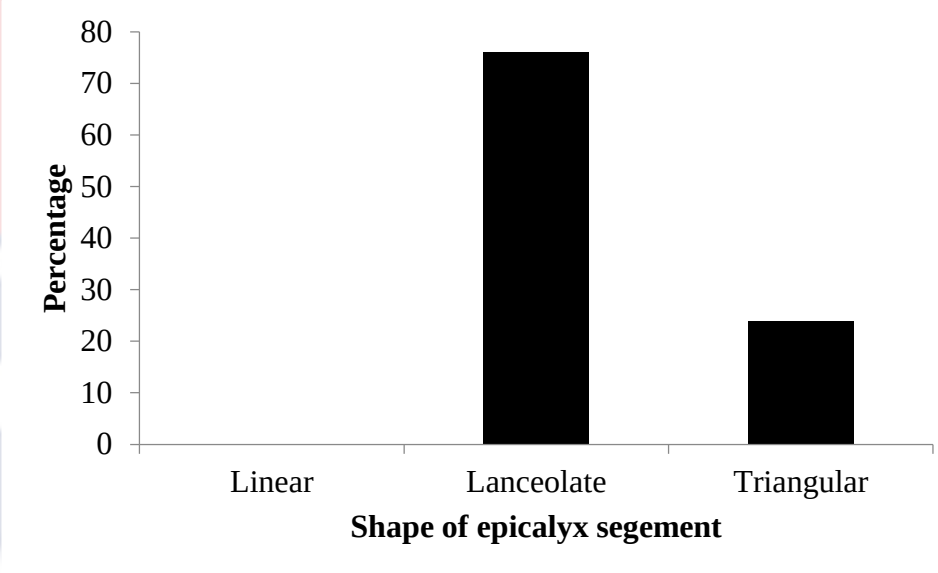


Figure 3.10 Variation in the shape of epicalyx segment

Triangular shape epicalyx **Lanceolate shape**

Figure 3.11 Variation in shape of epicalyx segment

3.4 Fruit Characteristics

3.4.1 Fruit pubescence and Fruit Shape

The extent of pubescence on fruits varied significantly. A significant proportion (65%) of the plant population bore fruits with little hairs on them. Meanwhile, 21% of the population produced smooth fruits without hair, whereas 14% produced hairy fruits (Figure 3.12).

Moreover, it was observed that fruit shape depicted the widest diversity among the genotypes from short conical to long slender, curved or straight fruits and was scored from type 1 to type 15. The population was dominated by fruits with type 8 and type 2. However, few of the population bore fruits scored as type 3, 4, and 5 (Figure 3.13 and Figure 3.14).

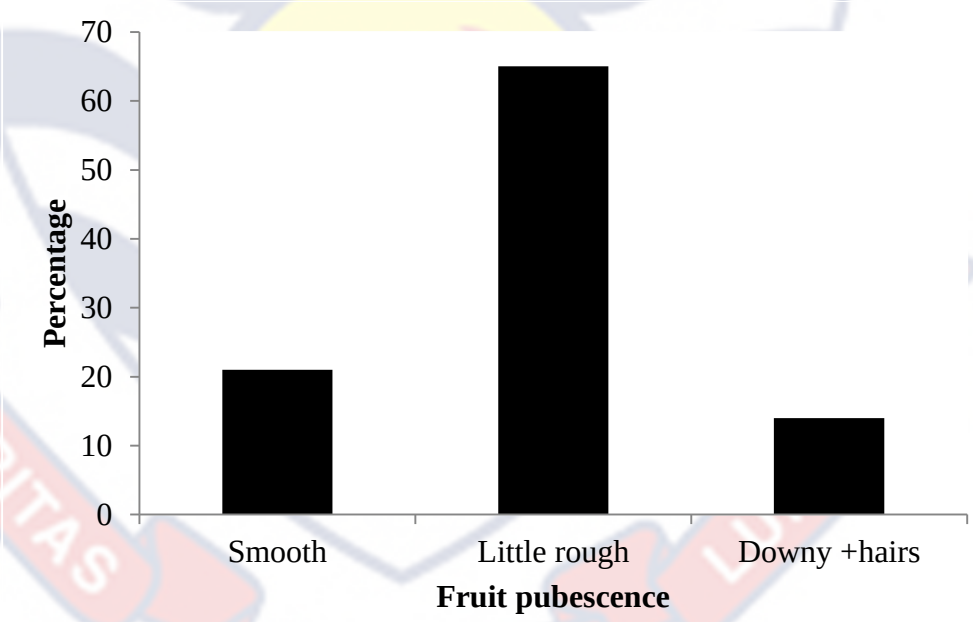


Figure 3.12 Variations in fruit pubescence

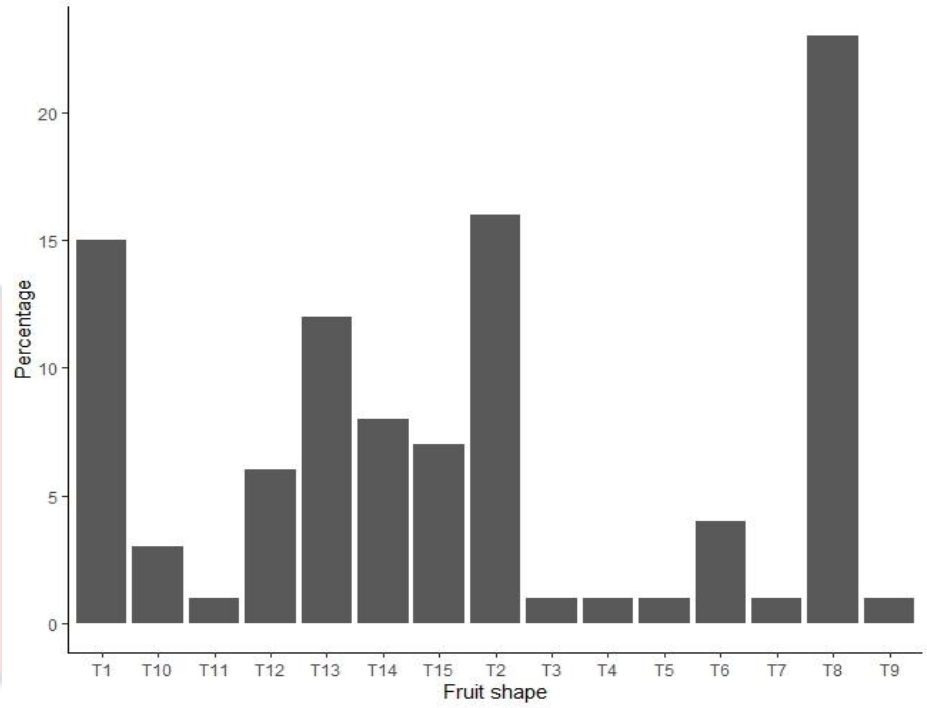


Figure 3.13 Variations in fruit shape

Figure 3.14 Variations in fruit shape

3.4.2 Fruit Colour

The result of the analysis of variance showed a significant variation ($p<0.001$) among the genotypes for fruit colours. Fruit colour diversity ranged from green to purple (Figure 3.15 and Figure 3.16). About 69% of the collected germplasms were characterized by green fruits, and 12% of the accessions produced fruits with green + purple spots. However, Siengu maana (1%) had purple fruit colouration (Figure 3.15 and Figure 3 16).

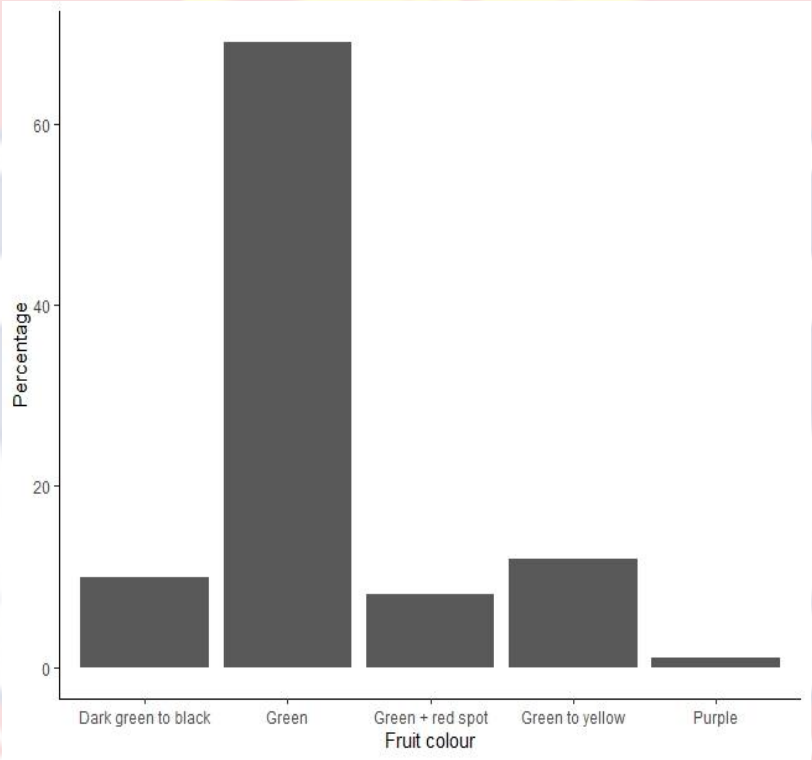


Figure 3.15 Variation in fruit colour

Green Green + purple spot Purple

Figure 3.16 Variation in fruit colour

3.4.3 Fruit orientation

Fruit orientation differed among the genotypes. The result revealed that 86% of the collected germplasm bore fruits that were erect on the main stem of the plant whiles 13% of the genotype produced fruits that were horizontal on the main stem. However, 1% of the genotype bore fruits drooping on the main stem (Figure 3.17 and Figure 3.18).

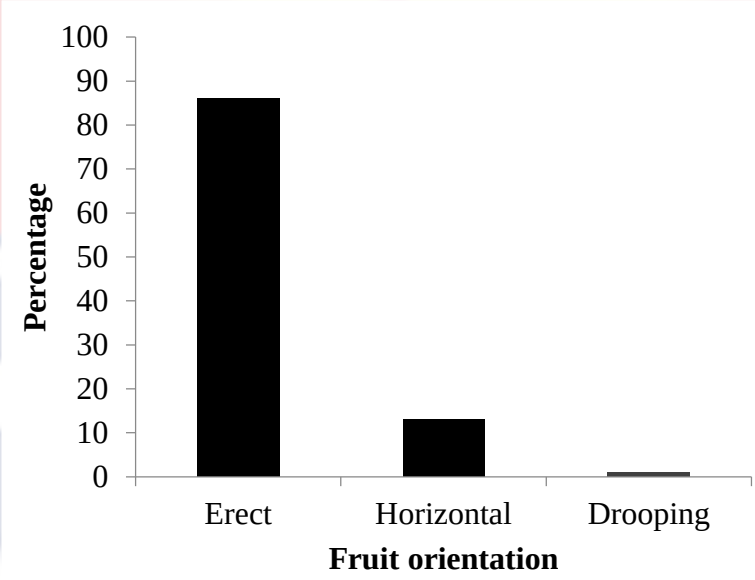


Figure 3.17 Variations in fruit orientation.

Erect position Horizontal Drooping

Figure 3.18 Variations in fruit orientation/ position on the main stem

3.5 Variability in Quantitative Agro- morphological Traits of Okra Genotypes

The results showed significant ($p<0.001$) differences among the genotypes for all quantitative traits. Days to first flowering ranged from 41.2 to 148.9, with a mean of 68.6 days. Okra genotypes Dagara saalu, Asontem ASH, Sepaale Were, and Sepaale Wuro recorded the shortest number of days to flowering (Table 3.6). Conversely, Okra genotypes GH4511, GH5293 and Fabae recorded the most extended number of days to first flowering. The result showed that the average days to 1st flowering was 68.6 days, and about 25% of the genotypes required more than the average days to produce 1st flowering. The days taken for genotypes to attain 50% flowering ranged from 47.2 to 151.2 days, with Dagara saalu, Nyubalsi, and Clemson genotypes recording the shortest number of days to reach 50% flowering (Table 3.6). Moreover, the hundred seed weight varied from 2.3 g to 6.0 g with a mean of 3.9 g. Okra genotypes Penkruma produced the highest 100 seed weight, followed by Osofo and Bropo. Moreover, Penkruma, followed by GH5793 and G7, had the most dry pods per plant. Furthermore, the height of plants varied from 12.3 to 95.6 cm, with a population average of 48.2. Okra genotype 0K11P30 produced the tallest height at flowering, followed by the Keta genotype and Asontem ASH (Table 3.6).

Table 3.6 Means of Quantitative Agro-morphological traits among the 100 Okra genotypes

ACCESSIONS	MP(cm)	STD(cm)	DFF (days)	50%FL(days)	FFN	FFrPN	FL(cm)	FW(cm)	NFP	NS/F	100SWT(g)
Hihaho	67.9	1.4	62.2	71.3	9.9	10.6	7.7	2.3	5.1	61.7	4.1
AKD3	39.7	1.0	56.2	60.3	8.3	8.0	6.2	3.7	3.6	51.6	5.1
Alama	72.9	1.3	54.0	62.1	9.1	9.0	6.2	2.9	5.2	53.4	3.4
Maanpeli	30.3	1.1	61.0	67.2	7.1	7.7	4.6	2.9	2.9	71.6	3.0
MR OFFEI	44.5	1.5	57.7	66.6	6.4	6.1	9.8	2.1	4.4	78.6	4.1
5	50.3	1.5	56.8	61.9	6.5	7.1	6.2	2.3	3.9	48.9	3.1
Bropo	36.7	2.2	72.2	84.3	7.3	7.0	12.2	2.5	6.7	75.3	5.4
Fabae 008	27.9	1.8	138.5	146.1	19.1	20.0	14.5	2.6	4.9	70.7	4.4
Mangbaa	40.6	1.3	58.9	66.7	5.2	5.2	5.8	2.6	5.8	56.9	4.5
Wun mana	26.9	1.6	60.7	72.3	5.9	6.1	6.1	3.5	4.6	40.2	4.2
OK11PT25	30.1	1.2	85.5	91.0	8.8	10.1	7.3	3.4	2.4	69.9	3.4
Asontem tiatia	42.0	1.2	50.7	58.5	7.0	6.9	7.3	2.5	4.2	74.5	3.2
G6	32.2	0.8	70.7	86.0	9.6	10.0	5.2	2.3	2.6	31.5	3.7
BBN8	42.2	1.1	65.5	69.8	6.8	7.4	7.2	2.6	4.3	54.4	4.6
Ayigbe	59.4	1.1	61.9	70.5	9.4	9.6	7.2	2.7	4.2	57.0	4.1
57	43.9	1.3	54.9	66.5	8.4	9.1	5.2	1.9	3.0	25.5	3.0
Penkruma	40.9	2.0	101.2	109.3	17.6	17.5	15.5	3.0	9.0	94.3	6.0
14	45.5	1.1	58.7	64.0	7.5	7.4	9.4	2.3	3.8	68.2	3.9
EJS 1	41.1	1.2	58.0	67.0	7.3	8.6	7.4	2.1	4.0	47.8	4.0
FNBAC11	35.7	1.1	59.0	61.8	6.3	6.9	6.8	2.1	3.3	46.7	4.5
39	67.0	1.2	63.5	70.9	11.2	11.5	5.7	2.1	4.1	61.2	4.1
AKD8	56.2	1.3	60.9	64.3	8.0	8.5	6.9	2.0	3.9	59.5	3.2
Paapa	56.8	1.4	57.7	63.0	10.4	10.3	6.8	3.4	5.6	93.4	4.5
BBN3	40.5	1.5	70.2	75.5	11.3	12.7	6.0	2.7	3.9	53.4	3.9
Sengevi	59.7	1.3	73.9	78.8	13.0	13.5	3.2	3.3	2.7	97.8	3.2
Tamale 2E	54.2	1.5	58.5	61.9	7.2	7.6	6.2	2.5	5.9	77.1	3.4
SGKP3	65.2	1.2	67.2	70.3	11.5	11.9	8.6	2.0	5.0	33.4	3.3
Ejisu 001	74.7	1.3	68.9	72.8	9.5	10.0	7.2	2.0	3.9	52.6	3.5
21	53.6	1.2	62.2	70.5	8.5	9.4	7.4	2.7	4.0	49.1	3.7

Table 3.6 cont'd

ACCESSIONS	MP(cm)	STD(cm)	DFF (days)	50%FL(days)	FFN	FFrPN	FL(cm)	FW(cm)	NFP	NS/F	100SWT(g)
Bropo Asontem	72.1	1.7	65.0	71.8	7.7	8.8	5.2	2.9	4.0	64.7	4.0
Tamale 2H	47.0	1.4	67.3	70.1	10.9	12.0	6.3	2.3	4.6	72.6	4.2
Zedulie kopiene	36.5	1.2	60.0	68.7	4.7	4.7	5.6	3.1	3.5	83.5	3.8
AKD11	51.0	1.3	59.2	62.6	5.8	6.3	9.2	1.9	4.3	52.0	4.4
GH3734	31.2	1.2	61.4	64.4	8.1	7.7	8.6	2.5	3.1	66.2	3.4
Ayisha BA	38.2	1.2	66.9	72.4	8.1	8.2	4.4	3.3	2.6	61.4	2.4
51	51.1	1.2	58.7	61.4	8.8	8.6	9.7	2.0	5.4	81.3	4.3
Siengu Maana	58.2	1.0	55.1	58.1	5.4	7.4	17.1	2.3	3.0	56.9	5.0
50	63.7	1.7	61.9	63.9	7.1	7.2	9.6	2.3	6.6	81.2	4.2
FUNAAB 2	51.1	1.4	59.8	61.0	7.7	7.4	8.9	2.5	5.0	67.6	4.3
Nyufulma	30.0	1.2	68.0	73.7	4.2	4.7	4.4	2.7	4.1	40.8	3.9
G1	52.9	1.3	58.7	60.5	7.1	7.4	9.6	1.8	4.5	68.5	4.3
3	25.1	1.1	70.0	74.3	8.4	8.4	6.4	2.3	4.0	39.8	3.7
Sepale Were	43.8	1.1	47.5	65.4	5.4	6.7	3.7	2.5	2.2	62.1	3.1
Adesheman	56.4	1.2	54.7	67.5	6.6	6.4	6.4	2.5	3.1	68.0	3.6
Baabo	49.5	1.2	53.1	66.9	7.9	7.6	5.5	2.3	4.0	77.8	4.7
33	49.6	1.4	65.2	72.0	6.0	6.3	6.4	2.2	4.0	65.2	3.7
24	48.6	1.4	51.1	64.8	4.8	6.2	6.5	2.7	4.5	64.4	3.5
YELEEN	74.1	1.7	66.1	71.3	9.8	10.7	6.5	2.4	5.6	81.4	4.3
55	72.0	1.6	57.1	63.4	6.9	8.1	10.0	2.0	6.1	75.1	4.1
Avata	61.1	1.2	66.8	71.5	9.7	10.5	6.2	2.3	2.8	50.8	4.1
OK11P13	45.0	1.4	62.4	65.2	8.5	8.8	7.7	2.1	4.2	51.7	3.7
Asontem ASH	92.5	1.4	63.0	63.3	5.9	6.0	6.7	2.2	7.0	79.2	3.7
G7	52.2	1.7	68.2	70.1	11.0	12.6	7.6	2.5	7.0	44.2	4.3
OK11P3	95.6	1.4	59.7	65.0	8.0	7.9	6.1	2.9	5.9	77.9	4.5
Nkruma Fitaa	39.6	1.2	57.5	62.2	8.7	9.0	7.8	2.2	3.9	40.8	3.5
Owni Maana	46.7	1.0	77.7	87.6	11.0	12.1	4.8	2.0	2.2	64.2	3.9
Kobonmani	50.5	1.4	58.8	65.0	8.3	8.2	5.6	3.0	3.1	54.2	2.9
6	39.8	1.2	55.4	62.2	7.6	7.4	6.6	3.1	4.2	58.3	3.5
Tamale 2A	48.6	1.8	73.1	73.5	13.3	13.6	5.5	2.7	3.5	60.9	3.4

Table 3.6 cont'd

ACCESSIONS	MP(cm)	STD(cm)	DFF (days)	50%FL(days)	FFN	FFrPN	FL(cm)	FW(cm)	NFP	NS/F	100SWT(g)
AFRIYIE	42.0	1.4	55.4	59.7	8.0	8.3	8.5	1.9	4.2	59.0	4.0
CLEMSON	12.3	0.9	51.0	55.7	6.7	7.0	1.7	1.6	0.6	84.3	2.3
G12	16.1	1.3	71.8	76.0	7.0	6.5	8.5	2.2	1.7	51.3	4.7
Asontem CR	40.0	1.2	44.0	61.7	4.1	4.4	8.9	1.8	3.4	33.1	4.4
GH4373	45.5	2.0	118.9	126.0	24.8	25.3	6.7	3.8	5.4	72.3	4.6
Bosikese 002	74.1	1.4	49.5	68.2	4.2	6.6	6.2	2.8	4.3	61.3	4.0
AKD1	58.4	1.4	54.3	63.1	6.5	6.7	7.6	1.9	4.8	60.8	4.2
Sepaale	36.9	1.1	64.3	70.1	7.5	8.7	1.3	1.5	1.4	87.0	2.4
K8PT14	38.6	1.2	58.7	69.5	8.8	10.2	5.7	1.8	2.3	55.3	4.1
GH5293	30.5	1.6	143.4	150.5	18.8	18.8	8.2	2.6	5.2	80.8	4.3
Kran fono	40.9	1.4	64.8	70.6	12.5	12.7	3.6	2.6	2.7	43.5	4.9
AMO/96/218	38.7	1.1	88.3	87.8	7.5	9.2	3.8	2.4	4.5	40.3	3.5
GH 3760	37.7	1.8	100.4	106.9	12.3	12.8	12.0	2.3	5.1	50.2	4.0
47	56.2	1.6	64.2	64.7	9.2	9.0	8.6	2.1	4.9	39.8	3.7
GH2041	35.7	1.8	83.4	83.4	12.3	12.3	5.0	3.3	4.2	62.0	3.8
Akorofu	62.9	1.4	65.5	66.1	8.7	10.9	6.7	2.4	4.3	71.5	3.5
GH5793	47.4	1.8	133.1	141.3	19.9	20.0	11.5	2.9	8.8	63.6	3.7
OSOFO	26.4	1.7	75.0	73.1	8.2	8.4	8.9	2.1	5.2	46.1	5.5
Sepale Wuro	73.2	1.3	46.7	61.2	5.7	5.5	10.3	2.5	3.1	51.3	3.8
GH6105	31.7	1.6	77.3	92.8	9.0	10.7	9.0	2.7	4.1	44.8	3.8
Nyubalsi	38.9	1.2	49.0	54.1	6.2	8.9	5.0	2.6	2.1	46.6	3.0
Essoumtem	34.9	1.3	66.8	76.9	8.6	8.7	5.9	2.8	2.4	31.8	5.1
Keta	94.1	1.1	65.9	69.2	11.3	10.9	6.4	2.5	4.8	81.5	4.3
Ayisha Ash	49.1	1.2	62.6	69.8	8.6	8.5	6.7	3.1	4.5	42.2	2.7
GH4499	37.1	1.7	138.4	144.7	19.8	20.4	6.9	3.5	4.1	59.0	3.6
Abapa	46.6	1.5	74.1	81.7	7.9	8.5	6.3	2.1	2.7	34.7	4.5
AKD 9	47.0	1.2	58.9	65.9	5.3	8.9	9.6	2.4	5.1	62.6	3.9
Nkran Nkruma	79.0	1.5	66.8	72.2	13.9	13.6	8.3	2.7	4.1	79.2	4.0
GH4511	44.6	1.9	146.9	151.2	22.3	21.9	8.7	2.1	4.6	73.0	4.0

Table 3.6 cont'd

ACCESSIONS	MP(cm)	STD(cm)	DFF (days)	50%FL(days)	FFN	FFrPN	FL(cm)	FW(cm)	NFP	NS/F	100SWT(g)
GH1094	40.0	1.8	133.2	148.7	21.5	22.8	9.1	2.9	5.3	76.9	5.2
Asante Aba	49.6	1.5	65.9	70.2	8.8	8.4	6.6	2.6	5.4	84.5	3.6
GH4376	29.8	1.5	128.8	133.9	18.3	18.8	9.2	3.2	3.1	61.3	4.7
Dagara Saalu	41.4	0.9	41.2	47.3	4.1	6.3	4.7	2.5	2.0	36.9	4.0
EDUB 004	56.0	1.2	62.8	66.1	5.7	6.4	5.7	2.4	3.6	64.7	3.7
BBN11	37.8	1.0	56.8	60.4	5.3	6.3	4.9	2.4	3.1	52.7	3.9
Wun mansala	23.9	1.4	63.2	73.8	4.1	4.8	7.1	3.8	3.5	60.9	4.6
G 11	40.8	1.3	55.6	65.3	6.4	7.1	6.4	2.7	5.4	66.8	3.4
25	42.7	1.3	54.1	67.3	6.0	8.2	6.7	2.7	5.3	61.4	4.0
Asante Nkruma	55.8	1.2	66.3	70.4	10.3	10.8	6.3	3.1	3.9	82.2	4.2
CRI 1	64.4	1.2	54.6	61.1	5.7	6.0	7.2	2.3	4.0	76.2	3.9
Mampong	71.8	1.5	61.3	66.4	7.3	8.3	6.6	2.1	4.1	77.9	3.8

MPH= maximum plant height (cm); STD = stem diameter (cm); DFF = days to first flowering (days); 50%FL = days to fifty percent flowering; FFN = first flowering node; FFrtPN = first fruit producing node; FL = fruit length (cm); FW = fruit width (cm); NFP = number of fruits per plant; NS/F = number of seeds per fruit; 100SWT (g) = hundred seed weight (g)

3.5.1 General clustering of okra quantitative and qualitative morphological traits into groups

A cluster diagram obtained from the quantitative and qualitative morphological characters produced four main cluster groups of okra genotypes. Cluster I recorded the least number of okra genotypes, Clemson and Sepaale, which differed from genotypes in other clusters by having yellow petal colouration and green + red vein leaf rib and petiole colour (Figure 3.19). Cluster II consisted of nine (9) okra genotypes distinctly differing from other clusters by having a long period of maturity, thus taking over a hundred days to flower (late genotypes), which was sub-divided into two sub-clusters B1 and B2 (Figure 3.19). Moreover, seven of the ten collected germplasm from Bunsu, Ghana, were grouped in this cluster.

Also, cluster III, the largest cluster with forty-eight (48) okra genotypes, is made up of okra genotypes that vary from genotypes in other clusters by having relatively shorter days to flower and green fruit colour. Cluster III was subdivided repeatedly into sub-cluster C1 and C2, each with twenty-four (24) genotypes (Figure 3.19). Cluster IV was the second largest cluster with forty-one okra germplasms. Cluster IV was discriminated into two sub-clusters, D1 and D2.

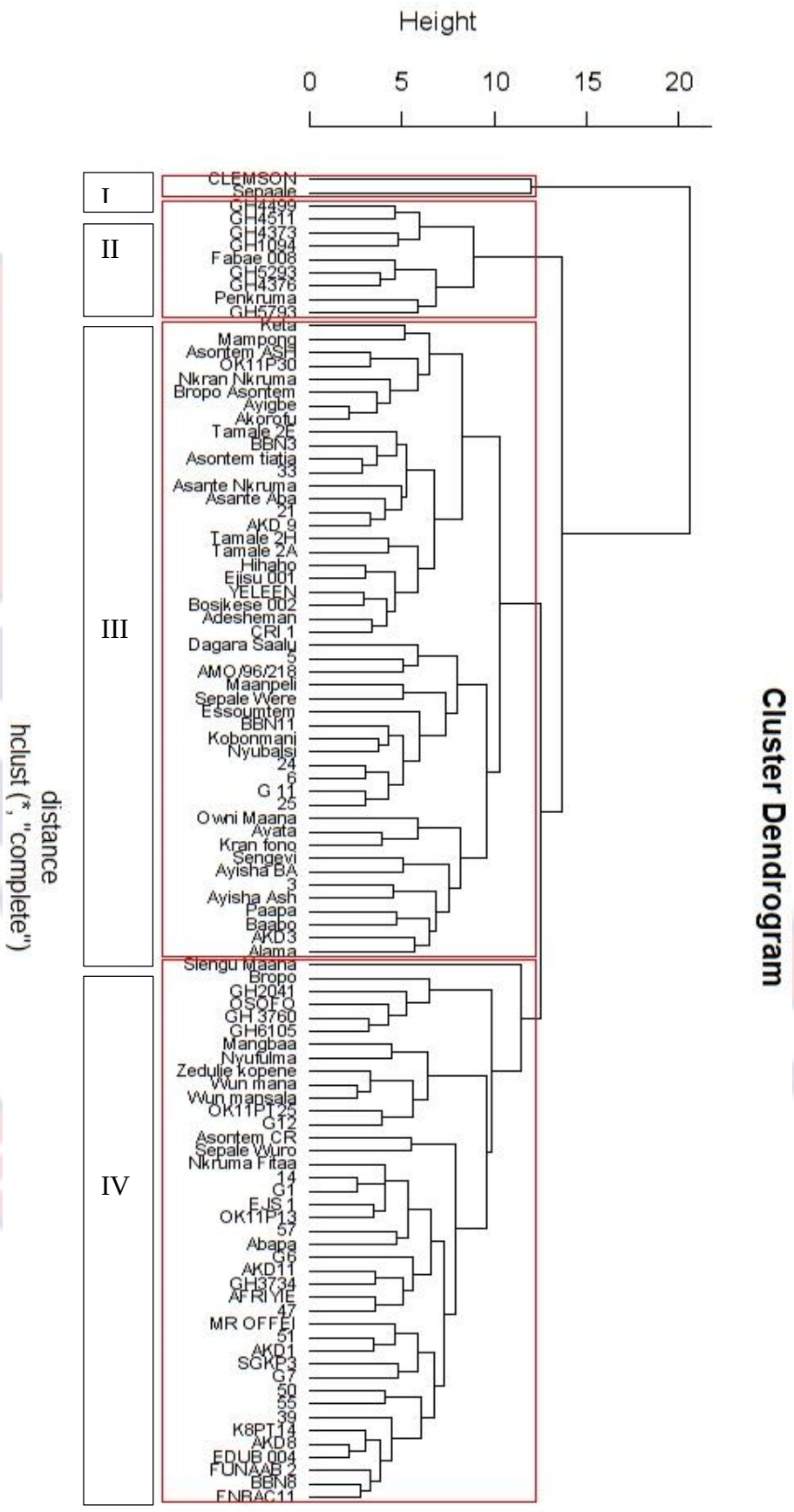


Figure 3.19 Morphological dendrogram showing the relationship among 100 okra genotypes revealed by cluster analysis

3.5.2 Principal components analysis

The first two PCs accounted for up to 58.85% of the total variation (Table 3.7). The first principal component (PC1) explained 38.4.4% of the total variance observed, and this was correlated to variation in the incidence of *Podagrica* spp., stem girth, length of fruit, hundred seed weight, number of fruits per plant, and incidence of okra mosaic disease. These parameters recorded the highest loadings. The other characters, such as days to first flowering, fruit width, length of internode, number of seeds per fruit, plant height and days to 50% flowering, had comparatively lower effects on the first PC. The second principal component (PC2) accounted for 20.41% of the variations, with days to first flowering, length of internode, plant height, and 50% flowering being the characters with the highest loadings. The third PC accounted for 10.15% of the total variation, mainly due to days to first flowering, number of seeds per fruit, plant height, incidence of okra mosaic disease, days to 50% flowering, and internode length. However, the hundred seed weight and fruit width had negative weight on PC3. The fourth principal component (PC) accounted for 8.24% of the total variation and was positively associated with fruit width (0.66) and the number of seeds per fruit. Fruit length and number of fruits per plant had negative weight on PC4 (Table 3.7).

3.5.3 Molecular Characterization of 100 okra genotypes using SSR Markers

Six of the thirteen SSR primers used to measure genetic diversity across the 100 okra genotypes were polymorphic, representing forty-six percent. These six primers were used for the diversity studies, and they

generated 613 scorable and readable bands across the genome of the 100 okra germplasm with sizes of amplified allelic loci ranging from 100 to 1500 bp. The primer pair AEKVR-117 amplified the most DNA polymorphic bands (159), while AEKVR-183 amplified the least number of DNA polymorphic bands (69) (Table 3.8). The number of alleles varied from 1 (AEKVR-187) to 4 (AEKVR-117 and AEKVR-165). The polymorphic information content (PIC) of a locus ranged from 0.08 for AEKVR-187 to 0.93 for AEKVR-183, with a mean of 0.72. Approximately 83% of the primers had above 0.5 PIC values. About 83% of the SSR loci had PIC values greater than 0.6. Expected heterozygosity ranged from 0.07 for AEKVR-183 to 0.92 for AEKVR-187, with a mean of 0.29, as shown in Table 3.8.

Table 3.7 The loadings and proportion of variation of the seven principal components among the study genotypes

Characters	PC1	PC2	PC3	PC4	PC5	PC6	PC7
DFF	0.28	0.39	0.37	0.02	0.23	0.2	0.07
FL	0.3	-0.04	-0.18	-0.59	0.16	0.25	-0.33
FW	0.26	0.02	-0.28	0.66	0.3	-0.21	0.07
HSWT	0.31	-0.08	-0.39	-0.12	0.47	-0.27	-0.26
INTL	0.07	-0.54	0.26	0.03	0.32	0.27	0.16
NFP	0.35	-0.12	0.09	-0.26	-0.01	-0.4	0.27
NSF	0.24	-0.2	0.38	0.28	-0.26	-0.12	-0.75
PH	0.1	-0.55	0.28	-0.01	0.15	-0.11	0.24
SI	-0.37	-0.01	0.13	-0.16	0.46	-0.38	-0.04
STD	0.37	0.11	0.11	-0.13	-0.12	-0.47	0.25
IP	-0.35	0.14	0.37	-0.12	0.19	-0.38	-0.18
50%FL	0.28	0.4	0.37	0.03	0.26	0.21	0.08
SD	**2.15**	**1.56**	**1.1**	**0.99**	**0.87**	**0.76**	**0.74**
Variance	**4.61**	**2.45**	**1.22**	**0.99**	**0.76**	**0.58**	**0.55**
% variance	**38.44**	**20.41**	**10.15**	**8.24**	**6.34**	**4.83**	**4.57**
%Cumulative	**38.45**	**58.86**	**69.01**	**77.25**	**83.59**	**88.42**	**92.99**

PH= maximum plant height; STD = stem diameter; DFF = days to first flowering; 50%FL = fifty percent flowering; FL = fruit length; FW = fruit width; NFP = number of fruits per plant; NSF = number of seeds per fruit; 100SWT (g) = hundred seed weight; INTL = internode length; NRF =number of ridges per fruit; IP =incidence of *Podagrica* spp

Table 3.8 Assessment of genetic diversity among 100 Okra genotypes using nine cowpea primers resolved on 2% agarose gel.

Primer/Name	Sample size	Alleles	Heterozygosity	PIC	No. of bands
AEKVR-117	100	4	0.32	0.68	159
AEKVR-119	100	3	0.18	0.82	99
AEKVR-108	100	3	0.14	0.86	102
AEKVR-165	100	4	0.08	0.92	88
AEKVR-183	100	3	0.07	0.93	69
AEKVR-187	100	1	0.92	0.08	96
Mean	100	3	0.29	0.72	102.17

3.5.4 Molecular Cluster Analysis (Dendrogram) based on Molecular data

The dendrogram depicts the data from the six polymorphic primers, which clustered the genomes of the 100 okra genotypes into five large groups based on Gower's dissimilarity index at 0.27(Figure 3.20). Cluster I consisted of five okra genotypes: Dagara saalu, F003, K8PT14, G7 and F002. Cluster II was the second largest cluster, with 33 okra genotypes. Cluster II was discriminated into two sub-clusters, B1 and B2. However, five (5) ties (100% similar) were recorded among okra genotypes Sepaale (Nandom, Upper west) and GH4373 (Bantama, Ashanti), AMO/96/218 and AKD1 (same source, CRI- Kwadaso), Tamale 2A (Tamale) and Kobonmani (WA), Akorofu (Worawora, Volta) and Sepaale Were (Nandom, Upper west) and 24 and 3 (same source CRI- Kwadaso). Moreover, genotypes Asontem ASH (Kobreso, Ashanti) and Baabo (Nyamebekyere, Ahafo), G11 (CRI- Kwadaso), and Siengu maana (Zanlerigu, Upper East) recorded a Gower dissimilarity index of about 0.01 (Figure 3.20).

Also, Cluster III, the third largest cluster, recorded 20 okra genotypes that varied genetically from other clusters. Cluster III was further discriminated into two sub-clusters, C1 and C2, with two ties or duplicates. The duplicates are Wunmansala (Kpalung, Northern) BBN (CRI-Kwadaso),

Owni Maana (Zanlerigu, Upper East) and G (CRI-Kwadaso) with 100% similarity index (Figure 3.20).

Cluster IV recorded the least number of okra genotypes with only two (2) accessions: Mampong (Bosikese, Ahafo) and F004 (Techiman, Bono East), while cluster V recorded the most significant number of okra genotypes with forty (40) accessions. Moreover, cluster V was divided into two sub-clusters, E1 and E2. The analysis revealed that genotypes Ejisu 001(Ejisu, Ashanti) and GH1094 (PGRRI-Bunsu), CRI 1 and OSOFO (same source, CRI-Kwadaso) were duplicates within cluster V. Similarly, genotypes 5 (CRI-Kwadaso) and GH4511 (PGRRI-Bunsu), Asante Aba (Adugyama, Ahafo), F001 (Tanoso, Bono East) and BBN11 (CRI-Kwadaso), Alama (Adabokrom, Western North) and GH4499 PPGRRI-Bunsu), Sengevi (Agortime, Volta) and Nkruma fitaa (Kutre No.2, Bono) were also found to be duplicates with a similarity index of 100% (Figure 3.20).

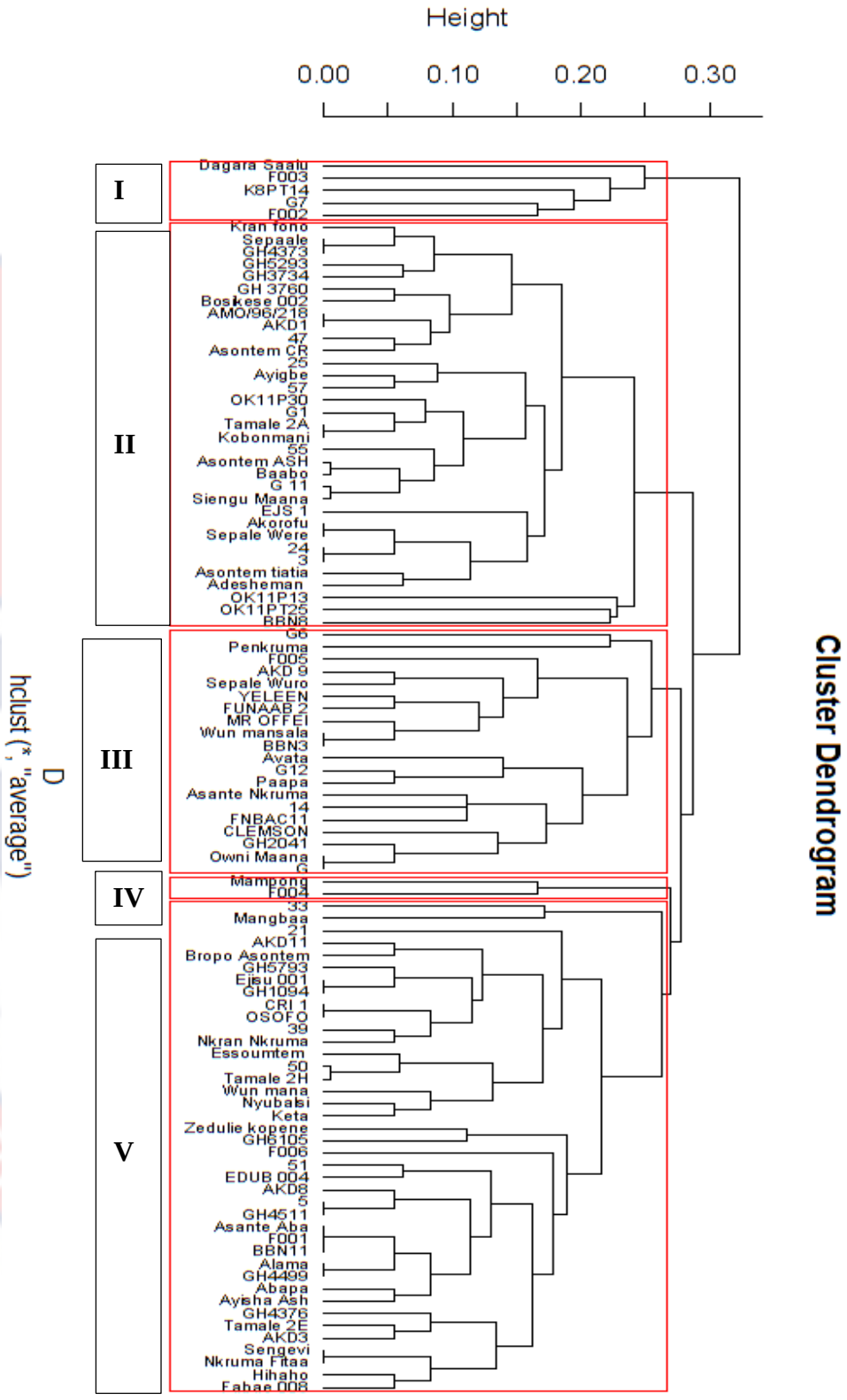


Figure 3.20 Molecular dendrogram showing the relationship among 100 okra genotypes revealed by cluster analysis

3.5.5 Phenotypic and Genotypic Variations

The result of the variability studies revealed significant differences among the genotypes for the studied traits. The estimated phenotypic variations (PV), genotypic variations (GV) and environmental variations for the 16 quantitative traits of 100 okra genotypes are presented in (Table 3.9). The phenotypic variation ranged from 0.09 to 485.88. The highest phenotypic variances were estimated for days to first flowering and were followed by days to 50% flowering. Meanwhile, stem diameter recorded the lowest phenotypic variance (Table 3.9). The genotypic variance ranged from 0.03 to 366.62. Days to first flowering recorded the highest genotypic variance, followed by days to 50% flowering (Table 3.9). Similarly, the result showed that environmental variance ranged from 0.07 to 277.96. The number of seeds per fruit recorded the highest environmental variance, followed by plant height (Table 3.9).

3.5.6 Phenotypic and genotypic coefficient of variation

The result of the genetic analysis showed that the estimated phenotypic coefficient of variation (PCV) ranged from 18.28% to 244.40%: Okra mosaic virus disease incidence and *Podagrica* spp. incidence were observed to have the most significant phenotypic coefficient of variation. Similarly, the hundred seed weight recorded the lowest phenotypic coefficient of variation, followed by fruit width (Table 3.9).

The result also revealed that the genotypic coefficient of variation (GCV) ranged from 7.49% to 167.57%. The okra mosaic virus disease incidence had the highest estimate of the genotypic coefficient of variation. It

was followed by the incidence of *Podagrica* spp. with an estimate of 56.16% (Table 3.9). The analysis again revealed that the environmental coefficient of variation (ECV) ranged from 15.15% to 177.39%. Okra mosaic virus incidence was found to have the largest environmental coefficient of variation. This was followed by the incidence of *Podagrica* spp. (Table 3.9).

Table 3.9 Variance parameters for sixteen characters in okra genotypes

Traits	Mean	EV	GV	PV	ECV(%)	GCV(%)	PCV(%)
Days to first flowering	68.64	119.26	366.62	485.88	15.91	27.90	32.12
Days to 50% flowering	74.87	128.74	341.28	470.02	15.15	24.67	28.96
Plant height (cm)	48.23	144.25	129.36	273.61	24.90	23.59	34.30
Stem diameter (cm)	1.36	0.07	0.03	0.09	19.15	11.75	22.47
Internode length (cm)	4.40	1.57	1.44	3.01	28.49	24.06	39.42
First flowering node	9.07	6.79	11.64	18.43	28.75	37.64	47.36
First fruit-producing node	9.60	6.77	11.39	18.16	27.11	35.15	44.39
Fruit length	7.18	6.04	0.31	6.35	34.25	7.72	35.11
Fruit width	2.52	0.18	0.09	0.27	16.82	11.95	20.63
Number of ridges per fruit	1.36	0.18	0.15	0.32	31.18	28.16	42.01
Pedicel length	1.53	0.31	0.08	0.40	36.71	18.87	41.27
Number of fruits per plant	4.18	1.62	0.63	2.25	30.46	18.93	35.86
Number of seeds per fruit	61.40	277.96	46.40	324.36	27.15	11.09	29.33
100 seed weight	3.94	0.43	0.09	0.52	16.68	7.49	18.28
Incidence of *Podagrica* spp.	0.81	0.63	0.21	0.84	98.34	56.16	113.24
Incidence of okra mosaic virus	0.39	0.47	0.42	0.89	177.93	167.57	244.40

PV=Phenotypic variation, GV= Genotypic variation, EV= Environmental variation PCV=Phenotypic Coefficient of Variation, GCV=Genotypic Coefficient of Variation,

3.5.7 Estimates of Heritability and Genetic Advance

Estimates of heritability in a broad sense and genetic advance as a percent of the mean (GAM) for the 16 quantitative traits are presented in (Table 3.10). Heritability values ranged from 4.84% for fruit length to 75.45% for days to first flowering. Seven out of the sixteen (16) studied traits, representing 43.75%, had low values of heritability estimates, while 5 out of

the sixteen studied traits, representing 31.25%, had medium estimates of heritability. Meanwhile, days to first flowering, days to 50% flowering, first flowering node, and first fruit-producing node representing 25% of the studied trait recorded high heritability estimates (Table 3.10).

The analysis revealed that genetic advance as a percent of the mean ranged from 3.5% for fruit length to 100% for incidence of okra mosaic disease. Ten of the sixteen traits representing 62.5% had high estimates of genetic advance as percent of the mean. In contrast, three of the studied traits representing 18.75% recorded moderate values of genetic advance as a percent of the means (Table 3.10).

Table 3.10 Estimation of heritability and genetic advance of different parameters of okra

Traits	H^2	GA	GAM (5%)
Days to first flowering	75.45	34.26	49.92
Days to 50% of flowering	72.61	32.43	43.31
Plant height (cm)	47.28	16.11	33.41
Stem diameter (mm)	27.33	0.17	12.65
Internode length (mm)	47.77	1.71	38.79
First flowering node	63.16	5.59	61.63
First fruit-producing node	62.70	5.50	57.34
Fruit length (cm)	4.84	0.25	3.50
Fruit width (mm)	33.54	0.36	14.26
Number of ridges per fruit	44.92	0.53	38.89
Pedicel length (mm)	20.90	0.27	17.78
Number of fruits per plant	27.87	0.86	20.59
Number of seeds per fruit	14.31	5.31	8.64
100 seed weight (g)	16.80	0.25	6.33
Severity of Podagrica spp	24.59	0.46	57.37
Severity of okra mosaic virus	47.01	0.91	236.68

H^2=Heritability in broad sense, GA=Genetic advance, GAM=Genetic Advance as Percent of Mean

3.5.8 Correlation coefficient for fruit yield and other yield components traits

Pearson`s correlation of the characters studied is presented in (Figure 3.21). The phenology traits (days to first flowering, days to fifty percent flowering, fruit length, fruit diameter, plant height, fruit width, number of seeds per plant, hundred seed weight and number of fruits per plant) were positively associated. The analysis revealed that the number of fruits per plant was highly significant and positively correlated ($p < 0.01$ or $p<0.001$) with plant height, stem diameter, number of seeds per fruit, fruit length, and hundred seed weight (Figure 3.21). Moreover, hundred seed weight showed a negative and significant ($p < 0.01$) association with *Podagrica* spp. and okra mosaic disease incidence. A significant positive ($p< 0.001$) association was calculated between days to 50% flowering and days to first flowering (Figure 3.21).

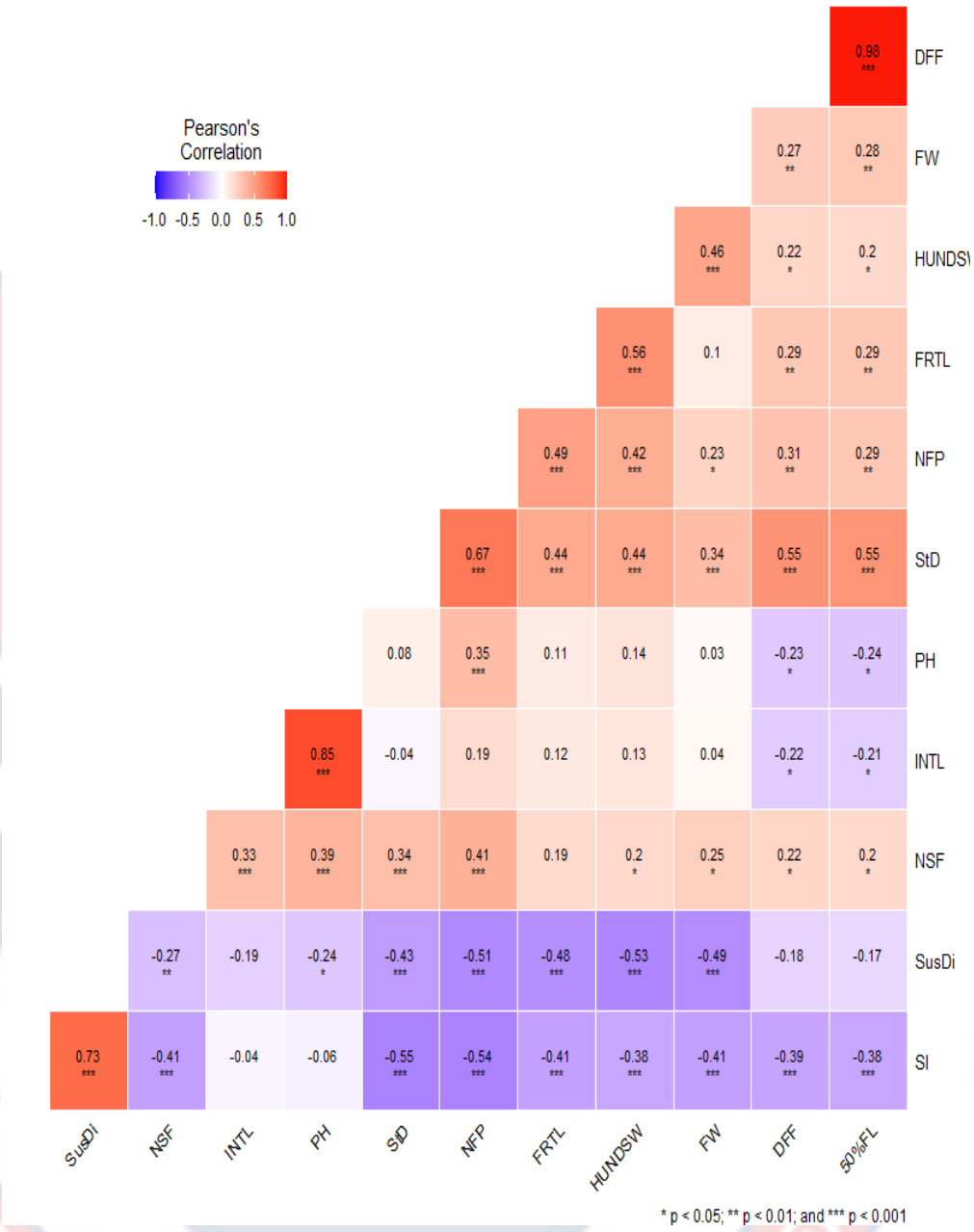


Figure 3.21 Pearson correlation coefficient for different traits

3.6 Discussions

The variability observed for the current study could be exploited through selective breeding to improve okra cultivars for desired traits. The results of this study supported those of Amoatey *et al*. (2015) and Hazem *et al.* (2013), who found significant variations across okra genotypes for most of the parameters under investigation. Differences in qualitative traits among the

germplasm provide a promising prospect for selection. The presence of a large number of green fruits (69%) among the studied germplasm confirmed the findings of Muluken *et al*. (2015), who observed that a larger proportion of the collected germplasm out of the 25 genotypes studied produced green fruits (72%). However, the findings of the present studies are contrary to the observation made by Adeoluwa and Kehinde (2013), who found purple fruit colour as predominant in the population (48.57%) followed by green fruit colouration (42.85%). The discrepancies in the result could be attributed to the differences in the germplasm and the selection location.

Cluster analysis aids in the reduction of some individual variables by grouping them into clusters and presenting them in the form of a dendrogram using the similarity-dissimilarity coefficient (Doumbia, 2012). Molecular markers, morphological traits, or a mix of the two can all be used to measure genetic diversity. The study of genetic diversity based on morphological characteristics has proven less trustworthy than diversity based on DNA markers, which are more reliable and independent of environmental variables. Among the 100 okra genotypes, the average SSR alleles per locus detected was 3.00. This is comparatively similar to numbers reported in studies by Schafleitner *et al*. (2013), Fougat *et al.* (2015)) with SSR markers, Gulsen *et al*. (2007) with SRAP markers, Akash *et al.* (2013) with AFLP markers and Prakash *et al*. (2011) with RAPD markers. The polymorphic information content (PIC) of a locus ranged from 0.08 for AEKVR-187 to 0.93 for AEKVR-183, with a mean of 0.72. The PIC values of primer AEKVR-183 were the highest, making it the most informative primer combination. Similar work was carried out for the creation and characterisation of SSR markers in

gossypium, with the mean PIC value being 0.65 (John *et al*. 2012). In another study in cotton, genetic diversity was examined, with PIC values ranging from 0.34 to 0.86 and a mean value of 0.80.

Moreover, Fougat *et al*. (2015) found comparable results from 24 okra accessions with slightly lower PIC values (0.00 to 0.89). Differences in the results may be attributed to variations in the markers used and the experimental crops. The highest heterozygosity of 0.92 reported by primer AEKVR-187 might reflect changes in the okra genome, which, despite being self-pollinating, may have undergone some hybridization during open-field agriculture.

The cluster analysis results based on qualitative and quantitative morphological and molecular traits grouped the 100 okra genotypes into four and five main clusters, respectively. This suggests that some individuals have similar characteristics. The dendrogram constructed from the morphological and molecular data also revealed that the genetic relationship among germplasm did not depend on the geographical origin of the collected okra germplasm, indicating free flow and adaptation of okra accessions across Ghana. These findings agree with earlier reports of Mishra *et al.* (1996), Reddy *et al.* (2012), Ab.Mazid *et al*. (2013) in okra and Elameen *et al*. (2008) in sweet potato. Some okra accessions clustered based on morphological similarities were re-grouped into different clusters and sub-clusters using the SSR markers. This situation could be attributed to environmental or physiological responses of the morphological tools. Moreover, the molecular dendrogram revealed that out of the 100 okra genotypes studied, 27 were deemed duplicates with a 100% similarity index. In contrast, the remaining 73

genotypes had varying degrees of similarity index. These findings are consistent with Almajali *et al*. (2012), who used ISSR markers to detect duplication in the fig germplasm. Sharma *et al*. (2015) used SSR markers to detect duplication among grapefruit germplasm.

All traits under investigation had larger phenotypic variances and phenotypic coefficients of variation than their corresponding genotypic variances and coefficients of variation. This indicates that the apparent variation is not only due to the genotypes but also the influence of the environment, and selection for these traits may be misleading. The environmental effect could be due to heterogeneity in soil fertility status and other unpredictable factors. These findings are in consonance with earlier works on okra by Thirupathi *et al.* (2012), Reddy *et al.* (2012b), Mohapatra *et al.* (2007) and Adekoya *et al.* (2014), who reported that most of the traits exhibited highly phenotypic variance and coefficient of variation higher than their respective genotypic variances. PCV and GCV estimates in the current studies were categorized based on Sivasubramanian and Madhavamenon (1973) as low (<10%), moderate (10-20%) and high (> 20%). Moderate values for GCV (10-20) were calculated for hundred seed weight, number of seeds per fruit, number of fruit per plant and number of ridges per fruit. Moderate PCV and GCV values showed that these characters were controlled more by the genetic factors. Hence, these characters were amenable to selection for further improvement. This research confirms the findings of Das *et al*. (2012), Thirupathi *et al*. (2012) and Ehab *et al.* (2013), who reported moderate PCV and GCV values of okra characters. However, the high magnitude (>20%) of PCV and GCV for days to first flowering, days to 50% flowering, plant height,

internode length, first flowering node and first fruit-producing node suggested greater phenotypic and genotypic variability among the populations. It indicated that these characters can be improved through phenotypic selection. By extension, it also meant greater potential for favourable advances in selecting these attributes than others (Eid, 2009; Ndukauba *et al*., 2015).

Broad sense heritability is an estimate of the total contribution of the genotypic variance to the total phenotypic variance. Estimates of heritability in the broad sense in the current study ranged from 4.84% for fruit length to 75.45% for days to first flowering. Johnson *et al*. (1955) indicated that heritability estimates were classified as < 30 values were low, 30 - 60 values were moderate and > 60 values were high. Accordingly, heritability estimate in a broad sense was high (>60%) for days to first flowering (75.45%), days to 50% flowering (72.61%), first flowering node (63.16%) and first fruit-producing node (62.70%). A high heritability, close to 1, indicates that genetics explain much of the variation; a low heritability, near zero, indicates that most of the variation is due to environmental factors. Heritability estimates give an insight into the extent of genetic control to express a particular trait and phenotypic reliability in predicting its breeding value (Ndukauba *et al*., 2015). This research agrees with Hazem *et al.* (2013), who reported high broad sense heritability for days to first flowering; Singh *et al.* (2006) and Mohapatra *et al.* (2007), who observed high magnitude (>60%) of heritability estimates for days to 50% flowering in okra. However, the findings disagree with those of Mihretu *et al.* (2014) and Pradip *et al.* (2010), who reported high heritability estimates for plant height in okra. Moreover, Anteneh (2017) noted high broad sense heritability estimates for the characters

of 25 okra germplasm except moderate heritability for days to emergence and days to first flowering. The disparity in results could be attributed to differences in the genetic materials. If the heritability of a character is very high, around 80% or more, the selection for such a character is reasonably easy. This is because there would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotype expression of the trait (Singh *et al.*, 1990).

The genetic advance as a percent of the mean (GAM) at 5% selection intensity for the current studies was estimated between 3.30% for fruit length and 236.68% for the severity of okra mosaic virus disease. Similarly, Mihretu *et al*. (2014b) also reported a genetic advance between 5.94% for the number of epicalyx and 198.15% for the number of primary branches. As reported by Johnson *et al.* (1955) and Sibsankar *et al.* (2012), high heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual than heritability alone. High heritability and genetic advance as a percent of the mean were obtained for days to first flowering, days to fifty percent flowering, first flowering node and first fruit-producing node. This indicates the predominance of additive genetic components governing these traits; hence, phenotypic selection will improve the characters. It provides better information than each parameter alone and also an expression of additive gene action and amenable for selection (Salesh *et al.*, 2010; Sibsankar *et al.*, 2012).

The presence of significant and positive associations for the number of fruits/plants and most yield component traits suggested that increasing these attributes could invariably increase fruit yield. The findings of positive

correlation are also confirmatory of results by Niranjan and Mishra (2003), Alam and Hossain (2006), Mehta *et al.* (2006) and Pal *et al.* (2010) on okra. Hazra and Basu (2000) suggested that component breeding would be particularly successful if significant yield characteristics were positively correlated, as was discovered in this study. Genes governing two positive and significantly correlated traits were similar, and environmental factors played a small part in expressing these traits that justified the possibility of correlated response to selection. The presence of negative and significant association observed for hundred seed weight with respect to incidence of *Podagrica* spp. and okra mosaic diseases implied that the selection of traits negatively correlated will favour one trait while suppressing others. This is in accordance with the findings of Jaiprakash and Ravindra (2004) on okra. Henry and Krishna (1990) also noted that characters that negatively correlate with one another would be complex to select for in characterising desirable traits. Those with a negative association but non-significant correlation will be disregarded in the selection for crop variety improvement.

3.7 Conclusion

The morphological traits and the 6 SSR markers used showed a wide genetic variability among the 100 okra genotypes studied. This provides an opportunity to select promising genotypes for desirable characteristics for breeding programmes, exploiting these genotypes for future breeding programmes. The dendrogram constructed from the morphological data and the 6 SSR markers revealed that the genetic relationship among germplasm did not depend on the geographical origin of the collected okra germplasm,

indicating informal germplasm exchange among farmers across Ghana. The molecular analysis revealed that 27 of the 100 collected germplasms were duplicates or genetically similar with a 100% similarity index. Moreover, okra genotypes Penkruma recorded the most dry pods per plant and the highest seed weight. It was also observed that Dagara saalu and Asontem ASH were the early maturing genotypes out of the 100 okra accessions.

CHAPTER FOUR

4.0 Assessment of breeding value and Gene Action of okra [*Abelmoschus esculentus* (L.) Moench] Germplasm under low-N and high-N Conditions

4.1 Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] stands out among vegetables due to its excellent nutritional content, broad adaptability, widespread popularity, year-round availability, and export potential. Despite okra's enormous contribution and benefits to many economies in West and Central Africa, okra production has been restricted by abiotic and biotic stresses. Inputs use in agriculture, notably soil N, are one of the abiotic stresses that affect okra productivity due to its high cost, resulting in inadequate application and decreasing soil fertility (Sanchez, 2010). Since many crops require a lot of energy to produce, adding nitrogen (N) fertilizer often results in the greatest input cost per crop, and energy price influences this cost (Rothstein, 2007). Since the advent of chemical fertilizers, the main goal has been to enhance yield production per unit area of land. N fertilizers were applied at levels nearly at the economic optimum (Firbank, 2005). The inherently low fertility quality of the soils and the unavailability of low N tolerant genotypes continue to be the key issues limiting okra production, particularly in SSA. This has resulted in a tremendous and varying yield reduction across many farms in Ghana. Using N-fertilizers to improve soil fertility has become essential to ensuring the world can feed billions of people (Abdul-Elkader *et al.,* 2010). However, the development of okra hybrids with high N use efficiency in a sustainable manner to reduce the excessive utilization of N fertilizers associated with the high cost and the direct impact

of these chemicals on the environment is critical. Therefore, developing and releasing such hybrids to our resource-poor farmers is the surest way of protecting the environment and mitigating food insecurity in Ghana.

To establish a solid foundation for a breeding programme designed to improve yield and nitrogen use efficiency in okra hybrid, a thorough understanding of the general combining ability (GCA) and specific combining ability (SCA) of a breeding population is critical (Begna, 2020). Such knowledge of combining ability is essential for selecting suitable parents for hybridization and identifying promising hybrids to develop improved varieties for diverse agro-ecologies. Estimate of combining ability using North Carolina Design II (NCD II) has been extensively used to provide data on the performance of parental populations and their heterotic pattern in crosses, identify heterotic groups, and forecast the performance of new populations (composites) derived from such crosses (Miranda, 1985). The present study was initiated with the following specific objectives:

i. Determine the combining ability of the collected okra parental genotypes under low soil N, high-N and across research conditions.
ii. Assess the nature of gene action influencing okra fruit yield in low-N and high-N soil conditions.
iii. Evaluate the okra single cross hybrids for high yield, stability and tolerance under low-N.

4.2 Materials and methods

4.2.1 Germplasm Source

Twelve (12) okra accessions, which were used in earlier investigations, were used for the current study. These parental accessions were chosen based on their resistance to biotic and abiotic stress factors. The description of the genetic materials is presented in Table 4.1

Table 4.1 Description of the Germplasms used in North Carolina Design II

ENTRIES	ACCESSIONS	SOURCE
1	25	CSIR Kwadaso
2	Paapa	Adamsu
3	SGKP3	CSIR Kwadaso
4	Mampong	Bosikese
5	50	CSIR Kwadaso
6	EDUB	New Edubiasi
7	G1	CSIR Kwadaso
8	OSO-5	Kwadaso
9	Baabo	Nyamebekyere
10	Tamale 2E	CSIR Kwadaso
11	Asontemtiatia	Akumadan
12	Hihaho	Gbogbme

4.2.2 Generation of North Carolina Design II Crosses

The twelve (12) screened okra genotypes selected based on tolerance to biotic and abiotic factors were planted in a nursery at the Horticulture Division of CSIR-Crops Research Institute, Kwadaso, Kumasi. These were crossed using North Carolina Design II (NCD II) mating design with four sets of three genotypes to generate 36 single cross hybrids in the 2020 and 2021 cropping seasons. Genotypes from one set (Set A) were utilized as females and crossed with genotypes from other sets (Set B) used as males (Table 4.2). Each genotype had an equal chance of being utilized as a female parent in one group and a male parent in another (Table 4.2).

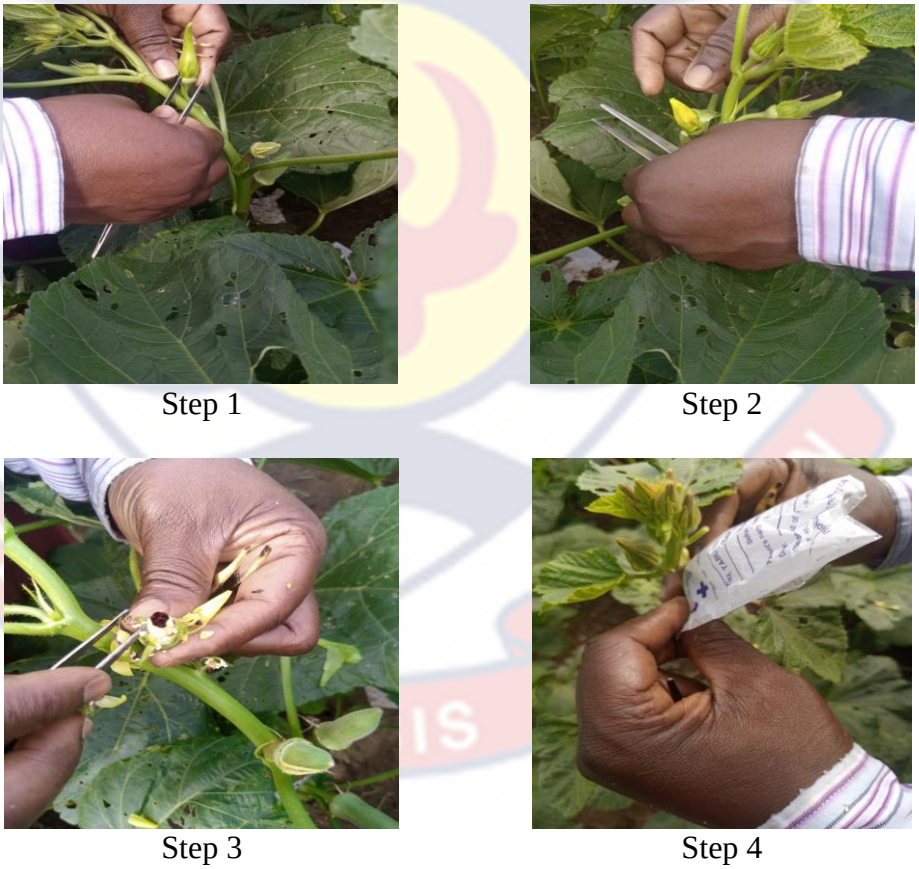
Table 4.2 North Carolina Mating Design II

	SET B MALES				SET C MALES		
SET A FEMALES	4	5	6	SET B FEMALES	7	8	9
1	1×4	1×5	1×6	4	4×7	4×8	4×9
2	2×4	2×5	2×6	5	5×7	5×8	5×9
3	3×4	3×5	3×6	6	6×7	6×8	6×9
	SET D MALES				SETA MALES		
SET C FEMALES	10	11	12	SET D FEMALES	1	2	3
7	7×10	7×11	7×12	10	10×1	10×2	10×3
8	8×10	8×11	8×12	11	11×1	11×2	11×3

4.2.3 Emasculation and Pollination Techniques in okra

Okra produces flowers that contain male and female parts on the same plant (bisexual) and are fertilized by their pollen. Emasculation is carried out a day before anthesis/flower opening, and it is done preferably in the early morning between 6 am and 9 am. At this stage, the sepals have started to separate, and the anthers and corolla are beginning to change from light to yellow. In the process of emasculation ten plants from each genotype were selected as the parents of the next generation. The first step in the emasculation process is the identification of matured flower buds/sepals (Figure 4.1). The second step is carefully making an incision through the calyx of the developed bud with a sterilized sharp forceps/knife to detach the petals by making a cut close to the receptacle. The third step involves grasping the base of the anthers and the petals with forceps inserted between the sepals, removing them with a firm but steady pull as a group with the surrounding corolla. The last step is to fold back the calyx and seal it with a zip bag to prevent insect pollination (Figure 4.1).

The stigma is fully receptive at this stage, allowing for pollination even immediately after emasculation. Pollination was carried out early the following morning by wiping ear cotton buds with the desired pollen and applying pollen from the chosen male parents to the receptive stigma of the emasculated flower. After emasculation and pollination, flower buds were carefully labelled to provide information on the pollen donor and recipients and covered with zip bags to prevent contamination of the pollinated plants (Figure 4.2). Zip bags from each cross were removed after the fruit set a day after pollination. Fruits were monitored till they were fully matured. Harvesting was carefully done, and each successful cross was kept in well-labelled brown envelopes.



Step 1 Step 2

Step 3 Step 4

Figure 4.1 Pictorial presentation of the process of okra emasculation at CSIR-CRI, Kwadaso, during the 2020 cropping season

Figure 4.2 Experimental field for hybrids generation

4.2.4 Determination of hybridization success

The success of the hybridization process was evaluated by examining the flower buds of the pollinated plant 1-3 days after hybridization. Depending on the genotypes, fertilized flowers developed fruit capsules 2 to 4 days after pollination, whereas unsuccessful fertilization resulted in flower abortion a few days after pollination. Failed fertilization was depicted by a change in the colour of fruit capsules from green to brown. In a case where the fruit capsule remained green, it indicated the success of the pollination process. The success of fertilization after pollination depended mainly on the night temperature. Cool night temperatures encouraged fruit set, whereas warm night temperatures resulted in the abortion of fruits. The percentage fruit set for each cross was mathematically estimated using the method of Nunekpeku *et al.*, (2012).

$$FS\ (\%) = \frac{NFF}{NFP} \times 100$$

Fruit set percentage = (FS)

Number of fruit formed = (NFF)

Number of flowers pollinated = (NFP)

4.2.5 Experimental site and field design

The research was undertaken in two separate environments, Jacobu and Akumadan, in the major and minor cropping seasons. Jacobu is in the Amansie central district, located in the forest belt and Akumadan in the Offinso north district located in the transitional zone both in the major and minor cropping season between March to December 2021. Jacobu is on latitude 06º 21' North and longitude 01º39' West with an elevation of 194 meters above sea level. In contrast, Akumadan is located on latitude 07º 22' North and longitude 01º55 ' West with an elevation of 342 meters above sea level. Both locations experience bimodal annual rainfall distribution patterns. The mean annual rainfall at Jacobu is between 1500mm and 1800mm, with a mean relative humidity of about 70%. The mean minimum and maximum temperatures are about 20°C and 32°C, respectively, with a mean of 28°C.

Moreover, the mean annual rainfall in Akumadan ranges between 700mm and 1500mm, with mean relative humidity reaching as high as 90% between late May and early June. The area experiences a mean minimum temperature of about 30°C around March and April, with a mean monthly temperature of 27°C. It is a major okra producing centre in the Ashanti region (MOFA, 2021). The soil for both locations is moderately drained sandy loam. The land was ploughed to a depth of about 30 cm with a tractor-mounted plough and harrowed to break down large clods of soil to a fine tilth in the

2021 major and minor seasons. The area was lined and well-demarcated/ pegged.

The experimental designs were 10 × 4 and 4 × 3 alpha lattice designs with three replications for hybrids and parental genotypes trial at each location. Parental trial (low N. and high N.) was established adjacent to the hybrid trials (low N. and high). Each entry was planted in a one-row plot of 3.6m long; hills were spaced at 0.40m while rows were spaced 0.6m apart, with one guard row on either side. Two seeds were sown per hill and thinned to one plant two weeks after emergence, giving a population of 5,227.63 on an area of 1,254.6m^2. Table 4.3 presents the mean monthly temperature, rainfall and relative humidity of area.

Table 4.3 Mean monthly temperature (ºC), rainfall (mm) and relative humidity (%) during the growing period at Jacobu and Akumadan

	Location: Jacobu					Location: Akumadan				
Months	Temperature		Rainfall	Relative humidity		Temperature		Rainfall	Relative humidity	
	Min.	Max.	(mm)	Min.	Max.	Min.	Max.	(mm)	Min.	Max.
April	24.2	33.8	1.9	55	89	21	38.1	4	40	94
May	24.1	33.4	4.1	57	90	21.1	36.7	3.7	44	88
June	23.1	31.5	6.2	62	79	20	34	5	56	95
July	22.9	30.1	3.3	65	91	20.4	33	1.5	58	88
August	22.7	29.7	2.9	69	91	21.5	32.9	2.8	49	94
September	22.8	30.3	10.4	68	92	20.5	32.6	13.4	61	75
October	22.3	31.1	8.2	59	92	21	34.5	7.3	59	73

4.2.6 Evaluation of genetic materials on low-nitrogen and high-nitrogen soil conditions

Thirty-six hybrids, four checks, and 12 parental accessions were evaluated in two blocks at each location, Jacobu and Akumadan (both in major

and minor seasons). Low nitrogen block was separated from high N field by 3m alleys. Low-N evaluation was achieved by applying N-fertilizer at 30 kg/ha. At the same time, the high N field received 100 kg N/ha (Figure 4. 3). Sulphate of ammonia was applied as a form of nitrogen. However, every trial received 60kg/ha of single super phosphate (P_2O_5) and muriate of potash (K_2O) at planting.

Depletion of soil available N at both locations was achieved by continuously growing maize uniformly on the trial at an increased density without applying any substance as a fertilizer. All plants were harvested when they reached maturity, and the stover was taken out of the field to stop the organic material from degrading and releasing nitrogen (Bänziger *et al*., 2000). Soil samples were collected from 0 to 15 cm deep before the beginning of each crop season from each experimental site and analyzed at the CSIR-SRI laboratory at Kwadaso, Kumasi, Ghana, to determine the initial level of nitrogen. The analyzed soil samples revealed that the soil pH at Jacobu and Akumadan were 6.46 and 4.7, respectively (Table 4.4). The findings of the soil chemical and physical characteristics at Jacobu and Akumadan in the 2021 major and minor cropping seasons are presented in Table 4.4

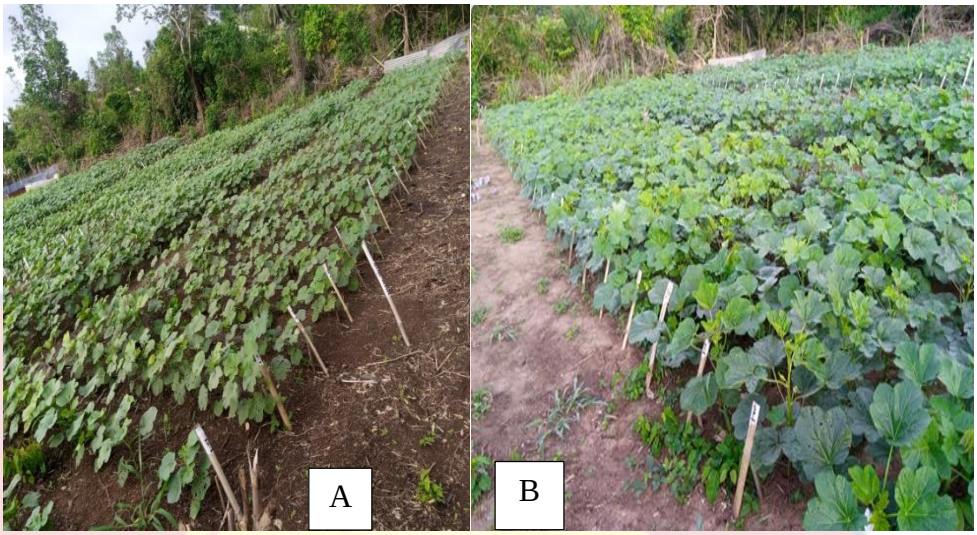


Figure 4.3 Pictorial presentation of the performance of hybrids under low N and high N conditions. A: low nitrogen field and B: high N nitrogen field

Table 4.4 Soil chemical and physical properties at Jacobu and Akumadan experimental sites

	Locations		Landon(1991) interpretation	
	Jacobu	Akumadan		
Soil Properties	**0-15cm**	**0-15cm**	**High**	**Low**
PH 1:2.5	6.46	4.7	>6.5	<5.8
Organic Carbon (%)	1.88	1.24	>10.0	<4.0
Organic Matter (%)	3.23	2.13		
Total Nitrogen (%)	0.17	0.07	>0.5	<0.2
Exchangeable cations (me/100g)				
Ca	6.6	4.8	>10.0	<4.0
Na	0.02	3.33	>1.0	<1.0
Mg	1.81	0.82	>4.0	<0.5
K	0.7	0.37	>0.6	<0.2
Available P (mg/kg)	12.52	6.48	>50.0	<15.0
Particle size (%)				
Sand	74	69.87		
Silt	10	21.45		
Clay	16	4.33		

4.2.7 Agronomic practices

Golan SL TM and Sunpyrifos 48% EC insecticide were used to control *Podagrica* spp. and grasshoppers, respectively, the most notorious and predominant insect pests at the field. *Panicum maximum* which were the predominant weed at the area was controlled by using a traditional hoe. Earthing up was also done to provide support for plants. Fertilizers were applied accordingly.

4.2.8 Data collected

Quantitative traits were randomly recorded from five plants per row, leaving the border plants grown at both ends of the row. The following quantitative traits were measured and recorded: plant height, plant width, number of branches, leaf area, days to first flowering, days to fifty percent flowering, fruit length, fruit with, number fruits per plant, sliminess and chlorophyll content.

4.2.9 Data Analysis

Data collected and recorded for all the variables measured were first subjected to Analysis of Variance (ANOVA) using SAS statistical software. Location and season were viewed as the environment, while low nitrogen and high N growing conditions were considered the research conditions (treatments). Data obtained under low-N and high-N growing conditions were first subjected to a separate Analysis of Variance (ANOVA) using the general linear model approach (PROC GLM) in the Statistical Analysis System (SAS) (SAS Institute, 2012). Additionally, combined ANOVA was carried out across

the test environments. Environments replicate within environments, and the incomplete blocks within replicates × environment interaction were regarded as random factors in the ANOVA for each and across study conditions, whilst the entries (hybrids) were considered fixed factors.

The entry means were corrected for block effects following the lattice design (Cochran and Cox, 1960), and the means were separated using standard error (S.E.). An initial ANOVA was carried out for each research condition and across research conditions to understand the variation brought about by the hybrid (not partitioned) and hybrid environment interaction. The means for each study condition and across the research conditions were then plotted using the NCD II ANOVA for all data gathered using PROC GLM in SAS (SAS Institute, 2012). The NCD II mating design was based on the following general linear model:

$$X_{ijklm} = \mu + S_i + g_i(S_l) + g_j(S_l) + h_{ij}(S_l) + E_m + r_k(SE)_{lm} + (SE)_{lm} + (E_g)_{im}(S_l) + (E_g)_{jm}(S_l) + (E_h)_{ijm}(S_l) + e_{ijklm}$$

Where:

$Xijklm$= the observed value of the ith female's and jth male's offspring in the kth replication of set l and the mth environment.

μ= population mean, Sl= mean effect of the lth set,

$gi(Sl)$= GCA impact shared by all hybrids of the ith female nestled in the lth set, $gj(Sl)$= GCA effect shared by all hybrids of the jth male nested within lth set, $hij(Sl)$= SCA effect of hybrid from the ith female and jth male nested within lth set, Em= mean effect of the mth environment, $rk(SE)lm$ = effect of the kth replication nested within the lth set and mth environment,

$(SE)lm$ = Set effect and environment interaction,

$(Eg)im\ (S)\ and\ (Eg)\ (Sl)$ = environmental and GCA interactions nested within sets E (E_h)(S_l) = environment and SCA interaction nested within sets, $eijklm$= the experimental error (Singh and Chaudhary, 1985).

In the NCD II ANOVA, the variance resulting from hybrids (sets) was divided into variations resulting from male (sets), female (sets), and female-male (sets) interaction. Moreover, the F-test was computed for male, female and male × female by utilizing the mean squares of their respective interaction with the environment. General combining ability (GCA) is represented by the major effects of male (sets) and female (sets). In contrast, specific combining ability (SCA) is characterised by the interaction of females and males (sets). (Hallauer and Miranda, 1988). The proportion of the sum of squares for the crossings attributable to general combining ability (GCA) and specific combining ability (SCA) was determined for each trait as stated below.

Contribution of GCA-male (%) = [ssm / (ssm + ssf + ssmf) x 100]

Contribution of GCA-female (%) = [ssf / (ssm + ssf + ssmf) x 100]

Contribution of SCA (%) = [ssmf / (ssm + ssf + ssmf) x 100]

Where:

ssm = sum of squares attributable to males in the sets,

ssf = sum of squares attributable to females in the sets,

ssmf = sum of squares attributable to male × female sets interaction.

Standard errors for GCAs effects were calculated as described by Cox and Frey (1984):

SE GCA = [MSfe (f-1) / mfer] ½ or [MSme (m-1) / mfer] ½

SE SCA = [MSfme (m-1)(f-1) / mfer]½

Where, MSfe, MSme, and MSfme are the respective female x environment, male x environment, and female x male x environment interaction mean squares multiplied by the appropriate proportion of total number of observations (female x male x replicate x environment). The significance of the GCA-male, GCA-female, and SCA effects of the parental accession was assessed using relative standard errors. To determine the relative significance of cytoplasmic effects, it was also necessary to compare the mean squares of the GCA male and GCA female using the F test or variance ratio, as advised by Kearsey and Pooni (1996). SAS PROC Varcomp was used to provide restricted maximum likelihood (REML) estimates of the okra genotypes and hybrids' phenotypic and genotypic variances, which were then used to calculate the broad-sense heritability for the different features.

$H^2 = \sigma^2 G/(\sigma^2E/re + \sigma^2GE/e + \sigma^2G)$

Where;

σ^2 G = genotypic variance,

σ^2 E = environmental variance,

σ^2GE = genotype × environment interaction variance,

r = number of replications,

e = number of environments (Fehr, 1991).

According to the method described by Matzingar *et al*. (1962) in the formulas, the mid-parent (MPH) and better parent heterosis (BPH) values for a cross were calculated for each characteristic.

MPH = [(F1-MP)/MP] × 100

BPH = [(F1-BP)/BP] × 100

Where;

F1 = Mean of the hybrid,

MP = the mean of the parents that constituted the hybrids and

BP = the mean of the better parent.

MPH and BPH were averaged across low N environments and high N environments.

4.3 Results

4.3.1 Analysis of variance of fruit yield and other agronomic traits of okra hybrids under low-nitrogen, high nitrogen and across environments

Across low N environment, the analysis revealed significant ($p<0.001$) variations among the genotypes (G) and environment (E) main effects for fruit yield and all the studied characters except (G) and (E) mean square for fruit width. However, there was no significant genotype by environment interaction (GEI) for fruit yield and the measured traits (Table 4.5). Except for fruit length, the ANOVA also showed significant set effects for fruit yield and other agronomic characteristics (Table 4.5). Partitioning the hybrid components of variation into a male set (GCA-male), female set (GCA-female), and male × female interaction (SCA) showed highly significant ($p<0.001$) differences among GCA-male, GCA-female and SCA mean squares for fruit yield and all measured traits except fruit width. The estimated heritability in the broad sense ranged from 74% for fruit length to 99% for fruit yield and yield relating traits. Narrow sense heritability estimates varied from 40% for plant width to 70% for plant height. Fruit yield had a narrow sense heritability estimate of 58 % (Table 4.5).

Across high nitrogen conditions, the results showed highly significant ($p<0.001$) differences among the genotypes (G) and environment (E) main effects for fruit yield and all studied traits except (G) main effect for leaf area (Table 4.6). However, genotype by environment interaction (GEI) was significant for the number of fruits per plant, days to first flowering and days to 50% flowering (Table 4.6). The results showed significant set effects for fruit yield and all yield components except for fruit length, plant girth, and leaf area. Moreover, significant GCA-males and GCA-females were observed for fruit yield and all measured traits except leaf area. The result also showed significant variations for SCA mean squares for all the traits studied except fruit width and leaf area (Table 4.6). The broad sense heritability values range was 53% for leaf area and 99% for fruit yield and related components. Heritability in the narrow sense ranged from 31% for leaf area to 67% for plant height (Table 4.6).

Across the research environment (low N and high N), the results revealed highly significant ($p<0.001$) variations among genotypes (G) and environment main effects for fruit yield and all studied traits (Table 4.7). However, GEI was significant for the number of fruits per plant and leaf area (Table 4.7). The results revealed significant set effects for fruit yield and most yield component traits except fruit length and leaf area. Similarly, highly significant ($p<0.001$) differences were observed for GCA-males, GCA-females and SCA for fruit yield and all measured traits except GCA-females and SCA for fruit width (Table 4.7). Estimates of broad sense heritability across low N and high N conditions differed from 74% for leaf area to 99% for days to first flowering and days to fifty percent flowering. Narrow sense

heritability estimates varied from 37% for leaf area to 72% for plant height (Table 4.7).

4.3.2 Proportion of combining ability effects (Mode of gene action) under contrasting environments

The ratio of the GCA component to total genetic variation based on the sum of squares was used to assess the relative contributions of GCA and SCA effects. The more predictable a hybrid's performance is based on GCA, the closer the ratio gets to one (Baker, 1978). Under low nitrogen environments, the sum of squares of GCA contributions to total genetic diversity for hybrids varied from 53.69% for plant height to 90.81% for the number of fruits per plant. The SCA sum of squares ranged from 9.19 % for number of fruits per plant to 45.31% for plant height (Figure 4.4). For fruit yield and all other measured agronomic parameters, GCA effects had a higher contribution than SCA. GCA controlled 86.09% of the overall sum of squares for fruit yield (Figure 4.4).

Under a high nitrogen environment, the proportion of GCA effects to each genotypic sum of squares varied from 57.46 % for leaf area to 91.49 % for fruit length. The SCA sum of squares ranged from 8.51% for fruit length to 42.54% for leaf area (Figure 4.5). The effects of GCA on fruit yield and all other measured traits were more remarkable than that of the SCA effects. The contribution of GCA to the overall sum of squares was 81.08% for fruit yield.

Table 4.5 Mean squares and estimates of heritability for fruit yield and other agronomic parameters of okra evaluated under low-N conditions in 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	FW	PH	PW	LA
ENV	3	60.68**	176.25**	34.01*	41.01**	15.85**	1.56	3442.96**	0.46**	979320.71**
SET	3	31.65**	105.31**	72.61**	147.40**	0.30	2.13*	3334.65**	0.27**	435781.55**
ENV* SET	9	0.49	3.39	0.78	0.80	0.08	0.64	8.41	0.03	1987.30
REP(ENV*SET)	24	0.73	3.65	8.21	6.97	1.46	0.26	159.46	0.05	4412.87
BLOCK(ENV*SET)	64	0.69	3.44	9.71	6.30	2.30*	0.64	159.68	0.05	3646.62
HYBRID GENOTYPES	35	9.09**	32.60**	139.10**	221.0**	8.69**	0.89	1664.09**	0.20**	256140.42**
MALE (SET)	11	6.77**	27.53**	83.13**	66.13**	7.36**	0.84	451.91	0.17**	467208.17**
FEMALE (SET)	11	14.96**	64.78**	201.14**	218.95**	10.72**	0.99	1127.85**	0.20**	448369.22**
FEMALE *MALE (SET)	25	3.51**	9.34**	70.12**	81.94**	8.03**	1.03	1362.70**	0.13**	184221.44**
HYBRID * ENV	105	0.24	2.06	8.28	4.63	0.18	0.69	22.16	0.02	2634.86
ENV*MALE (SET)	33	0.21	2.17	2.33	1.54	0.08	1.21	20.62	0.01	1559.75
ENV*FEMALE (SET)	33	0.23	2.54	1.79	2.57	0.27	0.89	33.62	0.02	1395.64
ENT*FEMALE*MALE (S)	75	0.23	1.49	1.93	2.95	0.07	0.84	22.48	0.01	2503.10
ERROR	192	0.85	3.72	10.96	10.55	1.71	0.78	282.65	0.05	3456.27
Heritability (NS)		**0.58**	**0.56**	**0.66**	**0.60**	**0.47**	**0.48**	**0.70**	**0.40**	**0.50**
Heritability (BS)		**0.99**	**0.99**	**0.99**	**0.99**	**0.74**	**0.77**	**0.99**	**0.79**	**0.99**

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; Env = environment; Rep = replication; FY(t/ha) = fruit yield in tons/hectare; NFP = number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL = fruit length; FW = fruit width/diameter; PH = plant height; PW = plant width/diameter; LA = leaf area; NPP = number of plants per plot; NPH; number of plants at harvest**

Table 4.6 Mean squares and estimates of heritability for fruit yield and other agronomic parameters of okra evaluated under high-N conditions in 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	FW	PH	PW	LA
ENV	3	130.69**	251.90**	96.51**	99.85**	52.00**	0.81**	5852.31**	0.99**	1517652.65**
SET	3	16.24**	34.65**	51.04**	28.10*	1.51	1.72**	3290.30**	0.13	99693.15
ENV* SET	9	0.30	1.06	2.41*	26.96	1.02	0.02	46.31	0.04	3363.75
REP(ENV*SET)	24	1.92*	7.80**	12.94*	33.26**	1.96	0.14**	189.84	0.05	3900.25
BLOCK(ENV*SET)	64	1.84*	5.18*	8.16	20.02**	2.60**	0.09*	144.87	0.05	118998.82
HYBRID GENOTYPES	35	14.69**	734.24**	202.82**	238.63**	10.51**	0.43**	2829.01**	0.28**	229213.65
MALE (SET)	11	6.72**	14.54**	113.28**	99.30**	7.20**	0.31**	1286.18**	0.25**	127347.42
FEMALE (SET)	11	36.33**	60.50**	184.66**	222.40**	22.04**	0.40**	2947.23**	0.34**	311805.22
FEMALE *MALE (SET)	25	10.05**	14.37**	71.01**	90.23**	2.72*	0.10	722.44**	0.34**	325103.44
HYBRID * ENV	105	0.32	8.96*	2.32**	9.48*	0.38	0.02	17.26	0.03	199837.33
ENV*MALE (SET)	33	0.23	2.04	2.02	7.47	0.26	0.02	10.00	0.03	7314.75
ENV*FEMALE (SET)	33	0.31	2.06	1.38	2.47	0.16	0.04	13.02	0.04	796005.30**
ENT*FEMALE*MALE (SET)	75	0.39	1.51	1.76	10.35	0.37	0.02	10.99	0.04	4751.51
ERROR	192	1.24	3.96	7.01	12.49	1.49	0.06	144.38	0.07	207171.40
Heritability (NS)		**0.57**	**0.58**	**0.60**	**0.59**	**0.52**	**0.64**	**0.67**	**0.49**	**0.31**
Heritability (BS)		**0.99**	**0.99**	**0.98**	**0.99**	**0.98**	**0.98**	**0.99**	**0.98**	**0.53**

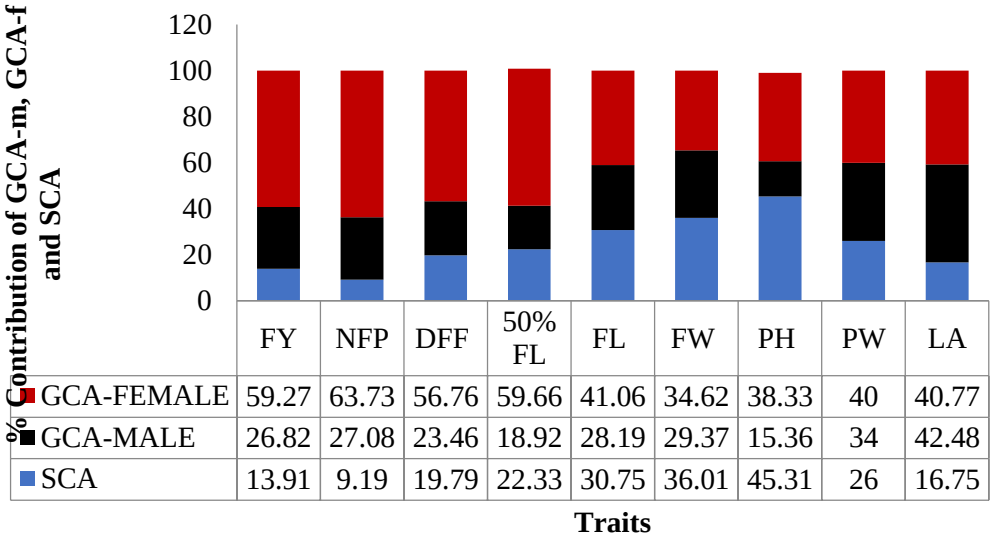
***, ** = Significant at 0.05 and 0.01 probability levels, respectively; Env = environment; Rep = replication; FY(t/ha) = fruit yield in tons/hectare; NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL = fruit length; FW = fruit width/diameter; PH = plant height; PW = plant width/diameter; LA = leaf area; NPP = number of plants per plot; NPH; number of plant at harvest**

Across research environments, the effects of GCA on the hybrid genotypic sum of squares were more significant than the effects of SCA. The contribution of GCA to the total sum of squares for fruit yield across the environment was 88.07 % (Figure 4.6). The proportion of the GCA sum of squares to the corresponding genotypic sum of squares ranged from 67.64 % for leaf area to 91.26 % for the number of fruits produced per plant. The SCA sum of squares ranged from 8.75% for the number of fruits /plants to 32.3% for leaf area (Figure 4.6).

Table 4.7 Mean squares and estimates of heritability for fruit yield and other agronomic parameters of okra evaluated across high-N and low-N conditions in 2021 major and minor growing season at Jacobu and Akumadan

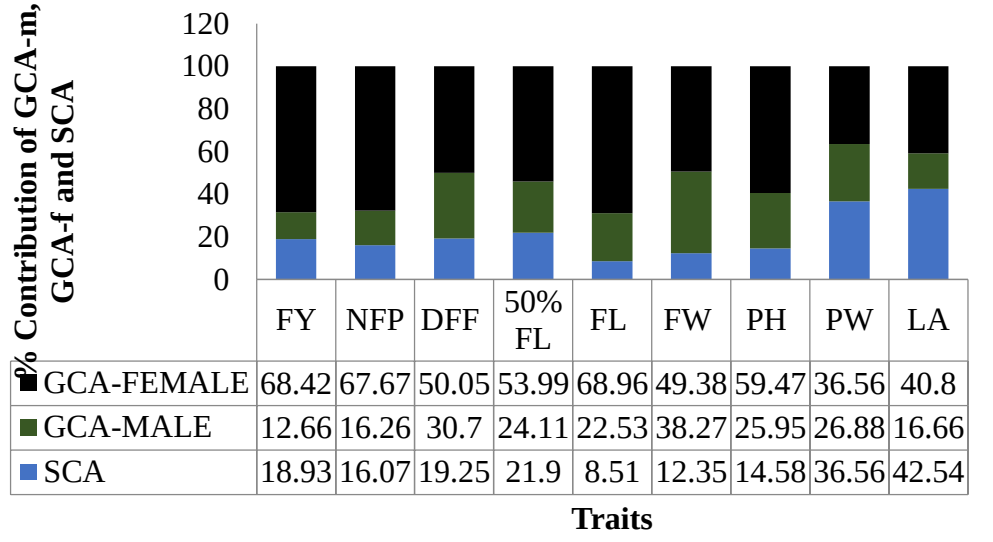
SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	FW	PH	PW	LA
ENV	3	619.17**	625.08**	673.74**	1172.08**	127.14**	1.21**	26999.07**	2.75**	4290171.08**
SET	3	44.82**	125.72**	113.57**	141.31**	0.75	3.69**	6121.35**	0.30**	131627.54
ENV* SET	9	0.78	3.94	2.81	16.78	0.62	0.31	95.39	0.05	59985.76
REP(ENV*SET)	24	1.32	5.72*	10.58	20.11**	1.71	0.20	174.65	0.05	4156.56
BLOCK(ENV*SET)	64	1.27*	4.31	8.94	13.16	2.45**	0.36	152.27	0.05	61322.72
HYBRID GENOTYPES	35	17.70**	419.05**	309.09**	425.92**	14.79**	0.88**	3871.87**	0.36**	222320.04**
MALE (SET)	11	9.87**	30.55**	169.84**	127.77**	9.45**	0.78**	1279.20**	0.28**	237926.66**
FEMALE (SET)	11	44.33**	115.51**	338.21**	407.35**	29.90**	0.75	3727.19**	0.42**	315999.96**
FEMALE *MALE (SET)	25	7.34**	14.00**	104.06**	134.08**	6.87**	0.46	1430.41**	0.32**	265042.57**
HYBRID * ENV	105	1.39	54.41**	12.09	10.86	1.82	0.46	105.65	0.04	124350.08**
ENV*MALE (SET)	33	0.71	3.45	5.66	9.24	0.88	0.58*	78.68	0.04	54750.35
ENV*FEMALE (SET)	33	1.23	3.37	8.16	7.02	0.59	0.49	69.69	0.04	405196.75**
ENT*FEMALE*MALE (S)	75	1.15	2.68	6.88	11.14	0.75	0.46	107.88	0.04	38006.59
ERROR	192	1.05	3.84	8.99	13.09	1.60	0.42	213.51	0.06	105313.80
HERITABILITY (NS)		0.56	0.56	0.63	0.60	0.50	0.55	0.72	0.44	0.37
HERITABILITY (BS)		0.95	0.98	0.99	0.99	0.88	0.88	0.98	0.89	0.74

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; Env = environment; Rep = replication; FY (t/ha) = fruit yield in tons/hectare; NFP = number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL = fruit length; FW = fruit width/diameter; PH = plant height; PW = plant width/diameter; LA = leaf area; NPH = number of plants at harvest**



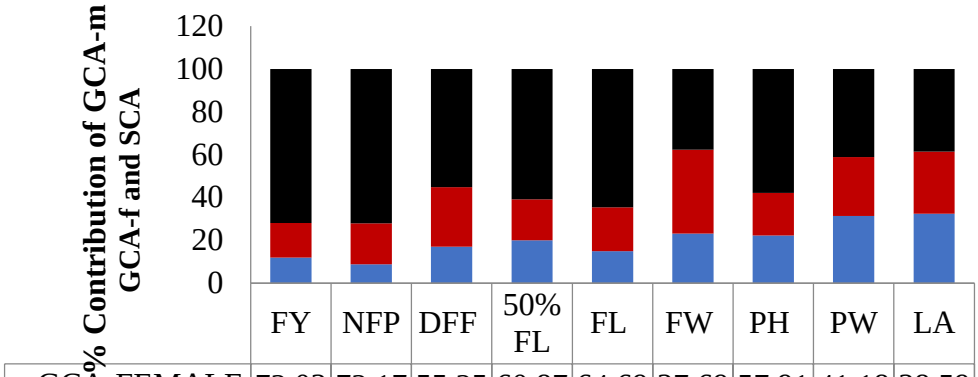
	FY	NFP	DFF	50% FL	FL	FW	PH	PW	LA
GCA-FEMALE	59.27	63.73	56.76	59.66	41.06	34.62	38.33	40	40.77
GCA-MALE	26.82	27.08	23.46	18.92	28.19	29.37	15.36	34	42.48
SCA	13.91	9.19	19.79	22.33	30.75	36.01	45.31	26	16.75

Figure 4.4 Percentage of the sum of squares based on genotypes for fruit yield and agronomic parameters of okra genotypes attributed to general combining ability (GCA-male and GCA-female) and specific combining ability (SCA) estimates under low-N conditions.



	FY	NFP	DFF	50% FL	FL	FW	PH	PW	LA
GCA-FEMALE	68.42	67.67	50.05	53.99	68.96	49.38	59.47	36.56	40.8
GCA-MALE	12.66	16.26	30.7	24.11	22.53	38.27	25.95	26.88	16.66
SCA	18.93	16.07	19.25	21.9	8.51	12.35	14.58	36.56	42.54

Figure 4.5 Percentage of the sum of squares based on genotypes for fruit yield and agronomic parameters of okra genotypes attributed to general combining ability (GCA-male and GCA-female) and specific combining ability (SCA) estimates under high N conditions.



	FY	NFP	DFF	50% FL	FL	FW	PH	PW	LA
GCA-FEMALE	72.03	72.17	55.25	60.87	64.69	37.69	57.91	41.18	38.59
GCA-MALE	16.04	19.09	27.75	19.09	20.45	39.2	19.87	27.45	29.05
SCA	11.93	8.75	17	20.04	14.86	23.12	22.22	31.37	32.36

Traits

Figure 4.6 Percentage of the sum of squares based on genotypes for fruit yield and agronomic parameters of okra genotypes attributed to general combining ability (GCA-male and GCA-female) and specific combining ability (SCA) estimates across low-N and high N conditions. FY = fruit yield; NFP= number of fruits per plot; NFPLA = number of fruits per plant; DFF = days to first flowering; 50%F = fifty percent flowering; FL = fruit length; FW = fruit width; PH = plant height; PW = plant width; LA = leaf area; NPP = number of plants per plot; NPH = number of plants at harvest

4.3.3 Analysis of variance of fruit yield and other agronomic traits of okra parental genotypes in diverse environments

Under low N condition, the ANOVA revealed highly significant ($p<0.001$) differences among the parental genotypes for fruit yield and all other traits (Table 4.8). Similarly, there were significant ($p<0.001$) environmental variations for fruit yield and the studied traits except for days to first flowering, days to 50% flowering, fruit width and plant width. Moreover, Genotype by environment interaction significantly ($p<0.05$) differed for fruit yield and number of fruits per pant (Table 4.8).

Across the high N environment, there were significant differences ($P<0.001$ or $p< 0.05$) among genotypes and environment main effects for all measured traits except environment main effects for leaf area. Moreover, GEI significantly varied for only fruit yield (Table 4.9).

The ANOVA of parental accessions evaluated across the research environment (low N and high N) revealed highly significant ($p<0.001$) differences for genotypes (G) and environment main effects for fruit yield and all studied traits (Table 4.10). Moreover, there was significant ($p<0.001$) genotype × environment interaction for fruit yield (Table 4.10).

Table 4.8 Mean squares and heritability estimates of okra parental genotypes evaluated under low nitrogen conditions during the 2021 major and minor seasons at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL (cm)	FW (cm)	PH (cm)	PW	LA
ENV	3	10.54**	142.10**	2.86	1.75	11.06**	0.06	1309.85**	0.05	471944.83**
REP(ENV)	8	0.15	2.29**	3.19	7.67	2.64**	0.06	72.23	0.05*	3108.64
BLOCK(ENV*REP)	16	0.07	1.05*	6.45	10.95	0.72*	0.02	128.95**	0.02	3706.39
ENTRY	11	17.25**	39.50**	317.08**	209.63**	6.36**	0.71**	2977.97**	0.08**	131237.88**
ENV* ENTRY	33	0.21*	0.80*	1.41	3.80	0.17	0.01	11.75	0.01	1435.87
ERROR	72	8.41	0.46	11.16	9.48	0.37	0.04	77.85	0.02	6487.91
Heritability (NS)		**0.58**	**0.56**	**0.66**	**0.6**	**0.47**	**0.48**	**0.7**	**0.4**	**0.5**
Heritability (BS)		**0.99**	**0.99**	**0.99**	**0.99**	**0.74**	**0.77**	**0.99**	**0.79**	**0.99**

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area;**

Table 4.9 Mean squares and heritability estimates of okra parental genotypes evaluated under high nitrogen conditions during the 2021 major and minor season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL cm)	FW(cm)	PH (cm)	PW	LA
ENV	3	52.04**	100.72**	22.34**	71.69**	12.13**	0.28**	2728.05**	0.50**	243199.17
REP(ENV)	8	0.42*	3.86	6.49	9.42	1.19*	0.04	159.67*	0.09**	1138801.76**
BLOCK(ENV*REP)	16	0.21	1.79	8.41	7.99	0.73	0.03	48.01	0.02	1132341.58**
ENTRY	11	15.50**	38.39**	266.4**	263.48*	13.93**	0.77**	4647.57**	0.07*	669736.33*
ENV* ENTRY	33	0.36*	1.95	2.14	6.22	0.40	0.02	90.90	0.02	394171.63
ERROR	72	0.20	2.09	6.84	9.35	0.54	0.03	75.06	0.03	383991.02
Heritability (NS)		0.57	0.58	0.6	0.59	0.52	0.64	0.67	0.49	0.31
Heritability (BS)		0.99	0.99	0.98	0.99	0.98	0.98	0.99	0.98	0.53

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area;**

Table 4.10 Mean squares and heritability estimates of okra parental genotypes evaluated across high and low N conditions during the 2021 major and minor season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	FW	PH	PW	LA
ENV	3	170.49**	258.33**	164.14**	602.57**	25.28**	0.16**	3149.78**	0.36**	717685.18**
REP(ENV)	8	0.29*	3.08**	4.84	8.55	1.92**	0.05	115.95	0.07**	570955.20**
BLOCK(ENV*REP)	16	0.14	1.42	7.43	9.47	0.72*	0.03	88.48	0.02	568023.98**
ENTRY	11	31.48**	74.84**	573.76**	464.23**	18.29**	1.43**	7432.46**	0.09**	620888.76**
ENV* ENTRY	33	0.43**	1.61	2.91	5.56	0.53	0.02	71.57	0.02	195272.57
ERROR	72	0.16	1.28	9.00	9.42	0.45	0.04	76.46	0.03	195239.47
HERITABILITY (NS)		0.56	0.56	0.63	0.6	0.5	0.55	0.72	0.44	0.37
HERITABILITY (BS)		0.95	0.98	0.99	0.99	0.88	0.88	0.98	0.89	0.74

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; FY= Fruit yield (t/ha NFP= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area;**

4.3.4 Effects of general combining ability (GCA effects)

GCA-male effects for fruit yield under low N conditions varied from -0.64 for G1 to 0.59 for Tamale 2E, while GCA-female effects varied from -0.14 for accession 25 to 0.16 for both Paapa and Tamale 2E (Table 4.11). Out of the 12 okra parental genotypes, only genotype Tamale 2E (best general combiner) showed a significant positive GCA-male effect of 0.59 for fruit yield (Table 4.11). In addition, GCA- male effects for days to first flowering varied from -3.06 for parental genotype 25 to 6.21 for Mampong. Okra genotype 25 and Tamale 2E (best general combiners) recorded a significant negative GCA-male effect of -3.06 and -3.02 for the days to first flowering, respectively (Table 5.10). For days to fifty percent flowering, parental genotypes G1 (-2.03), Paapa (-0.85), 50 (-1.27), Baabo (-1.05) and Asontemtiatia (-1.36) showed a significant negative GCA-female effect under low nitrogen stress. For fruit length genotypes, SGKP3 and Mampong were the top general combiners with GCA-male estimates of 3.92 and 4.92, respectively (Table 4.11). Furthermore, genotypes Hilhaho (1.69), Mampong (1.59), Tamale 2E (1.36), and SGKP3 (1.33) had significant and positive GCA-female effects for fruit length.

Across high N conditions, the effects of GCA-male for fruit yield differed from - 0.97 for G1 to 1.07 for Hilhaho, while GCA-female effects for fruit yield ranged from -0.05 for EDUB to 0.02 for both hilhaho and paapa (Table 4.12). Among the 12 okra genotypes studied, Paapa, Baabo and Hilhaho had the same significant positive GCA-female effects of 0.2, followed by OSO-5 with positive GCA-female effects of 0.01 for fruit yield. Moreover, genotypes Hilhaho and Paapa recorded a significant positive GCA-

male effect of 1.07 and 0.89 for fruit yield, respectively. Furthermore, significant positive GCA-male effects were recorded by okra genotype Hilhaho (1.60) for the number of fruits per plant. Similarly, okra genotypes SGKP3 (1.06), G1 (0.95) and Paapa (0.90) showed a significant positive GCA-female effect for number of fruits per plant (Table 4.12). Four out of the twelve parental genotypes studied had significant negative GCA-female effects for days to first flowering. These are genotypes G1 (-1.87), 25 (1.86), 50 (1.12) and Paapa (1.02). For days to 50% flowering, parental genotype 25 (-2.14) recorded a significant negative GCA-male. Moreover, genotypes G1 (-1.87), 25 (-1.35), Baabo (-1.17) and 50 (-1.30) were the best general combiners in terms of days to fifty percent flowering for GCA-female (Table 4.12).

Across low N and high N conditions, the effect of GCA-male for fruit yield ranged from -0.87 for G1 to 0.82 for Hilhaho (Table 4.13). Of the twelve parental genotypes, Hilhaho depicted a significant positive GCA male effect of 0.82 for fruit yield. GCA male effects for days to first flowering ranged from -2.69 for Tamale 2E to 5.53 for Mampong, while GCA-female effects varied from -1.88 for G1 to 2.38 for Mampong. Out of the twelve parental genotypes, G1 (1.88), Paapa (1.14), 50 (1.14) and 25 (1.63) were the best general combiners with significant negative effects of GCA-female for days to first flowering (Table 4.13).

Table 4.11 Estimates of general combining ability for fruit yield and yield component characters of okra parental genotypes evaluated under low-N conditions during 2021 major and minor seasons

	YIELD		NFP		DFF		50%FL		FL		PH	
Parents	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	-0.64*	0.08	-1.01	0.06	1.29	-0.08	1.52	-2.03**	1.52	-2.03**	-7.15*	-40.87**
Paapa	0.10	0.16	0.07	0.10	-2.17	-0.06	-1.45	-0.85*	-1.45	-0.85*	-26.82*	3.30
SGKP3	-0.35	0.02	-0.75	0.01	4.81**	0.03	3.92*	1.33**	3.92*	1.33**	58.45**	35.81**
Mampong	-0.25	-0.13	-0.46	-0.08	6.21**	0.10	4.92**	1.59**	4.92**	1.59**	0.43	43.41**
50	-0.17	0.02	-0.31	0.02	0.41	-0.03	0.49	-1.27**	0.49	-1.27**	34.16**	10.63
EDUB	-0.23	-0.12	-0.37	-0.08	-1.00	0.06	-1.06	0.54	-1.06	0.54	-27.90*	7.04
OSO-5	0.49	-0.13	0.87	-0.08	-2.52	0.02	-2.46	0.03	-2.46	0.03	-40.24**	-3.12
25	0.07	-0.14	-0.03	-0.09	-3.06*	-0.05	-2.89	0.02	-2.89	0.02	-22.15	-18.18*
Baabo	0.17	0.08	0.31	0.04	-0.14	-0.04	0.37	-1.05*	0.37	-1.05*	14.62	-20.06**
Tamale 2E	0.59*	0.16	1.06	0.09	-3.02*	0.00	-3.33	1.36**	-3.33*	1.36**	-54.28**	5.76
Asontemtiatia	-0.22	0.04	-0.15	0.02	-2.19	-0.05	-1.32	-1.36**	-1.32	-1.36**	13.60	1.35
Hihaho	0.44	-0.05	0.76	-0.02	1.38	0.09	1.27	1.69**	1.27	1.69**	77.28**	-13.05

***, ** = Significant at 0.05 and 0.01 probability levels, respectively NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; PH = plant height (cm)**

Table 4.12 Estimates of general combining ability for fruit yield and yield component characters of okra parental genotypes evaluated under high-N conditions in the 2021 major and minor growing season at Jacobu and Akumadan.

	YIELD		NFP		DFF		50%FL		FL		PH	
PARENTS	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	-0.97*	0.00	-1.46*	0.95**	0.77	-1.87**	0.79	-1.87**	0.04	0.63**	-11.86	-1.27
Paapa	0.89*	0.02*	0.11	0.90**	-1.13	-1.06**	-0.84	-0.81	-0.44	0.33**	-13.04*	-1.29
SGKP3	-0.55	0.01	-0.73	1.06**	3.79**	0.48	4.46**	0.24	0.00	-0.36**	13.94*	-1.47
Mampong	-0.76	0.00	-1.09	-0.37	4.54**	2.71**	4.37**	2.45**	0.07	0.05	23.94**	9.10**
50	-0.33	0.00	-0.34	-0.08	-0.49	-1.12*	-0.37	-1.30**	0.02	-0.07	3.93	-4.32
EDUB	0.06	-0.05**	-0.22	-0.35	-1.43	0.63	-2.10	0.83	0.10	0.53**	-7.63	4.87**
OSO-5	-0.13	0.01	-0.22	-0.79**	-1.60	0.04	-1.76	0.73	0.19	-0.26**	-8.96	-6.25**
25	0.35	-0.01	0.37	0.12	-1.92	-1.86**	-2.14**	-1.35**	0.00	-0.05	-4.95	-1.59
Baabo	0.58	0.02**	0.75	-0.10	-0.33	-0.19	-0.24	-1.17**	-0.17	-0.25	12.15*	-2.61
Tamale 2E	0.59	-0.02**	1.09	-0.42**	-2.19	0.57	-2.10	0.29	0.12	-0.07	-15.56*	-1.04
Asontemtiatia	0.07	0.01	0.12	-0.30	-1.09	-0.16	-0.78	-0.25	-0.12	-0.43**	-3.58	0.49
Hihaho	1.07**	0.02**	1.60**	-0.33	1.08	1.83	0.91	2.21	0.18	-0.03	11.62	4.36

Table 4.13 Estimates of general combining ability for fruit yield and yield component characters of okra parental genotypes evaluated across low N and high- N conditions during the 2021 major and minor growing season at Jacobu and Akumadan.

	YIELD		DFF		50%FL		FL		PH	
PARENTS	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	-0.87*	1E-15	1.08	-1.88**	1.23	-1.95**	-0.03	-4.77**	-10.12*	-16.77*
Paapa	0.05	2E-15	-1.66	-1.14*	-1.12	-0.83*	-0.52*	-0.65	-10.76*	-13.83
SGKP3	-0.50	1E-15	4.47**	0.60	4.35**	0.79	0.06	4.17**	11.34*	47.12**
Mampong	-0.56	-1E-15	5.53**	2.38**	4.73**	2.02**	0.06	-7.59**	24.65**	33.45**
50	-0.28	-2E-16	-0.10	-1.14*	0.01	-1.28**	0.03	3.81**	3.53	7.23
EDUB	-0.12	-1E-15	-1.29	1.07*	-1.73	0.69	0.02	-0.76	-7.27	-2.72
OSO-5	0.21	-2E-15	-2.11	0.17	-2.17	0.38	0.50	5.50**	-9.72*	19.77*
25	0.22	-1E-15	-2.56	-1.63**	-2.59	-0.67	-0.08	-0.57	-4.10	-15.82*
Baabo	0.42	4E-16	-0.26	-0.80	0.08	-1.11**	-0.10	4.72**	7.90	-15.59*
Tamale 2E	0.67	9E-16	-2.69	0.60	-2.83	0.83*	0.04	-1.18	-14.39*	-3.12
Asontemtiatia	-0.05	2E-16	-1.68	-0.49	-1.08	-0.81*	-0.18	-0.91	-2.74	-2.49
Hihaho	0.82*	-5E-16	1.27	2.25**	1.12	1.95**	0.21	-1.77	11.68*	-37.22*

***, ** = Significant at 0.05 and 0.01 probability levels, respectively NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; PH = plant height (cm)**

4.3.5 Specific combining ability of hybrids

Under low nitrogen conditions, favourable SCA estimates (significant and positive) were observed for hybrids such as Tamale 2E × G1, Hilhaho × Paapa, Mampong × Baabo, EDUB × OSO-5, OSO-5 × Tamale, OSO-5 × Asontemtiatia, and OSO-5 × Hilhaho for fruit yield (Table 4.14). Cross Hilhaho × Paapa recorded the highest positive and significant SCA effect of 1.74 among these hybrids and was followed by EDUB × OSO-5 with an SCA estimate of 1.45. Desirable SCA estimates (significant and positive) for number of fruits per plants were obtained for crosses Tamale 2E × G1, Hilhaho × Paapa, Mampong × Baabo, EDUB × OSO-5, OSO-5 × Tamale, OSO-5 × Asontemtiatia and OSO-5 × Hilhaho with the highest SCA effects detected for Hilhaho × Paapa (3.08) and was followed by EDUB × OSO-5. Hybrid crosses Asontemtiatia × G1, Hilhaho × Paapa, SGKP3 × 50 and EDUB × Baabo (best specific combiners) recorded significant and negative SCA estimates for days to first flowering (Table 4.14)

Across high N environments, significant positive SCA effects for fruit yield were observed for crosses Tamale × SGKP3, Asontemtiatia × Paapa, Asontemtiatia × SGKP3, Asontemtiatia × G1, Hilhaho × Paapa, EDUB × OSO-5, 25 × Hilhaho and Baabo × Tamale (best specific combiners) (Table 4.15). Hilhaho × Paapa recorded the highest positive SCA effects of 2.28 and was closely followed by Asontemtiatia × G1 with an SCA estimate of 2.18. Significant positive SCA estimates were also recorded for the number of fruits per plant. For days to first flowering, Tamale × G1, Asontemtiatia × G1, 50 × 25 and EDUB × OSO-5 had significant and negative SCA effects (Table 4.15).

Across the environment, hybrid crosses Asontemtiatia × G1, Hilhaho × Paapa, and EDUD × OSO-5 had significant and positive SCA effects on fruit yield (Table 4.16). Hybrid cross Hilhaho × Paapa had the highest significant and positive SCA effect for fruit yield and was followed by EDUB × OSO-5 and Asontemtiatia × G1 with an estimate of 1.69, 1.66 and 1.16, respectively. Furthermore, hybrid crosses Tamale 2E × G1, Asontemtiatia × G1, Hilhaho × Paapa, and EDUB × OSO-5 had positive and significant SCA effects on number of fruits per plant.

Table 4.14 Specific combining ability estimates of hybrids for fruit yield and yield component characters under low nitrogen conditions

HYBRIDS	YIELD	NFP	DFF	50%FL	LA	FL	FW	PH	NBP
G1 × Mampong	0.06	0.17	0.88	-0.25	-191.83**	0.08	0.01	13.94**	-0.13
G1 × 50	-0.45	-0.69	-0.33	0.39	-95.58**	-0.11	-0.02	0.62	0.24
G1 × EDUB	-0.75	-1.26	-0.58	-1.22	250.66**	-0.14	0.03	-11.12*	-0.10
Tamale × G1	1.25**	2.15**	-2.90	-4.93**	-215.39**	-0.08	0.07	-7.76	-0.08
Tamale × Paapa	-0.42	0.49	-1.11	-2.91	-17.09	0.25	-0.04	-0.01	-0.73**
Tamale × SGKP3	0.14	0.72	-2.61	-4.12*	-182.05**	-0.10	0.01	-2.96	-0.30
Asontemtiatia × G1	0.02	0.82	-0.38	-2.36	-120.41**	0.28	0.02	-2.85	-0.98**
Asontemtiatia × Paapa	0.10	0.13	-1.88	-3.41	-184.79**	0.08	0.06	-0.01	-0.04
Asontemtiatia × SGKP3	0.57	0.98	0.39	1.76	-46.68**	-0.05	-0.07	7.47	0.59**
Asontemtiatia × G1	0.63	1.41	-5.47**	-5.19**	234.72**	-0.16	-0.03	-9.13	-0.32
Hilhaho × Paapa	1.74**	3.08**	-4.70**	-4.39*	220.42**	0.05	-0.04	-1.88	0.21
Hilhaho × SGKP3	0.50	0.96	2.36	1.58	-77.06**	0.15	0.02	7.24	-0.20
Paapa × Mampong	-0.24	-0.58	-0.41	-2.30	99.72**	-0.32	0.03	0.06	-0.27
Paapa ×50	0.19	0.96	-2.87	-3.75*	-151.11**	-0.02	0.04	-5.95	0.44*
Paapa × EDUB	-0.36	-0.84	-0.61	-2.06	0.11	-0.07	0.07	1.88	0.00
SGKP3 × Mampong	-0.73	-1.24	4.09*	4.52*	-173.24**	-0.01	0.01	-5.35	-0.78**
SGKP3 × 50	0.04	-0.07	-3.56*	-3.54	159.80**	0.21	-0.04	12.05*	-0.65**
SGKP3 × EDUB	0.51	0.71	1.45	0.09	-162.87**	-0.05	-0.05	-6.06	-1.10*
Mampong × OSO-5	-0.95*	-1.91**	0.33	-0.08	-171.15**	-0.05	0.04	-3.01	-0.95**
Mampong × 25	-0.44	-0.70	-1.65	-1.45	31.32	-0.21*	-0.05	11.78*	0.08
Mampong × Baabo	1.39**	2.64**	2.04	2.74	90.00**	0.19	0.18	4.51	-0.56**
50 × OSO-5	-0.45	-1.26	-1.67	-1.92	-18.31	-0.07	0.21	-2.56	0.52**

Table 4.14 cont'd

HYBRIDS	YIELD	NFP	DFF	50%FL	LA	FL	FW	PH	NBP
50 × 25	-0.44	-1.13	-2.71	-2.00	82.15**	0.11	0.00	-6.56	-0.05
50 × Baabo	-0.05	0.59	1.14	0.83	159.54**	0.02	-0.04	5.06	0.62**
EDUB × OSO-5	1.45**	2.98**	0.53	-0.42	213.53**	-0.01	-0.03	-7.35	0.11
EDUB × 25	-0.75	-1.43	-2.32	-2.11	134.81**	-0.05	0.05	-8.10	0.29
EDUB × Baabo	-0.39	-0.73	-5.15**	-6.07**	-225.63**	-0.03	0.00	-6.53	0.78**
OSO-5 × Tamale	0.91*	2.28**	-1.40	-0.50	-120.46**	0.85*	-0.01	-6.17	-0.11
OSO-5 × Asontemtiatia	1.14**	2.08**	-2.06	-3.32	18.57	0.15	-0.03	-0.90	-0.93**
OSO-5 × Hilhaho	1.15**	2.09**	-1.64	-4.45*	160.24**	-0.10	-0.06	-3.52	-0.69**
25 × Tamale	0.09	0.38	-2.08	-5.16**	57.26**	-0.10	0.00	1.83	-0.81**
25 × Asontemtiatia	0.59	0.78	-1.63	-3.71	-116.32**	0.12	-0.02	2.93	-0.75**
25 × Hilhaho	-0.23	-0.65	-1.45	-3.14	-51.00**	-0.15	0.00	-12.48*	-0.11
Baabo × Tamale	0.22	0.77	0.04	1.20	-181.76**	0.11	-0.06	4.62	-0.25
Baabo × Asontemtiatia	0.17	0.62	-0.93	-2.91	114.09**	0.13	-0.01	0.18	-0.27
Baabo × Hilhaho	0.01	0.29	2.63	1.77	-158.57**	-0.22	0.00	12.87**	-0.67**

***, **, Significant at 05and 0.01 probability levels, respectively; Yield= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; LA= leaf area; FL= fruit length; FW = fruit width; PH = plant height (cm); NBP = number of branch plant**

Table 4.15 Specific combining ability effects of hybrids for fruit yield and yield component characters under high-N environments

HYBRIDS	YIELD	NFP	DFF	50%FL	LA	FL	FW	PH	NBP
G1 × Mampong	-0.86	-0.89	2.88	2.22	9.78	0.14	-0.03	19.07**	0.19
G1 × 50	-0.79	-1.52	-0.90	-0.61	-20.95	-1.09**	-0.10	-10.30	-0.19
G1 × EDUB	-0.47	-0.88	-2.99	-3.05	22.61	1.10**	0.25**	-2.12	0.27
Tamale × G1	0.92	1.30	-3.76*	-3.07	14.48	0.39	0.29**	4.01	0.21
Tamale × Paapa	-0.13	-0.10	-2.23	-2.99	-1.93	0.96**	0.10	-8.31	-0.40
Tamale × SGKP3	1.11*	2.33**	-1.83	-2.44	-12.25	0.31	0.05	-2.99	-0.43
Asontemtiatia × G1	0.05	0.15	-1.36	-1.57	-13.49	1.49**	0.09	0.27	0.09
Asontemtiatia × Paapa	1.17*	1.46	-2.97	-2.52	14.81	0.68	0.18*	7.46	0.67*
Asontemtiatia × GKP3	1.20*	1.86*	2.42	2.28	42.27	-0.53	-0.11	13.29*	0.19
Asontemtiatia × G1	2.18**	3.10**	-5.14**	-6.08**	4.55	0.56	-0.02	3.63	0.25
Hilhaho × Paapa	2.28**	2.93**	-2.49	-2.30	0.37	0.13	0.02	4.29	1.59**
Hilhaho × SGKP3	0.91	1.63*	-0.96	-1.59	4.35	0.22	0.09	-2.59	-0.23
Paapa × Mampong	0.09	-0.35	-1.72	-1.68	-6.98	-1.69**	0.08	12.75*	-0.45
Paapa ×50	-0.63	-0.36	-1.16	-1.52	18.58	-0.12	-0.18*	-2.66	1.19**
Paapa × EDUB	0.24	0.17	-1.40	-1.76	-17.96	-0.23	0.17*	-8.60	0.26
SGKP3 × Mampong	-0.58	-0.93	6.00**	5.83**	12.50	0.63	0.09	7.53	-2.15**
SGKP3 × 50	-0.44	-0.96	-2.52	-2.19	-1.05	0.11	-0.02	6.57	-1.53**
SGKP3 × EDUB	0.11	0.78	0.61	1.43	3.58	0.21	-0.05	9.94	-0.60
Mampong × OSO-5	-1.38**	-2.15**	-0.92	-0.06	4.71	-0.38	0.15	5.17	-1.18**
Mampong × 25	0.31	0.49	-2.69	-2.97	-16.89	0.23	-0.03	7.69	1.72**
Mampong × Baabo	-0.18	0.13	5.19**	4.51*	8.34	0.15	0.01	9.75	-2.05**
50 × OSO-5	-1.50**	-1.97*	3.06	3.39	-22.24	-0.54	-0.09	-7.34	-0.49
50 × 25	-1.08*	-1.04	-3.54*	-3.37	1.19	0.50	0.07	1.74	-0.83*

Table 4.15 continued

HYBRIDS	YIELD	NFP	DFF	50%FL	LA	FL	FW	PH	NBP
50 × Baabo	0.95	1.10	-2.01	-2.19	6.68	-0.01	-0.01	20.62**	0.69*
EDUB × OSO-5	2.60**	2.84**	-4.40**	-3.38	-1.75	0.78*	0.00	-12.65*	0.71*
EDUB × 25	-0.10	0.04	-2.31	-2.12	6.31	-0.19	0.13	-12.80*	-0.05
EDUB × Baabo	-0.68	-0.68	-3.03	-6.53**	3.50	-0.09	0.17*	3.50	1.18**
OSO-5 × Tamale	0.12	0.43	-2.20	-2.38	16.62	0.24	-0.04	-7.64	0.28
OSO-5 × Asontemtiatia	0.73	0.75	-1.16	-1.51	-8.52	0.02	0.08	1.66	-1.66**
OSO-5 × Hilhaho	0.71	1.07	-2.53	-2.45	1.69	1.19**	0.01	4.79	-1.30**
25 × Tamale	-0.95	-1.26	-1.01	-2.09	-24.03	0.32	0.09	-7.89	-1.06*
25 × Asontemtiatia	0.77	0.89	-1.73	-2.41	-10.92	0.58	-0.08	8.97	-0.33
25 × Hilhaho	1.31*	1.08	-2.54	-2.96	2.49	-0.50	0.05	-6.04	1.03*
Baabo × Tamale	1.23*	1.39	-1.10	-1.69	7.40	0.26	-0.08	14.04*	-0.40
Baabo × Asontemtiatia	0.69	1.05	0.11	0.28	-10.93	0.22	-0.10	14.23*	-0.39
Baabo × Hilhaho	0.17	0.85	0.19	0.35	3.29	-0.81*	-0.05	19.07**	-1.22**

***, **, Significant at 05and 0.01 probability levels, respectively; Yield= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; LA= leaf area; FL= fruit length; FW = fruit width; PH = plant height (cm); NBP = number of branch plant**

Table 4.16 Specific combining ability effects of hybrids for fruit yield and other agronomic traits across low- N and high-N conditions

HYBRIDS	YIELD	NF/P	DFF	50%FL	LA	FL	FW	PH	NBP
G1 × Mampong	-0.34	-0.35	1.91	1.01	-25.86	0.17	0.01	16.25**	0.03
G1 × 50	-0.46	-1.02	-0.64	-0.10	-61.90	-0.54	-0.05	-4.01	0.02
G1 × EDUB	-0.51	-1.03	-1.75	-2.12	93.63	0.19	0.12	-6.22	0.09
Tamale × G1	0.88	1.63*	-3.29**	-3.92*	-14.56	0.01	0.18	-1.55	0.07
Tamale × Paapa	-0.22	0.17	-1.62	-2.89	-5.12	0.69	-0.01	-3.27	-0.56*
Tamale × SGKP3	0.47	1.42	-2.13	-3.21	-60.69	-0.05	0.05	-2.33	-0.36
Asontemtiatia × G1	0.06	0.50	-0.87	-1.95	-43.94	0.96*	0.06	-1.32	-0.43
Asontemtiatia × Paapa	0.58	0.82	-2.43	-2.93	-1.28	0.38	0.12	3.42	0.32
Asontemtiatia × SGKP3	0.73	1.39	1.43	2.01	82.72	-0.53	-0.10	10.42*	0.39
Asontemtiatia × G1	1.16*	2.18**	-5.40**	-5.65**	60.02	-0.07	-0.04	-3.42	-0.03
Hilhaho × Paapa	1.69**	2.93**	-3.69*	-3.35	48.67	0.09	-0.04	0.57	0.91**
Hilhaho × SGKP3	0.56	1.23	0.69	-0.07	-6.57	0.28	0.07	2.05	-0.21
Paapa × Mampong	-0.12	-0.49	-0.98	-1.91	5.01	-1.00*	0.04	6.32	-0.37
Paapa ×50	-0.18	0.29	-2.01	-2.54	2.64	-0.01	-0.02	-3.81	0.82**
Paapa × EDUB	-0.10	-0.37	-0.94	-1.83	-38.00	-0.11	0.12	-2.56	0.13
SGKP3 × Mampong	-0.56	-1.05	4.95**	5.08**	-13.62	0.21	0.05	0.27	-1.47**
SGKP3 × 50	-0.13	-0.46	-3.21*	-2.91	30.11	0.35	-0.04	8.68	-1.10**
SGKP3 × EDUB	0.24	0.72	0.93	0.69	-29.17	-0.01	-0.08	1.02	-0.85**
Mampong × OSO-5	-0.98	-1.98**	-0.44	-0.22	-26.22	-0.21	0.08	-0.07	-1.07**
Mampong × 25	-0.07	-0.12	-2.35	-2.35	-26.22	-0.24	-0.09	8.61	0.90**
Mampong × Baabo	0.57	1.39	3.42*	3.46	36.46	0.32	0.19*	5.85	-1.32**
50 × OSO-5	-0.83	-1.58*	0.72	0.74	-48.53	-0.29	0.20*	-4.81	0.00

Table 4.16 continued

HYBRIDS	YIELD	NF/P	DFF	50%FL	LA	FL	FW	PH	NBP
50 × 25	-0.66	-1.07	-3.10*	-2.70	19.43	0.33	0.00	-2.68	-0.45
50 × Baabo	0.43	0.87	-0.40	-0.72	46.80	0.02	-0.09	11.90*	0.64**
EDUB × OSO-5	1.66**	2.83**	-1.84	-1.88	44.75	0.25	-0.02	-9.27	0.41
EDUB × 25	-0.38	-0.67	-2.28	-2.08	44.08	-0.16	0.11	-9.72	0.11
EDUB × Baabo	-0.38	-0.63	-4.07**	-6.23**	-38.05	-0.08	0.06	-1.44	0.97**
OSO-5 × Tamale	0.48	1.30	-1.77	-1.38	5.52	1.30**	-0.01	-6.29	0.08
OSO-5 × Asontemtiatia	0.78	1.33	-1.61	-2.33	-15.01	0.17	0.01	0.65	-1.30**
OSO-5 × Hilhaho	0.74	1.47	-2.01	-3.36	35.40	0.22	-0.05	0.76	-1.00**
25 × Tamale	-0.29	-0.38	-1.51	-3.52	-40.82	-0.04	0.03	-2.53	-0.94**
25 × Asontemtiatia	0.58	0.83	-1.67	-2.96	-51.58	0.40	-0.05	5.78	-0.54*
25 × Hilhaho	0.43	0.21	-1.90	-2.96	-11.00	-0.39	0.01	-8.95	0.46
Baabo × Tamale	0.63	1.06	-0.52	-0.27	-19.72	0.27	-0.09	8.44	-0.33
Baabo ×Asontemtiatia	0.35	0.80	-0.44	-1.30	6.60	0.29	-0.04	6.26	-0.34
Baabo × Hilhaho	0.03	0.52	1.47	1.03	-22.98	-0.58	-0.02	14.94**	-0.95**

***, **, Significant at 05and 0.01 probability levels, respectively; Yield= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; LA= leaf area; FL= fruit length; FW = fruit width; PH = plant height (cm); NBP = number of branch plant**

4.4 Discussions

The preponderance of GCA (GCA-male + GCA-female) effects over SCA for fruit yield and yield component characters for each and across environments suggested that the additive gene effect was more significant than the non-additive gene effects. This also implied that the contribution of GCA was enormous towards the inheritance of the characters measured for the 36 single cross hybrids evaluated. The findings suggested that superior hybrids could be produced through hybridization of parents with significant and positive GCA effects. The findings are in consonance with an earlier report by Kumar *et al.* (2017), who reported that crude fibre, number of seeds per fruit, plant height, and other traits were influenced mainly by additive gene action. Additionally, the findings agreed with those of Ramesh and Singh (1999), El-Gendy and El-Sherbeny (2005), and El-Sherbeny *et al*. (2005), who found that for most economic characters of okra, additive genetic variance (2A) was more significant than nonadditive genetic variance (2D). However, this result is contradictory to those of Solanky and Singh (2010), El- Gendy *et al.* (2012) and El-Gendy and Sherbeny (2013), who discovered that non-additive genetic variance was greater than the additive genetic variance for okra plant height, branch count, pod yield, and the number of pods per plant. The discrepancy between the current findings and those of the researchers mentioned above may be attributed to different testing conditions (N stress level) or genotypic variations among the set of genotypes used in the experiments. GCA contributed 86.09 percent of the sum of squares for fruit yield under low N in the current study. For high N and across the environment, GCA accounted for 81.08% and 88.07% of the overall sum of squares, respectively. To ascertain

the contributions of the accessions to their hybrids, GCA effects or additive gene effects of a character's parental genotypes are useful.

A significant objective of the current research was to assess the combining ability of the twelve okra parental accessions under low-N and high-N environments. In a recurrent selection process to develop populations that are tolerant to low-N, parental accessions of okra with highly significant and positive estimates of GCA for fruit yield in low nitrogen soil have the likelihood of passing on desirable genes for fruit yield to the progeny. Moreover, such okra parental accessions could also enhance the current populations and create hybrid and synthetic types tolerant to low nitrogen for commercialization. The okra accession Tamale 2E had a significant positive GCA-male effect on fruit yield under low nitrogen environment, indicating that this okra accession when utilized as male parents would pass on advantageous genes for increased fruit yield to their offspring. The reported positive and significant estimates of GCA-male and GCA- female for fruit yield of parental accessions Paapa and Hilhaho under high N environment signified that these parental accessions could transmit beneficial genes for enhanced fruit yield to their young ones across the testing conditions when utilized as either male or female parents. Thus, these parents may be considered in future breeding programmes to produce desirable segregants for fruit yield and its component characters. Moreover, the observed significant negative GCA-male effects for days to fifty percent flowering displayed by parental accessions 25 and Tamale 2E under low N environments indicates that this parental line would contribute favourable genes for earliness when used as a male parent. Furthermore, accessions Paapa, 50 and 25 had

significant negative GCA –female effects and would contribute desirable alleles to their progenies when used as females across high N environment.

The occurrence of significant SCA is a consequence of fluctuations in dominance relationships among parents (Wassimi *et al.,* 1986). According to the current study, significant and positive SCA effects were observed for hybrids such as Tamale 2E × G1, Hilhaho × Paapa, Mampong × Baabo, EDUB × OSO-5, OSO-5×Asontemtiatia and OSO-5 × Hilhaho under low nitrogen environment. Coincidentally, three of these hybrids; Tamale 2E × G1, Hilhaho × Paapa, and EDUB × OSO-5, were among the best single cross hybrids selected under a low nitrogen environment. This implied that choosing parents for hybrid production solely based on favourable estimations of SCA may not be beneficial as significant and positive estimates of SCA are not necessarily indicative of excellent performance in hybrids. Thus, Menkir *et al*. (2004) suggested that selection of single cross hybrids based on high SCA as well as average fruit yield is more practicable. Moreover, all hybrid crosses which exhibited significant and positive SCA estimates for fruit yield, in each and across the research environments, involved at least one good general combiner. Corresponding to these findings, Das *et al*. (2013) reported that positive SCA effects were discernible in the hybrids involving both parents possessing significant positive GCA effects. These good × good combinations could result in the capitalization of non- additive (Dominance × dominance variance) effects over the super structure of the additive gene effects. Hybrids involving both the parents possessing significant positive GCA effects (good × good) with higher significant SCA effects for number of fruits per plant and fruit yield in okra have been earlier reported by Aulakh *et al*. (2012),

Medagam *et al.* (2012), Katagi *et al*. (2015), Raghuvanshi *et al*. (2011), Wammanda *et al*. (2010), Singh, (2011), Prakash *et al.* (2002) and Dabhi *et al*. (2010). These hybrids could be exploited through heterosis breeding and may also give transgressive segregants in subsequent generations; therefore, it would be worthwhile to use them for improvement in fruit yield *per se.*

According to Hallauer and Miranda (1988), when compared to the diallel, the NCD II allows for the utilization of more parental genotypes and enables the paternal and cytoplasmic (maternal) effects to be calculated. The proportion of the GCA-male and GCA-female mean squares was employed in the current investigations to calculate the cytoplasmic and paternal effects (Kearsey and Pooni, 1996). The contributions of GCA-female and GCA-male to hybrids varied depending on the trait and conditions. Superior GCA-female to GCA-male effects for yield and yield component characters in nitrogen-deficient soils, high N and across research environments suggested that cytoplasmic effects might have modified these traits. The effects of low-N and high-N environments on the contributions of GCA-male and GCA-female to fruit diameter and plant girth did not differ significantly, indicating that maternal and paternal effects were equally important in the inheritance of these traits. The findings showed that under each and across research environments, maternal (cytoplasmic) influences contributed to the inheritance of fruit yield, number of fruits per plant, days to first flowering, days to fifty percent flowering, fruit length and plant height. These findings also suggest that to maximize the benefits of maternal inheritance on their progeny under each research environment genotypes with larger magnitudes of GCA-female effects than GCA-male effects for fruit yield, prolificacy, and yield component

traits could be made female parents in the process of hybridization. On the contrary, a larger magnitude of GCA-male than GCA-female for leaf chlorophyll content and leaf area under low-N conditions indicated that paternal genotypes played a more significant role in determining these traits. To maximize prolificacy under high N conditions, it also signifies that using male parents should be based on genotypes with significant GCA-male estimates for fruit yield. This suggests that paternal influences controlled prolificacy when production parameters were not constrained.

The importance of genetics in a trait is measured by its heritability. A high heritability, close to 1, suggests that genetics accounts for a large portion of the variation in a trait between different germplasm; a low heritability, close to zero, indicates that most of the variation is due to environmental factors. Furthermore, broad-sense heritability (H^2 = VG/VP) quantifies the fraction of phenotypic variation owing to genetic values, which may include dominance and epistasis effects. Narrow-sense heritability, h^2 = VA/VP, on the other hand, reflects only the amount of genetic variation owing to additive genetic values (VA). Estimates of heritability, as stated by Johnson *et al*. (1955) were classified as < 30 values were low, 30 - 60 values were moderate and > 60 values were high. In general, estimates of heritability in the broad sense (H^2) were higher than those of the narrow sense (h^2) for all the studied characters. The current studies agreed with the findings of Abed *et al*. (2020), who reported higher estimates of broad sense heritability than narrow sense heritability estimates. Moreover, high broad sense heritability estimates were observed for fruit yield, number of fruits per plant, days to first flowering, days to fifty percent flowering, fruit length, fruit diameter, plant height and

plant width under low soil nitrogen, high N and across research conditions indicating that phenotypic selection of these characters might be used to achieve genetic gains. The high broad sense estimates of heritability, as observed in the current study, showed that GCA was more important for these characters, which agreed with the findings of Saryam *et al.* (2015), Sundaram (2015), Khajuria *et al*. (2015); Shivaramegowda *et al.* (2016); Jadhav *et al*. (2016) and Kerure *et al*., (2017). The above heritability estimates were based on a broad sense, and hence, the total genetic variance may include dominance and epistatic components, which are not available for selection. On the contrary, a large magnitude of narrow sense heritability (h^2) values was found for fruit yield and most yield components under low N and high N environments. Moreover, moderate narrow sense heritability was obtained for plant-width and leaf area under high N conditions. Very low heritability reveals the ineffectiveness of direct selection for improving the traits, while moderate heritability suggests improvement through selection. It is, however, significant to note that, in selecting genotypes that tolerate low-N, information on fruit yield, fruit number per plant, days to first flowering and leaf chlorophyll content should be considered. Moreover, high heritability in the narrow sense (h^2) values indicates the relative importance of additive gene action in inheriting the studied traits.

4.5 Conclusion

The results of the study on combining ability for fruit yield and other agronomic qualities showed that additive gene effect was more significant than the non-additive gene effect and that GCA significantly contributed to the transmission of the studied characters for the 36 hybrids assessed. The results further revealed that parental genotypes Hilhaho, Baabo and Paapa were the top general combiners under high N conditions. Moreover, parental genotype Tamale 2E was the leading general combiner for fruit yield under low N conditions. These genotypes will likely transmit desirable alleles to their hybrids and could benefit breeding programmes. However, seven hybrid crosses manifested significant and positive SCA effects for fruit yield in tons/ha under each and across the research environment. Of these, three among the top seven were Hilhaho × Paapa, Tamale 2E × G1 and Mampong × Baabo. High broad sense heritability estimates characterized fruit yield and most yield component traits. Moreover, maternal effects influenced fruit yield, and most traits

CHAPTER FIVE

5.0 Combining Ability Studies and Gene Action of Okra [*Abelmoschus esculentus* (L.) Moench] Germplasm for Tolerance to Okra Leaf curl and Mosaic virus diseases under low Nitrogen and high Nitrogen Conditions

5.1 Introduction

Okra [*Abelmoschus esculentus* (L.) Moench] yields in Ghana range from 1.5 to 4.5 t/ha on average, compared to 30 t/ha in agriculturally developed nations (SRIDMOFA, 2007). This significant yield deficit between potential and actual yield is attributed to abiotic (fertility) and biotic stresses like pests and diseases.

The okra leaf curl virus (OLCV) and okra mosaic virus (OMV) are the two main diseases that have been reported in Ghana (Bi-Kusi, 2013; Asare-Bediako *et al*., 2014a and b). In Ghana, OMVD is among the most severe and pervasive viral infections of the crop (Asare Bediako *et al*., 2014a and b). The flea beetle (*Podagrica* spp) spreads the illness which is brought about by the okra mosaic virus (Asare-Bediako *et al*., 2014), while OLCV is disseminated by the whitefly (*Bemisia* tabaci) (Brunt *et al*., 1996). According to Basu (1995), OLCV infection can result in yield losses of up to 80%, whereas OMV infection has been linked to yield losses of up to 90% (Alegbejo *et al*., 2008). These economic losses resulting from poor fruit quality and a decreased market price are significant.

By using chemicals to suppress *Podagrica* species and the white fly as well as cultural techniques such as crop rotation, intercropping, and manipulating plant density, OMD and OLCD incidence and severity can be decreased. However, these measures have not been efficient in managing the

diseases. Chemical application is expensive and rarely viable for farmers with limited resources. Moreover, using chemicals harm the environment and human and animal health. It would be more affordable to control OMD and OLCD if a more environmentally friendly option, such as resistant hybrids, was developed and used.

For a breeding program to be successful, the parents must be chosen correctly. Combining ability analysis makes it possible to estimate the magnitude of gene action for disease resistance and nitrogen-efficient genotypes, which is crucial in creating a successful breeding program. However, no work has been done on combining ability and gene action for OMD and OLCD resistance in Ghana under low-N environment. To find the best parents for the generation of hybrids, North Carolina mating design II has been successfully employed in genetics research to determine the inheritance of a trait among a collection of genotypes. The present study was initiated with the following specific objectives:

i. Determine the general and specific combining ability of parents for resistance to OLCD, OMD and *Podagrica* spp. under low and high N environments.
ii. Assess the gene action effects conditioning the expression of OMD, OLCD and *Podagrica* spp. under low-N and high-N environment.
iii. II Identify superior genotypes and hybrids that are resistant to OMD, OLCD and *Podagrica* spp. under low-N and high-environment

5.2 Materials and Methods

5.2.1 Study Location and Germplasm Source

The study was conducted at two locations in the major and minor growing seasons of the 2021 cropping year at Jacobu and Akumadan. Twelve okra accessions, four checks, and 36 hybrids were grown and monitored. The detailed parental information is presented in Chapter 4, section 4.2.1, Table 4.1.

5.2.2 Pest control

The field was left for one month for diseases and insect pest infestation before spraying was effected. At this stage, the infestation and the population of the *Podagrica* and white fly (*Bemisia tabaci*) were very high. This gave way to scoring the *Podagrica* spp. and diseases across the various locations (Table 6.3). Golan SL TM and Sunpyrifos 48% EC insecticide were used to control grasshoppers, white flies (Akumadan location) and *Podagrica* spp., the most devastating and predominant insect pests at the field.

5.2.3 Assessment of incidence of *Podagrica* species, okra mosaic disease and leaf curl disease

The incidence of okra *Podagrica* spp was assessed based on the extent of leaf area damaged by the *Podagrica* spp. *Podagrica* spp. incidence was calculated as the ratio of infected plants to the total number of sampled plants expressed as a percentage. OMD and OLCD incidence was also determined as the number of okra plants manifesting the visual symptoms of the disease defined as a percentage of the total number of plants observed. The disease

incidence within the okra field was calculated using a method described by Sankara and Acharyya (2012) based on a visual inspection of symptoms as follows:

$$\textbf{PDI} = \frac{\text{Number of diseased plants}}{\text{The total number of plants observed}} \times 100$$

PDI= Percentage of Disease Incidence (Sankara and Acharyya, 2012)

5.2.4 Assessment of severity of okra mosaic and leaf curl disease

The severity indices for okra mosaic disease and okra leaf curl disease were assessed by adopting the formula of Galanihe *et al.* (2004) as

$$DSI = (P \times Q)/ (M \times N)] \times 100$$

Where: P = severity score, Q = number of infected plants having the same score; M = Total number of plants observed, N = Maximum rating scale number. Table 6.1 and 6.2 presents a visual scale for scoring the severity of OMD and OLCD, respectively.

Table 5.1 Visual scale for rating severity of okra mosaic virus disease

Disease scoring rate	Description
0	Healthy, asymptomatic plant
1	Mild mosaic, mottle or chlorosis on leaves
2	Moderate chlorosis and mosaic without significant leaf distortion
3	Score 1 or 2 plus leaf malformation
4	Severe chlorosis, mottle or mosaic plus stunting of the whole plant
5	Score 4 plus drying and leaf drop

Table 5.2 Visual scale for rating severity of okra leaf curl virus disease

Disease scoring rate	Description
0	No symptom
1	No visible disease symptom
3	Top leaves curled and slight dwarfing of plant.
5	All leaves curled and slight dwarfing of plants.
7	Severe curling of leaves, dwarfing of plants, and the proliferation of auxiliary branches

Table 5.3 Visual scale for rating severity of *Podagrica* spp. disease

Disease score	% Damage	Description
0	0	No apparent damage
1	25	About a quarter (1/4) of total leaf area Damaged
2	50	About half (1/2) of total leaf area damaged
3	75	About three quarters (3/4) of total leaf area damaged
4	95	Only a few leaves are green and stem green
5	100	All leaves and stems eaten by pest

5.2.5 Parameters measured

Data was scored on the incidence of *Podagrica* spp., the incidence of okra mosaic disease, the incidence of okra leaf curl disease, the severity of *Podagrica* spp., the severity of okra mosaic disease and the severity of okra leaf curl disease.

5.2.6 Statistical Analysis

Data recorded for the incidence of *Podagrica* spp., okra mosaic disease, okra leaf curl disease, severity of *Podagrica* spp., okra mosaic disease and okra leaf curl were transformed using the $\log_{10}$. Subsequently, combining ability analysis was carried out as described in Chapter 4, section 4.2.9.

5.3 Results

5.3.1 Analysis of variance of okra mosaic and leaf curl disease under low-N, high-N and across environments

Across low N environments, the ANOVA of the single cross hybrids differed significantly ($p<0.05$) for genotype main effect (G) and environment (E) main effect for all the measured traits except E mean squares for IP and SOMD (Table 5.4). However, no significant genotype × environment (GEI) interaction existed for the measured traits. When the hybrids' components of variation were decomposed into female set (GCA-female), male set (GCA-male) and male × female interaction (SCA), the ANOVA showed significant ($P< 0.05$) differences for GCA-male and GCA-female for all evaluated traits except for GCA-female for SOMD (Table 5.4). Conversely, SCA mean squares showed no significant variations for the investigated characters. Heritability estimates for broad sense ranged from 91% for SOMD to 93% for IP and SP. Narrow sense heritability estimates varied from 46% to 53% (Table 5.4).

Across a high nitrogen environment, the ANOVA showed significant ($p<0.05$) variations for G and E main effects for all the studied traits except E mean square for incidence and severity of OLCD (Table 5.5). However, there was no significant genotype × environment interaction (GEI) for the studied traits (Table 5.5). Moreover, the ANOVA showed significant GCA-males mean squares for the incidence and severity of OLCD. Also, there was a significant GCA-female mean square for SP (Table 5.5). The magnitude of broad sense heritability values differed from 84% to 95%. Narrow sense heritability estimates varied from 46% to 66% (Table 5.5).

Across low N and high N environments, the ANOVA showed significant ($p<0.05$) variations for G and E main effects for all the studied characters except E mean square for incidence and severity of OLCD (Table 5. 6). However, GEI was not significant for the measured traits (Table 5.6). Furthermore, the results showed significant GCA-male and GCA-female effects for all the traits except GCA-male for incidence and severity of OMD. Moreover, except for the incidence and severity of *Podagrica* spp., there was a significant SCA mean square for the studied traits. Estimates of broad sense heritability across low N and high N conditions differed from 86% for the severity of OMD to 94% for the incidence of OLCD. Heritability in the narrow sense varied from 46% for severity of OLCD to 57% for severity of OMD (Table 5.6).

Table 5.4 Heritability estimates and mean squares of OMD and OLCD evaluated under low nitrogen conditions in 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	IP	SP	IOMD	IOLCD	SOMD	SOLCD
ENVIRONMENT	3	281.60	1.07*	325.52*	137.45*	0.53	0.79*
SET	3	177.71	0.52	150.74	109.78	0.47	0.39
ENV* SET	9	74.19	0.26	102.77	57.66	0.24	0.13
REP(ENV*SET)	24	57.54	0.15	40.67	75.97	0.09	0.17
BLOCK(ENV*SET)	64	72.17	0.22	60.49	108.86	0.15	0.30
HYBRID GENOTYPES	35	242.10**	0.67**	238.68**	198.91**	0.59**	0.53**
MALE (SET)	11	242.51*	0.68*	212.67*	225.03*	0.55*	0.54*
FEMALE (SET)	11	456.34**	1.21**	237.09*	244.27*	0.43	0.71*
FEMALE *MALE (SET)	25	163.18	0.57	171.41	127.02	0.41	0.34
HYBRID * ENV	105	73.98	0.21	75.65	74.24	0.16	0.20
ENV*MALE (SET)	33	57.89	0.20	91.18	103.10	0.21	0.24
ENV*FEMALE (SET)	33	66.15	0.14	64.07	63.23	0.15	0.18
ENT*FEMALE*MALE	75	97.24	0.26	79.22	59.74	0.14	0.17
ERROR	192	122.31	0.38	110.85	100.17	0.26	0.27
HERITABILITY (NS)		0.47	0.47	0.51	0.46	0.53	0.49
HERITABILITY (BS)		0.93	0.93	0.91	0.92	0.91	0.92

Table 5.5 Heritability estimates and mean squares of OMD and OLCD evaluated under high nitrogen conditions in the 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	IP	SP	IOMD	IOLCD	SOMD	SOLCD
ENVIRONMENT	3	2314.72**	6.07**	342.53*	169.92	1.08*	0.28
SET	3	54.18	0.09	150.68	11.53	0.35	0.05
ENV* SET	9	36.54	0.19	48.22	78.24	0.20	0.22
REP(ENV*SET)	24	103.42	0.22	58.98	101.61	0.18	0.36
BLOCK(ENV*SET)	64	95.10	0.23	93.63	111.36	0.25	0.33
HYBRID GENOTYPES	35	224.84**	1.09**	188.76**	204.15**	0.56**	0.49*
MALE (SET)	11	197.61	0.48	90.24	301.64**	0.18	0.79**
FEMALE (SET)	11	257.18	0.73*	197.22	83.32	0.61	0.20
FEMALE *MALE (SET)	25	186.08	0.47	206.38*	114.56	0.45	0.44
HYBRID * ENV	105	86.39	0.47	70.91	64.12	0.25	0.18
ENV*MALE (SET)	33	84.75	0.19	50.95	41.74	0.17	0.13
ENV*FEMALE (SET)	33	86.48	0.32	51.70	72.95	0.24	0.19
ENT*FEMALE*MALE	75	122.89	0.33	62.93	84.42	0.18	0.25
ERROR	192	125.14	0.32	106.03	0.32	0.28	0.28
HERITABILITY (NS)		0.52	0.52	0.58	0.47	0.66	0.46
HERITABILITY (BS)		0.93	0.91	0.84	0.95	0.84	0.93

Table 5.6 Heritability estimates and mean squares of OMD and OLCD evaluated across research environments in the 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	IP	SP	IOMD	IOLCD	SOMD	SOLCD
ENVIRONMENT	3	1456.17**	3.77**	385.48**	138.22	1.11**	0.48
SET	3	69.32	0.22	263.84	29.10	0.72	0.08
ENV* SET	9	70.68	0.25	70.08	71.42	0.20	0.20
REP(ENV*SET)	24	80.48	0.18	49.82	88.79	0.14	0.27
BLOCK(ENV*SET)	64	83.64	0.22	77.06	110.11	0.20	0.31
HYBRID GENOTYPES	35	276.93**	0.75**	305.82**	323.42**	0.85**	0.80**
MALE (SET)	11	309.37*	0.81*	200.50	397.43**	0.45	0.97**
FEMALE (SET)	11	393.18**	1.23**	304.45*	250.93*	0.72*	0.75*
FEMALE *MALE (SET)	25	160.03	0.53	236.56*	180.97*	0.58*	0.59*
HYBRID * ENV	105	95.87	0.27	80.19	70.67	0.22	0.19
ENV*MALE (SET)	33	79.81	0.22	75.54	80.54	0.20	0.21
ENV*FEMALE (SET)	33	111.18	0.30	68.17	69.32	0.21	0.18
ENT*FEMALE*MALE	75	121.37	0.33	81.10	70.44	0.18	0.21
ERROR	192	123.79	0.35	108.44	99.76	0.27	0.28
HERITABILITY (NS)		0.48	0.49	0.56	0.47	0.57	0.46
HERITABILITY (BS)		0.91	0.90	0.87	0.94	0.86	0.93

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; Env = environment; Rep = replication; IP = incidence of Podagrica; SP = severity of Podagrica; IOMD = incidence of okra mosaic disease; IOLCD = incidence of okra leaf curl disease; SOMD = severity of okra mosaic disease and SOLCD = severity of okra leaf curl disease**

5.3.2 Estimates of breeding value (GCA effects)

Across low nitrogen environment, GCA-male effects for incidence of OLCD varied from -0.18 for Tamale 2E to 0.17 for SGKP3, while GCA-female effects ranged from -0.15 for Baabo to 0.17 for Tamale 2E (Table 5.7). Similarly, GCA-female effects for severity of OLCD ranged from -0.05 for Baabo to 0.04 for Tamale 2E. Okra genotypes SGKP3, 50, and Baabo were resistant to OLCD with negative GCA–female effects (Table 5.7). However, four of these genotypes, Paapa, Baabo, Tamale 2E and 25, were the best general combiners with significant and negative GCA-male effects for the incidence of OLCD. Moreover, the GCA-female effect for the incidence of OMD ranged from -0.18 for Mampong to 0.10 for OSO-5. Similarly, okra genotypes SGKP3, Mampong, and Tamale 2E were the best general combiners for both incidence and severity of OMD with significant and negative GCA- female effects (Table 5.7).

Across the high N environment, the GCA male effect for incidence of OLCD ranged from -0.14 for Paapa to 0.12 for Asontemtiatia. In contrast, the GCA-female effect varied from -0.21 for Paapa to 0.18 for Tamale 2E for the incidence of OLCD (Table 5.8). Similarly, the GCA-female effect for severity of OLCD varied from -0.07 for Paapa to 0.05 for Tamale 2E, while GCA-male estimates ranged from - 0.05 for Paapa to 0.06 for Asontemtiatia. Parental genotypes Paapa, OSO-5 and 25 were the best general combiners with negative and significant GCA-female effects for both incidence and severity of OLCD and were identified as the tolerant genotypes. Conversely, Paapa, 25 and Baabo were also identified as resistant genotypes with significant and negative GCA-male effects for both incidence and severity of OLCD. The

GCA-female effect for the incidence of OMD varied from - 0.06 for OSO-5 and 25 to 0.08 for SGKP3, while the GCA-female estimate for the severity of OMD varied from -0.02 to 0.03. Parental genotypes EDUB, OSO-5 and 25 were identified as the best female general combiners with significant GCA-female estimates for the incidence of OMD while G1, EDUB and 25 were the most resistant genotypes with significant GCA-female effects for the severity of OMD (Table 5.8).

Across low N and high N environments, the GCA-female effect for the incidence of OLCD varied from -0.12 for Paapa to 0.17 for Tamale 2E. In contrast, the GCA-female effect ranged from -0.04 for Paapa to 0.05 for Tamale 2E for the severity of OLCD (Table 5.9). Significant and negative GCA-female effects were observed for the reaction of genotypes to the incidence and severity of OLCD. Accessions Paapa, OSO-5 and Baabo were the best female general combiners for incidence and severity of OLCD (Table 5.9). Also, okra genotypes Paapa, Baabo, Tamale and 25 were the best male general combiners for the severity of OLCD. Moreover, GCA-female effects for incidence of OMD varied from -0.07 for Mampong to 0.05 for Hilhaho, while GCA-male effect ranged from 0.13 for Tamale2E to 0.14 for Mampong and G1. Okra genotypes Mampong, EDUB, and Tamale 2E were the most resistant female genotypes for both incidence and severity of OMD (Table 5.9).

Table 5.7 General combining ability effects of okra mosaic disease, leaf curl disease and *Podagrica* spp of okra parental genotypes evaluated under low nitrogen conditions during the 2021 major and minor season

	IOLCD		IOMD		I.*Podagrica*		SOMD		S.*Podagrica*		SOLCD	
Parents	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	0.02	0.03	0.08	0.03	0.002	-0.05	0.03	0.01	0.003	-0.02	0.00	0.01
Paapa	-0.10**	-0.03	-0.02	0.08**	0.000	0.09**	-0.01	0.03**	0.000	0.02	-0.01	-0.01
SGKP3	0.17**	-0.13**	0.00	-0.05*	0.001	-0.16**	0.00	-0.03**	0.001	-0.05**	0.01	-0.03**
Mampong	0.11	0.02	0.08	-0.18**	0.001	-0.01	0.03	-0.05**	0.003	-0.02	0.01	0.02*
50	0.14**	-0.08**	-0.03	0.01	-0.001	-0.04	-0.01	-0.01	-0.002	-0.02	0.02	-0.02*
EDUB	0.04	0.05	0.03	-0.02	0.000	-0.02	0.01	0.00	0.000	0.01	0.00	0.02*
OSO-5	-0.02	-0.03	-0.05	0.10**	-0.001	0.08*	-0.02	0.03**	-0.002	0.04**	0.00	-0.02*
25	-0.08*	0.12**	0.01	0.07*	0.002	0.11**	0.00	0.03**	0.002	0.03*	-0.01	0.03**
Baabo	-0.16**	-0.15**	0.02	-0.02	0.000	-0.02	0.01	-0.01	0.000	-0.01	-0.01	-0.05**
Tamale 2E	-0.18**	0.17**	-0.08	-0.07*	-0.002	-0.16**	-0.03	-0.02*	-0.005	-0.05**	-0.01	0.04**
Asontemtiatia	0.05	0.03	0.03	-0.01	0.001	0.10**	0.01	0.00	0.003	0.04**	0.00	0.01
Hihaho	0.00	0.01	-0.06	0.05*	-0.002	0.07*	-0.02	0.01	-0.004	0.03*	0.00	0.01

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; IP = incidence of *Podagrica*; SP = severity of *Podagrica*; IOMD = incidence of okra mosaic disease; IOLCD = incidence of okra leaf curl disease; SOMD = severity of okra mosaic disease and SOLCD = severity of okra leaf curl disease**

Table 5.8 General combining ability effects of okra mosaic disease, leaf curl disease and Podagrica spp of okra parental genotypes evaluated under high N conditions during the 2021 major and minor growing season

	IOLCD		IOMD		I. *Podagrica*		SOMD		S. *Podagrica*		SOLCD	
Parents	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	0.06*	0.05	0.12	-0.02	0.11	0.01	0.04	-0.02**	0.03	0.00	0.03**	0.02
Paapa	-0.14**	-0.21**	-0.02	-0.01	0.03	0.10**	-0.01	0.00	0.00	0.02**	-0.05**	-0.07**
SGKP3	0.05*	-0.02	0.11	0.08**	0.03	-0.05*	0.05*	0.01	0.01	0.00	0.02*	0.01
Mampong	0.03	0.11**	0.13	0.05**	0.05	-0.05*	0.05	0.03**	0.02	0.00	0.01	0.03*
50	0.06*	0.02	0.00	0.01	0.02	0.02	0.00	0.00	0.01	0.00	0.01	0.00
EDUB	0.03	-0.03	-0.06	-0.05**	-0.04	-0.14**	-0.02	-0.02**	-0.01	-0.05**	0.01	-0.01
OSO-5	0.00	-0.14**	0.00	-0.06**	0.05	-0.01	0.00	-0.01	0.02	0.01	0.00	-0.04**
25	-0.06*	-0.08*	-0.09	-0.06**	-0.07	0.01	-0.04	-0.02**	-0.02	-0.01	-0.03*	-0.02*
Baabo	-0.07**	0.02	-0.05	0.06**	-0.08	0.05*	-0.02	0.01	-0.03	0.01*	-0.03**	0.01
Tamale 2E	-0.07**	0.18**	-0.12	-0.02	-0.06	-0.08**	-0.04	0.01	-0.02	-0.02**	-0.02	0.05**
Asontemtiatia	0.12**	0.06	0.02	-0.03	0.03	0.02	0.00	0.00	0.01	0.01	0.06**	0.01
Hihaho	-0.02	0.04	-0.05	0.05**	-0.07	0.10*	-0.01	0.01	-0.03	0.02**	-0.01	0.00

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; IP = incidence of *Podagrica*; SP = severity of *Podagrica*; IOMD = incidence of okra mosaic disease; IOLCD = incidence of okra leaf curl disease; SOMD = severity of okra mosaic disease and SOLCD = severity of okra leaf curl disease**

Table 5.9 General combining ability effects of okra mosaic disease, leaf curl disease and *Podagrica* spp of okra parental genotypes evaluated across low N and high conditions in the 2021 major and minor growing season

	IOLCD		IOMD		I. Podagrica		SOMD		S. Podagrica		SOLCD	
Parents	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**	**GCA-m**	**GCA-f**
G1	2E-15	0.04	0.14*	0.01	0.05	-0.02	0.04*	0.00	0.02	-0.01	0.02	0.01
Paapa	-6E-15	-0.12**	-0.02	0.04**	0.01	0.10**	-0.01	0.02**	0.00	0.02*	-0.05**	-0.04**
SGKP3	5E-15	-0.08**	0.07	0.01	0.02	-0.10**	0.02	-0.01*	0.01	-0.02*	0.04**	-0.01
Mampong	3E-15	0.06*	0.14*	-0.07**	0.03	-0.03	0.04*	-0.01*	0.01	-0.01	0.03*	0.02**
50	5E-15	-0.03	-0.03	0.01	0.00	-0.01	-0.01	0.00	0.00	-0.01	0.04**	-0.01
EDUB	2E-15	0.01	-0.01	-0.03**	-0.01	-0.08**	0.00	-0.01*	0.00	-0.02*	0.01	0.00
OSO-5	-5E-16	-0.08**	-0.04	0.02	0.00	0.04	-0.01	0.01*	0.00	0.03**	-0.01	-0.03**
25	-3E-15	0.02	-0.04	0.01	0.00	0.06*	-0.02	0.00	0.00	0.01	-0.03**	0.01
Baabo	-6E-15	-0.06*	-0.02	0.02	-0.03	0.01	0.00	0.00	-0.01	0.00	-0.05**	-0.02**
Tamale 2E	-6E-15	0.17**	-0.13*	-0.05**	-0.04	-0.12**	-0.04*	-0.01*	-0.02	-0.04**	-0.03**	0.05**
Asontemtiatia	4E-15	0.04	0.03	-0.02	0.02	0.06*	0.01	0.00	0.01	0.02*	0.04**	0.01
Hihaho	-6E-16	0.02	-0.08	0.05**	-0.04	0.09**	-0.02	0.01*	-0.02	0.02*	-0.01	0.01

***, ** = Significant at 0.05 and 0.01 probability levels, respectively; IP = incidence of *Podagrica*; SP = severity of *Podagrica*; IOMD = incidence of okra mosaic disease; IOLCD = incidence of okra leaf curl disease; SOMD = severity of okra mosaic disease and SOLCD = severity of okra leaf curl disease**

5.3.3 Estimate of specific combining ability (SCA)

Positive and negative SCA effects were recorded among hybrid crosses under each and across research environments. Under low nitrogen conditions, 23 of the 36 okra hybrids had negative SCA effects for the incidence of *Podagrica* spp. (IP) (Table 5.10). Out of the 23 single cross hybrids that manifested negative SCA effects, only crosses Paapa × Mampong (-0.258), Tamale × G1 (-0.238) and Hilhaho × SGKP3 (-0.238) had negative and significant SCA effects and were found to be tolerant to *Podagrica* spp. (IP). Conversely, hybrid cross SGKP3 × Mampong (susceptible) recorded the highest significant and positive SCA effect for *Podagrica* spp. and was observed to be the worst specific combiner (Table 5.10). Also, Hybrid Cross Paapa × Mampong had significant and negative SCA effects for their reaction to the incidence and severity of OMD. In contrast, Mampong × OSO-5 (susceptible) had the highest positive and significant SCA effects for both incidence and severity of OMD. Moreover, out of the 36 hybrids, only hybrid cross Asontemtiatia × Paapa (tolerant) showed a significant and negative SCA effect for the incidence of OLCD, while OS-5 × Tamale (susceptible) recorded the highest significant and positive SCA effect for OLCD (Table 5.10).

Across high N environment, 22 out of the 36 hybrids manifested a negative SCA effects for the incidence of OLCD (Table 5.11). However, hybrid crosses Paapa × EDUB (-0.257), Hilhaho × Paapa (-0.247) and Asontemtiatia × Paapa (-0.247) had the highest negative and significant SCA effects for incidence of OLCD while cross OSO-5 × Tamale 2E (most susceptible) recorded the highest significant and positive SCA effect for the incidence of OLCD. Furthermore, crosses, Hilhaho × SGKP3 (-0.212) and

EDUB × OSO-5 (-0.220), were the best specific combiners for the incidence of *Podagrica* spp. (Table 5.11).

Across low N and high N environments, hybrid cross Asontemtiatia × Paapa (-0.265) was the best specific combiner and was followed by Paapa × EDUB (-0.231), OSO-5 × Asontemtiatia (-0.197), 25 × Asontemtiatia (-0.197), Baabo × Asontemtiatia (-0.197), G1 × 50 (-0.188) and EDU × OSO-5 (-0.173) for both incidence and severity of OLCD. In contrast, cross OSO-5 × Tamale 2E was the worst specific combiner with the highest positive and significant SCA effect for the incidence of OLCD (Table 5.12). For the incidence of *Podagrica* spp., crosses Hilhaho × SGKP3 (-0.265) and Asontemtiatia × G1 (-0.217) were the best specific combiners, while cross Mampong × OSO-5 had the highest positive and significant SCA effect. Moreover, cross EDUB × OSO-5 was the best specific combiner for the incidence of OMD, while Mampong × OSO-5 had the highest positive and significant SCA effect (Table 5.12)

Table 5.10 Specific combining ability effects for okra mosaic, leaf curl disease and *Podagrica* spp under low- N environments

Hybrids	IOLCD	I.Podagrica	SOLCD	SOMD	S.Podagrica	IOMD
G1 × Mampong	0.05	0.13	0.02	0.01	0.03	0.07
G1 × 50	-0.18	0.21	-0.06	0.02	0.07	0.07
G1 × EDUB	0.02	-0.06	0.01	-0.02	-0.01	-0.05
Tamale × G1	-0.14	-0.24*	-0.04	-0.03	-0.08	-0.13
Tamale × Paapa	-0.03	0.01	0.00	-0.01	-0.01	-0.08
Tamale × SGKP3	-0.18	-0.11	-0.02	-0.01	-0.03	0.03
Asontemtiatia × G1	0.05	0.07	0.02	0.02	0.03	0.07
Asontemtiatia × Paapa	-0.19*	-0.13	-0.06	-0.02	-0.05	-0.03
Asontemtiatia × SGKP3	-0.14	-0.13	-0.03	-0.04	-0.04	-0.12
Asontemtiatia × G1	-0.07	-0.17	-0.02	-0.03	-0.05	-0.08
Hilhaho × Paapa	-0.03	-0.05	-0.01	0.02	-0.01	0.05
Hilhaho × SGKP3	-0.02	-0.24*	-0.01	-0.04	-0.07	-0.13
Paapa × Mampong	-0.03	-0.25 *	-0.00	-0.08 *	-0.08*	-0.22*
Paapa ×50	-0.12	-0.01	-0.04	-0.02	-0.00	-0.02
Paapa × EDUB	-0.14	-0.02	-0.04	-0.01	0.03	-0.02
SGKP3 × Mampong	0.16	0.28 *	0.05	-0.03	0.08 *	-0.11
SGKP3 × 50	0.18	-0.08	0.04	0.02	-0.04	0.10
SGKP3 × EDUB	0.01	-0.02	-0.01	-0.01	-0.01	-0.02
Mampong × OSO-5	0.18	0.26 *	0.05	0.13**	0.12 **	0.33**
Mampong × 25	0.11	-0.02	0.02	-0.01	-0.00	-0.03
Mampong × Baabo	0.01	0.02	0.00	0.00	0.01	0.03
50 × OSO-5	0.12	-0.05	0.03	0.00	-0.02	0.03
50 × 25	0.19	0.03	0.06	0.01	0.01	0.02
50 × Baabo	-0.03	0.01	-0.02	-0.02	0.00	-0.05
EDUB × OSO-5	-0.11	-0.06	-0.04	-0.02	-0.03	-0.07
EDUB × 25	0.06	0.10	0.01	0.04	0.02	0.12
EDUB × Baabo	-0.14	-0.13	-0.04	-0.03	-0.04	-0.08
OSO-5 × Tamale	0.29**	-0.07	0.07 *	0.01	-0.02	0.04
OSO-5 × Asontemtiatia	-0.14	-0.01	-0.04	-0.02	-0.01	-0.04
OSO-5 × Hilhaho	-0.12	-0.19	-0.03	-0.03	-0.06	-0.10
25 × Tamale	0.01	-0.11	-0.01	-0.02	-0.05	-0.05
25 × Asontemtiatia	-0.14	0.04	-0.04	-0.02	-0.00	-0.07
25 × Hilhaho	-0.12	0.14	-0.04	0.00	0.05	0.05
Baabo × Tamale	-0.07	-0.14	-0.02	-0.04	-0.05	-0.13
Baabo × Asontemtiatia	-0.17	-0.11	-0.05	-0.02	-0.03	-0.08
Baabo × Hilhaha	-0.02	0.14	0.01	0.05	0.04	0.13

Table 5.11 Specific combining ability effects for okra mosaic, leaf curl disease and Podagrica spp under high-N environments

Hybrids	I.OLCD	I.Podagrica	S.OLCD	S.OMD	S.Podagrica	IOMD
G1 × Mampong	-0.00	0.14	0.01	0.02	0.06	0.08
G1 × 50	-0.12	0.11	-0.03	-0.00	0.02	-0.01
G1 × EDUB	-0.14	-0.19	-0.03	-0.02	-0.06	-0.06
Tamale × G1	-0.05	-0.07	-0.01	-0.02	-0.01	-0.08
Tamale × Paapa	-0.01	0.06	0.02	0.01	0.02	0.00
Tamale × SGKP3	0.01	-0.09	-0.00	0.00	-0.03	0.03
Asontemtiatia × G1	0.02	-0.04	0.02	-0.01	-0.01	-0.06
Asontemtiatia × Paapa	-0.25*	-0.14	-0.07	-0.01	-0.05	-0.06
Asontemtiatia × SGKP3	-0.10	-0.09	0.01	0.01	-0.01	0.05
Asontemtiatia × G1	-0.19	-0.12	-0.06	0.00	-0.05	0.02
Hilhaho × Paapa	-0.25*	0.02	-0.07	-0.01	0.02	-0.02
Hilhaho × SGKP3	0.14	-0.21 *	0.05	-0.01	-0.05	-0.06
Paapa × Mampong	0.13	-0.03	0.02	0.00	0.00	-0.01
Paapa ×50	-0.14	-0.03	-0.03	-0.01	-0.01	-0.05
Paapa × EDUB	-0.26*	-0.06	-0.07	0.00	-0.02	0.02
SGKP3 × Mampong	0.07	-0.18	0.01	-0.00	-0.05	-0.02
SGKP3 × 50	0.01	0.11	0.01	0.02	0.02	0.07
SGKP3 × EDUB	0.07	-0.03	0.02	-0.01	-0.02	-0.02
Mampong × OSO-5	-0.05	0.08	-0.02	0.02	0.03	0.06
Mampong × 25	-0.01	-0.03	-0.01	-0.01	-0.01	-0.00
Mampong × Baabo	0.07	-0.01	0.02	-0.01	-0.01	-0.03
50 × OSO-5	-0.03	0.05	-0.00	-0.00	0.03	-0.04
50 × 25	0.01	0.04	-0.00	-0.00	0.01	0.00
50 × Baabo	-0.11	-0.05	-0.04	0.00	-0.01	0.00
EDUB × OSO-5	-0.17	-0.22*	-0.06	-0.01	-0.06	-0.08
EDUB × 25	-0.11	-0.15	-0.02	-0.02	-0.04	-0.11
EDUB × Baabo	0.13	0.16	0.04	0.01	0.04	0.11
OSO-5 × Tamale	0.29 *	0.06	0.09*	0.01	0.02	0.01
OSO-5 × Asontemtiatia	-0.19	-0.10	-0.06	-0.00	-0.03	-0.02
OSO-5 × Hilhaho	-0.05	0.09	-0.03	-0.00	0.02	0.01
25 × Tamale	0.09	-0.14	0.02	-0.00	-0.05	-0.02
25 × Asontemtiatia	-0.19	-0.15	-0.06	-0.02	-0.03	-0.04
25 × Hilhaho	0.02	-0.09	-0.01	-0.01	-0.01	-0.04
Baabo × Tamale	0.01	-0.13	0.06	-0.00	-0.02	-0.03
Baabo × Asontemtiatia	-0.13	-0.13	-0.04	-0.01	-0.04	-0.06
Baabo × Hilhaha	-0.19	-0.01	-0.06	0.00	-0.01	0.04

Table 5.12 Specific combining ability effects for okra mosaic, leaf curl disease and *Podagrica spp.* across low N and high - N environments

Hybrids	I.OLCD	I.Podagrica	S.OLCD	S.OMD	S.Podagrica	IOMD
G1 × Mampong	0.04	0.16	0.01	0.03	0.05	0.09
G1 × 50	-0.19*	0.16	-0.05	0.00	0.05	0.02
G1 × EDUB	-0.06	-0.15	-0.01	-0.02	-0.04	-0.10
Tamale × G1	-0.12	-0.17	-0.03	-0.04	-0.05	-0.13
Tamale × Paapa	-0.03	0.05	0.01	0.01	0.02	-0.03
Tamale × SGKP3	-0.12	-0.11	-0.02	0.00	-0.03	0.05
Asontemtiatia × G1	0.04	0.01	0.03	-0.00	0.01	-0.02
Asontemtiatia × Paapa	-0.27**	-0.17	-0.08**	-0.02	-0.06*	-0.08
Asontemtiatia × SGKP3	-0.15	-0.14	-0.01	-0.02	-0.03	-0.03
Asontemtiatia × G1	-0.15	-0.22*	-0.05	-0.01	-0.05	-0.01
Hilhaho × Paapa	-0.16	-0.00	-0.05	0.01	0.01	0.02
Hilhaho × SGKP3	0.07	-0.27**	0.03	-0.03	-0.07*	-0.11
Paapa × Mampong	0.06	-0.15	0.01	-0.01	-0.04	-0.09
Paapa ×50	-0.15	-0.01	-0.05	-0.02	-0.00	-0.05
Paapa × EDUB	-0.23 *	-0.04	-0.07*	-0.00	0.01	0.01
SGKP3 × Mampong	0.15	0.06	0.05	-0.02	0.02	-0.08
SGKP3 × 50	0.13	0.03	0.04	0.04	-0.00	0.11
SGKP3 × EDUB	0.05	-0.03	0.01	-0.01	-0.02	-0.03
Mampong × OSO-5	0.08	0.19*	0.03	0.07*	0.08**	0.22*
Mampong × 25	0.06	-0.03	0.02	-0.02	-0.01	-0.03
Mampong × Baabo	0.04	0.01	0.01	-0.02	0.00	-0.03
50 × OSO-5	0.06	0.01	0.02	0.00	0.01	-0.02
50 × 25	0.12	0.05	0.05	0.01	0.02	0.02
50 × Baabo	-0.09	-0.01	-0.03	-0.01	-0.00	-0.02
EDUB × OSO-5	-0.17*	-0.17	-0.06*	-0.03	-0.05	-0.12*
EDUB × 25	-0.02	-0.04	-0.01	-0.01	-0.02	-0.04
EDUB × Baabo	-0.02	0.01	-0.01	-0.00	0.00	0.04
OSO-5 × Tamale	0.36**	0.01	0.10**	0.02	0.00	0.04
OSO-5 × Asontemtiatia	-0.20*	-0.05	-0.06*	-0.01	-0.02	-0.04
OSO-5 × Hilhaho	-0.11	-0.04	-0.04	-0.01	-0.02	-0.04
25 × Tamale	0.06	-0.17	0.01	-0.01	-0.06	-0.05
25 × Asontemtiatia	-0.20*	-0.09	-0.06*	-0.02	-0.03	-0.08
25 × Hilhaho	-0.07	0.00	-0.04	-0.01	0.02	-0.01
Baabo × Tamale	0.01	-0.17	-0.01	-0.03	-0.04	-0.10
Baabo × Asontemtiatia	-0.20*	-0.15	-0.06*	-0.03	-0.04	-0.10
Baabo × Hilhaha	-0.12	0.06	-0.03	0.03	0.01	0.10

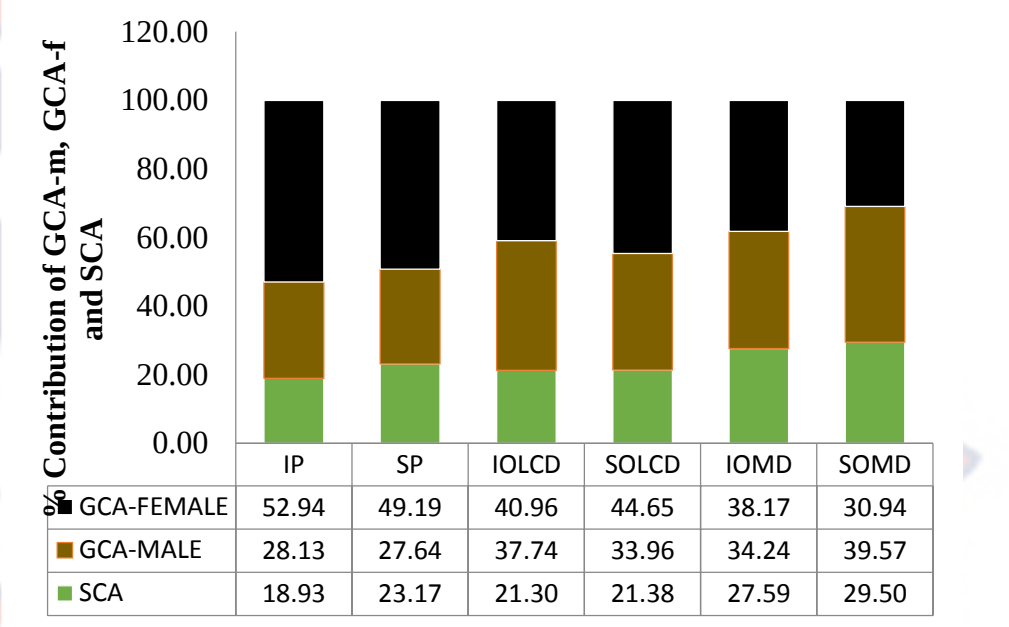
5.3.4 Proportion of combining ability effects under contrasting environments

The ratio of the GCA component to total genetic variation using the sum of squares method was used to determine the relative contributions of GCA and SCA effects. Under low nitrogen environments, the GCA sum of squares varied from 70.51% for the severity of okra mosaic disease to 81.07% for the incidence of *Podagrica* spp. while the SCA sum of squares ranged from 18.93% for the incidence of *Podagrica* spp. to 29.50% for the severity of okra mosaic disease (Figure 5.1). The proportionate contribution of GCA sum of squares was more significant than that of the SCA sum of squares for all measured parameters. GCA accounted for 81.07% of the total variance for incidence of *Podagrica* spp., 76.83% for the severity of *Podagrica* spp., 78.70% for the incidence of okra leaf curl disease, 78.61% for the severity of okra leaf curl disease, 72.41% for incidence of okra mosaic disease and 70.51% for severity of okra mosaic disease (Figure 5.1).

Across high nitrogen environment, the proportion of general combining ability effects to each genotypic sum of squares varied from 58.21 percent for the incidence of okra mosaic disease to 77.07 % for the incidence of okra leaf curl while SCA components ranged from 22.93 % for the incidence of okra leaf curl disease to 41.79 % for the incidence of okra mosaic disease (Figure 5.2). The proportionate contribution of the GCA sum of squares was greater than that of the SCA sum of squares for all measured parameters. GCA accounted for 70.96 % of the total variance for the incidence of *Podagrica* spp., 72.02% for the severity of *Podagrica* spp., 77.07 % for the incidence of okra leaf curl disease, 69.23% for the severity of okra leaf curl

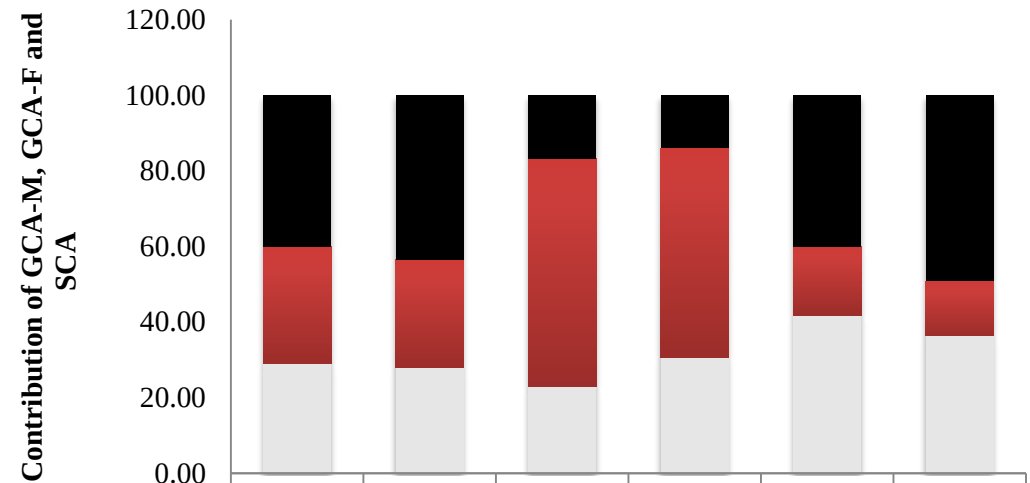
disease, 58.21% for incidence of okra mosaic disease and 63.71% for severity of okra mosaic disease (Figure 5.2).

Across low and high-nitrogen environments, GCA effects on the hybrid genotypic sum of squares were higher than the effects of SCA (Figure 6.3). The proportion of GCA was 81.45% for the incidence of *Podagrica* spp., 79.38% for the severity of *Podagrica* spp., 78.18% for the incidence of okra leaf curl disease, 74.46% for the severity of okra leaf curl disease, 68.10% for incidence of okra mosaic disease and 66.85% for the severity of okra mosaic disease (Figure 5.3).



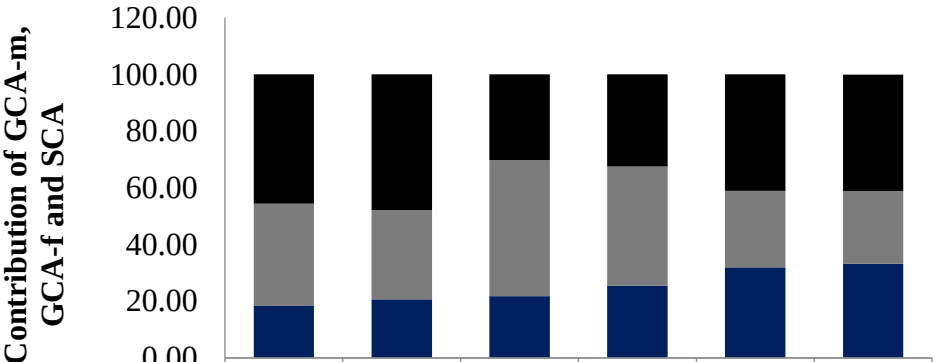
	IP	SP	IOLCD	SOLCD	IOMD	SOMD
GCA-FEMALE	52.94	49.19	40.96	44.65	38.17	30.94
GCA-MALE	28.13	27.64	37.74	33.96	34.24	39.57
SCA	18.93	23.17	21.30	21.38	27.59	29.50

Figure 5.1 Percentage of the sum of squares (genotypic) of okra diseases attributable to GCA-f, GCA-m and SCA under low-N environments. IP =Incidence of *Podagrica* spp., SP = Severity of *Podagrica* spp, IOLCD = Incidence of okra leaf curl disease, SOLCD = Severity of okra leaf curl disease, IOMD = Incidence of okra mosaic disease, SOMD = Severity of okra mosaic disease



	IP	SP	IOLCD	SOLCD	IOMD	SOMD
GCA-FEMALE	40.13	43.45	16.68	13.99	39.94	49.19
GCA-MALE	30.83	28.57	60.39	55.24	18.27	14.52
SCA	29.04	27.98	22.93	30.77	41.79	36.29

Figure 5.2 Percentage of the sum of squares (genotypic) of okra diseases attributable to GCA-f, GCA-m and SCA under high-N environments.



	IP	SP	IOLCD	SOLCD	IOMD	SOMD
GCA-FEMALE	45.58	47.86	30.26	32.47	41.06	41.14
GCA-MALE	35.87	31.52	47.92	41.99	27.04	25.71
SCA	18.55	20.62	21.82	25.54	31.90	33.14

Figure 5.3 Percentage of the sum of squares (genotypic) of okra diseases attributable to GCA-f, GCA-m and SCA across low-N and high environments. IP =Incidence of *Podagrica* spp., SP = Severity of *Podagrica*s spp., IOLCD = Incidence of okra leaf curl disease, SOLCD = Severity of okra leaf curl disease, IOMD = Incidence of okra mosaic disease, SOMD = Severity of okra mosaic disease

5.4 Discussions

Assessment of general and specific combining ability of crops is essential for yield enhancement and stress tolerance (Ali *et al.*, 2014). The study discovered significant GCA and SCA effects for all characters, which suggested that additive and non-additive gene actions influence the inheritance of *Podagrica* spp. infestations, leaf curl disease, and okra mosaic virus disease. This means that both additive and non-additive gene action can be exploited through crosses and recurrent selection programs to increase disease tolerance. Positive GCA effects are typically associated with susceptibility, while negative GCA effects are usually associated with resistance (Owolade *et al.*, 2006; Bokmeyer *et al.*, 2009). Okra genotypes SGKP3, 50, and Baabo showed a high degree of resistance to OLCD with significance and negative GCA –female effects under low N. This suggested that in a recurrent selection program to create hybrids that are resistant to OLCD under low-N conditions, these genotypes have a high probability of passing on favourable genes for resistance to their offspring. Moreover, the observed significant and negative GCA-female for Mampong, SGKP3 and Tamale 2E implied that these genotypes have immunity against okra mosaic diseases (OMD) under low N environment and could contribute desirable alleles to their progenies when used as female parents. Also, SGKP3 and Mampong were also observed to have immunity against *Podagrica* spp. and could be chosen for resistance breeding programmes under low N environments since their cross progenies showed a propensity to lessen infection. Similarly, Mampong, SGKP3 and Tamale were identified as the most resilient genotypes to OMD across low N environments with significant and negative GCA-male effects and could be

deployed for future breeding programmes in hot spot areas. Genotypes with significant negative GCA values for OMD, OLCD and *Podagrica* spp. suggest that they possibly possess desirable alleles for resistance and would be needed to develop new varieties resistant to the studied pests and diseases.

Specific combining ability effects are usually used to identify the best cross-combinations for hybrid production. It is vital to note that in the parental crosses of each of these hybrids, there were either one or both high general combiners. It was also found that the best cross combination regarding SCA effects always had one or both high general combiners as parents. Across low nitrogen conditions, hybrid cross Paapa × Mampong had significant and negative SCA effects for OMD. Similarly, Tamale 2E × G1, Hilhaho × SGKP3 and Paapa × Mampong showed high resistance to *Podagrica* spp. with negative and significant SCA effects. Moreover, only Asontemtiatia × SGKP3 was identified as the best hybrid with resistance to the incidence of OLCD. It would be desirable to deploy these hybrids to increase disease and pest resistance. They could be used for heterosis breeding and produce transgressive segregants in later generations. According to Falconer and Mackay (1996), significant SCA effects suggested that the level of resistance of hybrids was either higher or lower than predicted based on the GCA of the two parents involved in the cross, and these effects are attributed to dominant gene action. Across high N environment, hybrids Asontemtiatia × Paapa, Hilhaho × Paapa and Paapa × EDUB showed high degree of tolerance to OLCD with significant and negative SCA effects. Similarly, crosses Hilhaho × Paapa and EDUB × OSO-5were the best tolerant hybrids for *Podagrica* spp. Also, hybrid crosses Asontemtiatia × Paapa, Paapa × EDUD, EDUB × OSO-5,

OSO-5 × Asontemtiatia, 25 × Asontemtiatia and Baabo × Asontemtiatia were resistant to OLCD across low N and high N environment.

In the present studies, the maternal and paternal effects were calculated using the GCA-male to GCA-female mean square ratio (Kearsey and Pooni, 1996). The contributions of GCA-female and GCA-male to hybrids varied depending on the trait and conditions. Superior GCA-female to GCA-male effects for the measured characters in nitrogen deficient soils, high N and across research environment suggested maternal effects might have modified these traits. The findings showed that under low N, all the traits were maternally modified except SOMD, which was influenced by paternal effects. Similarly, under high N and across the research environment, maternal (cytoplasmic) influences contributed to the inheritance of all the traits under study except the incidence and severity of OLCD, which were paternally inherited. The larger GCA-female effects for the tested traits under each and across the research environment suggested that cytoplasmic involvement conditioned the inheritance of this group of hybrids since GCA-male effects were smaller for the measured traits than GCA-female. Additionally, hybrids with significant negative GCA-female effects for these characteristics should be utilized as females to pass on resistance to their offspring. On the contrary, a larger magnitude of GCA-male than GCA-female for SOMD suggested that paternal inheritance was more important in determining these characters under a low N environment.

The preponderance of GCA effects over SCA for OMD, OLCD and *Podagrica* spp. under each and across environments implied that additive gene action conditioned the inheritance of OMD, OLCD and *Podagrica* spp.

resistance. Because additive gene effects predominated over non-additive gene effects, as demonstrated by the high GCA: SCA ratios calculated for all the characters in the current study, recurrent selection would be an effective strategy for trait improvement. GCA accounted for 81.07% of the total variance for the incidence of *Podagrica* spp., 76.83% for the severity of *Podagrica* spp., 78.70% for the incidence of okra leaf curl disease, 78.61% for the severity of okra leaf curl disease, 72.41% for incidence of okra mosaic disease and 70.51% severity of okra mosaic disease. A similar trend was obtained under high N and across research conditions, which showed the significance of the additive genes in the expression of the traits.

5.5 Conclusion

The study found significant GCA and SCA effects for all the traits, indicating that both additive and non-additive gene actions conditioned the inheritance of okra mosaic virus disease, leaf curl disease and *Podagrica* spp. infestations. However, the importance of additive gene action outweighed non-additive gene action at each and across research conditions and that, and general combining ability was a major determinant of the heritable variation. The result revealed that maternal influences play a significant part in the inheritance of most traits under each and across research conditions. It was observed that okra genotypes SGKP3 and Tamale 2E had immunity (good combiners) against OLCD, OMD and *Podagrica* infestation under low N conditions. Under a high N environment, genotypes OS-5 and 25 were identified as the most tolerant genotypes against the two biotic factors, OMD and OLCD while EDUB and Tamale were observed to be the most resilient

genotypes against *Podagrica* spp. Similarly, the okra genotype Tamale 2E was observed to be concurrently resistant to the three stress conditions. This suggested that these genotypes had advantageous alleles and tended to lessen the severity and incidence of OMD, OLCD, and *Podagrica* spp. infections. Furthermore, Single cross hybrids such as Paapa × Mampong, Tamale 2E × SGKP3 and Hilhaho × SGKP3 were the best tolerant hybrids against the incidence of *Podagrica* spp. under low N environment. Also, Paapa × Mampong had immunity against OMD, while hybrid cross Asontemtiatia × Paapa was the most resistant hybrid against incidence of OLCD under low N.

CHAPTER SIX

6.0 Performance of okra [*Abelmoschus esculentus* (L.) Moench] parental accessions and their hybrids under low and high nitrogen conditions

6.1 Introduction

Okra [*Abelmoschus esculentus* (L.) satisfies the nutritional needs of people from all socioeconomic backgrounds and fits in well with farming practices in all agro ecological zones of the region. Approximately 32.8 percent of the world's okra is produced in Africa. West and Central African nations contribute over 75% of all the okra produced in Sub-Saharan Africa (SSA) (Kumar and Reddy, 2016).

Despite the significant benefits and contributions of okra to numerous economies in West and Central Africa, the production of okra has been constrained by scarce input sources, resulting in generally low fruit yields (Ibrahim and Hamma, 2012). According to Siemonsma and Kouame (2004), one of the main abiotic factors influencing the production of most vegetables, including okra, is poor soil nutrition particularly low soil nitrogen. Additionally, the unavailability of okra hybrids in Ghana and the high cost and insufficient fertilizer application by farmers with limited resources are major factors that reduce productivity in the sub-region (Fischer *et al*., 2014). This has caused a significant and variable yield drop on numerous farms in Ghana. This is true even in cases where high-yielding cultivars have been planted.

The genetic ability of the parental accessions that make up the hybrid determines how successfully okra accessions and their hybrids perform, especially when the accessions combine exceptional performance with high heritability estimates for critical agronomic variables (Betrán *et al.,* 2003).

Hence to combat food insecurity in SSA, low-N tolerant hybrid development and commercialization are essential. To do this, it is necessary to choose okra accession that is low-N tolerant and can grow in both low-N and high-N environments. According to Lafitte and Edmeades (1994a), this might be accomplished by choosing cultivars with increased N-use efficiencies or cultivars with greater N-use efficiencies in terms of N-uptake or N-use. Plants that thrive well in low soil nitrogen levels should produce more biomass. These plants should also have minimal impacts of N deficit on plant height, leaf area, and chlorophyll content, as well as an effective distribution of biomass and N to the yield (Lafitte and Edmeades, 1994a). The identification of genotypes that are low-N tolerant for hybrid development in low-N and high-N environments is crucial. The objectives of the present study were

I. Assess the performance of the okra hybrids and their parental genotypes under low-N, optimum, and across research environments.
II. To identify nitrogen-efficient hybrids and parental genotypes for future hybridization programme
III. Assess the magnitude of heterosis for fruit yield
IV. Determine the correlation between fruit yield and other yield components

6.2 Materials and Methods

6.2.1 Genetic materials

A selected group of twelve (12) okra accessions screened from a group of hundred (100) accessions from diverse sources in Ghana after characterization were selected based on their tolerance to biotic and abiotic factors (Table 4.1).

These twelve parental lines, 36 hybrids, and four other checks constituted the germplasm for the current study.

Table 6.1: Characteristics of the okra parental genotypes evaluated during the 2021 major and minor cropping season

ACCESSIONS	FY	NFP	DFF	50%FL	FL	FW	PH
50	7.15	11.70	54.67	58.92	9.59	1.91	82.38
Paapa	7.01	11.83	54.58	60.42	7.67	2.56	64.13
Tamale 2E	6.86	10.94	55.17	59.92	8.51	2.18	68.51
25	6.80	11.42	53.33	59.00	8.92	1.85	86.34
Baabo	6.63	10.01	53.42	58.17	8.15	2.27	64.19
SGKP3	5.59	9.40	60.50	66.33	8.28	1.76	92.03
G1	5.32	9.15	56.83	61.75	9.55	1.88	60.97
Mampong	5.18	8.58	65.33	69.83	9.98	1.84	112.66
EDUB	4.98	7.66	59.42	63.67	9.73	1.84	99.04
Hihaho	4.98	8.34	65.67	71.17	9.98	1.84	107.24
OSO-5	4.55	7.63	54.92	59.00	9.43	1.86	74.73
Asontemtitia	4.38	7.52	52.33	57.25	6.38	1.81	61.72
MEANS	**5.78**	**9.52**	**57.18**	**62.12**	**8.85**	**1.97**	**81.16**
LSD	**0.36**	**1.18**	**2.13**	**2.49**	**0.6**	**0.13**	**7.05**

FY= Fruit yield; NFP = Number of fruits per plant; DFF = Days to first flowering; 50%FL = 50% Flowering; FL = Fruit length; FW = Fruit width; PH = Plant height

6.2.2 Generation of North Carolina Design II Crosses

The generation of the hybrids through NCD II is vividly explained in Chapter Four, section 4. 2.2 and Table 4.2.

6.2.3 Agronomic practices

Golan SL TM and Sunpyrifos 48% EC insecticide were used to control Podagrica spp. and grasshoppers, respectively which were, the field's most notorious and predominant insect pests. Panicum maximum, the dominant weed in the area, was controlled using a traditional hoe. Earthing up was also done to provide support for plants.

6.2.4 Data collected

Quantitative traits were randomly recorded from five plants per row, leaving the border plants grown at both ends of the row. The following quantitative traits were measured and recorded: plant height, plant width, number of branches, leaf area, days to first flowering, days to fifty percent flowering, fruit length, fruit with, number fruits per plant, sliminess and leaf chlorophyll content.

6.2.5 Statistical Analysis

Data collected and recorded for all the variables measured were first subjected to Analysis of Variance (ANOVA) using the "Carolina" function of the 'agricolae' package in R statistical software, version 4.2.3. Treatment means were separated by the Least Significant Difference at 5% probability level. Location and season were viewed as the environment and season, respectively. Low nitrogen and high N growing conditions were the research conditions (treatments). Data acquired under low-N and high-N growing conditions were initially subjected to a separate Analysis of Variance (ANOVA). Additionally, combined ANOVA was performed in each of the cases.

Genetic analysis, such as genotypic variance and phenotypic variance, among the traits were calculated using the 'variability' package in R. The "heterosis" function in the 'agricolae' package in R was used to determine the heterosis. Moreover, the 'metan' package in R was used to determine the correlation coefficient among the traits studied.

Hybrids were regarded as fixed factors in the ANOVA, while incomplete blocks within replicates × environment interaction, environments, and replicates within environments were all considered as random variables. The statistical model was

$$yklmi = \mu i + Eki + R(E)kli + Gmi + GEkmi + \epsilon klmi$$

Where $yklmi$ is the observed measurement of trait i with mean effect μi, Eki is the effect of environment k on trait i, (E) is the effect of replication l within environment k on trait i, Gmi is the effect of genotype m on trait i, $GEkmi$ is the effect of the interaction between genotype m and environment k on trait i, and $\epsilon klmi$ is the experimental error effect associated with genotype m and replication l within environment k on trait i. According to the experimental design (Cochran and Cox, 1960), the entry means were corrected for block effects, and means were separated using standard error (S.E).

6.3 Results

6.3.1 Parental and hybrids mean performance and analysis of variance of fruit yield and other traits under contrasting environments

Across low N environment, the ANOVA of the parental and single cross hybrids for the 2021 major and minor season showed significant variations for genotypes (G) and environment (E) mean squares for fruit yield and all other characters except G and E main effects for leaf chlorophyll content, number of branches per plant, and plant width (Table 6.2). Additionally, significant ($p<0.05$) differences were observed for the various seasons (S) and environment × season (E × S) interactions for fruit yield and number of fruits per plant. Moreover, there was no significant interaction for

genotype × season (G × S) and genotype × environment (G × E) for fruit yield (Table 6.2). Environment contributed 92.03% to the overall sum of squares for fruit yield. Furthermore, genotype and GEI each contributed 7.76% and 0.22%, respectively, to total sum of squares (Table 6.3).

Fruit yield of hybrids under low N varied from 1.03 t/ha for SGKP3 × EDUB to 6.99 t/ha for hybrid cross Hilhaho × Paapa with a mean of 2.85 t/ha (Table 6.4). Hybrid cross Hilhaho × Papaa produced the highest fruit yield of 6.99t/ha, followed by hybrid cross Tamale 2E x G1 with a fruit yield of 5.67t/ha (Table 6.4). Contrarily, crosses SGKP3 × EDUB and Mampong EDUB were the worst yield-performing hybrids. Moreover, the fruit yield of parental accessions ranged from 1.04 for Asontemtiatia to 4.28 for Tamale 2E, with a population mean of 2.05 t/ha. Genotype Tamale 2E produced the highest fruit yield and was followed by Paapa (Table 6.5). Thirty percent of the hybrids performed better in terms of fruit yield than the best check (Hybridus) and 6.25% of same performing better than the best parental genotype (Tamale 2E). The analysis also revealed a higher percentage reduction in fruit yield among susceptible hybrids and parental accessions than among tolerant hybrid crosses and parental accessions.

Table 6.2 Mean squares of hybrids evaluated under low nitrogen conditions during the 2021 major and minor seasons at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	CC	PH	PW	NBP
REP	2	0.51	5.82	84.25***	93.66***	43.00**	534.93	23.4	0.57	0.1
GENOTYPE	47	14.26***	48.14***	272.69***	355.16***	12.57*	842.7	2475.2***	0.46	5.33***
ENVT	1	169.22***	658.56***	55.63*	78.03**	85.52**	2571.76	13906.2***	0.28	0.98
SEASON	1	27.13***	198.22***	4.17	4	59.07*	2057.76	267.3	0.21	1.58
GENOTYPE * SEASON	47	0.18	3.91	2.24	2.62	7.64	726.99	24.2	0.29	0.45
GENOTYPE * ENVT	47	0.4	1.52	1.77	3.07	7.64	765.63	19.3	0.28	0.11
ENVT * SEASON	1	6.76**	13.05*	16.34	1.17	0.01	1502.53	19.4	0.29	0.31
GENOTYPE* ENVT*SEASON	47	0.53	1.92	1.33	3.32	7.92	788.96	12.6	0.29	0.09
RESIDUALS	382	0.64	2.91	10.63	9.93	8.94	741.62	202.6	0.33	0.55

FY= fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length ; CC = chlorophyll content; PH = plant height (cm); PW = plant width; NBP = number of branches per plant

Table 6.3 Proportions of the total variation attributed to the sources of variation for fruit yield of okra hybrids evaluated under low, high N and across research conditions in the major and minor seasons of 2021 at Jacobu and Akumadan

Source	Df	Sum of Squares	% Contribution to Sum of squares
		Low N	
REP	2	0.51	
GENOTYPE	47	14.26	7.76 %
ENVT	1	169.22	92.03 %
SEASON	1	27.13	
GENOTYPE * SEASON	47	0.18	
GENOTYPE * ENVT	47	0.4	0.22 %
ENVT * SEASON	1	6.76	
GENOTYPE* ENVT*SEASON	47	0.53	
RESIDUALS	382	0.64	
		High N	
REP	2	10.22	
GENOTYPE	47	25.96	4.71 %
ENVT	1	525.04	95.23 %
SEASON	1	24.34	
GENOTYPE * SEASON	47	0.61	
GENOTYPE * ENVT	47	0.33	0.06 %
ENVT * SEASON	1	8.64	
GENOTYPE* ENVT*SEASON	47	0.44	
RESIDUALS	382	1.12	
		Across environments	
REP	2	3.59	
GENOTYPE	47	17.32	5.09 %
ENVT	1	322.77	94.85 %
SEASON	1	5.17	
GENOTYPE * SEASON	47	0.19	
GENOTYPE * ENVT	47	0.22	0.06 %
ENVT * SEASON	1	0.02	
GENOTYPE* ENVT*SEASON	47	0.37	
RESIDUALS	382	0.53	

Table 6.4 Performance of hybrids and four checks evaluated under low-N environments during the 2021 major and minor seasons

HYBRIDS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
Hilhaho × Paapa	6.99	18.25	54.17	60.83	8.19	1.48	75.75	935.74	52.08	2.00
Tamale 2E × GI	5.67	15.51	51.67	55.67	7.37	1.13	46.23	493.29	83.62	2.00
OSO-5 × Asontemtiatia	4.34	10.17	53.08	58.25	9.18	1.28	56.48	730.70	51.82	3.00
OSO-5 × Hilhaho	4.28	10.15	57.02	67.08	57.08	1.35	53.43	874.53	50.81	4.00
OSO-5 × Tamale 2E	4.24	10.48	53.83	61.17	7.13	1.28	50.36	589.56	51.65	4.00
Mampong × Baabo	3.89	9.49	66.17	71.75	8.77	1.33	95.70	803.50	48.60	4.00
Hilhaho × G1	3.82	9.41	53.33	60.00	7.19	1.50	67.33	950.26	49.58	1.00
EDUB × OSO-5	3.78	9.81	57.42	62.50	7.69	1.43	52.38	928.91	50.26	2.00
Hilhaho × SGKP3	3.63	8.87	61.75	67.00	8.72	1.56	86.34	633.73	49.05	2.00
Tamale 2E × SGKP3	3.38	8.91	52.08	56.50	7.26	1.33	51.79	527.14	47.68	2.00
25 × Asontemtiatia	3.35	7.88	53.00	57.42	8.38	1.33	67.73	593.76	50.61	3.00
Baabo × Tamale 2E	3.18	8.26	57.75	65.75	8.38	1.37	75.38	527.32	49.94	2.00
Okra hybrids (Check 1)	3.17	7.17	50.60	56.00	9.78	1.56	85.79	637.68	50.04	3.00
Asontemtiatia × SGKP3	3.05	7.99	56.08	64.58	6.45	1.63	75.02	664.58	47.76	3.00
Baabo × Asontemtitia	2.99	8.04	56.67	61.50	8.48	1.58	70.23	827.67	49.11	3.00
Tamale 2E × Paapa	2.95	8.77	53.58	57.75	8.95	1.33	55.23	694.62	50.00	1.00
25 × Tamale 2E	2.95	7.52	51.33	52.58	7.18	1.37	66.44	769.98	50.88	4.00
Paapa × 50	2.90	8.14	52.58	59.00	7.34	1.22	52.79	558.76	48.48	2.00
Essountem (Check)	2.76	6.31	48.50	72.58	8.65	1.64	67.50	840.72	47.39	4.00
Baabo × Hilhaho	2.75	7.66	60.58	66.33	6.81	1.27	84.96	550.86	47.78	3.00
Asontemtiatia × Paapa	2.69	7.16	53.58	59.25	8.04	1.38	65.29	524.36	48.96	3.00

Table 6. 4 cont'd

HYBRIDS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
G1 × EDUB	2.66	6.95	64.25	68.33	7.67	1.44	67.84	546.82	47.57	2.00
Hire (check)	2.58	6.11	49.17	62.42	7.49	1.67	64.96	757.22	48.26	4.00
Asontemtiatia × G1	2.50	7.86	55.17	60.33	9.02	1.32	61.99	589.72	46.96	3.00
50 × Baabo	2.47	7.42	59.42	65.33	7.93	1.48	75.88	874.11	46.68	4.00
25 × Hilhaho	2.40	6.29	53.33	58.00	6.95	1.37	49.82	660.07	46.45	2.00
SGKP3 × 50	2.30	6.21	58.83	64.58	8.94	1.52	88.88	874.41	47.98	4.00
Paapa × Mampong	2.28	6.39	55.33	60.50	5.90	1.42	59.78	813.41	47.85	4.00
Paapa × EDUB	2.16	6.09	55.08	60.75	7.12	1.25	61.88	712.29	47.88	2.00
EDUB × Baabo	2.04	5.95	55.92	56.67	7.60	1.32	53.33	483.06	46.98	2.00
CLEMSON (Check)	2.03	4.98	50.42	51.45	10.03	1.22	50.32	522.63	46.78	4.00
G1 × Mampong	1.88	6.10	60.17	65.58	8.10	1.51	75.93	517.42	46.38	3.00
50 × OSO-5	1.84	5.29	56.50	62.50	7.53	1.55	67.03	693.54	46.17	5.00
50 × 25	1.84	5.43	55.33	62.42	8.36	1.44	62.38	795.53	46.03	1.00
Mampong × 25	1.76	5.74	62.25	67.42	6.83	1.53	104.15	743.92	42.98	2.00
G1 × 50	1.48	5.27	58.75	66.25	7.19	1.47	60.44	610.88	46.04	3.00
EDUB × 25	1.45	5.05	54.33	60.75	7.47	1.20	51.51	848.99	43.25	3.00
SGKP3 × Mampong	1.33	4.85	67.08	72.92	7.88	1.47	68.66	536.30	45.11	3.00
Mampong × EDUB	1.23	4.45	64.42	68.83	7.63	1.87	86.97	538.37	40.74	5.00
SGKP3 × EDUB	1.03	4.55	58.58	64.58	7.06	1.43	46.81	966.65	48.88	4.00
MEAN	**2.85**	**7.67**	**55.27**	**62.14**	**7.86**	**2.04**	**66.52**	**693.57**	**49.80**	**3.00**
LSD (P≤0.05)	**0.72**	**1.53**	**2.81**	**2.86**	**1.05**	**0.65**	**13.09**	**52.40**	**23.90**	**0.05**

FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; FW = fruit width; PH = plant height (cm); LA = leaf area; CC = Chlorophyll content; SL = Sliminess

Table 6.5 Performance of okra parental genotypes evaluated under low-N environments

ACCESSIONS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
Tamale 2E	4.28	8.64	58.75	66.75	6.96	2.03	58.75	685.50	49.58	1.00
Paapa	3.60	7.99	57.50	68.25	7.12	2.47	58.75	855.93	49.17	2.00
Baabo	3.04	6.82	55.67	65.33	7.93	2.26	51.61	870.54	49.27	2.00
50	2.85	7.47	62.08	68.67	7.72	1.83	76.84	725.93	47.55	4.00
25	2.20	6.21	57.08	67.83	7.48	1.92	71.14	872.44	47.68	5.00
Hihaho	1.44	4.85	69.00	76.33	8.65	1.74	90.39	678.38	42.93	1.00
Mampong	1.39	4.75	69.75	77.58	8.37	1.82	92.52	820.27	41.48	5.00
SGKP3	1.32	4.12	65.50	74.75	7.81	1.93	79.91	825.28	41.56	2.00
G1	1.14	4.17	60.42	69.83	7.86	1.81	50.14	577.53	39.26	3.00
OSO-5	1.13	4.12	58.17	65.25	7.94	1.83	62.59	761.90	41.55	4.00
EDUB	1.13	4.25	63.25	69.75	7.64	1.87	81.76	873.20	40.33	3.00
Asontemtiatia	1.04	4.34	55.33	64.50	6.05	1.65	58.58	645.38	37.51	3.00
MEANS	**2.05**	**5.64**	**61.04**	**69.56**	**7.63**	**1.93**	**69.41**	**766.02**	**43.99**	**3.00**
LSD (P≤0.05)	**0.28**	**0.55**	**2.72**	**2.51**	**0.5**	**0.17**	**7.18**	**65.55**	**2.25**	**0**

FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); LA = leaf area; CC = Chlorophyll content ; SL = Sliminess

Figure 6.1 Variations in okra mucilage content

Days to first flowering varied from 48.50 days for Essountem (best check) to 67.08 days for SGKP3 × Mampong and OSO-5 × Hilhaho, with a population mean of 55.27. Among all the hybrids, cross 25 × Tamale 2E and Tamale 2E × G1 recorded the shortest days to flowering (Table 6.4). Fruit sliminess (mucilage content) ranged from a scale of 1 to 5, with (1 being very slimy and 5 not slimy). Hybrid crosses Hilhaho × G1 and Tamale 2E × Paapa produced the highest content of fruit mucilage (Table 6.4).

Across high N environments, the result significantly ($P<0.05$) differed for G and E main effects for fruit yield and all other studied characters. Similarly, there were significant differences among the various seasons (S) for fruit yield and all other characters except days to 50% flowering and number of branches per plant. Moreover, significant interactions were observed for environment × season (E × S) for fruit yield and most other traits (Table 6.6). The environment contributed 95.23% of the total sum of squares for fruit

yield, whereas the genotype and GEI contributed 4.71% and 0.06%, respectively (Table 6.3).

The fruit yield of the hybrids under high N environments ranged from 4.45 t/ha for Mampong × EDUB to 10.14 t/ha for Hilhaho × Paapa (Table 6.7). Hilhaho × Paapa was the best hybrid in terms of fruit yield and was followed by Hilhaho × G1. Conversely, hybrid cross Mampong × EDUB recorded the lowest fruit yield. Almost thirty-one percent (31%) of the hybrids produced higher fruit yield than the best check (Hybridus) (Table 6.7). Furthermore, 31.25% of the hybrids produced higher fruit yield than the best parental accessions (genotype 50) under high N environment. Fruit yield among parental accessions also differed from 4.38 t/ha for Asontemtiatia to 7.15 t/ha for parental genotype 50. Genotypes 50, Paapa and Tamale2E were the best-performing genotypes among the twelve parental genotypes for fruit yield. On the contrary, Asontemtiatia and OSO-5 were the two worst-performing parental genotypes under high N environment for fruit yield (Table 6.8). Days to first flowering ranged from 43.92 for Essountem (check) to 63.58 for SGKP3 × Mampong. Furthermore, days to first flowering among the accessions varied from 52.3 for Asontemtiatia to 65.67 for Hilhaho (Table 6.8).

Table 6.6 Mean squares of hybrids evaluated under high nitrogen conditions during 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	CC	PH	PW	NBP
REP	2	10.22***	5.55	146.18***	78.69**	3.85	9.3	1369.5***	0.48***	2.45
GENOTYPE	47	25.96***	54.72***	250.03***	302.2***	10.2***	80.4***	4440.9***	0.32***	14.04***
ENVT	1	525.04***	981.88***	82.51**	193.67**	39.95***	10976.9***	19075.3***	1.32***	149.55***
SEASON	1	24.34**	63.53***	126.56***	25.84	141.71***	187.3***	3735.7***	0.58**	2.36
GENOTYPE * SEASON	47	0.61	2.15	3.8	11.18	0.67	24.5***	63.8	0.04	0.69
GENOTYPE * ENVT	47	8.33*	1.51	1.34	8.3	0.36	5.3	20.1	0.03	0.59
ENVT * SEASON	1	8.64**	5.47	105.06***	200.69***	2.6	265.3***	2761.2***	2.13***	46.41***
GENOTYPE* ENVT*SEA	47	0.44	1.62	1.37	7.3	0.43	5.5	17.2	0.03	3.88***
RESIDUALS	382	1.12	3.67	7.6	12.61	1.42	2.2	126.2	0.06	1.02

FY= fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; CC = chlorophyll content; PH = plant height (cm); PW = plant width; NBP = number of branches per plant

Table 6.7 Performance of okra hybrids and four checks evaluated under high-N environments during 2021 major and minor seasons at Jacobu and Akumadan

HYBRIDS	FY	NFPLANT	DFF	50%FL	FL	FW	PH	LA	CC	SL
Hilhaho x Paapa	10.14	45.60	52.00	56.25	9.68	2.04	106.73	1015.30	53.78	2
Hilhaho x G1	10.04	38.70	49.25	52.25	10.18	1.99	106.03	1055.00	54.87	1
EDUB x OSO-5	9.46	41.76	47.50	52.00	10.35	2.13	69.71	1062.30	54.48	2
Hilhaho x SGKP3	8.70	39.86	53.58	57.00	9.79	2.13	99.51	1011.10	54.01	2
Baabo x Tamale 2E	8.55	13.71	52.00	55.75	9.48	1.96	117.48	1090.20	52.48	2
Tamale 2E x SGKP3	8.44	14.46	49.42	53.00	9.83	2.42	71.91	900.90	52.74	2
25 X Hilhaho	8.40	12.40	48.92	52.50	8.78	2.07	79.33	999.10	51.32	2
Tamale 2E x GI	8.23	13.35	47.42	52.33	9.92	2.70	79.25	1155.40	52.22	2
Asontemtia x SGKP3	8.00	12.99	54.92	59.42	8.63	1.93	100.98	1449.20	52.01	4
Baabo x Asontemtitia	7.98	12.74	53.25	57.83	9.43	1.93	117.68	915.70	53.36	3
Asontemtia x Paapa	7.97	12.55	49.33	54.33	10.03	2.27	94.86	1187.80	53.48	3
Okra hybrids (Check 1)	7.91	17.56	50.33	54.92	11.44	2.15	105.17	852.70	54.32	3
25 x Asontemtiatia	7.84	12.19	49.75	53.08	10.03	1.92	95.07	871.40	51.61	3
Baabo x Hilhaho	7.43	12.53	53.33	57.92	8.25	1.99	122.77	1051.00	51.53	3
50 x Baabo	7.33	11.71	50.92	55.08	9.37	1.98	116.17	1075.70	50.43	4
OSO-5 x Asontemtiatia	7.30	11.44	50.67	54.42	9.57	2.09	83.38	909.30	51.98	3
OSO-5 x Hilhaho	7.29	11.79	49.25	53.42	10.92	2.01	86.67	1006.50	51.28	4
Tamale 2E x Paapa	7.13	11.83	49.00	52.42	10.58	2.47	66.33	999.20	52.83	1
Paapa x EDUB	6.93	11.14	51.00	55.08	8.66	2.53	68.55	818.00	50.67	2
Asontemtiatia x G1	6.80	11.14	51.00	55.33	10.95	2.16	87.32	918.40	50.45	3
Paapa x Mampong	6.77	10.58	50.67	55.17	6.98	2.42	90.95	922.50	49.92	4
OSO-5 x Tamale 2E	6.67	11.11	49.58	53.50	9.83	1.95	73.63	746.60	51.90	4

Table 6.7 cont'd

HYBRIDS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
EDUB × 25	6.62	10.68	49.67	53.33	9.24	2.28	69.55	1087.80	50.76	3
SGKP3 × EDUB	6.24	10.97	58.00	63.75	9.60	1.89	114.98	1025.60	46.44	2
Mampong × 25	6.22	10.29	55.25	59.00	9.68	2.01	122.61	856.70	48.54	2
25 × Tamale 2E	6.03	9.86	50.50	53.42	9.73	2.12	77.38	746.60	48.17	4
Paapa × 50	6.02	10.57	51.25	55.33	8.78	2.12	74.78	1165.80	47.65	2
EDUB × Baabo	6.01	9.89	48.92	49.67	9.35	2.33	86.64	1061.00	49.39	2
Hire (check)	5.94	20.45	52.17	56.17	9.25	2.07	79.83	1023.70	51.19	4
Mampong × Baabo	5.71	9.90	63.42	66.92	9.60	2.05	124.78	1096.90	48.21	4
SGKP3 × 50	5.66	9.07	54.75	59.92	9.48	1.93	111.44	981.50	47.12	4
SGKP3 × Mampong	5.51	9.11	63.58	68.42	10.08	2.05	112.44	1110.50	48.78	3
G1 × EDUB	5.21	8.43	51.25	55.33	10.66	2.35	76.53	1193.00	47.54	4
50 × 25	5.20	9.38	49.33	53.83	9.95	2.08	96.37	1023.40	47.33	1
G1 × 50	4.88	7.75	53.42	57.92	8.14	1.93	67.95	778.40	46.98	3
G1 × Mampong	4.80	8.42	57.33	60.92	9.56	2.02	98.75	1070.90	46.13	3
50 × OSO-5	4.76	8.37	56.17	61.00	8.76	1.88	86.85	800.40	45.88	5
Essountem (Check)	4.63	16.20	43.92	47.25	7.75	2.16	81.76	882.40	47.92	4
CLEMSON (Check)	4.59	18.70	59.45	71.42	11.25	2.13	50.63	738.90	48.05	4
Mampong × EDUB	4.45	7.43	57.08	62.08	8.98	2.23	119.98	1062.30	46.17	5
MEAN	6.84	14.38	52.37	56.44	9.56	2.12	92.32	1002.80	50.35	3.00
LSD (P≤0.05)	0.89	3.18	2.18	2.96	0.99	0.21	9.39	330.49	2.26	0

FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area; CC = Chlorophyll content; SL = Sliminess

Table 6.8 Performance of okra parental genotypes evaluated under high N environments during the 2021 major and minor seasons at Jacobu and Akumadan

ACCESSIONS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
50	7.15	11.70	54.67	58.92	9.59	1.91	82.38	836.40	54.10	4
Paapa	7.01	11.83	54.58	60.42	7.67	2.56	64.13	1024.40	51.30	2
Tamale 2E	6.86	10.94	55.17	59.92	8.51	2.18	68.51	984.00	53.06	1
25	6.80	11.42	53.33	59.00	8.92	1.85	86.34	955.70	52.73	5
Baabo	6.63	10.01	53.42	58.17	8.15	2.27	64.19	1631.20	50.35	2
SGKP3	5.59	9.40	60.50	66.33	8.28	1.76	92.03	877.00	48.31	2
G1	5.32	9.15	56.83	61.75	9.55	1.88	60.97	614.60	47.93	3
Mampong	5.18	8.58	65.33	69.83	9.98	1.84	112.66	850.00	48.39	5
EDUB	4.98	7.66	59.42	63.67	9.73	1.84	99.04	961.80	48.17	3
Hihaho	4.98	8.34	65.67	71.17	9.98	1.84	107.24	772.30	47.79	1
OSO-5	4.55	7.63	54.92	59.00	9.43	1.86	74.73	878.20	48.39	4
Asontemtiatia	4.38	7.52	52.33	57.25	6.38	1.81	61.72	1206.00	46.90	3
MEANS	**5.78**	**9.52**	**57.18**	**62.12**	**8.85**	**1.97**	**81.16**	**965.97**	**49.78**	**3**
LSD (P≤0.05)	**0.36**	**1.18**	**2.13**	**2.49**	**0.6**	**0.13**	**7.05**	**504.3**	**2.33**	**0.11**

FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; FW = fruit width; PH = plant height (cm); LA = leaf area; CC = Chlorophyll content; SL = Sliminess

Across low N and high N conditions, the combined ANOVA significantly ($P<0.05$) varied for G and E main effects for fruit yield and all other characters except G mean square for chlorophyll content and E mean square for plant width. Similarly, significant seasonal (S) variations were observed for fruit yield and all measured traits except days to first flowering, days to 50% flowering, and the number of branches per plant. Moreover, the ANOVA revealed significant interaction among environment × season (E × S) for number of fruits per plant and most traits except fruit length and fruit yield ((Table 6.9)). Environment, genotype, and GEI each contributed 94.85%, 5.09%, and 0.06% to the overall sum of squares for fruit yield (Table 6.3).

The yield of the hybrids under each and across the environment varied from 2.84 t/ha for Mampong × EDUB to 7.61 t/ha for Hilhaho × Paapa with a mean of 4.81 t/ha. Hybrid crosses Hilhaho × Paapa and Hilhaho × G1 were the high-yielding hybrids. The number of fruits per plant ranged from 5.94 for Mampong × EDUB to 21.44 for Hilhaho × Paapa. Hybrid cross Hilhaho × G1 also produced considerable number of fruits per plant (Table 6.10). Furthermore, fruit yield differed from 2. 71 t/ha for Asontemtiatia to 5.57 t/ha for parental genotype Tamale 2E. Genotypes Tamale 2E, Paapa and 50 were the best-performing genotypes for fruit yield among the twelve parental genotypes (Table 6.11). Conversely, Asontemtiatia and OSO-5 recorded the lowest fruit yield.

Table 6.9 Mean squares of hybrids evaluated across low nitrogen and high nitrogen conditions during 2021 major and minor growing season at Jacobu and Akumadan

SOURCE	DF	FY(T/HA)	NFP	DFF	50%FL	FL	CC	PH	PW	NBP
REP	2	3.59**	2.96	98.57***	68.67***	18.03**	103	421.2*	0.52**	1.61*
GENOTYPE	47	17.32***	46***	249.15***	313.44***	8.53***	241	3048.4***	0.29***	7.78***
ENVT	1	322.77***	812.11***	68.41***	129.39***	60.6***	6043.8***	16388.9***	0.1	31.57***
SEASON	1	5.17**	121.3***	21.2	2.38	95.94***	871.7*	1500.4***	0.37*	0.02
GENOTYPE * SEASON	47	0.19	1.38	1.4	3.65	2.09	212.3	24.5	0.07	0.26
GENOTYPE * ENVT	47	0.22	0.65	0.76	2.42	1.97	204.3	11.6	0.08	0.23
ENVT * SEASON	1	0.02	8.99*	51.06**	58.14**	0.71	757.6*	579.3*	1.0**	9.78***
GENOTYPE* ENVT*SEA	47	0.37	0.88	0.63	2.88	2.02	198.8	6.5	0.08	0.82**
RESIDUALS	382	0.53	2.22	5.96	6.53	3.06	184.4	97	0.09	0.51

FY= fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering; 50%FL = days to 50% flowering; FL= fruit length; CC = chlorophyll content; PH = plant height (cm); PW = plant width; NBP = number of branches per plant

Table 6.10 Performance of okra single cross hybrids plus four checks evaluated across low N and high N environments

Hybrids	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
Hilhaho x Paapa	7.61	21.44	53.08	58.54	8.94	1.97	91.24	975.50	52.80	2.00
Hilhaho x G1	6.93	18.61	51.29	56.13	8.68	1.94	86.68	1002.64	66.76	1.00
EDUB x OSO-5	6.62	11.76	52.46	57.25	9.02	2.06	61.05	969.99	52.37	2.00
Tamale 2E x GI	6.43	11.93	49.54	54.00	8.64	2.50	62.74	824.32	52.15	2.00
Hilhaho x SGKP3	6.16	11.55	57.67	62.00	9.25	2.10	92.93	843.42	51.53	2.00
Tamale 2E x SGKP3	5.91	11.69	50.75	54.75	8.45	2.23	61.85	714.03	50.21	2.00
Baabo x Tamale 2E	5.86	10.69	54.88	60.75	8.93	1.85	96.43	808.76	51.21	2.00
OSO-5 x Asontemtiatia	5.82	10.81	51.88	56.33	9.37	1.95	69.93	820.01	50.29	3.00
OSO-5 x Hilhaho	5.78	10.97	51.46	55.25	9.45	1.86	70.05	940.53	51.04	4.00
25 x Asontemtiatia	5.59	10.04	51.38	55.25	9.20	1.88	81.40	732.59	51.11	3.00
Okra hybrid (Check 1)	5.54	17.99	45.08	55.46	10.61	2.17	95.48	745.20	52.18	3.00
Asontemtia x SGKP3	5.53	10.49	55.50	62.00	7.54	1.82	88.00	1056.89	49.88	3.00
Baabo x Asontemtitia	5.49	10.39	54.96	59.67	8.54	1.92	93.95	871.68	51.23	3.00
OSO-5 x Tamale 2E	5.46	10.79	51.71	57.33	8.48	1.93	62.00	869.09	51.78	4.00
25 X Hilhaho	5.40	9.34	51.13	55.25	7.87	2.00	64.57	829.60	48.88	2.00
Asontemtia x Paapa	5.33	9.85	51.46	56.79	9.03	2.28	80.08	856.07	51.22	3.00
Baabo x Hilhaho	5.09	10.09	56.96	62.13	7.53	1.97	103.86	800.95	49.66	3.00
Tamale 2E x Paapa	5.04	10.30	51.29	55.08	9.76	2.19	60.78	846.90	51.41	1.00
50 x Baabo	4.90	9.56	55.17	60.21	8.65	1.96	96.03	974.88	48.56	4.00
Mampong x Baabo	4.80	9.69	64.79	69.33	9.18	2.46	110.24	950.17	65.91	4.00
Asontemtiatia x G1	4.65	9.50	53.08	57.83	9.98	2.13	74.65	754.07	48.70	3.00
Paapa x EDUB	4.55	8.61	53.04	57.92	7.89	2.42	65.22	765.13	49.27	2.00

Table 6.10 cont'd

Hybrids	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
Paapa × Mampong	4.53	8.48	53.00	57.83	6.44	2.28	75.36	867.94	48.88	4.00
25 × Tamale 2E	4.49	8.69	51.54	54.67	8.45	2.05	71.91	758.30	49.52	4.00
Paapa × 50	4.46	9.35	51.92	57.17	8.06	2.14	63.79	862.28	48.07	2.00
SGKP3 × EDUB	4.45	8.96	61.13	66.04	8.63	1.84	91.41	786.23	47.00	2.00
Hire (check)	4.26	13.23	47.17	59.29	8.37	2.04	72.40	890.44	49.73	4.00
EDUB × 25	4.03	7.86	52.00	57.04	8.35	2.24	60.53	968.39	47.00	3.00
EDUB × Baabo	4.03	7.92	50.13	52.67	8.48	2.23	69.99	772.04	48.18	2.00
Mampong × 25	3.99	8.01	58.75	63.21	8.26	1.90	113.38	800.32	45.76	2.00
SGKP3 × 50	3.98	7.64	56.79	62.25	9.21	1.86	100.16	927.94	47.55	4.00
CLEMSSON(Check)	3.69	14.87	57.58	72.00	8.20	2.12	74.63	861.58	47.65	4.00
50 × 25	3.52	7.40	52.33	58.13	9.15	2.05	79.37	909.46	46.68	1.00
SGKP3 × Mampong	3.42	6.98	65.33	70.67	8.64	2.06	90.55	823.41	46.95	3.00
G1 × Mampong	3.34	7.26	58.75	63.25	8.83	2.03	87.34	794.14	46.25	3.00
ESSOUNTEM(Check)	3.31	13.35	39.71	48.83	10.64	2.03	50.47	630.78	47.41	4.00
50 × OSO-5	3.30	6.83	56.33	61.75	8.15	2.44	76.94	746.97	46.03	5.00
G1 × 50	3.18	6.51	56.08	62.08	7.67	1.90	64.20	694.63	46.51	3.00
G1 × EDUB	3.12	6.49	54.92	59.96	8.86	2.24	61.67	1079.83	50.32	4.00
Mampong × EDUB	2.84	5.94	60.75	65.46	8.30	2.25	103.47	800.32	43.45	5.00
MEAN	**4.81**	**14.37**	**53.82**	**59.29**	**8.71**	**2.08**	**79.42**	**848.19**	**50.07**	**3.00**
LSD (P≤0.05)	**0.57**	**1.76**	**1.77**	**2.05**	**0.72**	**0.34**	**8.03**	**166.89**	**11.97**	**0.03**

FY= Fruit yield (t/ha); NFP= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area; CC = Chlorophyll content ; SL = Sliminess

Table 6.11 Performance of okra parental genotypes evaluated across low-N and high-N conditions

ACCESSIONS	FY	NFP	DFF	50%FL	FL	FW	PH	LA	CC	SL
Tamale 2E	5.57	9.79	56.96	63.33	7.73	2.10	63.63	834.80	51.32	1
Paapa	5.31	9.91	56.04	64.33	7.39	2.51	61.44	940.10	50.23	2
50	5.00	9.58	58.38	63.79	8.65	1.87	79.61	781.20	50.83	4
Baabo	4.84	8.41	54.54	61.75	8.04	2.26	57.90	1250.90	49.81	2
25	4.50	8.81	55.21	63.42	8.20	1.88	78.74	914.10	50.20	5
SGKP3	3.46	6.76	63.00	70.54	8.04	1.84	85.97	851.10	44.93	2
Mampong	3.28	6.67	67.54	73.71	9.18	1.83	102.59	835.10	44.94	5
G1	3.23	6.66	58.63	65.79	8.70	1.84	55.55	596.10	43.60	3
Hihaho	3.21	6.60	67.33	73.75	9.32	1.79	98.82	725.40	45.36	1
EDUB	3.05	5.96	61.33	66.71	8.69	1.85	90.40	917.50	44.25	3
OSO-5	2.84	5.88	56.54	62.13	8.69	1.85	68.66	820.00	44.97	4
Asontemtiatia	2.71	5.93	53.83	60.88	6.22	1.73	60.15	925.70	42.20	3
MEANS	**3.92**	**7.58**	**59.11**	**65.84**	**8.24**	**1.95**	**75.29**	**866.00**	**46.89**	**3**
LSD (P≤0.05)	**0.23**	**0.64**	**1.71**	**1.75**	**0.38**	**0.11**	**4.99**	**252.12**	**1.61**	**0.05**

FY= Fruit yield (t/ha); NF/PLOT=number of fruits per plant; NFPLANT= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area; CC = Chlorophyll content ; SL = Sliminess

6.3.2 Heterosis of the crosses for fruit yield (t/ha) under low N and high N conditions

The mid-parent heterosis under low N varied from -27.13% for 50 × 25 to 300% for OSO-5 × Asontemtiatia averaging 56.94%. Top hybrids with mid parent heterosis included OSO-5 × Asontemtiatia (300%), EDUB × OSO-5 (234.51%), OSO-5 × Hilhaho (233.07%), Hilhaho × G1 (196.12%), and Hilhaho × Paapa (177.38%). G1 × 50 (-25.81%), Tamale 2E × Paapa (-27.13%), and 50 × 25 (-27.13%) had the least estimates of mid-parent heterosis (-25.13%). Estimates of better parent heterosis varied from -48.07% for G1 × 50 to 234.51% for EDUB × OSO-5, with an average of 30.11%. EDUB × OSO-5 had the highest better parent heterosis (234.51%), followed by OSO-5 × Asontemtiatia (224.07%). The least estimates of mid-parent heterosis were observed by hybrid cross G1 × 50 (-48.07%), Paapa × EDUB (-40%) and Paapa × Mampong (-36.67%) (Table 6.12).

Across high N environments, mid-parent heterosis ranged from -25.45% for 50 × 25 to 98.53% for EDUBB × OSO-5, while better parent heterosis ranged from -33.43% for 50 × OSO-5 to 89.96% for EDUB × OSO-5 (Table 4.18). Hybrid crosses EDUB × OSO-5 recorded the highest mid-parent heterosis, followed by Hilhaho × Paapa (Table 6.13).

Table 6.12 Estimates of better parent and mid-parent heterosis for fruit yield (t/ha) under low N conditions at Jacobu and Akumadan in the 2021 major and minor seasons.

Parents and hybrids	Mean	Better parent heterosis%	Mid parent heterosis%
Tamale 2E	4.28		
Paapa	3.60		
Baabo	3.04		
50	2.85		
25	2.20		
Hihaho	1.44		
Mampong	1.39		
SGKP3	1.32		
G1	1.14		
OSO-5	1.13		
EDUB	1.13		
Asontemtiatia	1.04		
Hilhaho × Paapa	6.99	94.17	177.38
Hilhaho × G1	3.82	165.28	196.12
EDUB × OSO-5	3.78	234.51	234.51
Hilhaho × SGKP3	3.63	152.08	163.04
Baabo × Tamale 2E	3.18	-25.7	-13.82
Tamale 2E × SGKP3	3.38	-21.03	20.71
25 × Hilhaho	2.40	9.09	31.87
Tamale 2E × G1	5.67	32.48	109.23
Asontemtiatia × SGKP3	3.05	131.06	158.47
Baabo × Asontemtiatia	2.99	-1.64	46.57
Asontemtiatia × Paapa	2.69	-25.23	-15.95
25 × Asontemtiatia	3.35	52.27	106.79

Table 6.12cont'd

Parents and hybrids	Mean	Better parent heterosis%	Mid parent heterosis%
Baabo × Hilhaho	2.75	-9.54	22.77
50 × Baabo	2.47	-18.75	-16.13
OSO-5 × Asontemtiatia	4.34	224.07	300
OSO-5 × Hilhaho	4.28	197.22	233.07
Tamale 2E × Paapa	2.95	-31.07	-25.13
Paapa × EDUB	2.16	-40	-8.67
Asontemtiatia × G1	2.50	119.3	129.36
Paapa × Mampong	2.28	-36.67	-8.61
OSO-5 × Tamale 2E	4.24	-0.93	56.75
EDUB × 25	1.45	-34.09	-12.91
SGKP3 × EDUD	1.03	-21.97	-16.74
Mampong × 25	1.76	-20	-1.95
25 × Tamale 2E	2.95	-31.07	-8.95
Paapa × 50	2.90	-19.44	-10.08
EDUB × Baabo	2.04	-32.89	-2.16
Mampong Baabo	3.89	27.96	75.62
SGKP3 × 50	2.30	-19.3	10.31
SGKP3 × Mampong	1.33	-4.32	-1.85
G1 × EDUB	2.66	133.33	134.36
50 × 25	1.84	-35.44	-27.13
G1 × 50	1.48	-48.07	-25.81
G1 × Mampong	1.88	35.25	48.62
50 × OSO-5	1.84	-35.44	-7.54
Mampong × OSO-5	1.23	-11.51	-2.38
Mean		**30.11**	**56.94**
Max		**234.51**	**300**
Min		**-48.07**	**-27.13**

Table 6.13 Estimates of better parent and mid-parent heterosis for fruit yield (t/ha) under high N conditions at Jacobu and Akumadan in the 2021 major and minor seasons.

Single cross okra hybrids	Mean	Better parent heterosis%	Mid parent heterosis. %
50	7.15		
Paapa	7.01		
Tamale 2E	6.86		
25	6.80		
Baabo	6.63		
SGKP3	5.59		
G1	5.32		
Mampong	5.18		
EDUB	4.98		
Hihaho	4.98		
OSO-5	4.55		
Asontemtiatia	4.38		
Hilhaho × Paapa	10.14	44.65	69.14
Hilhaho × G1	10.04	88.72	68.74
EDUB × OSO-5	9.46	89.96	98.53
Hilhaho SGKP3	8.70	55.64	64.62
Baabo × Tamale 2E	8.55	24.64	26.76
Tamale 2E × SGKP3	8.44	23.03	35.58
25 × Hilhaho	8.40	23.53	42.61
Tamale 2E × G1	8.23	19.91	35.14
Asontemtiatia × SGKP3	8.00	43.11	60.48
Baabo × Asontemtiatia	7.98	20.36	44.96
Asontemtiatia × Paapa	7.97	13.69	39.95
25 × Asontemtiatia	7.84	15.29	40.25
Baabo × Hilhaho	7.43	12.07	27.99
50 × Baabo	7.33	2.52	6.37

Table 6.13 cont'd

Single cross okra hybrids	Mean	Better parent heterosis%	Mid parent heterosis. %
OSO-5 × Asontemtiatia	7.30	60.44	63.49
OSO-5 × Hilhaho	7.29	46.39	52.99
Tamale 2E × Paapa	7.13	1.71	2.81
Paapa × EDUB	6.93	-1.14	15.6
Asontemtiatia × G1	6.80	27.82	40.21
Paapa × Mampong	6.77	-3.42	11.07
OSO-5 × Tamale 2E	6.67	-2.77	16.91
EDUB × 25	6.62	-2.65	12.39
SGKP3 × EDUD	6.24	11.63	18.07
Mampong ×25	6.22	-8.53	3.84
25 × Tamale 2E	6.03	-12.1	-11.71
Paapa × 50	6.02	-15.8	-14.97
EDUB × Baabo	6.01	-9.35	3.53
Mampong × Baabo	5.71	-13.88	-3.3
SGKP3 × 50	5.66	-20.84	-11.15
SGKP3 × Mampong	5.51	-1.43	2.32
G1 × EDUB	5.21	-2.07	1.17
50 ×25	5.20	-27.27	-25.45
G1 × 50	4.88	-31.75	-21.73
G1 × Mampong	4.80	-9.77	-8.57
50 × OSO-5	4.76	-33.43	-18.63
Mampong × OSO-5	4.45	-14.09	-12.4
Mean		**11.52**	**21.6**
Max		**89.96**	**98.53**
Min		**-33.43**	**-25.45**

6.3.3 Pearson correlation coefficient between okra fruit yield and fruit components characters

Under low N conditions, the results revealed that fruit yield was significant ($p<0.01$) and positively associated with the number of fruits/plant ($r= 0.89$), leaf chlorophyll content ($r= 0.11$), fruit length ($r=0.12$) and leaf area ($r= 0.09$) but negatively correlated with days to first flowering ($r= 0.34$), days

to fifty percent flowering (r= 0.35) and incidence of *Podagrica* spp (Table 6.14).

Under high N, fruit yield of okra was significant ($p<0.01$) and positively linked with traits such as number of fruits per plant (r= 0.86), plant height (r= 0.18), plant width (r= 0.16), fruit length (r= 0.20), fruit width (r= 0.26), leaf chlorophyll content (r= 0.71) and leaf area (r= 0.09). However, fruit yield was significant ($p<0.01$) and negatively correlated with days to first flowering (r= 0.36), days to fifty percent flowering (r= 0.34), the incidence of okra *Podagrica* (0.22) and incidence of okra mosaic virus disease (0.21) (Table 6.14).

Across research conditions, fruit yield was significant ($p<0.01$) and positively correlated with the number of fruits per plant (r= 0.88), plant height (r=0.45), plant width (r= 0.18), fruit length (r=31), fruit width (r= 0.10), and leaf chlorophyll content (r= 0.15). On the contrary, fruit yield is significant ($p<0.01$) and negatively linked with days to fifty percent flowering (r=0.55) and leaf area (r=0.19). (Table 6.14)

Table 6.14 Pearson correlation of fruit yield and yield component characters under contrasting environments

Fruit yield			
Trait	**Low N**	**Optimum N**	**Across**
50%FL	-0.35**	-0.34**	-0.55**
DFF	-0.34**	-0.36**	-0.49**
PH	0.07	0.18**	0.45**
PW	-0.06	0.16**	0.18**
IMV	-0.01	-0.21**	-0.02
IP	-0.2**	-0.22**	-0.01
CC	0.11*	0.71**	0.15**
FW	0.02	0.26**	0.1**
FL	0.12**	0.2**	0.31**
LA	0.09*	0.09*	-0.19**
NFP	0.89**	0.86**	0.88**

*, **, Significant at 0.05 and 0.01probabilities, respectively; NFPLANT= number of fruits per plant; DFF = days to first flowering ; 50%FL = days to 50% flowering ; FL= fruit length; FW = fruit width; PH = plant height (cm); PW = plant width; LA = leaf area; CC = Chlorophyll content ; SL = Sliminess; IP = incidence of Podagrica spp; IMV = incidence of okra mosaic virus

6.4 Discussions

As evidenced by soil nitrogen levels and crop responses, using farms previously deficient in nitrogen resulted in severe N stress. The data indicated that okra fruit output increased in direct proportion to increased N fertilization (high N). The significant differences observed among environments and genotypes' main effects on fruit yield and the majority of the characters under low-N and high N suggested the presence of genetic variability among the parental genotypes and hybrids. The testing environments were also distinctive and could show the hybrids' genetic variations. This offers opportunities to choose acceptable genotypes with high means for all the desired traits. This corroborates the findings of Ariyo (1993) and Adeniji (2003) who mentioned the role of environmental factors and differences in the genetic makeup of different varieties in yield determination of okra. The non-significant genotype

× environment (G × E) interaction observed for fruit yield among the genotypes under each and across research conditions indicated that the genotypes exhibited consistency throughout all research conditions, and their genetic potential affected how well they performed under both high-nitrogen and low-nitrogen conditions.

On the contrary, genotype × environment interaction effects under high-N environments were significant for fruit yield, which implied that the different environments were distinct and that the genotypes would not be consistently chosen across the environments. This also suggested that environmental variations affected how fruit yield varied among genotypes. This is consistent with earlier works by Ramya and Senthilkumar (2010), Kachhadia *et al.* (2011), Srivastava *et al*. (2011) and Alake and Ariyo (2012). The current research also revealed that the environment's influence on the total sum of squares was enormous for fruit yield for each and across research conditions for the genotypes. As Badu-Apraku *et al.* (2007) stated in maize production, the significant environmental effects demonstrated the tremendous variability of the test conditions. They emphasized the need for genotype testing in various locations over the years. Similarly, the significant seasonal (S) effects observed among the genotypes for fruit yield and most traits under each and across the environment implied a wide variation among the various seasons. Furthermore, the observed significant genotype × season (G × S) interaction for chlorophyll content under high N conditions indicates that environmental effects significantly influenced the expression of these traits.

The assessment of the 36 single cross hybrids, four checks and 12 parental accessions under low-N and high-N environments were critical to determining high-yielding genotypes. Low N is a limiting constraint to commercial okra production in depleted soils. Breeding for nitrogen-efficient genotypes has been comparatively slow or neglected, probably due to a lack of genotypic variance for nitrogen-efficient genotypes. The current study's findings showed that low N stress resulted in decreased fruit yield, number of fruits/plant, length of fruits, plant height, leaf chlorophyll content, leaf area, and extended days to first flowering and days to fifty percent flowering. Plant height, number of branches per plant, fresh pod length and width, number of pods per plant, and pod weight are all factors that determine pod productivity in okra (Akinyele and Osekita 2006; Abd El-Fattah *et al*., 2020).

In the present study, a higher fruit yield, prolificacy and high leaf chlorophyll content indicated tolerance to low N. These traits are useful for selecting potential genotypes for breeding programmes to develop nitrogen-efficient hybrids. They can improve okra yield in nitrogen-depleted soils. Under low N stress, more tolerant genotypes experienced less yield loss. Thus, Hilhaho × Paapa and Tamale 2E × G1 hybrids were noted as the most N-tolerant hybrids under low-N conditions. These hybrids were naturally capable of delivering excellent results in low-N and high-N conditions. These hybrids outperformed the best check by 30% (okra hybrids) and all the other checks under low N conditions. These results suggested that the first two hybrids, Hilhaho × Paapa and Tamale 2E × G1, would be necessary for increasing okra yield and productivity under low-N conditions and should be evaluated in other places before being made available for cultivation by farmers with

limited resources. According to the findings, the low-N condition was harsh enough to separate between hybrids that can tolerate low-N and those that are susceptible. Mampong × EDUB was one of the five hybrids with the lowest yields in low-nitrogen and high-nitrogen conditions. Other research may employ this hybrid as a susceptible check. The parental genotypes Tamale 2E, Paapa, and Baabo were tolerant to low N environments. They were characterized by reduced plant height, increased chlorophyll content, broad leaf area, extended fruit length, high number of fruits per plant, and number of fruits per plot. However, there were an extended number of days to flowering and number of days to 50% flowering under low nitrogen conditions.

Under high N environments, the best hybrids were Hilhaho × Paapa and Hilhaho × G1. Coincidentally, Hilhaho × Paapa was among the top nitrogen-efficient hybrids evaluated under low -N conditions. These findings provided evidence that the top hybrids selected for the study will consistently produce more fruit in a given production location and season. Hilhaho × Paapa and Hilhaho × G1 had fruit yields of 10.14 and 10.04 tons/ha, respectively, under high N conditions (100 kg N/ha). This result is similar to the finding of Kurup *et al*. (1997), who reported that N rates up to 100 kg /ha could increase fruit weight per okra plant.

In every hybrid breeding effort, superior heterosis for fruit yield is crucial. According to the current study, mid-parent heterosis and better-parent heterosis were 56.94% and 30.11% in low N environments and 21.6% and 11.52% in high N environments, respectively. As revealed by the heterosis analysis, the results showed that mid-parent and better-parent heterosis were not constant for the single cross hybrids in low-N and high-N environments.

When compared to high N environment, they were higher in low N situations. The lower performance of parental genotypes under a low N environment might cause increased heterosis estimations under low N. Moreover, mid-parent heterosis values were higher than the corresponding heterotic estimates of better parents across low-nitrogen and high-nitrogen environments. Negative heterosis among some single cross-hybrids could be attributed to the combination of parents' undesirable genes. The substantial heterosis in fruit production across these germplasms suggests that these materials have a lot of potential for producing hybrids. The findings also imply that heterosis breeding can significantly boost okra yield.

Correlation of traits serves as a measure and forms the basis of selection, giving direction and magnitude of association between the traits studied. The significant positive correlation between fruit yield and the yield component traits suggests an association among the characters. It may support the utilization of these characteristics, particularly leaf chlorophyll content, fruit length, leaf area, and number of fruits per plant as a basis for selection under low N conditions. Under high N, the fruit yield of okra was significant and positively linked with most of the yield component traits. In okra, fresh pod yield is a complex trait influenced by several yield component variables (dos Santos Fariasa *et al.* 2019; Shi *et al.* 2020). Secondary traits, including stem diameter, plant height, fruit length, fruit width, leaf chlorophyll content and leaf area, were found to be critical in improving fruit yield in the current study. This suggested that increasing these attributes could invariably increase fruit yield.

6.5 Conclusion

Genetic variations were observed among genotypes, environment and the various seasons. Okra genotypes were consistent and stable across the test environment, as evidenced by the non-significant genotype x environment interaction (G × E). The assessment of the performance of okra hybrids under different growing conditions is crucial. Hilhaho × Paapa and Tamale 2E × G1 were selected as the top hybrids tolerant to low N and recommended for further release testing. These hybrids are naturally capable of delivering exceptional results in low- and high-nitrogen environments. The parental genotypes Tamale 2E, Paapa and Baabo were selected as the top genotypes tolerant to low-N. Under high-N environments, the best hybrids were Hilhaho × Paapa and Hilhaho × G1. A significant positive correlation existed between fruit yield and most yield component traits. Most hybrid crosses expressed heterosis on low-nitrogen and high-nitrogen soil conditions. Moreover, mid-parent heterosis values were higher than the corresponding heterotic estimates of better parents across low-nitrogen and high-nitrogen environments.

CHAPTER SEVEN

7.0 CONCLUSIONS AND RECOMMENDATIONS

7.1 Conclusions

Okra is a powerhouse of valuable nutrients and an underutilized crop widely grown in Asia, South America and Africa. The nutritional composition of okra makes it a vital source of nutrition to reduce malnutrition in Asia and sub-Saharan African countries (SSA). Abiotic and biotic factors such as low soil N and disease and pests are to blame for low yield. Therefore, it is essential to develop hybrids resistant to viral infections and tolerant to low soil N. This study was undertaken to (1) assess genetic diversity and relationship among 100 okra germplasm using morphological characters and SSR markers, (2) determine the performance and heterosis of the okra hybrids and their parental genotypes for yield and fruit quality under low-N, high-N, and across the four research conditions (3) Assess the breeding value and mode of gene action of selected okra genotypes for yield under low, high-N and across the four research conditions, (4) determine the combining ability of the selected okra genotypes for resistance to OMD, OLCD and *Podagrica* spp of hybrids in low N, high N and across the four research conditions .

The results of the diversity studies indicated wide genetic variability among the 100 okra germplasms studied and 27 out of the 100 collected germplasm were duplicates. The dendrogram constructed from the morphological data and the 6 SSR markers revealed that the genetic relationship among germplasm did not depend on the geographical origin of the collected okra germplasm, indicating free flow and adaptation of okra accessions across Ghana. The results further showed that moderate to high

heritability estimates coupled with high magnitude of genetic advance were recorded for most traits studied.

Studies on G × E interaction are necessary to determine the stability and performance of genotypes and hybrids bred for growing in a broader or specific growing environment. The combined ANOVA of the okra accessions (parents) and hybrids evaluated under each and across research conditions showed wide genetic variability in the study locations to allow phenotypic selection.

Because the performance of parental genotypes is not a strong measure of their performance in hybrid combinations, combining ability studies for fruit yield and other agronomic traits were carried out under low and high N. conditions. GCA appeared to influence inherited characters tested considerably, and additive gene effect was more significant than non-additive. Parental genotypes with significant general combining ability estimates for fruit yield and other agronomic variables may pass desirable genes to their F1s, which may be advantageous in a breeding programme. Superior GCA-female to GCA-male estimates for fruit yield and yield component traits on low N and high N and across research environments suggested that cytoplasmic effects might have modified these traits. Parental genotypes Tamale 2E was identified as the high-yielding genotype, the best general combiner for fruit yield and resistant to OLCD, OMD and *Podagrica* spp. under low- N environment. This implied that this genotype has immunity against the two viral diseases and *Podagrica* spp. under a low N environment and could contribute desirable alleles to their progenies. Similarly, hybrid

cross Hilhaho × Paapa, Tamale 2E ×G1 and Hilhaho × G1 were selected as the superior high-yielding hybrids under low, high N and across environments.

Moreover, hybrid cross Hilhaho × Paapa was the best specific combiner under each and across the research environment. However, hybrid cross Asontemtiatia × Paapa was resistant to OLCD under each and across environments. Also, Hybrid cross Paapa × Mampong was resistant to OMD with significant and negative SCA effect while cross Hilhaho × SGKP3 recorded the most significant and negative SCA effect under each and across the research environment. These hybrids were naturally capable of delivering excellent results under low- and high-nitrogen environments.

7.2 Recommendations

1. The SSR markers and morphological traits employed in the present study revealed a high level of genetic diversity among the 100 genotypes of okra and should be exploited for the okra improvement programme.
2. Heritability alongside genetic advance as a percent of means or correlations of fruit yield with secondary traits across low-N and high-N environments could be utilized as a trustworthy resource to find low-N tolerant genotypes.
3. The Parental genotypes Tamale 2E, Paapa and Baabo were identified as low N tolerant genotypes. These parental genotypes might be valuable sources of alleles for introgression of genes for low-N tolerance in population enhancement.

4. The hybrids Hilhaho × Paapa and Tamale 2E × G1, identified as the best low-N tolerant hybrid across the locations, should be further tested under low-N conditions to confirm their stability. These two hybrids also recorded positive and significant SCA effects for fruit yield for each and across the research environment.

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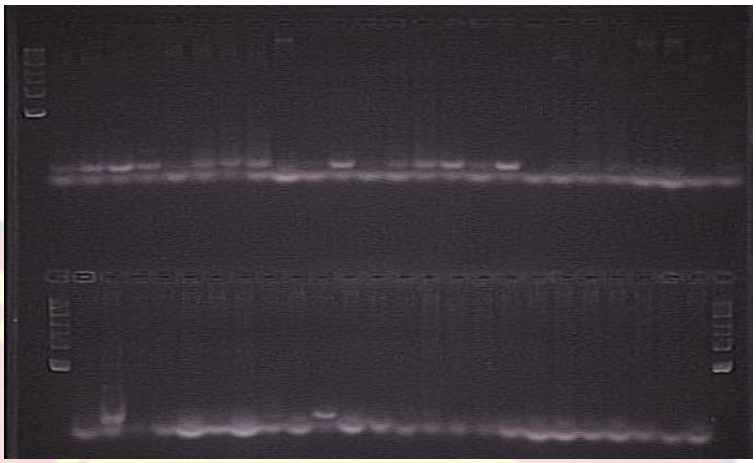
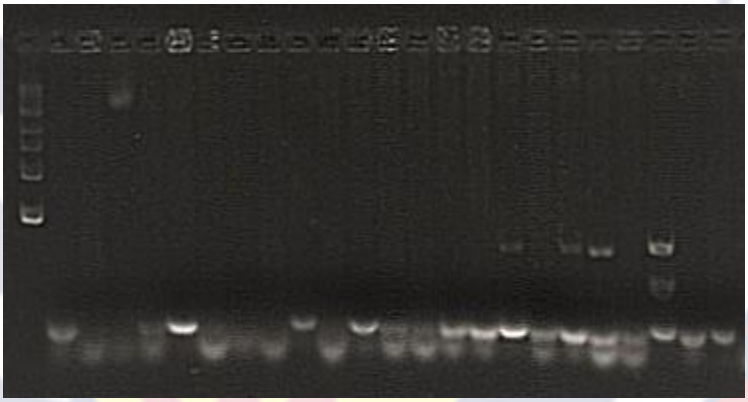
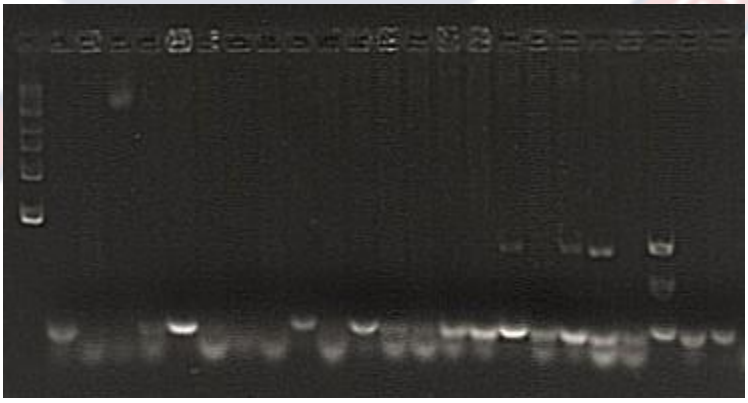
APPENDICES



Appendix 1: Showing SSR primerAEKVR-117 image on visual gel



Appendix 2: Showing SSR primerAEKVR-119 image on visual gel



Appendix 3: Showing SSR primerAEKVR-165 image on visual gel