

MAKERERE UNIVERSITY
SCHOOL OF GRADUATE STUDIES

**VARIABILITY IN PHENOTYPIC TRAITS AND RESISTANCE TO BLAST IN
INTERSPECIFIC FINGER MILLET PROGENIES**

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DECLARATION

This thesis is an original presentation of my research. Contributions of others are clearly indicated by acknowledgement and referencing the literature.

This thesis study was guided by Associate Professor Patrick Okori, Department of Crop Production, College of Agricultural and Environmental, Makerere University and Dr. Moses Biruma

Sign..... Date.....

In my capacity as the supervisor of the candidate's thesis, I certify that the above statements are true to the best of my knowledge.

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SUMMARY

Finger millet (*Eleusine coracana* (L.) Gaertn. ssp. *coracana*) is an important food, food security and cash crop in eastern and southern Africa where small-scale farmers grow it in low input farming systems. The crop has food security, nutritional, cultural, medicinal, and economic value with high industrial potential. Use of host plant resistance is the most feasible and economical viable means of managing finger millet blast especially for resource-poor farmers. The purpose of this study was to assess the performance of advance populations derived from three interspecific crosses between finger millet and two wild relatives *E. kigeziensis* and *E. africana*. F3 and F4 progeny deriving from these interspecific crosses i.e. *E. kigeziensis* X *E. coracana* (Pese 1), *E. africana* X *E. coracana* (Seremi 1) and *E. africana* X *E. coracana* (Seremi 3) were used. Two studies were conducted (i) on resistance to finger millet blast disease among F3 and F4 under controlled conditions of humid chambers and greenhouse using an aggressive *M. grisea* isolated obtained from Ngora in Eastern Uganda. The second study focused on variability of phenotypic traits (according to the finger millet descriptors, IPGR 1985) at two sites, Makerere University Agricultural Research Institute, MUARIK (MUARIK) and National Semi-Arid Resources Research Institute (NaSSARI) in NaSAARI. In both studies, experiments were established following the alpha lattice design.

Significant variations were observed among the finger millet accessions for various agronomic traits with the maturity and growth traits having the greatest contribution to the total phenotypic variation captured which was consistent with reports of previous studies. A number of accessions were identified for their good performance for specific traits; 36 for early flowering; 12 accessions for early maturity; 22 for more number of fingers; 10 for high basal tiller number and 24 accessions for long fingers, and 19 for tallness. 20 accessions were identified as multi-trait specific accessions, which were found to be sources of more than one trait. These accessions could be utilized for simultaneous transfer of multiple traits in finger millet improvement programme. Out of 48 accessions at F4 generation, of the finger millet interspecific progenies, a total of 39 accessions were identified as trait specific for six important yield-contributing traits. 21 Multi-trait specific accessions were identified, which were found to be sources for more than one trait.

Highly significant differences among the F3 interspecific progenies for the leaf blast ($P < 0.001$) were found, with the highest mean square variance recorded at 56 days after planting. The leaf blast severity ranged from 1.7 to 2.6 on a 1-5 scale compared to 2.2 on resistant check (Gulu E) and 3.2 on susceptible check (KATFMI). Among the 48 F3 progeny, nine lines (19%) were resistant, 38 lines (79%) were moderately resistant and only one line (2 %) was susceptible. No lines showed total immunity (highly resistant) and high susceptibility to the leaf blast disease. The minimum score was recorded on line 19c-b (1.7) followed by 19c, 24b, 13a, 6b, 2b, 20b, 24c-b and 22c-b all with a score of 1.9. All these were categorized as resistant. The maximum score was recorded on line 16c-b (2.6) categorized as susceptible, followed by 12a with a score of 2.4 and 26b, 8a, 1a, 17b, 18c-b, 7c-b, 5b, 25c-b all with a score of 2.3 and categorised as moderately resistant. Highly significant differences among the F4 interspecific progenies for the leaf blast ($P < 0.001$) were found with the highest mean square variance recorded at 56 days after planting. The leaf blast severity ranged from 1.8 to 2.7 on a 1-5 scale compared to 2.2 on resistant check (Gulu E) and 2.7 on susceptible check (SER 2). Among the 48 F3 progeny, five lines (10%) were resistant, 37 lines (77%) were moderately resistant and six lines (13 %) was susceptible. No lines showed total immunity (highly resistant) and high susceptibility to the leaf blast disease. The minimum score was recorded on line 25a (1.8) followed by 18b, 19b, 25c-b, 7b all with a score 1.9 and categorized as resistant. The maximum score was recorded on line 28a (2.7) followed by 22c-b, 23a, 14c, 20c with a score of 2.5 and categorized as susceptible. Significant differences among the F4 progeny for all the three forms of blast disease were found, with the highest mean square of variance being for Neck blast, followed by head blast and least leaf blast. Two lines (25a and 25c-b) were resistant to all the three forms of blast disease, thirteen lines (8b, 6b, 8a, 24b, 22b, 22a, 21b, 20b, 19c, 19c-b, 17b, 13c-b, 13a) were resistant to neck blast and head blast and moderately resistant to leaf blast; six lines (14c, 20c, 22c-b, 23a, 28a, 5b) were resistant to neck and head blast but susceptible to leaf blast.

The study also found that progeny deriving from the two different male wild parents remained distinct. Principle component analysis identified the key traits that could be used for selection i.e. the maturity traits such as days to 50% flowering and days to 50% maturity and phenological growth traits such as flag leaf length and plant height. Detailed results and discussions are presented in the thesis.

DEDICATION

To my mother Miss. Nantongo Jane and my little brother Abas Kabuye

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CHAPTER ONE

INTRODUCTION

1.1 Importance of Finger millet

1.1.1 Biology and eco-geographical distribution

Finger millet [*Eleusine coracana* (L) Gaertn.] is the main staple food of millions of poor people in the arid and semiarid tropical regions of Africa and Asia besides having high value for the straw (Hilu *et al.*, 1979). Finger millet is highly self-pollinated allotetraploid ($2n = 36$) derived from the wild tetraploid progenitor *E. coracana* subsp. *Africana* (Rao and Mushonga, 1985). Finger millet belongs to Poaceae family, Chloridoideae subfamily, and *Eleusine* genus. Production statistics for the nine cultivated millets are often combined so reliable estimates of the areas sown to individual millet species is difficult to find (FAO, 2011). It is estimated that finger millet accounts for 10% of 38 million ha sown to millets globally (Mgonja *et al.*, 2007). Finger millet is the most important millet grown in eastern and southern Africa and it serves as subsistence and a food security crop that is especially important for its nutritive and cultural value. It has wide adaptability to adverse agro-ecological conditions probably due to its C4 photosynthetic nature; with minimal inputs, tolerant to moisture stress, produced on marginal land where other crops cannot perform (Holt, 2000). Finger millet is grown in almost all agro-ecological areas of Uganda, but production is concentrated in the east, north and southwest agroecologies of Uganda; in these regions it is a basic staple food playing a very important role in meeting dietary needs (Oryokot, 2001). It can be cultivated in a wide range of soils and climates and because of its short growing season, it is of specific importance in semi- arid regions (Mbithi-Mwikya *et al.*, 2000). It is grown in an estimated annual area of 500,000 hectares producing 984,000 MT (FAO, 2011).

1.1.2 Finger millet production requirements

Finger millet is a short to medium day length plant with optimal photoperiod of 12-hours and grows well under moderate rainfall (500-1,000mm with optimum of 900mm), well distributed during the growing season without prolonged droughts, but with good distribution, it can tolerate rainfall as low as 130mm. Finger millet does not tolerate flooding. It grows best where average maximum temperatures exceed 27°C and average minimum do

not fall below 18°C, but can grow in temperatures up to 35°C. Dry weather is required for drying the grain at harvest as the crop is harvested at physiological maturity to avoid shattering on drying in the fields. Most of the world's finger millet is grown at intermediate elevations between 500 and 2,400 meters above sea level (masl), but it can grow from sea-level to over 2,400masl. In East Africa, it is grown mostly at 900masl (NRC, 1996 and Haore *et al.* 2007). Variation in the palaeo-climate of East Africa has been proposed as an explanation for the rapid diversification of allotetraploids in Eleusine (Liu *et al.*, 2011). Finger millet can grow on a variety of soils but does best on lateritic and well drained alluvial soils and tolerates some degree of alkalinity but not water logging (Obilana and Manyasa, 2002; de Wet 2006). The crop requires a well-prepared seedbed because of its small seed size, and inability to stand weed competition. Finger millet has wide adaptability to adverse agro-ecological conditions probably due to its C4 photosynthetic nature; with minimal inputs, tolerant to moisture stress, produced on marginal land where other crops cannot perform (Holt, 2000).

1.1.3 Significant to economies

Finger millet is being increasingly recognized as a highly nutritious food for the weak and immuno-compromised people (Takan *et al.* 2012). Finger millet has a good taste and is an excellent dietary source of methionine (an amino acid lacking in the diets of millions of the poor who live on starchy foods such as cassava, plantain, polished rice, and maize meal). It also contains minerals such as calcium, iron, phosphorus, and manganese (Holt, 2000). Finger millet is not only a source of cash for farmers, but also has the potential of saving foreign exchange, which would otherwise be required for the importation of other grains such as maize (Taylor *et al.*, 2006). Malted millet is extensively used in weaning food, infant food, and supplementary food formulations (Malleshi, 2005). In Africa, it is used to brew beer since its amylase enzymes readily convert starch to sugar, (Takan *et al.*, 2002; Duke, 1983). Finger millet straw is also a valuable livestock feed. It makes good fodder and contains up to 61% of total digestible nutrients (National Research Council 1996; Upadhyaya *et al.*, 2006).

1.2 Statement of the problem

Finger millet and sorghum are staple cereals in many semi-arid and tropic areas of the world, particularly in Sub-Saharan Africa because of its good adaptation to hard environments (Dicko *et al.*, 2005). Sorghum and millets are described as generally the most drought-tolerant cereal grain crops that require little input during growth and with increasing world

populations and decreasing water supplies, represent important crops for future human use especially with the current problem of climate change (ICRISAT, 1996; Taylor *et al.*, 2006). The semi-arid tropics are characterized by unpredictable weather, limited and erratic rainfall and nutrient-poor soils, which form a host of agricultural constraints (Maqbool *et al.*, 2001; Sharma and Ortiz, 2000).

Finger millet accounts for 8% of the area and 11% of production of all millets worldwide (Bennetzen *et al.*, 2003), however little has been done to improve its productivity (Fakrudin *et al.*, 2004; Bedis *et al.*, 2006; Upadhyaya *et al.*, 2006). There is limited information on finger millet improvement especially in sub-Saharan Africa particularly in Uganda. As such productivity is still low and communities dependent on the crop are vulnerable (Bezaweletaw *et al.*, 2006). Cultivated finger millet has a narrow genetic base, most probably owing to a bottleneck associated with its domestication (Dida *et al.*, 2008). In a study of East African finger millet landraces based on SSR markers and qualitative traits, the least genetic diversity was observed in Ugandan accessions (Manyasa, 2014). So there is need to expand this genetic base by tapping into the wild relatives of the crop. Crop wild relatives which include the progenitors of crops as well as other species more or less closely related to them, have been undeniably beneficial to modern agriculture, providing plant breeders with a broad pool of potentially useful genetic resources (Hajjar and Hodgkin, 2007). With the disappearance of several landraces from their natural habitats, a coherent and efficient system of germplasm development is needed to address the needs of small scale farmers (Bonham *et al.*, 2010).

Finger millet production is constrained by abiotic factors such as drought, declining soil fertility and biotic stresses such as blast (*Magnaporthe grisea*), leaf blight (*Helminthosporium nodulosum*), wilt, downy mildew (*Sclerospora graminicola*), smut (*Tolyposporium penicillariae*), cercospora leaf spot (*Cercospora penniseti*), and tar spot (*Puccinia substriata*) and lack of improved varieties (Bezaweletaw *et al.*, 2006).

Blast disease caused by *Magnaporthe grisea* (anamorph-*Pyricularia grisea* (Cooke) Sacc.) is the single most destructive disease of finger millet causing substantial yield losses to the crop. It affects the productivity, utilization and trade of finger millet within Eastern and Southern Africa (Mgonja *et al.*, 2007). Infection of the neck and head by the blast pathogen inhibit grain formation, causes shrivelling of grains, and in extreme cases causes yield losses

up to 90% (DFID, 2004). 10-50% losses have been reported in Kenya (Sreenivasaprasad *et al.*, 2007), 10-80% in Uganda (Esele, 1989), 80-90% in endemic areas in India (Nagaraja *et al.*, 2007). Effective management of finger millet Blast can best be achieved through development and use of host-plant resistance. Growing blast resistant varieties is most relevant and cost effective for the resource-poor farmers, who cannot afford other methods of disease control such as using fungicides. For proper use of host-plant resistance to develop resistant varieties, there is need to identify stable resistant sources. As the germplasm is the basic raw material, one has to rely upon a broad genetic base now and in the future, as a result the search for sources of high levels of host-plant resistance continues (Nagaraja *et al.*, 2007).

However due to the self-pollinated biology of the plant, the crop is subject to a limited gene pool including diversity for resistance to blast disease. This limited genetic pool thus compounds finger breeding, calling for the need to expand the gene pool through wide hybridization from cross fertile wild relatives especially those from gene pool 1 (i.e. cross fertile species (Gowda *et al.*, 2008). Wild relatives such as the mini-core accession IE 4709, an *africana* wild type finger millet is highly resistant to blast, has agronomically desirable characters and a rich source of Fe, Ca, Zinc (Zn) and protein (Upadhyaya *et al.* 2010). This type of accession could be involved in hybridization with agronomically superior accessions/breeding lines to combine blast resistance, grain nutrients and farmer and consumer preferred traits. Other sources include hybridization involving members of the genus *Eleusine*. The genus *Eleusine*, consists of the cultivated finger millet *E. corocana* sub spp *corocana* and the wild *E. corocana* sub spp *africana* and *E. kigeziensis* all allotetraploids with genome composition of AABB. Cross compatibility has been observed among these allotetraploid producing fertile hybrids (de Wet, 1991; Dida *et al.*, 2008). In earlier studies populations were derived from crosses between two wild relatives *Eleusine kigeziensis* and *E. Africana* spp and cultivated finger millets such as Adoke, Gulu E, DR 23, Seremi 1, Seremi 3 and Pese 1, NaSAARI 14 (Dramadri, 2013). Understanding the reaction to blast disease in these inter-species crosses is essential for efficient utilization of this resource. Breeding for better varieties is the most viable option to increase productivity in the resource poor farming systems where the crop is largely produced on small land unit.

1.3 Overall objective

To determine the potential of inter-specific crosses between *E. coracana* with *E. africana* and *E. kigeziensis* for improved production of finger millet in Uganda.

1.4 Specific objectives

1. To determine the variability among the interspecific progenies for various agronomic traits.
2. To determine the reaction of the inter-specific progeny to blast disease.

1.5 Hypotheses

1. F2 interspecific progenies have high variability for phenotypic traits that can be exploited to develop new high yielding varieties with farmer preferred traits.
2. The inter-specific progenies display varying levels of resistance to finger millet blast disease.

CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

Finger millet is an important cereal that belongs to the grass Poaceae family, subfamily Chloridoideae (Dida *et al.*, 2008). It has outstanding attributes as a subsistence food crop. The role of genetic variation from traditional landraces and wild species in the improvement of cultivated plants has been well recognized (Thomas and Mathur, 1991; Rao and Bramel, 2000). Morphological characterization has been effectively applied in many crops to generate germplasm references that are genetically diverse and these classical methods of estimating plant diversity are still utilized in crop species more so in finger millet where information on molecular markers for diversity studies is limited (Rao and Hodgkin, 2002; Lapitan *et al.*, 2007). Evaluation of germplasm for response to biotic and abiotic stresses and identification of farmer and market preferred traits are key factors in its effective utilization for improved crop productivity (Manyasa *et al.*, 2008). The main objective of this study was to determine the performance of inter-specific crosses between *E. coracana* with *E. africana* and *E. kigeziensis* in terms of yield and broadened genetic base.

2.2 Finger millet as a crop

2.2.1 Domestication of finger millet

Finger millet (*Eleusine coracana* (L.) Gaertn) is thought to have been domesticated in areas extending from western Uganda to the highlands of Ethiopia (Harlan, 1971; de Wet, 1995). It later spread to Asia reaching India about 3000 years ago and spread to southwest India in the Himalayas, Nepal and along the hills of southern Asia and east China. Finger millet belongs to the family Poaceae and subfamily Chloridoideae with two known sub-species, the cultivated *Eleusine coracana* subsp. *coracana* (L.) Gaertn and the wild type *E. coracana* subsp. *africana* (Kenn.-O'Byrne) (Upadhyaya, 2006). It is a tetraploid ($2n = 4x = 36$; AABB) (Dida *et al.*, 2008). Two diploid species *Eleusine indica*(L.)Gaertn (AA) and either *E. tristacya*(Lam.) Lam or *E. floccifolia*(Forssk.) Spreng (BB) were thought to be the genome donors (Hilu and de Wet, 1976; Hiremath and Salimath, 1992; Gupta *et al.*, 2010). However it is suggested that *E. coracana* descended from *E. africana*, a tetraploid, through mutation since the two species are cross compatible forming fertile hybrids (de Wet, 2006). Although

genomic data has confirmed a close genetic relationship between *E. coracana* and *E. indica*, no evidence of genetic association with *E. Floccifolia* has been found, strengthening the theory of mutation from *E. Africana* (Neves *et al.*, 2005). Based on vegetative, floral and seed morphology, finger millet was classified into three eco-geographical races viz: African highland race found in the East African highlands, lowland race found in the lowlands of Africa and south India and the Indian race found in north east India (Hilu and de Wet, 1976).

2.2.2 Taxonomy and gene pools

2.2.2.1. Finger millet systematics

Based on inflorescence compactness and shape, finger millet germplasm are classified into races and sub races. Species *E. coracana* consists of two subspecies *africana* and *coracana*. Subspecies *africana* consists of two wild races *africana* and *spontanea*; and subspecies *coracana* consists of four cultivated races namely *elongata*, *plana*, *compacta*, and *vulgaris*. Each of these races is further classified into subraces. The race elongate has three sub races; *laxa*, *reclusa* and *sparsa*; race *plana* also consists of three sub races; *seriata*, *confundere* and *grandigluma*; race *compacta* has no subrace, while the race *vulgaris* has four sub races, *liliacea*, *stellata*, *incurvata* and *digitata* (Prasada Rao *et al.*, 1993).

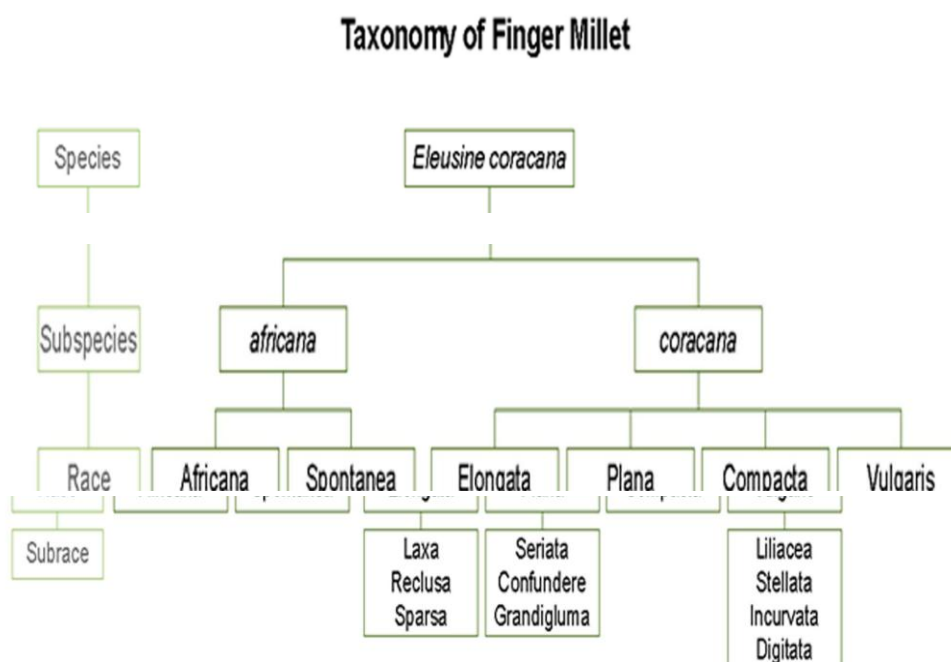


Figure 1: Classification of finger millet (source:

Further classification using inflorescence compactness and shape generates races and sub races of this important grass species. Species *E. coracana* consists of two subspecies *africana* and *coracana*. Subspecies *africana* consists of two wild races *africana* and *spontanea*; and subspecies *coracana* consists of four cultivated races namely *elongata*, *plana*, *compacta*, and *vulgaris*. Each of these races is further classified into subraces. The race *elongata* has three sub races; *laxa*, *reclusa* and *sparsa*; race *plana* also consists of three sub races; *seriata*, *confundere* and *grandigluma*; race *compacta* has no subrace, while the race *vulgaris* has four sub races, *liliacea*, *stellata*, *incurvata* and *digitata* (Prasada Rao *et al.*, 1993).

Sub species *africana* is a tufted annual, with slender and geniculately ascending culms that branch at the lower nodes. Flowering culms are up to 135 cm tall, with leaf blades up to 36 cm long and 10 mm wide. Inflorescence branches are 8- 17cm long and rarely more than 5 mm wide, with the Spikelets arranged in two rows on one side of the rachis. Spikelets have four to nine flowers and are 5-8 mm long. Glumes are shorter than spikelet, lanceolate - oblong in profiles, rarely over 5 mm long and narrowly winged along the keel *E. coracana* is predominately self- fertilized.

Sub species *africana* however crosses occasionally with subsp. *coracana* to produce fully fertile hybrids. Derivatives of such crosses are aggressive colonizers and are grouped under the race *spontanea*. There is another wild relative of finger millet, a tetraploid *E. kigeziensis* ($2n=4x=38$) which is endemic to southwestern Uganda and Rwanda (Phillips, 1972). It is a perennial, has one glume nerve and a dorsiventral caryopsis compression (Liu *et al.*, 2014). Subspecies *coracana* includes all cultivated finger millets. Plants are annual, tufted, and erect or with geniculately ascending culms that are up to 165 cm high and sometimes root from the lower nodes (De Wet *et al.*, 1984a).

2.2.2.2. Cross fertility: The gene pools

On the basis on cross fertility and following the biological concept of species, Eleusine germplasm has been classified into three gene pools; primary, secondary and tertiary. The primary gene pool includes all those taxa that easily cross with cultivated finger millet. This includes all variability in cultivated finger millet and its wild progenitor *E. africana* and weedy form *spontanea*. The secondary gene pool includes those species that also cross easily with cultivated finger millet but do not produce fertile hybrids (Hay *et al.*, 2013). It is now evident that cultivated finger millet is highly variable within its primary centre of origin in Africa and secondary centre in Indian sub-continent. Hybridization resulting in the formation of

allopolyploid species is a frequent mode of plant speciation and evolution (Paun *et al.*, 2009). 24% of crops are estimated to have arisen as a result of hybridization events (Meyer *et al.*, 2012). Finger millet breeding in Africa has been largely limited to pure line selection of landraces. Hybridization based breeding has been conducted in Uganda and India since the late 1960s- early 1970s and included the crossing of Indian and African cultivars in an attempt to widen the germplasm base (Dida *et al.*, 2008). Cultivated finger millet is cross-compatible with the wild sub-specie *africana* and with another allotetraploid, *E. kigeziensis* ($2n=4x=38$) (Hiremath and Salimath, 1991). Interspecific F1 hybrids of *E. intermedia* x *E. indica*, *E. intermedia* x *E. floccifolia* and *E. tristachya* x *E. intermedia* were successfully produced and studied for morphological and cytological details (Devarumath *et al.*, 2005).

Both wild finger millet (*Eleusine coracana* subspecies *africana*) and the cultivated finger millet (*Eleusine coracana* subspecies *coracana*) are important from the point of view of germplasm collection and conservation and form the primary gene pool. Natural hybridization between wild and cultivated finger millets has resulted in hybrid derivatives and in companion weeds of the crop in Africa. This no doubt has led to the generation of new diversity of intermediate forms. The weedy and wild forms are restricted to the closely related annual species (Prasada Rao *et.al*, 1993). The diploid wild species *E. indica*, *E. floccifolia* and *E. tristachya* form the secondary genepool and the tertiary genepool comprises species *E. intermedia*, *E. gaegeri*, *E. kigeziensis*, *E. multiflora* and *E. semisterlis* (*E. compressa*).

2.3 Diversity in finger millet

Whereas cultivated finger millet has a narrow genetic base (Dida *et al.*, 2007), a relatively high phenotypic variation has been reported. Phenotypic diversity was recorded in 2000 accessions from East Africa and India and effectively used to group the material into six races namely *africana*, *spontenea*-wild types, *elongate*, *plana*, *compacta* and *vulgaria* (Reddy *et al.*, 2009). High variability in most finger millet characteristics in all the four races including number of tillers per plant, maturity period, plant height, panicle length, grains per head, pigmentation and grain yield was reported (Upadhyaya *et al.*, 2007). In Ethiopia, 66 accessions were characterized and high variability among the accessions for all agronomic traits was reported (Bezaweleaw *et al.*, 2006).

Recent studies have reported a high and positive direct effect of productive tillers per plant and thousand grain weight, finger length, finger number, ear weight, number of grain per spikelet and culm diameter on grain yield (Lule *et al.*, 2012); high and moderate phenotypic coefficients of variability and genotypic coefficients of variability for number of productive tillers per plant and longest finger length, seed protein content, harvest index respectively, indicating large extent of genetic variability for these traits in the material. High heritability along with high genetic advance observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, seed protein content, harvest index and single plant grain yield, indicated involvement of additive gene action for these traits and phenotypic selection based on these traits in the segregating generations would likely to be more effective. Also they found that grain yield had positive correlation with number of productive tillers, finger length and harvest index (Priyadharshini *et al.*, 2011). Similar results have been reported on 230 accessions, with very high coefficient of variation at phenotypic and genotypic levels for productive tillers per plant and moderate for the traits viz., days to 50 % flowering, plant height, finger numbers per ear, finger length and grain yield per plant. From the results, high heritability coupled with high genetic advance observed in days to 50 per cent flowering, plant height, productive tillers per plant, finger numbers per ear, finger length and seed yield per plant, which indicates the predominance of additive gene effects, in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects (John, 2006; Ganapathy *et al.*, 2011). Other workers who have reported phenotypic variability of finger millet Mahto *et al.* 2000; Anatharaju, 2001; and Yazhini, 2006). The variability reported indicates the potential for finger millet improvement through selection. Improvement in any crop usually involves exploiting the genetic variability in specific traits. Concurrent improvement of such traits depends on the nature and degree of association between these traits.

2.4 Blast disease as a constraint to finger millet production

2.4.1 Importance of Finger millet blast disease

Finger millet blast is caused by an ascomycete fungus *Magnaporthe grisea* (Hebert) Barr. (anamorph: *Pyricularia grisea* (Cooke) Sacc. The disease is very prominent and affects the productivity, utilization and trade of finger millet within Eastern and Southern Africa (Mgonja *et al.*, 2007). It affects finger millet at all growth stages, from seedling stage

(causing lesions and premature drying of young leaves) to affecting the panicle causing neck and or finger blast (Takan *et al.*, 2002). The latter is the most destructive phase of the disease and can prevent grain set and cause seeds to shrivel (Pande *et al.* 1995). The disease was first recorded in Uganda in 1933 (Emechebe, 1975), however there is still limited knowledge on its control. The average loss due to blast in India has been reported to be around 28-36%, and in certain areas yield losses could be as high as 80-90% (Nagaraja *et al.*, 2007; Rao 1990). In east Africa losses of up to 80% have been reported (Holt 2000; Obilana, 2002; Takan *et al.*, 2002; Takan *et al.*, 2004).

2.4.2 Finger millet blast disease epidemiology and symptomology

Magnaporthe grisea is spread by air and seed with seed transmission being significant through seed movement (Kato *et al.*, 2000; Takan *et al.*, 2004). The pathogen reproduces both sexually and asexually. The sexual stage is rare and only the asexual stage has been found in the USA (Uddin, 2000). The pathogen is identified based on its morphological growth pattern and spore shape. The fungus produces greyish mycelium with conidiophores arising singly or in groups on the affected part. Conidiophores are slender, straight, greyish or dark grey, smooth bearing clusters of conidia, which are typically obpyriform or obclavate, hyaline and 2-septate.

The disease is polycyclic producing of millions of conidia (spores) within a short period (1 or 2 days) when conditions are conducive (Uddin, 2000; Ruiz, 2003). Conidia are produced and released during periods of high relative humidity (>89 % RH), and optimal temperature of 25-28°C and germinate within a few hours (Ruiz, 2003). Subsequently, infection takes place by development of an appressorium at temperatures of 16-25°C, which generates high turgor pressure and physical force, allowing the fungus to break the host cuticle and invade plant tissue within 10h (Talbot, 2003). The fungus appears to overwinter as mycelia in the infected living leaves or dead plant debris in the soil (Uddin, 2000). High temperature, high relative humidity and leaf wetness are critical environmental factors that influence disease development (Uddin, 2000; Ruiz, 2003).

The symptoms of finger millet blast disease include diamond shaped, greyish white lesions bordered by a brown margin that develop on leaves and black lesions on the inflorescence (Holt, 2000). Seedlings may die under epidemic conditions, and empty fingers and broken

pedicels may result in mature plants. The same pathogen can affect three sites of the plant i.e. leaf, neck and head causing leaf, neck and head blast respectively. Neck and finger blast reactions that are more destructive than leaf blast were considered important parameters for blast resistance (Takan, 2004; Nagaraja *et al.*, 2007; Nagaraja *et al.*, 2010).

2.5 Mechanism of resistance to blast disease

The mechanism of resistance to blast has been extensively studied using rice as the model plant. Monogenic resistance to rice blast is conditioned by the classical gene-for-gene interaction, where the host possesses a single dominant gene conditioning resistance against a race of the pathogen carrying a corresponding dominant avirulence gene (Hammond and Jones, 1997). Avirulence genes encode protein products that are recognized by plants (a pathogen-associated molecular pattern) possessing the appropriate resistance gene product. A study showed that resistance of a genotype to rice blast was based on epidermal and mesophyll hypersensitive reaction (HR). No papillae were formed and fungus spread was arrested in the epidermis by epidermal and mesophyll HR in the completely resistant accession. This may as well be the case in finger millet since the pathogens involved are quite similar (Bvindi, 2010).

Currently, two rice blast resistance genes, Pi-ta and Pib, have been cloned and characterized and a third locus, Pi-CO39 (t), is close to being identified (Bryan *et al.*, 2000; Chauhan *et al.*, 2002). The protein is therefore typical of the nucleotide-binding site leucine-rich repeat class of resistance gene (Hammond and Jones, 1997), although with some unusual characteristics including the presence of a duplication within the P-loop in the N terminus of the protein and some clustering of cysteine residues in one of the leucine-repeat sequences (Song and Goodman, 2007). The Pib gene is expressed in response to challenge with both compatible and incompatible strains of *M. grisea* and in response to certain environmental stresses (Wang *et al.*, 1999).

Studies on the mechanism of resistance to leaf, neck, and finger blast show that smaller leaf area, narrow leaf angle, fewer stomata, dwarf plant with better conversion efficiency of photosynthates from source to sink (harvest index), thick epidermis and cuticle on the leaf and neck, fewer chlorenchymatous strands, higher total phenols, and low quantities of total and reducing sugars contributed toward blast resistance in finger millet (Jain and Yadava, 2003).

In other studies resistant genotypes of finger millet have thicker epidermis and cuticle of leaves compared to highly susceptible cultivars (Kumar *et al.*, 2006). However, the highly resistant cultivars have significantly less stomata frequencies per mm and size when compared with highly susceptible cultivars. Therefore leaf area, leaf angle, number of stomata, plant height and harvest index contributed most towards blast resistance in finger millet (Jain *et al.*, 2002).

2.6 Sources of resistance to blast

Attempts have been made in Uganda to screen and select finger millet for resistance against leaf, neck and head blast (Bua and Adipala, 1995; Obilana, 2002). Some varieties showed consistency in resistance against leaf, neck and head blast due to different mechanisms which could be used in the formulation of selection indices in the selection of resistant genotypes for resistance breeding programmes against blast in finger millet (Jain and Yadava, 2003).

In an evaluation of 80 accessions, 58 of the 80 accessions were resistant to leaf blast and these resistant accessions represented one wild (*africana*) and four cultivated races (*vulgaris*, *plana*, *elongate* and *compacta*) of finger millet that originated from 13 countries in Asia and Africa and exhibited considerable diversity for agronomic traits, such as maturity period, plant height and panicle type (Babu *et al.*, 2012).

Surveys in western Kenya and Uganda indicate that dark seeded finger millet varieties with compact heads are more resistant to blast disease than light colour seeded and open headed varieties (Takan *et al.*, 2004). Sources of blast resistance have been reported in finger millet, and efforts have been made to incorporate resistance into improved cultivars and elite breeding lines (Seetharam and Halaswamy, 2003; Nagaraja *et al.*, 2008; Nagaraja and Mantur, 2007). The foregoing indicates variability for blast resistance, which can be incorporated in breeding Programmes, exists in finger millet germplasm.

2.7 Breeding for resistance to blast disease

Breeding for resistance to diseases is dependent on availability of sources of resistance to the disease. These sources could be cultivated genotypes or wild relatives of the crop. Blast resistance is often evaluated in the field in hot spot area under natural infection (Mgonja *et al.*, 2007; Nagaraja, 2010). However this sometimes provides opportunity for disease escapes leading to spurious resistance being identified (Thakur *et al.*, 2009). To avoid disease escape

artificial inoculation either in the field or in the greenhouse is carried out. Resistance is often assessed at the seedling stage, which did not correlate well with neck and finger infection. Hence, neck and finger blast are more destructive than leaf blast were considered important parameters for blast resistance (Nagaraja *et al.*, 2007). Breeding for blast resistant finger millet in Uganda was first reported in 1958 when a finger millet line, Mozambique 359 was used as a source of resistance (Rachie and Peters, 1977). Subsequent breeding activities have seen several blast resistant lines developed for example Gulu E, Seremi 1, Seremi 2, Pese 1, SX 8, and SEC 915 and subsequently released in East Africa (Lenné *et al.*, 2007; ICRISAT, 2013).

2.8 Sectional conclusion

Assessment and utilization of genetic variability is essential in plant breeding. Understanding the pattern of diversity and the genetic structure of gene pools is critical for effective management and use of germplasm resources. Progress in plant breeding depends on identification of new sources of genetic variation for beneficial traits, in such a way that a combination of alleles produces progenies with superior performance.

The identification of blast resistance through germplasm screening in Uganda is an indication of the existing potential of the region's finger millet germplasm which needs to be exploited for enhanced finger millet productivity. More blast resistant sources need to be identified to counter chances of resistance breakdown in the few improved resistant cultivars due to blast pathogen variability. The focus of this study is to identify such broad sources of genetic variation and identify their potential to be exploited for increased finger millet productivity.

CHAPTER THREE

MATERIALS AND METHODS

3.1 Study one: Determination of phenotypic variability among interspecific progenies of *Eleusine* species for various agronomic traits

3.1.1 Introduction

Assessment of variability present in any crop species is the essential pre-requisite for formulating an effective breeding programme. The existing variability can be used further to enhance the yield level of the cultivars following appropriate breeding strategies (Priyadharshini *et al.*, 2011). Understanding variability should also be coupled with knowledge of the associations between traits that contribute to finger millet yield through well-designed breeding. Knowledge of the diversity in the germplasm will also help in identification of diverse potential parents for hybridization to generate new cultivars with desired traits (Manyasa, 2013). The availability of diverse genetic resources is a prerequisite for genetic improvement of any crop including finger millet. Besides the availability of genetic resources, their characterization is essential for the effective utilization in crop improvement programs (Upadhyaya *et al.*, 2006). The purpose of this study was to identify new sources of genetic improvement for finger millet, this study was done to identify trait specific accessions for various phenotypic traits of agronomic importance in field conditions.

3.1.2 Description of study sites

The experiment was conducted at Makerere University Agricultural Research Institute MUARIK (MUARIK), located at 0°28'N and 32°37'E; 1200 m above sea level. The Station, receives an average rainfall of 1234 mm per year, has sandy clayey-loam soils rich in potash, low in Nitrogen and phosphorus, soil PH ranges between 5.5-6.0), and National Semi Arid and Resources Research Institute (NaSAARI) in NaSAARI (1°39'N and 33°27'E; 1038 m above sea level; average rainfall 1427mm per year; average temp 24°C).

3.1. 3 Study materials

The materials that were used for this study were F3 and F4 families from three previously generated interspecific crosses of allotetraploids wild types (*E. kigeziensis* and *E. africana*) and locally adapted susceptible and resistant finger millet cultivars (*E. corocana*);

32 families of *E. kigeziensis* X Pese 1, 2 families *E. africana* X Seremi 1 and 14 families of *E. africana* X Seremi 3. The choice of materials was guided by their useful traits such primary tillering, finger width, number of fingers, days to maturity and early flowering.

Table 1: Morphological characteristics of parents

Accession name	Altitude (masl)	DF	PHT	PG	P T	PL	LFL	LFW	NF
<i>E.kigeziensis</i>	1844m	48	128	G	12	15	13	0.5	12
<i>E.africana</i>	1263m	53	110	P	15	12	10	0.2	8
Pese 1	1038m	65	100	G	5	9	6	2.8	7
Seremi 1	1038	69	98	P	4	10	7	3.1	7
Seremi 3	1038	70	96	P	5	8	7	2.7	6

DF- days to 50% flowering(days), PHT- Plant height(cm), PG - Plant pigment PT- Productive tillers, PL- Panicle length(cm), LFL- longest finger length(cm), LFW – longest finger width(cm) NF- Finger numbers ES – Ear shape

3.1.4 Experimental design

48 lines at F3 was planted at MUARIK in Alpha lattice design, in 3 replications during the 2013 first rain season (March-June) for advancing F3 to F4 and then both F3 and F4 were planted at MUARIK and NaSAARI during the second rain season that runs from August to December in a side by side trial, in Alpha lattice design with 3 replications.

3.1.5 Field management

Each accession was grown in 2 rows of 2 m length with row-to-row spacing of 50cm and plant-to plant spacing within the row of 10cm with 3 replications in Alpha lattice. Plants were thinned to 10 plants /row at 15 days after planting and first weeding was done 2 weeks after emergence and second weeding was done 3 weeks later. The trial was planted in two seasons, March- June 2013 short rains and September- December 2013 long rain season. Sowing was done by hand drilling the seeds in furrows and three weeks after emergence, the plants were thinned to leave one plant per hill.

3.1.6 Data collection

The days to 50% flowering and physiological maturity were recorded on each plot when 50% of plants in the plot attained the respective stages. Physiological maturity was marked with prominent hard grain that did not crush into “milk” when rolled between thumb and forefinger. At the dough stage, plant height, number of fingers, finger length and width, flag length and width, finger numbers, primary and secondary tillers traits were recorded. Plant height (cm) was measured on five representative plants in a plot (ground level to tip of plant)

at physiological maturity and the average recorded. Number of fingers per ear for five plants was averaged and recorded; Finger length (cm) was recorded by measuring the length of the longest finger on the head for five plants and the average obtained. Finger width across the centre of the longest finger on the five plants was also averaged and recorded. Flag leaf length was measured on five representative plants (from base to the tip of the flag leaf) and the width (cm) across the centre of the leaf too was measured. Number of productive/ primary tillers (basal tillers that bear mature ears) and secondary tillers (culm branches) were counted and recorded averaged across five plants. Days to 50% maturity were also recorded when 50% of the heads were physiologically mature.

3.1.7 Data Analysis

The data was subjected to Analysis of variance (ANOVA) using the Residual Maximum Likelihood (REML) as implemented in GENSTAT statistical package (edition 14.0; Rothamsted Experiment Station, Harpenden, Herts AL52JQ, UK). The anova was fitted to a linear mathematical model for the balanced lattice i.e.

$$Y_{ijk} = \mu + b_i + r_j + g_k + (b/r)_{ij} + (g/b)_{ik} + e_{ijk} \dots\dots\dots(1)$$

Where Y_{ijk} = observed effects for i^{th} blocks, j^{th} replication and k^{th} genotypes μ = grand means for the experiment, b_i = effect of the i^{th} blocks r_j = effect of j^{th} replications g_k = effect of the k^{th} genotype $(b/r)_{ij}$ = effect of the i^{th} blocks within the j^{th} replication $(g/b)_{ik}$ = effect of the k^{th} genotype within i^{th} blocks e_{ijk} = lattice effective error or random error of the experiment.

Comparison between the two races of the interspecific crosses, *africana* (group A) and *kigeziensis* (group K) was done by subjecting their means of the quantitative traits to t-test to determine significance among groups; where the t-calculated value was compared with the t-critical value based on 0.05 probability level.

3.2 Study two: Reaction of the inter-specific progeny to finger millet blast disease

3.2.1 Introduction

Blast disease caused by *Magnaporthe grisea* (anamorph-*Pyricularia grisea*(Cooke) Sacc.) is a major problem and the most destructive disease of finger millet causing substantial yield losses to the crop. It has subsequently been reported to occur in all finger millet growing areas of East Africa (Obilana and Manyasa, 2002; Wanyera, 2007; Kisandu *et al.*, 2007). It is the major biotic constraint in finger millet productivity in the three East African countries. Most cultivated landraces are susceptible with grain yield losses of up to 60% (Pande, 1992; Obilana and Manyasa, 2002). Most of the cultivars grown by farmers are un-improved, with low grain yields and are susceptible to blast disease. Blast resistance is often evaluated in the field in hot spot areas under natural infection (Nagaraja, 2010). However this sometimes provides opportunity for escapes leading to spurious resistance being identified (Thakur *et al.*, 2009). To avoid disease escape artificial inoculation either in the field or in the greenhouse is carried out. The objective of this study was to identify interspecific progeny lines that are resistant to the finger millet blast disease.

3.2.2 Description of study site

This screen house study was carried out at MUARIK (section 3.1.2). This location was chosen because there are facilities for screen house study and is conveniently located within the study vicinity. A humidity chamber was used in this experiment because the disease development requires specific temperature and humidity levels. This experiment was established following the Alpha lattice design; five seedlings of each accession were tested in four replications (5 seedlings/ pot)

3.2.3 Raising the plants

The seedlings were raised in 15-cm diameter plastic pots (5seedlings/pot) filled with sterilized soil-sand-farm yard manure mix (2:1:1 by volume) in a greenhouse bay maintained at $28\pm 2^{\circ}\text{C}$. After 2 weeks, the seedlings were thinned to leave 5 seedlings per pot. At 30 days after planting, these were transferred into the humidity chamber set at a temperature of 21°C and humidity of $\geq 90\%$ for 24 hours before inoculation. The humidity was maintained high by misting three times a day and placing water troughs around the room.

3.2.4 Culture preparation and inoculation

Culture of *M. grisea* was obtained from diseased samples collected from finger millet fields at NaSSARI. The pathogen was purified through single-spore isolation and maintained on oatmeal agar (OMA) medium for further use. Mass multiplication of fungal spores for inoculation was achieved by growing the fungus on oatmeal agar (ref for manufacturer) in Petri dishes. The conidial concentration in the suspension was adjusted to 1×10^5 spores ml^{-1} for the inoculation, this was done to increase the disease pressure and intensity. Tween 20 (0.02%) was added to the suspension just before the inoculation to increase the adhesion of the spores on the leaves (Jia *et al.*, 2003).

The 31 day-old seedlings were inoculated by spray inoculation using an atomizer to apply the conidial suspension on the leaves of finger millet plants for the leaf blast screening. The conidial inoculum was applied just until the beginning of runoff from the foliage. Inoculated plants were placed in a moist chamber at $23 \pm 1^\circ\text{C}$. Forty eight hours after inoculation whilst still in the moist chamber, plastic pots each containing 10 inoculated finger millet plants was transferred to a greenhouse and exposed to high humidity ($>90\%$ RH) with additional misting for 10 days to allow for disease development. For the neck and head blast, re-inoculation of the plants was done at panicle initiation/emergence. The inoculated plants were then covered with polyethene bags for 24 hours to increase the relative humidity and moisture around the heads.

3.3 Data collection

The three phases of the disease (leaf, neck and finger) were separately scored (visual subjective scoring).

3.3.1 Leaf blast severity assessment

Blast severity was recorded at 7 days, 14 days and 21 days after inoculation using a 1-5 progressive scale (Takan *et al.*, 2002) a total of 4 times at weekly intervals. Disease rating scales were based on the per cent leaf area covered with blast lesions observed 7, 14 and 21 days after inoculation under greenhouse conditions. In scoring for foliar/leaf blast (LB) disease incidence, the scale used by (Takan *et al.*, 2002) was adopted where:

Table 2: Disease severity ratings for foliar/leaf Blast

Severity	Percent Severity	Status
1.0-1.4	0-5%	HR
1.5-1.9	6-10%	R
2.0-2.4	11-20%	MR
2.5-2.9	21-30%	S
3.0-3.5	>31	HS

HR=highly resistant; S = Susceptible; HS= highly susceptible; R= Resistant; MR= moderately resistant.

3.3.2 Neck blast severity assessment

Based on the relative lesion size on the neck a 1 to 5 progressive ratings scale was used that was developed by (Babu *et al.*, 2012) where, 1 = no lesions to pin head size of lesions on the neck region, 2 = 0.1 to 2.0 cm size of typical blast lesion on the neck region, 3 = 2.1 to 4.0 cm, 4 = 4.1 to 6.0cm, and 5 = >6.0 cm size of typical blast lesion on the neck region. The 1-5 rating scale was classified into four infection types (*i.e.* 1.0-2.0 = resistant; 2.1-3.0 = moderately resistant; 3.1-4.0 = susceptible and 4.1-5.0 =highly susceptible). Data was recorded in the greenhouse at physiological maturity on 5 randomly selected individual plants of each accession, 4 times at weekly intervals

3.3.3 Finger blast severity assessment

The finger blast severity estimate was recorded as visual percentage of blasted florets across all tillers of a plant on the same 5 randomly selected plants that were earlier rated for the neck blast severity in each row 4 times at weekly intervals (Babu *et al.*, 2012).

3.4 Data analysis

Data on leaf, neck and finger blast severity recorded from each pot in the screen house experiments. Statistical analysis of variance was performed following the Residual Maximum Likelihood (REML) on GENSTAT statistical package (edition 14.0; Rothamsted Experiment Station, Harpenden, Herts AL52JQ, UK). Analysis of phenotypic and genotypic variances and coefficient of variation, broad sense heritability and genetic advance were calculated as described (Singh and Chaundhary, 1977; Allard, 1960);

Genotypic variance (σ_g^2) = (MS_g - MS_{lee})/r. Where;

MS_g = mean square of genotypes (entries)

MS_{lee} = Mean square of lattice effective error

R = number of replications

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_{lee}^2$, ... (1)

where σ_g^2 = Genotypic variance, σ_{lee}^2 = Lattice effective error variance

Phenotypic coefficient of variance (PCV) = $(\sqrt{\sigma_p^2} / \bar{x}) * 100$... (2)

Where $\bar{x}$ = population mean for the trait considered.

Genotypic coefficient of variance (GCV) = $(\sqrt{\sigma_g^2} / \bar{x}) * 100$ (3)

Broad sense heritability (H^2) = $(\sigma_p^2 / \sigma_g^2) * 100$ (4)

Expected genetic advance under selection assuming a selection intensity of 5% was computed as follows;

$GA = K * O_p * H^2$ (5)

Where;

GA = expected genetic advance

K = Selection differential (2.056) at 5% selection intensity

O_p = phenotypic standard deviation

Genetic advance as percent of mean ($GA\%$) = $(GA / \bar{x}) * 100$(6)

CHAPTER FOUR

RESULTS

4.1 The phenotypic variability for quantitative traits among the wild finger millet progenies

The REML analysis of data for individual environments for F3 progeny showed significant differences for 6 traits out of 10 in MUARIK and 4 out of 10 in NaSAARI. However, the combined analysis showed significant genotypic difference for only one trait (Finger length) (Table 3). Significant variance in most of the traits in individual and combined analysis showed that the genotypes from the wild crosses were diverse and had sufficient scope for selection and utilization in finger millet improvement. Environments were significantly different for all the traits except 50% days to maturity, flag leaf length and number of fingers per inflorescence for the F3 accessions (Table 3). The variances due to genotype x environment were significant for all the traits (Table 3).

Analysis of data for individual environments for F4 progeny showed significant differences for 6 traits out of 10 in MUARIK and 8 traits out of 10 in NaSAARI. However, the combined analysis showed no significant genotypic difference for any trait in both environments (Table 5 and 6). Environments were significant for all the traits except plant height, number of fingers and primary tillers for the F4 accessions (Table 4).

The variances due to genotype x environment were highly significant for all the traits (Table 3 and 4). There was high significant interaction ($P \leq 0.01$ and $P \leq 0.001$) between genotypes and environment for all the traits (Tables 3 and 4) for both F3 progeny and F4 progeny. For the F3 progeny, highest mean squares were recorded in MUARIK for days to 50% flowering, days to 50% maturity, length of longest finger, plant height, number of fingers per main ear and secondary tiller number, while highest mean squares were recorded for traits flag leaf length, longest finger length and width in NaSAARI. F4 progeny showed highest mean squares in MUARIK for days to 50% flowering, days to 50% maturity, plant height, primary and secondary tillers. In NaSAARI, highest mean square was recorded for finger length and width, number of fingers per main ear and flag leaf length.

Table 3: Mean squares for the traits measured for F3 finger millet progeny evaluated at two locations during 2013 second rainy season.

Source of variation	df	Mean squares									
		DH	DM	FL (cm)	FW(cm)	FLL (cm)	FLW (cm)	PH (cm)	FN	PTN	STN
Location	1	22000***	302	282***	5.1***	2	16.7***	4588**	2.2	76.6+	94.7**
Genotype	48	38	20	0.99**	0.02	13	0.03	40	0.5	2.1	0.86
G X E	48	41**	38**	0.51***	0.03**	16***	0.03***	51**	1.5**	1.6**	0.68**
RESIDUAL	159	18	27	0.41	0.03	13	0.02	56	0.9	1.6	0.4
LEE		22	21	0.26	0.02	8	0.01	28	0.8	0.9	0.4
Mean		72.8	98.4	5.8	1.1	31.5	1.0	67.9	5.6	5.0	2.6
SEM		2.71	2.65	0.29	0.08	1.63	0.06	3.06	0.52	0.55	0.37
CV (%)		6.4	4.7	8.8	12.9	9.0	10	7.8	16.0	18.9	24.3

DM=Days to 50% maturity, DH=Days to 50% flowering , NF= Number of fingers / main ear, FL=Length of longest finger , FW=Width of longest finger ,FLL=Flag leaf length ,FLW=Flag leaf width , PIHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers.

Table 4: Mean squares for the traits measured for F4 finger millet progeny evaluated at two locations during 2013 second rainy season.

SOV	DF	TRAITS MS									
		DH	DM	FL(cm)	FW(cm)	FLL (cm)	FLW (cm)	PH	FN	PTN	STN
Environment	1	24914***	6616*	153***	0.50***	192*	17.3***	883	0.60	33	163***
Genotype	48	25	28	0.7	0.005	1258	0.009	540	5.40	0.5	0.0018
G X E	48	26**	57**	1.2**	0.009***	15**	0.01**	64**	0.67**	3.6***	0.5**
Residual	156	15	39	0.3	0.006	11	0.01	50	0.62	1.336	0.5
LEE		15	35	0.7	0.004	8	0.01	36	0.36	1.838	0.29
Mean		75	102	5.8	1.0	31.0	1.0	66.7	6.0	5.0	2.0
SEM		2.24	3.42	0.48	0.04	1.64	0.06	3.46	0.35	0.78	0.31
CV (%)		5.2	5.8	14.4	6.3	9.1	10	9.0	10	27.1	27

DM=Days to 50% maturity, DH=Days to 50% flowering, NF= Number of fingers / main ear, FL=Length of longest finger, FW=Width of longest finger, FLL=Flag leaf length, FLW=Flag leaf width, PHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers

Table 5: Mean squares of Genotype and Genotype X Environment estimated in the F3 interspecific crosses across two environments & pooled.

F3	MUARIK	NaSAARI	Pooled	
TRAIT	MS_g	MS_g	MS_g	MS_{g X e}
Earliness				
Days to 50% flowering	137***	6.2	38	41**
Days to 50% maturity	79	6.1	20	38**
Growth parameters				
Flag Leaf Length (cm)	19**	25.6*	13	16***
Flag Leaf Width (cm)	0.06**	0.029***	0.03	0.03***
Plant Height (cm)	79	57	40	51**
Yield parameters				
Finger length (cm)	1.19**	1.4***	0.99**	0.51***
Finger width (cm)	0.02	0.06*	0.02	0.03**
Finger Numbers	1.3	0.8	0.5	1.5**
Primary Tiller Number	3**	3	2.1	1.6**
Secondary Tiller Number	2.1***	0.4	0.86	0.68**

Table 6: Mean squares of Genotype and Genotype X Environment estimated in the F4 interspecific crosses across two environments & pooled.

	MUARIK	NaSAARI	Pooled	
TRAIT	MS_g	MS_g	MS_g	MS_{g X e}
Earliness				
Days to 50% flowering	73.97 ***	5 **	25	26**
Days to 50% maturity	115+	6	28	57**
Growth parameters				
Flag Leaf Length (cm)	9.69+	29 **	1258	15**
Flag Leaf Width (cm)	0.02	0.015 ***	0.009	0.01**
Plant Height (cm)	116 *	40	540	64**
Yield parameters				
Finger length (cm)	0.91***	2***	0.07	1.2**
Finger width (cm)	0.008	0.01*	0.005	0.009***
Finger Numbers	0.68	0.8+	5.40	0.6718**
Primary Tiller Number	7.4 ***	1.5 *	0.5	3.643***
Secondary Tiller Number	0.9	0.5 **	0.00179	0.5236**

4.1.1 Mean performance of interspecific finger millet progeny in different environments

Mean and range are simple and important measures of variability (Singh, 1983). Performance of the progeny in different environment was assessed by comparing the values of mean and range for particular traits. F3 progeny in MUARIK had highest range for six traits (Days to 50% flowering, Days to 50% maturity, flag leaf width, plant height, number of fingers, primary tiller number and secondary tiller number) while in NaSAARI Progeny showed highest range for three trait (finger width, flag leaf length and primary tiller number). Progeny had the same range difference for one trait (finger length) in both environments. F3 progeny showed greater mean in MUARIK for four traits (Days to 50% flowering, Days to 50% maturity, Flag Leaf Width, Secondary Tiller Number). Progeny had greater means for three traits in NaSAARI (Finger Length, Plant Height and Primary Tiller Number); the mean for three traits (Finger Width, Flag Leaf Length and Number of fingers) was approximately similar in both environments (Table 7).

Table 7: Range and Mean of Ten quantitative traits of F3 Progeny

TRAIT	MUARIK		NASAARI		POOLED	
	RANGE	MEAN	RANGE	MEAN	RANGE	MEAN
Days to 50% flowering	72-116	82.0	61-68	64.0	68-92	72.8
Days to 50% maturity	89-112	99.0	95-100	97.5	93-104	98.4
Finger Length (cm)	3.8-6.1	4.8	5.9-8.2	6.8	4.9-6.9	5.8
Finger Width(cm)	0.8-1.15	1.0	0.9-1.5	1.2	0.95-1.26	1.1
Flag Leaf Length (cm)	24-36	31.5	25.2-39.8	31.6	26.5-35.8	31.5
Flag Leaf Width (cm)	0.91-1.52	1.2	0.5-0.9	0.7	0.8-1.2	1.0
Plant Height (cm)	52.8-74.5	63.9	63-79.5	71.8	58-74	67.9
Finger Numbers	3.9-7.4	5.7	4.2-6.7	5.5	4.8-6.3	5.6
Primary Tiller Number	3-6.8	4.5	3.9-8.7	5.5	3.8-7.3	5.0
Secondary Tiller Number	1.8-5.6	3.2	1.5-2.9	2.1	1.9-4	2.6

F4 progeny in MUARIK had highest range for six traits (Days to 50% flowering, Days to 50% maturity, finger length, plant height, secondary tiller number and primary tiller number) while in NaSAARI Progeny showed maximum range for one trait only (flag leaf length). Progeny had the same range difference for three traits (finger width, flag leaf width and number of fingers) in both environments (Table 8).

Progeny at F4 showed greater mean in MUARIK for four traits (Days to 50% flowering, Days to 50% maturity, Flag Leaf Width, Secondary Tiller Number). Progeny showed greater mean for three traits in NaSAARI (Finger Length, Plant Height and Primary Tiller Number). The mean for three traits (Finger Width, Flag Leaf Length and Number of fingers) was approximately similar in both environments (Table 8).

Table 8: Range and Mean of Ten quantitative traits of F4 Progeny

TRAIT	MUARIK		NASAARI		POOLED	
	RANGE	MEAN	RANGE	MEAN	RANGE	MEAN
Days to 50% flowering	75-99	84.2	63-68	66	70-83	75
Days to 50% maturity	97-133	107	94-100	97	97-114	102
Finger Length (mm)	26-63	51	50-80	70	40-70	58
Finger Width(mm)	9-12	11	8-11	10	9-11	10
Flag Leaf Length (mm)	280-360	320	250-360	300	280-360	310
Flag Leaf Width (mm)	11-14	13	6-9	8	9-11	10
Plant Height (cm)	48-78	65	62-78	69	58-76	66.7
Finger Numbers	5-7.0	6	5-7.0	6	5.0-7.0	6
Primary Tiller Number	3-9.0	4	4-7.0	5	3.0-7.0	5
Secondary Tiller Number	2-5.0	3	0-3	1	1.0-3.0	2

4.1.2 Parameters for earliness

Locations were significantly different ($P \leq 0.001$) for days to 50% flowering of F3 progeny and F4 progeny (Tables 3 and 4). The overall means for the F3 progeny (Table 7) were 82 and 64 days for MUARIK and NaSAARI respectively and for F4 progeny (Table 8) were 84 and 66 days for MUARIK and NaSAARI respectively. However, the combined analysis revealed a mean of 73 days for F3 progeny and 75 days for F4 progeny (Tables 7 and 8) indicating that generally F3 progeny and F4 progeny took almost similar time to flower. The highest range for 50% days to flowering of F3 progeny and F4 progeny was in MUARIK for both generations (72-116 and 75-99 respectively) (Table 7 and 8).

No significant differences in among F3 accessions across both locations among F4 accessions for days to 50% harvest maturity were found. The overall means for F3 progeny (Table 7) were 99 days and 98 days in MUARIK and NaSAARI respectively and for F4 progeny (Table 8) were 107 days and 97 days in MUARIK and NaSAARI respectively. The F3 progeny took similar periods of time to mature in the two environments while F4 progeny

matured earlier in NaSAARI than they did in MUARIK. The highest range was observed to be in MUARIK at both F3 and F4 (89-112 and 97-133 respectively). F3 progeny and F4 progeny had similar range in NaSAARI (95-100 and 94-100 respectively). The combined analysis showed a mean of 98 days and 102 days and a range of 93-104 and 97-114 for F3 progeny and F4 progeny respectively, indicating that F3 progeny matured earlier than F4 progeny. Among the F4 progeny 12 accessions were found to mature in less than 100 days, Entry 44 was the earliest with 97 days but it was not different from progeny 40, 4, 32, 30, 25, 26, 24, 13, 46, 37 and 18.

4.1.3 Performance for growth parameters

Plants grown in NaSAARI were taller (72cm) than those at MUARIK (64cm) among the F3 accessions (Table 7). Among the F4 progeny there was slight difference in the means, 65cm and 69 cm in MUARIK and NaSAARI respectively (Table 8). In the combined analysis, the means of the F3 progeny was 67 cm and F4 progeny was 68 cm, showing no difference for this trait among the generations. The range for the F3 progeny was 53-75cm in MUARIK and 63- 80cm in NaSAARI while the F4 progeny had a range of 48-78cm (highest) in MUARIK and 62-78cm in NaSAARI, in the combined analysis the range of F3 progeny (58-74cm) was similar to that of F4 progeny (58-76cm) (Table 7 and 8).

Mean flag leaf length was similar in both environments for both F3 and F4 progeny (320mm in both environments and 320 mm and 300 mm in MUARIK and NaSAARI) respectively. The overall means for F3 progeny and F4 progeny were 320 mm and 310mm respectively. Among the F3 progeny a wider range was observed in NaSAARI (250-400 mm) compared to MUARIK (240-360 mm), similarly in F4 progeny a wider range was observed in NaSAARI (250-360 mm) compared to MUARIK (280-360 mm). Mean flag leaf width among the F3 progeny was higher in MUARIK (12 mm) than in NaSAARI (7 mm) (Table 5). Among the F4 progeny, mean was higher in MUARIK (13 mm) than in NaSAARI (8mm) (Table 6). The combined analysis showed a mean of 1 mm for both F3 progeny and F4 progeny. A wider range was observed in MUARIK (9-15 mm) than in NaSAARI (5-9 mm) for the F3 progeny; however the F4 progeny had a similar range both environments (11-14 mm and 6-9 mm). F3 progeny had a wider range (8-12 mm) than F4 progeny (9-11 mm) for this trait (Table 7 and 8).

4.1.4 Performance for yield parameters

The mean of the length of the longest finger for F3 progeny was 48mm and 68mm in MUARIK and NaSAARI respectively, and for F4 progeny was 51 and 70mm in MUARIK and NaSAARI respectively indicating that fingers were longer in NaSAARI for both generations. The mean was the same (58mm) for F3 progeny and F4 progeny in the combined analysis. The range for both F3 and F4 generation was the same in the two environments; also the range in the combined analysis for F3 and F4 is the same (4-7) (Tables 7 and 8). From the combined analysis entry 15 had the longest fingers at F4 and it was similar to 23 other accessions (Appendix 1) that were classified as having longest fingers.

The means of width of longest finger were similar in the two environments for both generations 10 mm and 12 mm for F3 and 11 mm and 10 mm for F4 in MUARIK and NaSAARI respectively; also in the combined analysis the overall mean (11mm and 10mm) was similar for both F3 and F4 progeny. Similarly like for the means the ranges were also not different (8-12mm in MUARIK and 9-15 in NaSAARI) for F3 progeny and 9-12mm and 8-11mm in MUARIK and NaSAARI for the F4 progeny. In the combined analysis the range was 10-13mm and 9- 11mm for the F3 progeny and F4 progeny respectively (Table 7 and 8).

The mean number of fingers per main ear was similar in the two environments for both F3 progeny and F4 progeny (6 fingers per inflorescence) giving also the same overall mean in the combined analysis. The ranges of the F3 progeny and F4 progeny were similar in both environments and were not very wide (4-7 fingers and 5-7 fingers respectively), this was also the same in the combined analysis.

The mean for primary tillers for the F3 accessions was higher in MUARIK (4.5 tillers) than in NaSAARI (5.5 tillers) but the mean for the F4 progeny was higher in NaSAARI (5 tillers) than in MUARIK (4 tillers). The overall mean for F3 and F4 was the same (5 tillers) in the combined analysis. A wide range was observed for this trait; 3- 6.8 tillers, 3.9 - 8.7 tillers and overall of 3.8 - 7.3 tillers for the F3 progeny in MUARIK, NaSAARI and combined respectively. Among the F4 progeny a wide range was observed; 3-9 tillers in MUARIK, 4-7 tillers in NaSAARI and 3-9 tillers in the combined analysis (Table 7 and 8).

A higher mean for secondary tillers was observed among the F3 progeny in MUARIK (3.2 tillers) than in NaSAARI (2.1 tillers), with a combined overall mean of 2.6 tillers. Similarly

among the F4 progeny, the highest mean was observed in MUARIK (3 tillers) compared to 1 tiller in NaSAARI, the overall mean from the combined analysis was 2 tillers. A wide range was observed among the F3 progeny in MUARIK (1.8-5.6 tillers) than in NaSAARI (1.5-2.9 tillers). Among the F4 progeny, a wider range was observed in MUARIK too (2-5 tillers) than in NaSAARI (0-3 tillers). A combined analysis revealed a range of 1.9-4 tillers for F3 progeny and 1-3 tillers for F4 progeny (Table 7 and 8).

4.1.5 Mean performance of the accessions according to their biological wild crosses

The mean values of the wild subspecies *E. africana* and *E. kigeziensis* at F3 significantly differed ($P \leq 0.05$) for all the traits except number of fingers per main ear and plant height in MUARIK, in NaSAARI the interspecific crosses differed for all traits except one trait (Days to 50% maturity). In a combined analysis, the wild races were significantly different for all traits except for two traits (number of fingers per main ear and plant height) (Table 9). *Eleusine africana* had higher mean for five traits; number of days to 50% flowering (87 days in MUARIK, 65 days in NaSAARI and 76 days in pooled), days to 50% harvest maturity (102.4 in MUARIK, 98 in NaSAARI and 100 in pooled) length of longest finger (54 mm in MUARIK, 78.4 mm in NaSAARI and 64mm in pooled), primary tiller number (5.5 in MUARIK, 6.1 in NaSAARI and 5.7 tillers in pooled), secondary tiller number (3.9 in MUARIK, 2.3 in NaSAARI and 3.1 in pooled) *E. kigeziensis*.

Table 9: Variation among interspecific finger millet hybrids for traits of agronomic importance in F3 progeny derived from *E. africana* & *E. kigeziensis*

	Traits	DF	NF	FL	FW	FLL	FLW	Pl.Ht	PTN	STN	DM
MUARIK											
MEAN	EA	87	5.9	5.4	0.9	29.7	1.1	63.8	5.5	3.9	102.4
	EK	78	5.5	4.5	1.02	32.6	1.3	63.9	3.9	2.8	97.5
VAR	EA	79.12	0.34	0.276	0.005	7.56	0.013	29.86	0.54	0.78	20.5
	EK	8.01	0.5	0.212	0.003	3.22	0.009	19.47	0.31	0.15	14.8
	T-VALUE	4.12s	2.1ns	6.07s	6s	3.98s	6.26s	0.09ns	7.97s	5.02s	3.8s
NASAARI											
MEAN	EA	65	5.2	7.48	1.19	29.3	0.66	69.5	6.1	2.3	98
	EK	64	5.6	6.45	1.28	32.9	0.79	73.3	5.2	1.9	97
VAR	EA	1.26	0.25	0.178	0.013	4.54	0.004	14.32	1.04	0.11	1.84
	EK	1.94	0.24	0.196	0.013	5.71	0.002	11.63	0.619	0.043	2.18
	T VALUE	3.27s	2.7s	8.03s	2.65s	5.56s	7.65s	3.5s	3.2s	4.6s	1.4ns
POOLED											
MEAN	EA	76	5.6	6.4	1.07	29.6	0.9	66.7	5.7	3.08	100
	EK	71	5.57	5.5	1.15	32.8	1.05	68.6	4.6	2.36	97
VAR	EA	24.53	0.11	0.12	0.004	4.26	0.004	13.69	0.56	0.32	5.66
	EK	3.19	0.15	0.13	0.003	2.08	0.003	6.97	0.23	0.06	3.93
	T VALUE	4.15s	0.19ns	8.69s	4.46s	5.71s	8.36s	1.93ns	5.99s	5.12s	4.49s

S= significant, ns= non-significant at $\alpha=0.05$ (T-test), DM=Days to 50% maturity, DH=Days to 50% flowering, NF= Number of fingers / main ear, FL=Length of longest finger, FW=Width of longest finger, FLL=Flag leaf length, FLW=Flag leaf width, PlHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers.

Progenies from *E. kigeziensis* had higher mean for three traits; width of longest finger (10.2mm in MUARIK, 12.8mm in NaSAARI and 11.5 mm in pooled), flag leaf length (326mm in MUARIK, 329mm in NaSAARI and 328mm in pooled), flag leaf width (13mm in MUARIK, 7.9mm in NaSAARI and 10.5mm in pooled) than progenies from *E. africana*. Two traits, number of fingers per main ear and plant height were not significantly different in MUARIK and in the pooled but were significantly different in NaSAARI only, with higher mean values for number of fingers (5.6) and taller plants (73.3cm) in *E. kigeziensis* than in *E. africana*.

The mean values of the progenies *E. africana* and *E. kigeziensis* at F4 significantly differed ($P \leq 0.05$) for only four traits (days to 50% flowering, flag leaf length, plant height and primary tiller number) in MUARIK, in NaSAARI the progenies differed for all traits except three traits (number of fingers per main ear, plant height and 50% days to harvest maturity). In a combined analysis, the wild races were significantly different for five traits (days to 50% flowering, length of longest finger, flag leaf length, primary and secondary tiller number). *E. africana* had higher mean for only two traits; number of days to 50% flowering (89days in MUARIK, 66 days in NaSAARI and 78 days in pooled), and primary tiller numbers (5.8 in MUARIK, 5.5 in NaSAARI and 5.7 in pooled) than the *kigeziensis* wild race. *E. Kigeziensis* had higher mean values for only flag leaf length in both locations and pooled (Table 10).

Number of fingers per main ear and days to 50% maturity were not significantly different between the wild races in any of the location even in the pooled analysis. Length of longest finger and secondary tiller number traits were significantly different only in NaSAARI and pooled but not in MUARIK, finger width and flag leaf width were significant only NaSAARI, plant height was significantly different only in MUARIK. Comparing the *E. africana* and *E. kigeziensis* progenies across generations, there was a similar trend of significant differences in the mean values for traits days to 50% flowering, flag leaf length, primary tiller numbers and secondary tiller numbers in both locations and in the pooled (Table 10).

Table 10: Variation among interspecific finger millet hybrids for agronomic trait in F4 progeny derived from *E. Africana* & *E. kigeziensis*

	Traits	DH	NF	FL	FW	FLL	FLW	Pl.Ht	PTN	STN	DM
MUARIK											
MEAN	EA	89	5.8	5.11	1.07	31.3	1.22	62.8	5.84	2.75	109
	EK	82	5.8	5.11	1.07	32.5	1.27	66.3	3.53	2.57	105
VAR	EA	17.79	0.22	0.18	0.002	2.99	0.01	34.17	1.92	0.49	61.49
	EK	13.62	0.24	0.34	0.003	2.98	0.004	34.7	0.57	0.21	26.93
	T-VALUE	5.9s	ns	ns	ns	2.5s	1.9ns	2.02s	6.52s	0.97ns	1.92ns
NASAARI											
MEAN	EA	66	5.7	7.44	0.95	29	0.7	68.6	5.47	1.4	96.7
	EK	65	5.9	6.05	1.01	31.2	0.79	68.4	4.87	0.97	97
VAR	EA	1.59	0.3	0.23	0.004	9.25	0.003	9.44	0.63	0.22	1.61
	EK	1.13	0.23	0.14	0.002	8.13	0.003	16.89	0.29	0.09	2.15
	T VALUE	3.1s	1.4ns	10.5s	3.5s	2.48s	5.5s	0.19ns	2.83s	3.5s	1.74ns
POOLED											
MEAN	EA	78	5.7	6.3	1	30.1	1	65.7	5.7	2.1	103
	EK	73	5.8	5.6	1	31.9	1	67.4	4.2	1.8	101
VAR	EA	5.81	0.12	0.08	0.002	3.06	0.002	11.59	0.416	0.22	14.06
	EK	4.47	0.13	0.14	0.001	2.78	0.002	15.61	0.235	0.06	6.11
	T VALUE	5.97s	0.94ns	7.3s	0ns	3.5s	0ns	1.58ns	8.53s	2.5s	2.01ns

S= significant, ns= non-significant at $\alpha=0.05$ (T-test), ***=significant at $P \leq 0.001$ **=significant at $P \leq 0.01$. *= significant at $P \leq 0.05$ (F-test), DM=Days to 50% maturity, DH=Days to 50% flowering, NF= Number of fingers / main ear, FL=Length of longest finger, FW=Width of longest finger, FLL=Flag leaf length, FLW=Flag leaf width, PlHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers.

4.1.6 Correlations among phenotypic trait

Seventeen out of 45 correlations were significant in NaSAARI, 10 in MUARIK and 18 in the pooled analysis (combined trait means across locations) (Tables 11-13). Days to 50% flowering (DH) had highly significant and positive correlation with length of longest finger (0.59 in NaSAARI and 0.64 in combined), primary tiller number (0.54 in NaSAARI, 0.5 in MUARIK and 0.66 in combined) and days to 50% maturity (0.68 in MUARIK and 0.72 in the combined analysis). However it had significant negative correlation with width of longest finger (-0.4 in NaSAARI and in combined) and plant height in MUARIK (-0.43).

Number of fingers per main ear had moderate significant and positive correlation with flag leaf length (0.38), flag leaf width (0.4) and plant height (0.39) in NaSAARI, however it had a significant negative correlation with flag leaf length in MUARIK. Length of the longest finger had a strong positive correlation with primary tillers (0.49 in NaSAARI, 0.64 in combined), a strong significant negative correlation with width of longest finger (-0.47 in NaSAARI, -0.46 in combined), with flag leaf width (-0.51 in NaSAARI, -0.46 in combined).

Flag leaf width had a significant positive correlation with flag leaf width (0.69 in NaSAARI, 0.43 in combined). Plant height had positive correlation with primary tiller only in NaSAARI (0.45), but moderate significant correlation with days to 50% maturity (-0.53 in MUARIK and -0.31 in combined). Primary tillers had a significant positive correlation with secondary tillers in MUARIK (0.33) and in combined analysis (0.51).

Table 11: Correlation coefficients of quantitative traits in the 48 finger millet lines at F4 in NaSAARI

	DH	NF	FL	FW	FLL	FLW	PlHt	PTN	STN	DM
DH	1.000									
NF	0.115	1.000								
FL	0.590***	-0.207	1.000							
FW	-0.400***	0.282*	-0.467***	1.000						
FLL	0.028	0.384**	-0.102	0.335*	1.000					
FLW	-0.158	0.395**	-0.512***	0.350*	0.690***	1.000				
PlHt	0.137	0.387**	0.076	0.142	0.292	0.073	1.000			
PTN	0.537***	0.193	0.487***	-0.317*	0.089	-0.209	0.450**	1.000		
STN	0.275	-0.152	0.453**	-0.243	-0.285	-0.360*	0.084	0.085	1.000	
DM	-0.166	-0.218	-0.200	0.035	-0.161	0.037	0.062	-0.018	0.038	1.000

DM=Days to 50% maturity, DH=Days to 50% flowering ,NF= Number of fingers / main ear, FL=Length of longest finger , FW=Width of longest finger ,FLL=Flag leaf length ,FLW=Flag leaf width , PlHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers

Table 12: Correlation coefficients of quantitative traits in the 48 finger millet lines at F4 in MUARIK

	DH	NF	FL	FW	FLL	FLW	PIHt	PTN	STN	DM
DH	1.000									
NF	0.074	1.000								
FL	0.064	-0.017	1.000							
FW	-0.146	-0.103	-0.236	1.000						
FLL	-0.232	-0.383**	0.241	0.058	1.000					
FLW	-0.346*	0.082	0.013	0.079	0.175	1.000				
PIHt	-0.433**	-0.174	0.083	0.053	0.280	0.312*	1.000			
PTN	0.500***	-0.003	-0.173	-0.123	-0.344*	-0.343*	-0.134	1.000		
STN	0.083	0.027	-0.182	0.036	-0.137	-0.192	0.004	0.334*	1.000	
DM	0.716***	0.151	0.010	-0.154	-0.056	-0.147	-0.526***	0.178	-0.064	1.000

DM=Days to 50% maturity, DH=Days to 50% flowering, NF= Number of fingers / main ear, FL=Length of longest finger , FW=Width of longest finger ,FLL=Flag leaf length, FLW=Flag leaf width, PIHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers.

Table 13: Correlation coefficients of quantitative traits in the 48 finger millet lines at F4 in pooled analysis

	DH	NF	FL	FW	FLL	FLW	PIHt	PTN	STN	DM
DH	1.000									
NF	0.040	1.000								
FL	0.640***	-0.151	1.000							
FW	-0.405**	-0.002	-0.463***	1.000						
FLL	-0.129	0.042	-0.125	0.236	1.000					
FLW	-0.407**	0.280*	-0.459**	0.175	0.433**	1.000				
PIHt	-0.262	-0.037	-0.107	0.145	0.233	0.217	1.000			
PTN	0.659***	-0.032	0.638***	-0.375**	-0.341*	-0.602***	-0.061	1.000		
STN	0.244	-0.191	0.265	-0.223	-0.334*	-0.304*	-0.050	0.509***	1.000	
DM	0.680***	0.102	0.304	-0.310	0.057	-0.113	-0.313*	0.292*	0.064	1.000

DM=Days to 50% maturity, DH=Days to 50% flowering, NF= Number of fingers / main ear, FL=Length of longest finger , FW=Width of longest finger ,FLL=Flag leaf length ,FLW=Flag leaf width , PIHt=Plant height, PTN=Number of Primary tillers, STN=Number of secondary tillers.

4.1.7 Regression coefficient between F4 and F3 progenies

Table 14: Regression coefficient (b) and narrow sense heritability (h^2) between F3 and F4 interspecific progenies of finger millet for quantitative traits observed across locations

TRAITS	Environment					
	NaSAARI		MUARIK		Pooled	
	b	h^2	b	h^2	b	h^2
Days to 50% flowering	0.39**	39	0.12	12	0.14	14
Days to 50% maturity	0.54***	54	0.38	38	0.49**	49
Number of fingers per main ear	0.10	10	0.21	21	0.17	17
Length of longest finger(cm)	0.61***	61	0.03	3	0.71***	71
Width of longest finger (cm)	-0.13	-	0.19	-	0.33	33
Flag leaf length (cm)	0.46***	46	0.23	23	0.53**	53
Flag leaf width (cm)	0.89***	89	0.50*	50	1.0***	100
Plant height (cm)	0.21	21	0.16	16	0.37**	37
Primary tiller number	0.25	25	0.41**	41	0.5***	50
Secondary tiller number	0.23*	23	0.21	21	0.39*	39

Regression coefficient b was highly significant and positive for; five traits in NaSAARI, two traits in MUARIK and seven traits in the combined (pooled) analysis as seen in table 12 above. Even though these traits were significant, some of them were very low to be meaningful, flag leaf width had the highest b-value in both locations and in the combined where b was +1 hence it was very consistent across environments. The other traits were inconsistent across environments, .

Narrow sense heritability (h^2) was calculated (Table 14 above) from the parent-offspring regression using genotype means within location and across location, since these were selfed lines and both parents (F3 in this case) were evaluated together with offspring (F4 in this case) in the same environment in a side-by-side field trial. Accessions revealed $\geq 50\%$ heritability for three traits in NaSAARI (days to 50% maturity, length of longest finger and flag leaf width), one trait (flag leaf width) in MUARIK and four traits (length of longest finger, flag leaf length, flag leaf width and primary tiller number) in the combined analysis. The rest of the traits had low heritability as seen in table 14.

4.1.8 Principle Component Analysis

Principal component analysis is used to provide reduced dimension model that would indicate measured differences among groups. For both generations F3 and F4, in all the two environments and also in the combined analysis, a large proportion of the total variation was explained by the first two principal components. Results of this analysis are presented in Tables 15 and 16.

Among the F3 generation, the first two principal components explained 82.5% variation in MUARIK, 83% in NaSAARI, and 79.8% variation in combined location. In MUARIK, the variability on the first principal component (64.9%) was accounted for by high negative loadings for plant height and flag leaf length whereas plant height contributed more to the variability on the second principal component (17.6%) with high negative loading. In NaSAARI, the variability on the first principal component (62.6%) was accounted for by high positive loadings for days to 50% flowering and days to 50% maturity. The 20.2% variability accounted by second principal component had high positive loading from plant height. In a combined analysis, the variability on the first principal component (60.2%) was accounted for by high positive loadings for days to days to 50% flowering and days to 50% maturity while the plant height and days to 50% flowering accounted for the variation for the second principal component (19.6%) with high positive loadings (Table 15).

Among the F4 progeny the first two principal components accounted for 86.6% variation in MUARIK, 83.2% variation in NaSAARI and 80.8% variation in combined analysis (Tables 16). In MUARIK, the variability on the first principal component (67.7%) was accounted for by high negative loadings for days to 50% flowering and days to 50% maturity, while the variability on the second principal component (18.9%) was accounted for high positive loadings for plant height, days to 50% flowering and days to 50% maturity. In NaSAARI, the variability on the first principal component (55.6%) was accounted for by high positive loadings for plant height and flag leaf length, the variability on the second principal component (27.6%) was accounted for by high negative loadings for flag leaf length. In the combined analysis, the variability on the first principal component (52.9%) was accounted for by high negative loading for plant height and positive loadings for days to 50% flowering and days to 50% maturity. The second principal component (27.9%) variability was accounted for by high positive loadings for plant height, days to 50% flowering and days to 50% maturity (Table 16).

Table 15: Principal component analysis of quantitative traits recorded on F3 progeny across the two locations.

F3	MUARIK		NaSAARI		Pooled	
Principal components	1	2	1	2	1	2
Eigen values	19.7	5.3	62	21.9	24	7.8
Proportion of variance (%)	64.9	17.6	62.6	20.4	60.2	19.6
Total variation	64.9	82.5	62.6	83	60.2	79.8
Eigen vectors (loadings)						
Days to 50% flowering	0.1151	0.1140	0.8614	0.1143	0.7908	0.3468
Days to 50% Maturity	0.0047	-0.0002	0.4486	0.1785	0.3682	0.2040
Length of longest finger (cm)	0.0619	0.0683	0.0158	0.0469	0.0560	0.0384
Width of longest finger (cm)	-0.0069	0.0046	-0.0020	-0.0013	-0.0078	0.0049
Flag leaf length (cm)	-0.4874	-0.8305	-0.1466	0.0616	-0.2690	-0.0087
Flag leaf width (cm)	-0.0131	-0.0126	-0.0067	-0.0026	-0.0108	-0.0012
Plant height (cm)	-0.8600	0.5030	-0.1799	0.9682	-0.3944	0.9112
Number of fingers per main ear	-0.0631	-0.0473	0.0059	0.0784	-0.0069	0.0346
Primary tiller number	0.0347	0.1878	0.0336	0.0674	0.0733	0.0704
Secondary tiller number	0.0197	0.0443	0.0379	0.0299	0.0501	0.0130

Table 16: Principal component analysis of quantitative traits recorded on F4 progeny across the two locations.

F4	MUARIK		NaSAARI		Pooled	
Principal component	1	2	1	2	1	2
Eigen values	76.1	21.3	15.9	7.9	19.9	10.5
Proportion of variance (%)	67.7	18.9	55.6	27.6	52.9	27.9
Total variation	67.7	86.6	55.6	83.2	52.9	80.8
Eigen vectors (loadings)						
Days to 50% flowering	-0.4900	0.3847	0.0456	0.0358	0.5027	0.4812
Days to 50% Maturity	-0.6840	0.3799	-0.0055	0.1274	0.5379	0.4533
Length of longest finger (cm)	0.0007	0.0147	0.0079	0.0469	0.0436	0.0499
Width of longest finger (cm)	0.0009	-0.0010	0.0034	-0.0052	-0.0031	-0.0023
Flag leaf length (cm)	0.0445	0.0803	0.4734	-0.8693	-0.0824	0.1366
Flag leaf width (cm)	0.0025	0.0018	0.0055	-0.0158	-0.0041	-0.0005
Plant height (cm)	0.5359	0.8353	0.8743	0.4666	-0.6654	0.7288
Number of fingers per main ear	-0.0091	-0.0094	0.0603	-0.0267	0.0056	0.0035
Primary tiller number	-0.0523	0.0568	0.0751	0.0556	0.0793	0.1027
Secondary tiller number	0.0004	0.0009	-0.0034	0.0525	0.0129	0.0095

4.1.9 Cluster Analysis for performance of the interspecific finger millet progenies

Clustering analysis was done using the group average method based on the performance of the progenies for the means of ten quantitative traits in the pooled data across the two

locations. Progenies from the same crosses with the same wild relative sub species clustered together in the major clusters (fig 2-3 and Table 17). Among the F3 progenies, three clusters were formed with most of the progenies (98%) placed into two major clusters 1 and 2. Cluster 1 had 30 (63.8%) accessions that were 92.4% similar and all were from the cross with *E. kigeziensis* (Appendix VII). The accessions in this cluster were early flowering and maturing, had the highest plant height, flag leaf length and width, widest fingers, least finger length, primary and secondary tillers numbers. Cluster 2 had 17 (36.8%) accessions that were 89.3% similar and they were mainly from the cross with *E. africana*. In this cluster, accessions had the longest mean length of fingers, highest primary and secondary tiller numbers (Appendix VIII). Cluster 3 had only one accession from the *E. africana* cross. It took the longest to flower and mature, had the least mean flag leaf length, plant height and number of fingers per main ear.

Analysis of the F4 progeny clustered the accessions into four clusters (fig 3), with most of the progenies (95.8%) placed in clusters 1 and 2. Cluster 1 had 31 (67.4%) accessions that were 90.8% similar, most deriving from the *E. kigeziensis* cross. (Appendix IX). The accessions in this cluster were generally earliest to flower and mature, had the highest mean number of fingers per main ear, least mean number of primary tillers and length of longest finger. Cluster 2 contained 15 (32.6%) accessions that were 89% similar with all of them belonging to the *E. africana* cross. Accessions in cluster 2 had moderate mean days to 50% flowering and maturity, highest primary and secondary tiller numbers and least flag leaf length (Appendix X). Cluster 3 had only one accession that was from the *E. kigeziensis* cross with the highest mean plant height, flag leaf length and least mean number of fingers per main ear. Cluster 4 had also one accession from the *E. africana* cross which took the longest to flower and mature, had the longest mean finger length, highest number of fingers per main ear and least mean plant height.

Cluster for F3 millet lines performance for 10 traits across location

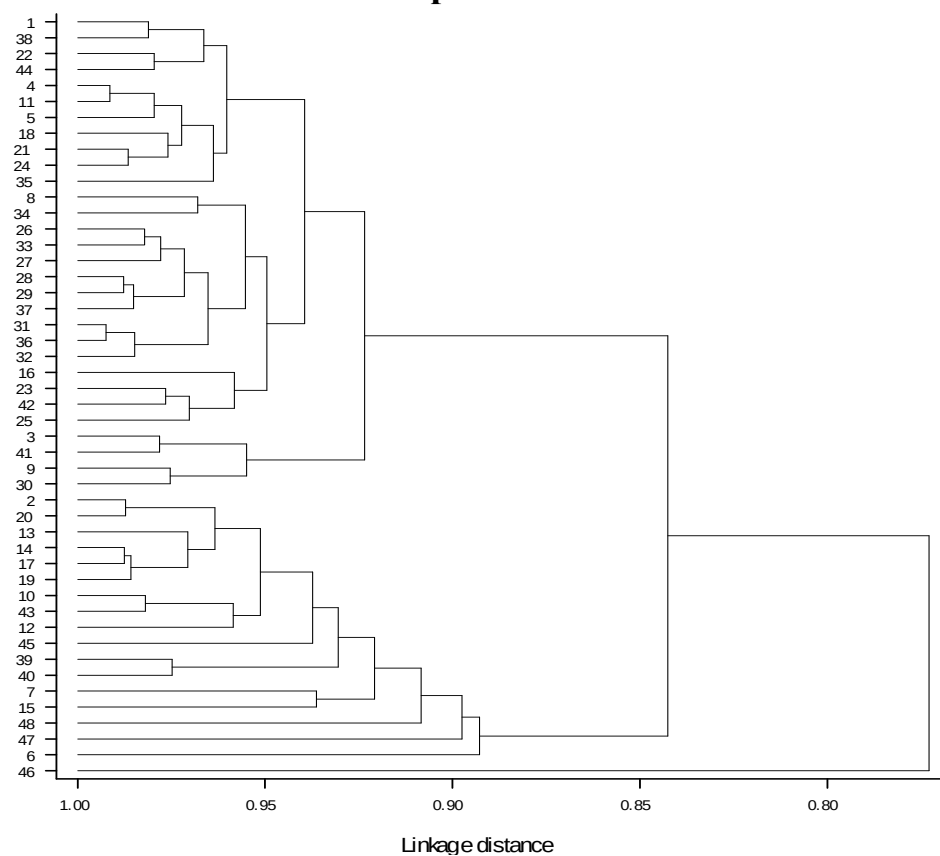


Figure 2: Dendrogram for 48 F3 finger millet Lines based on average linkage for 10 quantitative trait means across two locations.

Cluster of F4 millet lines trait performance across two locations

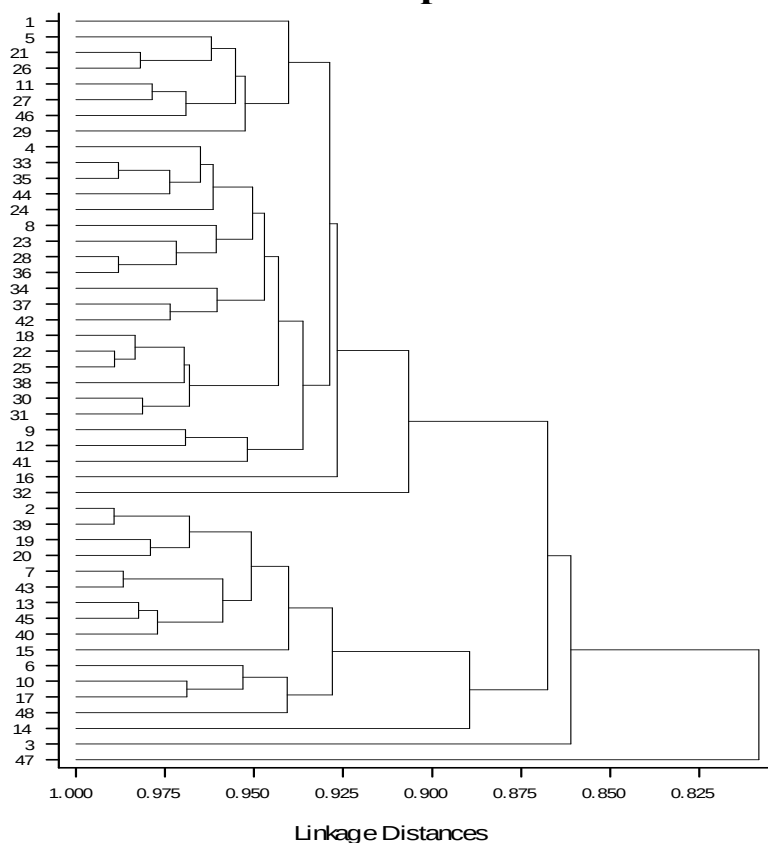


Figure 3 Dendrogram for 48 F4 finger millet Lines based on average linkage for 10 quantitative trait means across two locations

Table 17: Means of 10 quantitative traits within clusters determined from cluster analysis across locations.

	F3			F4			
				Clusters			
	1	2	3	1	2	3	4
No. of Genotypes	30	17	1	31	15	1	1
Trait means of lines in each cluster							
Days to 50% flowering	70.9	75.1	91.9	73	77.4	79	83
Days to 50% maturity	97.4	100.0	103.0	101.2	102.6	106	114
Flag leaf length	32.8	29.6	27.8	31.7	29.8	36.0	33.9
Flag leaf width	1.0	0.9	0.9	1.0	0.9	1.0	1.0
Plant height	68.6	67.1	58.0	67	65.9	75.2	58.1
Number of fingers per main ear	5.6	5.6	5.5	5.9	5.7	5	6
Length of longest finger	5.5	6.5	6.1	5.6	6.3	6.3	6.5
Width of longest finger	1.2	1.1	1.0	1.0	1.0	1.0	1.0
Primary tiller numbers	4.6	5.8	5.1	4	5.8	5	5
Secondary tiller numbers	2.4	3.2	2.5	2	2.2	2	2

4.2 The variability for Blast Resistance among the wild finger millet progenies in the screen house.

4.2.1 Resistance to Leaf Blast among the F3 progeny

Analysis of variance showed highly significant differences among the F3 interspecific progenies for the leaf blast ($P < 0.001$) with the highest mean square variance recorded at 56 days after planting. The leaf blast severity ranged from 1.7 to 2.6 compared to 2.2 on resistant check (Gulu E) and 3.2 on susceptible check (KATFMI) (Table 18). Among the 48 F3 progeny, nine lines (19%) were resistant, 38 lines (79%) were moderately resistant and only one line (2 %) was susceptible. No progeny showed total immunity and high susceptibility to the leaf blast disease. The minimum score was recorded on line 19c-b (1.7) followed by 19c, 24b, 13a, 6b, 2b, 20b, 24c-b and 22c-b all with a score of 1.9. All these were categorized as resistant. The maximum score was recorded on line 16c-b (2.6) categorized as susceptible, followed by 12a with a score of 2.4 and 26b, 8a, 1a, 17b, 18c-b, 7c-b, 5b, 25c-b all with a score of 2.3 and categorised as moderately resistant (Table 18).

Table 18: Best and worst 10 accessions among the F3 progeny

Accession	42 DAP	49 DAP	56 DAP	Mean Score	Reaction
Best 10 lines					
19c-b	1.4	1.7	2.0	1.7	R
19c	1.6	1.7	2.2	1.8	R
24b	1.5	1.9	2.2	1.9	R
13a	1.7	1.8	2.2	1.9	R
6b	1.4	1.9	2.5	1.9	R
2b	1.6	1.9	2.3	1.9	R
20b	1.2	2.0	2.5	1.9	R
24c-b	1.5	1.8	2.5	1.9	R
22c-b	1.3	2.1	2.2	1.9	R
1c-b	1.8	1.8	2.4	2.0	MR
Worst 10 lines					
26b	1.8	2.2	2.8	2.3	MR
8a	2.0	2.2	2.7	2.3	MR
1a	2.0	2.2	2.7	2.3	MR
17b	2.0	2.3	2.6	2.3	MR
18c-b	2.0	2.3	2.6	2.3	MR
7c-b	1.9	2.4	2.7	2.3	MR
12a	2.1	2.3	2.7	2.4	MR
5b	1.6	2.3	2.5	2.1	MR
25c-b	1.8	2.3	2.3	2.1	MR
16c-b	2.4	2.7	2.8	2.6	S
Commercial material					
Gulu E	1.8	2.1	2.8	2.2	MR
SER 1	1.8	2	2.8	2.2	MR
SER 2	2.1	2.8	3.4	2.8	S
OKIRING	2	2.2	2.7	2.3	MR
PESE 1	1.7	2.1	2.4	2.1	MR

SER 3	1.7	2.2	2.6	2.2	MR
KATFMI	2.8	3.4	3.6	3.3	HS
E11	1.9	3	3.4	2.8	S
Grand mean	1.81	2.13	2.55	2.2	

4.2.2 Resistance to leaf blast among F4 progeny

Analysis of variance showed highly significant differences among the F4 interspecific progenies for the leaf blast ($P < 0.001$) with the highest mean square variance recorded at 56 days after planting. The leaf blast severity ranged from 1.8 to 2.7 on a 1-5 scale compared to 2.2 on resistant check (Gulu E) and 2.7 on susceptible check (SER 2) (Table). Among the 48 F3 progeny, five lines (10%) were resistant, 37 lines (77%) were moderately resistant and six lines (13 %) was susceptible. No lines showed total immunity (highly resistant) and high susceptibility to the leaf blast disease (Table 19). The minimum score was recorded on line 25a (1.8) followed by 18b, 19b, 25c-b, 7b all with a score 1.9 and categorized as resistant. The maximum score was recorded on line 28a (2.7) followed by 22c-b, 23a, 14c, 20c with a score of 2.5 and categorized as susceptible (Table 19).

4.2.3 Resistance to Neck and Head Blast among the F4 progeny

Analysis of variance showed that there was significant difference among the progeny for neck blast ($p < 0.001$) and head blast ($p < 0.05$). All the lines (100%) were resistant to neck blast with a range of 1.0- 1.8 On a scale of 1-5 (Appendix XII). Head blast severity ranged from 1.8 to 2.4 on a scale of 1-5 compared to 1.9 of resistant check Gulu E and 3.4 of susceptible check E11. Twenty lines (42%) were resistant and twenty eight (58%) were moderately resistant. No lines were completely immune (highly resistant) and susceptible to head blast (Table 19-21).

Table 19: Table Summarizing the Reaction of Accessions to Blast

Category	Frequency of F3 progeny	Number of F4 Accessions		
	LB	LB	NB	HB
HR	00	00	00	00
R	09	05	48	20
MR	38	37	00	28
S	01	06	00	00
HS	00	00	00	00

LB=Leaf Blast; HR= highly resistant (1.0-1.4), R=Resistant (1.5-1.9), MR= moderately resistant (2.0-2.4), S= Susceptible (2.5-2.9), HS=highly susceptible (3.0-3.5). NB= Neck Blast; NB=Neck Blast;

HB=Head Blast; 1.0-2.0= Resistant, 2.1-3.0= moderately resistant, 3.1-4.0= Susceptible, 4.1-5.0= highly resistant.

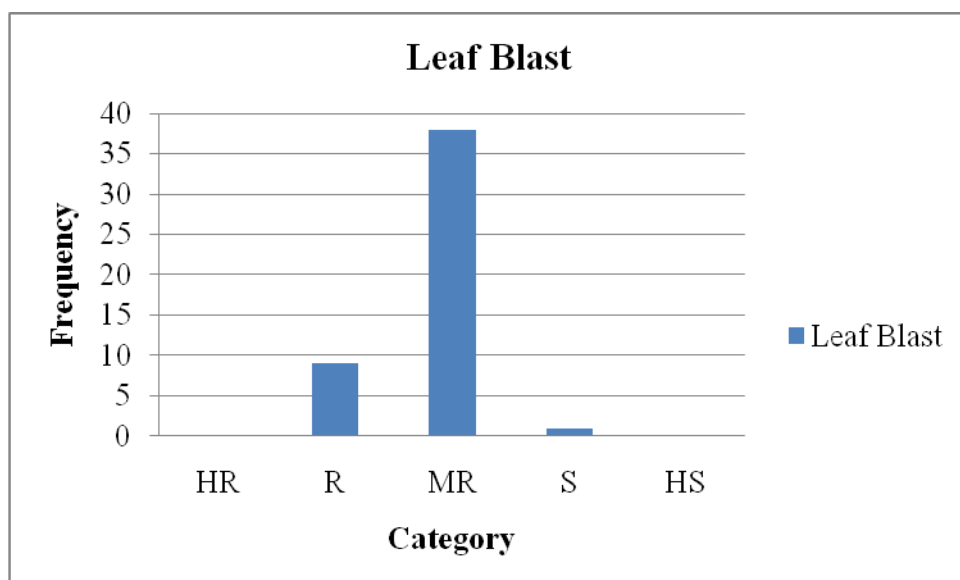


Figure 4: Frequency distribution for Leaf blast reaction categories among F3 progeny

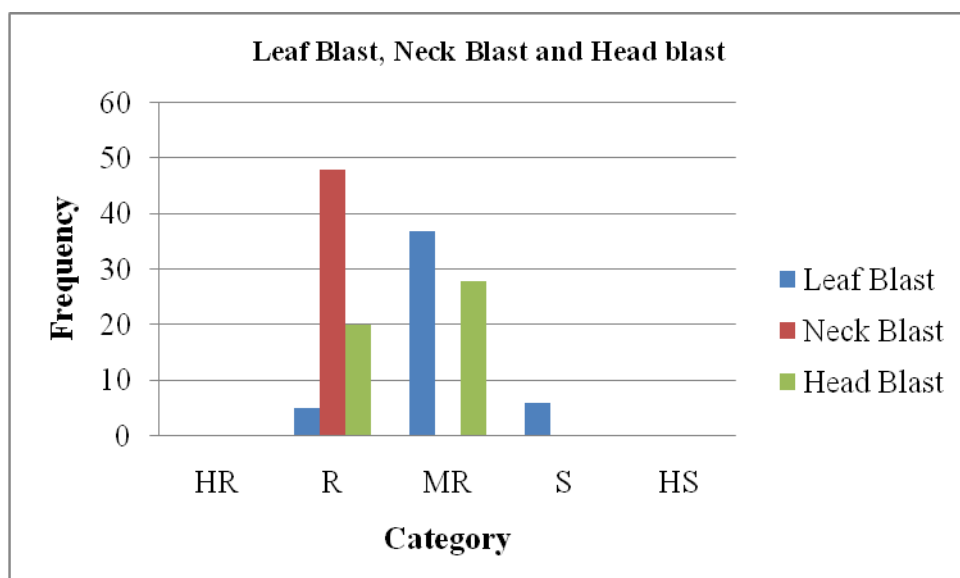


Figure 5: Frequency distribution for Leaf, Neck and Head blast reaction categories among F4 progeny

Table 20: Best and worst 10 performing accessions among the F4 progeny for leaf blast

Name	42 DAP	49 DAP	56 DAP	Mean score	Category
Best 10					
25a	2.1	2.1	2.3	1.8	R
18B	1.9	2.1	1.8	1.9	R
19b	1.9	2.1	1.6	1.9	R
25c-b	2.0	2.1	2.0	1.9	R
7b	2.2	2.0	2.2	1.9	R

8b	2.1	2.1	2.3	2.2	MR
1b	2.1	2.0	2.2	2.1	MR
8c-b	2.2	2.1	2.1	2.1	MR
6b	2.0	2.2	2.2	2.1	MR
10b	2.1	2.1	2.3	2.2	MR
worst 10					
26b	2.3	2.4	2.4	2.4	MR
1c-b	2.3	2.6	2.3	2.4	MR
19c	2.4	2.4	2.4	2.4	MR
12a	2.0	2.5	2.7	2.4	MR
20c	2.3	2.2	2.8	2.5	S
14c	2.5	2.5	2.4	2.5	S
23a	2.0	2.5	2.9	2.5	S
22c-b	2.3	2.7	2.4	2.5	S
5b	2.3	2.7	2.5	2.5	S
28a	2.2	2.9	3.0	2.7	S
commercial varieties					
GULU E	2.1	2.2	2.4	2.2	MR
PESE 1	2.2	2.2	2.3	2.3	MR
SER 1	2.1	2.2	2.6	2.3	MR
OKIRING	2.1	2.3	2.7	2.4	MR
SER 3	2.4	2.3	2.5	2.4	MR
KATFMI	2.1	3.2	2.6	2.6	S
SER 2	2.0	3.0	3.1	2.7	S
Grand mean	2.2	2.3	2.4	2.3	
SEM	0.1222	0.1324	0.1775	0.110	
LSD (5%)	0.34	0.37	0.49	0.31	
CV%	11.1	11.5	14.8	9.6	

Table 21: Best and worst 10 performing accessions among the F4 progeny for head blast

NAME	Head blast SCORE	Category
Best 10		
25c-b	1.8	R
20b	1.8	R
13a	1.8	R
24b	1.9	R
22b	1.9	R
6a	1.9	R
28a	1.9	R
22c-b	2.0	R
25a	2.0	R
21b	2.0	R
worst 10		

20c	2.3	MR
8a	2.3	MR
14b	2.3	MR
1b	2.3	MR
18B	2.3	MR
10b	2.3	MR
18c-b	2.4	MR
13c	2.4	MR
7b	2.4	MR
1c-b	2.4	MR
Commercial checks		
GULU E	1.9	R
PESE 1	1.9	R
SER 3	1.9	R
OKIRING	2.0	R
SER 1	2.1	MR
SER 2	2.5	MR
KATFMI	2.7	MR
E11	3.4	S
MEAN	2.1	
SEM	0.188	
LSD (5%)	0.523	
CV	17.61	

4.2.4 Resistance to the three forms of blast disease among the F4 progeny

Analysis of variance showed significant differences among the F4 progeny for all the three forms of blast disease with the highest mean square of variance being for Neck blast, followed by head blast and least leaf blast. Two lines (25a and 25c-b) were resistant to all the three forms of blast disease, thirteen lines (8b, 6b, 8a, 24b, 22b, 22a, 21b, 20b, 19c, 19c-b, 17b, 13c-b, 13a) were resistant to neck blast and head blast and moderately resistant to leaf blast; six lines (14c, 20c, 22c-b, 23a, 28a, 5b) were resistant to neck and head blast but susceptible to leaf blast (Appendix XII).

Table 22: Estimates of variance components, heritability and genetic advance in the test lines for the three forms of finger millet blast.

	Mean	O^2_g	O^2_p	h^2 (%)	PCV	GCV	GA	GA (%)
Leaf Blast	2.3	0.011	0.060	18.8	10.6	4.6	9.5	4.109
Neck Blast	1.3	0.064	0.147	43.7	29.5	19.5	34.5	26.507
Head Blast	2.1	0.015	0.156	9.7	18.8	5.9	7.9	3.748

O^2_g = Genotypic variance, O^2_p = Phenotypic variance, h^2 = Broad sense heritability, PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, GA = Genetic advance, GA (%) = Genetic advance as percentage of population mean.

The Phenotypic coefficient of variation estimates were higher than the Genotypic coefficient of variation estimates for all the three blast types. Moderate broad sense heritability and high genetic advance percentage were estimated for neck blast, low heritability and genetic advance were estimated for both leaf and head blast (Table 22). Correlation between head blast and neck blast was small but positive ($r^2 = 0.08$), head blast and leaf blast was negative (-0.05) and neck blast and leaf blast was negative too (-0.2). These correlations were non-significant and very weak.

CHAPTER FIVE

GENERAL DISCUSSION

5.1 Phenotypic variability for quantitative traits

The classical selection theory in breeding for quantitative traits heavily depends on availability of variation in the population for prediction of response to selection (Bernado, 2002). In this study a wide range of variation was observed in all the traits studied indicating existence of broad variability among the interspecific hybrid progenies that would provide an opportunity for genetic improvement through selection and hybridisation. These studies suggest that interspecific hybridization indeed increased the genetic variability. Similar findings were reported in finger millet studies on Ethiopian and Indian germplasm (Bezaweletaw *et al.*, 2006; Nandini *et al.*, 2010; Lule *et al.*, 2012). This provides adequate variation upon which to establish a breeding programme. Thus the purpose of increase variability through interspecific hybrids as was done in this project have expanded the genepool of finger millet improvement. In this study, the variance due to G x E interaction was greater than genotypic variance for most of the traits except length of longest finger, primary and secondary tiller numbers in F3; Flag leaf length, plant height and number of finger per main ear in F4. This is indicative of the relative importance of G x E for these traits as has been reported elsewhere (Mohan, 2003; Ganapathy *et al.*, 2011). Testing of these materials over a wide environment is thus critical to get materials with similar agroecological performance.

5.1.1 Mean performance for phenotypic traits in different environments

The two environments differed significantly indicating that choice of the environments was appropriate in expressing the variability of the interspecific progenies for various traits. In the pooled analysis of two environments, variance components due to G x E were estimated and tested against their respective standard errors and they were significant for all the traits indicating the genotypes had variation and their performance differed in different environments. Indeed comparisons of progeny performance based on rakings showed that an entry that flowered earliest in one location did not necessarily flower earliest in the second location. This corroborates other reports on morphological variation of finger millet (Dida *et al.*, 2008).

5.1.1.1 Earliness

Thus the significant variance in most of the traits in individual environments showed that the progenies from the interspecific crosses were diverse and had sufficient scope for selection and utilization in crop improvement program. Forty four accessions (92% of the total accessions) of the F3 accessions flowered within 68 -76 days with a pooled mean of 72.8 days, with the earliest five accessions (27, 30, 33, 9 and 35) flowering at 68 days across the two locations. Among the F4 generation accessions, 36 accessions (75% of the total accessions) flowered between 70-76 days. The five accessions 30, 24, 4, 31 and 22 recorded consistently early flowering (70 days) across both environments. Entry 30 was consistently early across both locations at both F3 and F4 generations. These accessions flowered earlier than East African finger millet germplasm that was characterized at ICRISAT, India (Gopal *et al.*, 2009). The material in this study had comparably similar means with those in other studies (Opole, 2012; Priyadharshini *et al.*, 2011; Nandini *et al.*, 2010). These results show that indeed earliness a common characteristic of wild plants was successfully introgressed in to the cultivated millet. Phenological traits such as appropriate early flowering and maturity are major components of crop adaptation, particularly in environments where the growing season is restricted by terminal drought and high temperatures (Subbarao *et al.*, 1995). Early flowering while a adaptive strategy for drought escape may however compromise yield especially if the plant size is limited. These accessions matured earlier than other materials in the studies done in Ethiopia and India and could be used as sources of earliness (Lule *et al.*, 2012; Ganapathy *et al.*, 2007; John, 2006).

5.1.1.2 Plant Height

Ten lines (9, 38, 30, 5, 32, 26, 25, 3, 41 and 48) were classified as tall among F3 and F4 progeny across locations. The taller lines could be evaluated in multi-location environment to find their suitability for fodder yield. However, the lines in the present study were shorter than those reported on germplasm collections from Ethiopia and India (Wolie *et al.*, 2013; Lule *et al.*, 2012; Ganapathy *et al.*, 2007). Again this shows the impact of inter specific hybridisation. In this case the means for F3 and F4 progeny were similar (68 cm) with similar number of primary tiller numbers (5 primary tillers) and secondary tillers (2-3) (Tables 5 & 6) are indicative of introgression of wild genome into cultivated finger millet. In other studies on fox tail millet, low number of tillers per plant have been reported in interspecific

hybrids involving finger millet and in foxtail millet (Opole, 2012; Vetriventhan, 2011; Nandini *et al.*, 2010)). However, higher ranges for number of tillers per plant have also been reported (Wolie *et al.*, 2013; Bharathi, 2011). The shorter stature would easily support the use of inorganic fertilizers and associated increase in yield. This was a crucial trait for the green revolution.

5.1.1.3. Ear traits

The mean number of fingers per main ear ranged from 5-7 fingers with a mean of 5.6 and 6 fingers among F3 progeny and F4 progeny respectively. The mean finger width was 10 mm and length (58mm). These traits were similar for both generations across both environments. These results compare with those reported in India and Ethiopia (Lule *et al.*, 2012; Krishnappa *et al.*, 2009; Gopal *et al.*, 2009). However the finger length reported in the current study was lower than that in other studies on finger millet (Wolie *et al.*, 2013; Priyadharshini *et al.*, 2011; Ganapathy *et al.*, 2007), perhaps due to limited soil amendments used. The stability of these traits across both environments however implies that they can be targeted for improvement for material determined for different agroecologies

5.1.2 Mean performance of the accessions according to their biological wild crosses

Mean number of days to 50% flowering was higher for progenies of *E. africana* than progenies of *E. kigeziensis* at both generations (Table 7 & 8). In other studies progeny derived *E. Africana* flowered later than those from other wild relatives such as *vulgaris*, *plana*, *compacta*, *elongata* and *spontanea* (Bharathi, 2011; Upadhyaya *et al.*, 2007)). It therefore suggests that *E. kigenziensis*, while falling within the same clade as *E. coracana* subsp. *coracana* and *africana*, *E. indica*, and *E. tristachya* (Neves *et al.*, 2005), flowers earlier.

Mean basal tiller number and length of longest finger, was higher for progenies of wild relative *E. africana* families in all locations and across locations at both F3 and F4 generation, than for progenies of *kigeziensis*. Finger width was higher in *kigeziensis* than in accessions of *africana* interspecific cross in F3 and there was no significant difference between the races at F4 generation for this trait. Flag leaf width and length were longer for wild relative *kigeziensis* than for *africana* interspecific crosses in this present study. These

findings are similar with a studies reported in India (Bharathi, 2011; Upadhyaya et al., 2007; Mgonja *et al.*, 2007). In general the progenies from the wild relative *E. africana* had the highest mean for most of the traits in both generations. This may be due to adaptive nature of this *E. africana* wild relative to lowlands compared to *E. Kigeziensis* this is well adapted for highlands. Indeed, both species have been reported to have been affected habitat-specific hypothesis which proposes divergences of the allotetraploid lineage within Eleusine in East Africa due to habitat-specific factors such as topographic uplift and increasing amplitudes of palaeoclimate variability at crucial geological periods (Liu *et al.*, 2011b).

5.1.3 Phenotypic correlation for ten quantitative traits

Understanding the correlation among traits is important to breeders in that improvement of one trait may impact positively or negatively on an associated trait. For effective simultaneous improvement of the key traits in crop productivity it is necessary to determine the magnitude of associations between the traits. In this multi location study, correlation coefficient analysis indicated the magnitude and direction (positive or negative) of the associations between the traits. The highest significantly strong positive correlation was recorded between days to 50% flowering and days to 50% physiological maturity (0.68) as expected because these two are maturity traits. This was also reported in a diversity study in Uganda (Dramadri, 2013). Significantly strong positive correlation was also recorded between days to 50% flowering and number of primary tillers and length of longest finger, this means early maturing accessions also had long fingers and many primary tillers; significant high positive correlation between number of primary and secondary tillers could improve yield since these are yield traits. High significant negative correlation was recorded between flag leaf width and primary tillers; days to 50% flowering and finger width and flag leaf width, this means late maturing accessions had narrow fingers and narrow flag leaves. Similar findings were reported by other authors in studies on finger millets (Manyasa, 2013; Bezawelataw, 2006). Traits that had positive correlation between each other could simultaneously be improved on saving time and resources in breeding programmes.

5.1.4 Narrow-sense Heritability (h^2)

Productive tillers per plant, finger length, flag leaf width and flag leaf length had high heritability ($\geq 50\%$), this concurs with another study done in Ethiopia. Traits with high heritability are known to be mainly under additive genetic control (Allard, 1960) and will therefore respond to selection. In finger millet, literature on narrow sense heritability estimates is quite limited. Days to 50% flowering and number of fingers per main ear and plant height had low heritability. Similar results have been reported in a study of F1 where low heritability was found for days to flowering (8%), plant height (7%), productive tillers per plant (18%) with higher non-additive genetic effects (Krishnappa *et al.*, 2009). Based on findings of this study improvement through selection will be faster for primary tillers per plant, finger length, flag leaf length and flag leaf width.

5.1.5 Principal component analysis

Principal component analysis was used to provide a reduced dimension model that would indicate measured differences among groups. For both generations F3 and F4, in all the two environments and also in the combined analysis, a large proportion of the total variation was explained by the first two principal components. Among the F3 generation, the first two principal components explained 82.5% variation in MUARIK, 83% in NaSAARI, and 79.8% variation in combined location. Among the F4 generation the first two principal components accounted for 86.6% variation in MUARIK, 83.2% variation in NaSAARI and 80.8% variation in combined analysis. The percentages of total variability accounted for by the two principal components in each of the location and pooled analysis for both generations was higher than the 59.63% on seven and 71% on six principal components but less than 91.5% by three principal components reported in India (Dramadri, 2013; Bharathi, 2011; Gopal Reddy *et al.*, 2009).

The first two principal components separate F3 generation accessions based on plant height (0.860) and flag leaf length (0.487) in MUARIK, days to 50% flowering (0.861), days to 50% maturity (0.449) and plant height (0.968) in NaSAARI. In pooled analysis, principal component separates the accessions based on days to 50% flowering (0.791) and maturity (0.368) and plant height (0.911). The F4 accessions are separated by the first two principal components based on days to 50% flowering (0.49), days to 50% maturity (0.684) and plant

height (0.835) in MUARIK; plant height (0.874) and flag leaf length (0.869) in NaSAARI; days to 50% flowering (0.503) and maturity (0.538) and plant height (0.728) in combined analysis. Considering principal components for all the two environments and combined, the maturity traits such as days to 50% flowering and days to 50% maturity and phenological growth traits such as flag leaf length and plant height occurred in the two environments in the first two principal components at both generations, indicate the importance of these traits and their contribution to evolution among finger millet germplasm. These traits could thus be used as a basis for selecting parents in a finger breeding programme for finger millet (Ashfaq *et al.*, 2012). Highest contribution by these maturity traits and growth parameters was also reported in a number of studies (Dramadri, 2013; Bharathi, 2011, Bezawelataw *et al.*, 2006).

5.1.6 Clustering

Cluster analysis was done using the group average method based on the performance of the progenies using means of ten quantitative traits from pooled data across the two locations MUARIK and NaSAARI. Two main clusters were found among the F3 progeny with 30 lines in Cluster 1 and 17 lines in cluster 2. Similarly two major clusters were found among the F4, also with 31 lines in cluster I and 18 lines in cluster 2. In both cases the materials clustered according to their male wild parent cross i.e. *E. Africana* ((labelled c or a) or *E. Kigeziensis* (labelled b or c-b). This clustering depicts the distinctiveness of these materials and could be manage the germplasm and guide their deployment in finger millet breeding programmes (Appendix VII-X).

5.1.7 Identification of trait specific accessions

In any crop, improvement of yield and other traits like quality, biotic and abiotic stresses can be achieved by identifying gene/trait specific sources. Identification of promising resources for the environment sensitive quantitative characters is a difficult task because such traits are highly environment interactive and require multi-environment testing to accurately characterize them (Upadhyaya *et al.*, 2010). However with the use of core and mini core collections, sources for high grain yield, high nutrients, tolerance to drought and disease have been identified to guide breeding activities (Upadhyaya *et al.*, 2011; Pande *et al.*, 2006; Kashiwagi *et al.*, 2005). Nevertheless there is need to further characterize any materials

deriving from these crosses. In this study, interspecific finger millet progenies at F3 & F4 were evaluated and led to the identification of novel materials that could be used in finger millet breeding. The number of accessions among the F4 generation that performed repeatedly better across the locations for the particular trait(s) were 36 for early flowering; 12 accessions for early maturity; 22 for more number of fingers; 10 for high basal tiller number and 24 accessions for long fingers, and 19 for tallness. 20 accessions were identified as multi-trait specific accessions which were found to be sources of more than one trait. These accessions could be utilized for simultaneous transfer of multiple traits in finger millet improvement programme. Out of 48 accessions at F4 generation, of the finger millet interspecific progenies, a total of 39 accessions were identified as trait specific for six important yield contributing traits (Table 17). 21 Multi-trait specific accessions were identified, which were found to be sources for more than one trait.

Table 23: Ten top performing F4 accessions for six quantitative traits

Trait	Range	Number of accessions	Top Ten Accessions
Days to 50% flowering	70-76 days	04	30***, 24**, 4**, 31**, 22**, 25**, 33, 32****, 21
Days to 50% maturity	≤ 99 days	12	44, 40***, 4**, 32***, 30***, 25**, 26**, 24**, 13, 46
Number of fingers/main ear	6-7 fingers	37	8, 11, 17***, 27, 26**, 48**, 32****, 14, 5, 29
Length of longest finger(cm)	≥ 6.0cm	24	43**, 3, 19**, 39**, 7, 6**, 47, 40***, 17***, 15
Number of primary tillers	6-7 tillers	10	40***, 19**, 43**, 10, 17***, 48**, 6**, 20, 39**, 2
Plant height (cm)	≥ 70cm	19	18, 30***, 25, 31**, 22**, 26**, 12, 32****, 3, 41

Accession identified for; **= two traits, ***= three traits, ****= four traits.

5.2 Reaction of the interspecific hybrid to blast

Significant differences ($P \leq 0.05$) in reaction of the test lines to blast was found. Over 50% of test lines were resistant to leaf, neck and head blast under artificial inoculation. This high percentage of resistance could present good source of genes for resistance to blast. Resistant genotypes developed symptoms slowly, perhaps indicative of reduced disease development commonly associated with multi gene based systems (horizontal resistance) (Van der plank, 1963). If this is true then the slow blasting genotypes identified in this study stand to have

long term resistance and may withstand the high blast pathogen variability (Takan *et al.*, 2012).

Among the F3 progeny, nine lines; 19c,24b,13a,6b,2b,20b,24c-b and 22c-b were found to be resistant to leaf blast, the best performing accessions for leaf blast among the study materials had a score of 1.7-2.0, this was better than a score of the resistant check (Gulu E) of 2.2 (moderately resistant). Even the materials identified as the worst performing for leaf blast were comparably more resistant than the susceptible check (KATFMI). At F4, five lines; 25a, 18b, 19b, 25c-b and 7b were resistant to leaf blast, all lines were resistant to neck blast and twenty lines were resistant to head blast. A similar trend was also observed among the F4 progenies, indicating stability of the disease resistance among the interspecific test lines. Hence these resistant accessions identified will be useful parents in breeding new lines with blast resistance. Sources of blast resistance have been reported in finger millet, and efforts have been made to incorporate resistance into improved cultivars and elite breeding lines (Nagaraja *et al.*, 2008; Nagaraja and Mantur, 2007). Genotypes (14c, 20c, 22c-b, 23a, 28a, 5b) that were susceptible to leaf blast and later showed resistance to neck and head blast could be due to changes in the physiological status of plant hence the expression of mature (adult) resistance as was reported in rice (Li *et al.*., 2007). Similar findings of adult resistance have been reported by other authors in finger millet and foxtail millet (Manyasa, 2013; Sharma *et al.*, 2013).

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) are useful in obtaining a measure of the genetic variability in the expression of the target traits. Higher GCV than PCV estimates would suggest that the phenotypic expression of the trait is more influenced by genes than the environment whereas higher PCV estimates would mean the trait is more influenced by the environment as was the case in this study. Moderate broad sense heritability and high genetic advance percentage were estimated for neck blast, low heritability and genetic advance were estimated for both leaf and head blast, this means selection for leaf and head blast should be done at later generation.

5.3 Correlations among the blast types

The correlations in this study among the blast forms were weak. This is similar to other finding by other authors of weak correlation and no correlations at all among leaf, neck and head blast in finger millet and foxtail millet, this could be attributed to non-linkage of leaf

and neck blast resistance in the cultivars involved (Babu *et al.*, 2013; Owere, 2013; Sharma *et al.*, 2013). However other studies have found high significant correlations among the blast forms (Manyasa, 2013; Babu *et al.*, 2013). These different findings could be attributed to variation in weather/ test conditions as the pathogen is known to be highly variable depending on the prevailing climatic conditions (Esele, 2002; Takan *et al.*, 2012). Also this means that using leaf blast to select for neck and head blast resistance should be done with caution.

CHAPTER SIX

CONCLUSIONS AND RECOMMENDATIONS

6.1 Conclusions

This study investigated phenotypic variability among the interspecific finger millet progenies and involved field evaluations to characterize phenotypic diversity among the selected finger millet accessions. Additionally, resistance to finger millet blast disease among these accessions was also studied. Significant variance in most of the traits in individual environments showed that the progenies from the interspecific crosses were diverse and had sufficient scope for selection and utilization in crop improvement program. Considering principal components, maturity traits such as days to 50% flowering and days to 50% maturity and the phenological traits such as the growth traits- flag leaf length and plant height could be used to guide selection of promising materials in breeding programmes involving interspecific hybrids such as was done in this study. These accessions could be utilized for simultaneous transfer of multiple traits in finger millet improvement programme.

Over 50% of the F4 accessions presented resistance to leaf, neck and head blast under artificial inoculation. This high percentage of resistance could present good source of resistance to blast. Resistant genotypes were slow in developing blast probably due to horizontal resistance, which may enable them to withstand blast pathogen variability for a longer time. Moreover, lines identified as the worst performing among the interspecific hybrids for leaf blast still developed less disease than the susceptible check (KATFMI), increasing opportunity for farmers to access resilient material than commercially available varieties currently in use. . Two lines (25a and 25c-b) were resistant to all the three forms of blast disease; thirteen lines (8b, 6b, 8a, 24b, 22b, 22a, 21b, 20b, 19c, 19c-b, 17b, 13c-b, 13a) were resistant to neck blast and head blast and moderately resistant to leaf blast. These resistant accessions identified will be useful parents in breeding new lines with blast resistance.

6.2 Recommendations

The variability among the finger millet accessions can be used for selecting most diverse parents for use in developing finger populations to be used in the breeding programme. This study was done for only one season in two locations; there is need for the accessions to be evaluated across seasons and in more locations to establish their stability across seasons. A nutrition study should also be conducted to ascertain the nutrient content of these interspecific progenies especially for nutrients such as Iron and Zinc, identification of genotypes with good sources of micronutrient content will be useful for alleviating micronutrient deficiency.

Blast pathogen races have been reported to differ between season in rice and between agro-ecologies in finger millet. It is therefore essential that these accessions are adequately screened for blast across seasons and agro-ecologies to ascertain stability of their resistance especially in humid and sub-humid finger millet production agro-ecologies where blast is prevalent. The new sources for blast resistance can be used for improving finger millet varieties with farmer-preferred traits.

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LIST OF APPENDICES

Appendix 1: Mean performance of F3 progeny for ten quantitative traits at NaSAARI, 2013 second rain season

ENTRY	Name	DH	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	64.2	98.5	6.2	6.5	1.4	34.2	0.8	70.2	4.8	1.8
2	15a	64.2	96.2	5.9	7.2	1.2	29.7	0.6	70.8	6.1	2.2
3	8c-b	66.0	97.4	5.1	7.5	1.4	31.7	0.8	72.7	6.3	1.9
4	13c-b	65.4	97.2	5.4	6.2	1.4	31.0	0.8	70.9	6.8	1.9
5	22c-b	64.6	99.5	6.6	6.7	1.4	35.0	0.8	75.0	5.6	1.9
6	14c	65.2	98.5	5.0	7.6	1.2	33.4	0.8	68.9	5.1	2.9
7	23a	63.0	97.5	5.2	7.0	1.2	26.7	0.5	65.6	4.6	2.0
8	4c-b	64.8	99.6	5.5	6.3	1.2	29.3	0.7	67.7	5.3	2.1
9	18c-b	63.9	96.6	5.1	6.5	1.4	30.0	0.8	69.3	4.7	1.6
10	18a	65.1	96.4	5.0	8.2	1.2	27.1	0.6	69.7	5.5	2.4
11	2c-b	62.7	95.2	5.6	6.7	1.2	33.4	0.8	72.2	5.3	1.9
12	13a	64.5	97.7	5.3	7.7	1.2	30.7	0.7	71.3	8.7	2.5
13	9a	65.2	98.0	5.1	6.9	1.2	27.9	0.6	72.1	7.0	2.1
14	22a	64.8	97.5	4.6	7.5	1.1	25.2	0.7	64.8	6.0	2.2
15	8a	64.5	96.7	6.4	6.7	1.0	32.9	0.7	71.7	5.2	2.1
16	19c-b	65.5	99.5	6.3	7.2	1.2	39.8	0.8	74.7	4.4	1.8
17	6a	64.0	97.4	5.4	7.1	1.3	29.4	0.6	70.6	6.1	2.9
18	7c-b	63.1	95.6	5.6	6.5	1.2	37.4	0.9	71.8	4.8	1.8
19	3a	65.3	100.3	5.0	7.4	1.3	29.5	0.6	73.6	6.2	2.1
20	25a	63.9	100.3	5.2	7.7	1.4	31.6	0.6	67.2	5.3	1.8
21	1b	62.4	95.3	5.9	6.3	1.2	30.4	0.8	70.1	5.5	2.0
22	14b	63.1	96.4	6.0	6.9	1.5	32.9	0.8	77.5	5.1	1.7
23	20b	62.7	96.3	5.4	6.6	1.2	34.3	0.8	76.4	6.2	2.3
24	22b	63.5	97.9	6.0	6.2	1.2	31.6	0.8	73.3	4.9	2.1
25	8b	62.4	96.5	4.9	6.3	1.1	34.4	0.8	77.6	4.0	2.4
26	19b	61.4	100.7	5.6	6.0	1.2	32.9	0.8	76.1	5.2	2.0
27	21b	63.0	96.4	5.7	6.0	1.3	31.6	0.8	69.4	4.6	2.1

28	24b	65.0	97.5	5.2	6.9	1.5	30.3	0.7	69.7	5.1	1.9
29	26b	63.5	98.7	5.7	6.3	1.3	30.5	0.8	76.2	3.9	2.0
30	2b	62.3	97.8	6.0	6.8	1.3	36.0	0.8	79.5	5.2	1.8
31	7b	63.0	97.1	4.9	5.9	1.3	31.3	0.8	70.0	4.7	1.5
32	6b	63.8	98.7	6.3	6.4	1.3	36.2	0.9	76.1	6.2	1.8
33	5b	60.8	96.6	5.2	5.9	1.2	32.9	0.8	71.0	4.0	1.9
34	10b	63.4	96.8	5.8	5.9	1.2	32.3	0.8	70.0	4.8	1.6
35	3b	62.7	95.2	6.7	6.2	1.2	31.3	0.7	76.3	6.8	1.7
36	17b	64.4	95.3	5.1	6.3	1.2	31.8	0.8	73.2	6.2	1.8
37	12b	63.1	99.1	5.1	5.9	1.3	31.1	0.8	75.5	4.6	2.2
38	18b	61.3	97.3	5.8	6.3	1.2	34.0	0.8	74.7	4.5	2.0
39	12a	65.3	99.6	5.0	8.1	1.2	30.4	0.6	63.7	6.0	2.5
40	1a	63.1	99.6	4.2	7.8	1.2	27.7	0.6	65.3	5.2	2.5
41	1c-b	66.9	97.5	5.0	7.6	1.5	32.6	0.8	78.3	4.8	2.1
42	25c-b	63.5	97.7	5.9	6.6	1.2	35.6	0.8	76.5	6.0	2.0
43	28a	64.5	97.5	5.1	7.8	1.2	29.8	0.7	69.8	6.1	2.5
44	16c-b	64.3	95.5	5.4	6.2	1.3	33.7	0.8	66.9	5.3	1.8
45	7a	65.6	96.4	5.3	8.0	1.3	27.3	0.6	73.5	7.1	2.5
46	13c	68.0	97.1	5.6	7.7	0.9	28.9	0.7	63.2	6.6	1.8
47	19c	65.9	96.4	5.0	7.2	1.2	29.0	0.7	71.4	5.5	2.8
48	20c	64.9	99.2	5.9	7.2	1.2	29.7	0.7	77.0	7.9	2.1
Mean		64.0	97.5	5.5	6.8	1.2	31.6	0.7	71.8	5.5	2.1
Min		60.8	95.2	4.2	5.9	0.9	25.2	0.5	63.2	3.9	1.5
Max		68.0	100.7	6.7	8.2	1.5	39.8	0.9	79.5	8.7	2.9
SEM		1.2	1.3	0.5	0.3	0.1	2.4	0.1	4.1	0.8	0.3
CV (%)		6.5	5.1	13.3	4.4	3.0	52.5	1.6	70.9	35.9	13.0

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers, SEM= Standard error of mean, CV= Co-variance

Appendix 2: Mean performance of F3 progeny for ten quantitative traits at MUARIK, 2013 second rain season

ENTRY	Name	DF	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	78.7	98.1	5.3	5.3	1.0	32.6	1.3	62.8	4.0	2.5
2	15a	81.6	102.0	5.5	5.7	0.9	32.2	1.2	59.3	5.0	3.6
3	8c-b	79.6	95.7	5.3	4.7	1.1	36.3	1.4	73.4	4.5	3.5
4	13c-b	78.9	96.9	7.0	5.0	0.9	34.5	1.3	62.4	4.0	3.1
5	22c-b	81.5	98.7	5.2	4.4	1.0	31.9	1.2	65.5	5.7	2.7
6	14c	96.5	106.8	5.5	5.5	1.0	34.6	1.3	64.9	4.5	4.5
7	23a	82.8	100.0	7.4	5.4	0.9	29.7	1.1	74.5	5.4	4.7
8	4c-b	79.2	99.0	5.6	4.8	1.1	30.9	1.3	60.4	3.4	3.4
9	18c-b	73.7	91.2	5.3	5.3	1.0	33.7	1.3	70.4	3.8	2.4
10	18a	82.2	99.5	6.4	5.7	0.9	30.9	1.2	62.4	6.0	5.0
11	2c-b	83.1	100.1	6.6	4.8	1.0	33.3	1.2	59.4	4.5	3.0
12	13a	78.3	93.3	5.9	5.4	0.9	30.9	1.3	61.5	6.0	4.0
13	9a	95.3	105.2	6.3	5.2	1.1	30.6	1.2	64.8	5.6	3.9
14	22a	84.2	101.4	6.7	5.7	0.9	29.7	1.1	68.5	5.9	3.4
15	8a	84.8	111.6	5.0	5.5	1.0	25.4	0.9	62.4	4.6	2.9
16	19c-b	80.7	95.8	4.1	4.4	1.0	31.8	1.1	58.0	3.4	2.5
17	6a	86.7	102.1	5.7	5.7	0.9	27.2	1.1	66.0	6.5	2.9
18	7c-b	76.2	101.0	6.5	4.7	1.0	32.1	1.3	63.4	3.5	2.5
19	3a	87.2	99.9	6.1	6.1	0.8	27.8	0.9	67.2	5.5	3.3
20	25a	82.0	100.5	6.5	5.6	0.8	33.7	1.2	69.9	5.9	3.9
21	1b	79.8	100.3	6.0	4.1	0.9	34.1	1.4	64.8	3.9	3.0
22	14b	81.2	100.8	6.1	4.1	1.0	34.8	1.5	59.3	4.1	2.9
23	20b	80.4	96.9	5.0	4.8	1.0	29.8	1.2	61.0	3.2	2.6
24	22b	81.8	96.5	6.5	4.6	1.0	32.0	1.4	69.3	4.5	3.1
25	8b	79.2	96.4	5.5	3.8	1.1	34.4	1.5	65.9	4.0	2.7
26	19b	78.6	96.7	5.9	4.7	1.1	28.8	1.4	66.4	3.7	2.8
27	21b	72.4	95.6	5.7	4.8	1.0	33.1	1.2	63.5	3.7	3.5
28	24b	77.3	98.8	5.3	4.1	1.0	30.8	1.3	66.7	3.6	3.4

29	26b	74.7	98.7	5.2	4.3	1.0	32.2	1.2	62.1	3.9	2.9
30	2b	73.1	89.0	4.8	5.3	1.1	32.9	1.5	60.9	3.7	2.2
31	7b	76.5	106.3	5.6	4.4	1.0	33.7	1.3	67.7	4.0	2.9
32	6b	79.7	102.3	4.7	3.8	1.0	31.2	1.3	66.1	4.1	2.6
33	5b	74.9	94.2	6.1	4.0	1.0	30.4	1.3	71.2	4.1	3.0
34	10b	79.5	103.1	4.4	3.9	1.0	29.6	1.2	53.7	3.0	3.0
35	3b	73.9	93.2	5.5	4.6	1.0	31.3	1.3	64.2	3.3	2.4
36	17b	80.0	104.9	5.4	4.2	1.1	31.7	1.3	63.6	3.4	2.7
37	12b	75.6	94.8	5.5	4.2	1.2	33.5	1.2	62.7	4.8	3.4
38	18b	77.6	93.3	6.0	5.1	1.1	34.1	1.3	65.3	3.6	1.8
39	12a	84.5	104.8	5.4	5.6	0.9	30.1	1.3	61.7	5.8	3.7
40	1a	82.2	100.7	5.5	5.4	1.0	30.6	1.1	55.5	5.0	3.1
41	1c-b	81.1	94.6	5.4	5.3	1.0	31.8	1.2	68.7	3.9	2.8
42	25c-b	79.1	95.4	3.9	3.8	1.0	33.6	1.4	55.7	3.8	2.7
43	28a	81.9	98.6	5.9	4.7	0.9	29.4	1.0	62.9	6.8	4.9
44	16c-b	80.3	95.2	6.1	4.5	1.1	35.6	1.5	64.2	5.0	2.7
45	7a	96.7	105.4	6.3	4.9	1.0	29.2	1.2	65.4	5.6	5.6
46	13c	115.8	108.9	5.4	4.5	1.0	26.8	1.1	52.8	3.7	3.1
47	19c	83.8	96.5	5.4	4.1	0.9	24.0	1.0	58.1	5.6	5.2
48	20c	82.8	106.9	6.2	6.1	1.1	32.5	1.2	71.3	5.2	2.7
Mean		81.6	99.3	5.7	4.8	1.0	31.5	1.2	63.9	4.5	3.2
Min		72.4	89.0	3.9	3.8	0.8	24.0	0.9	52.8	3.0	1.8
Max		115.8	111.6	7.4	6.1	1.2	36.3	1.5	74.5	6.8	5.6
SEM		4.1	4.4	0.7	0.4	0.1	1.8	0.1	5.0	0.7	0.5
CV(%)		61.8	59.4	29.7	12.0	1.7	30.1	2.4	50.7	33.7	19.1

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers

Appendix 3: Mean performance of F3 progeny for ten quantitative traits across locations, 2013 second rain season

ENTRY	Name	DF	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	71.5	98.3	5.8	5.9	1.2	33.4	1.0	66.5	4.4	2.1
2	15a	72.9	99.1	5.7	6.5	1.1	31.0	0.9	65.0	5.6	2.9
3	8c-b	72.8	96.5	5.2	6.1	1.3	34.0	1.1	73.0	5.4	2.7
4	13c-b	72.2	97.0	6.2	5.6	1.1	32.8	1.1	66.7	5.4	2.5
5	22c-b	73.0	99.1	5.9	5.5	1.2	33.4	1.0	70.2	5.6	2.3
6	14c	80.8	102	5.2	6.5	1.1	34.0	1.0	66.9	4.8	3.7
7	23a	72.9	98.7	6.3	6.2	1.0	28.2	0.8	70.0	5.0	3.4
8	4c-b	72.0	99.3	5.6	5.6	1.1	30.1	1.0	64.0	4.3	2.8
9	18c-b	68.8	93.9	5.2	5.9	1.2	31.9	1.0	69.8	4.3	2.0
10	18a	73.6	98.0	5.7	6.9	1.0	29.0	0.9	66.0	5.8	3.7
11	2c-b	72.9	97.7	6.1	5.7	1.1	33.4	1.0	65.8	4.9	2.4
12	13a	71.4	95.5	5.6	6.6	1.1	30.8	1.0	66.4	7.3	3.2
13	9a	80.3	101	5.7	6.0	1.1	29.3	0.9	68.4	6.3	3.0
14	22a	74.5	99.4	5.6	6.6	1.0	27.4	0.9	66.6	6.0	2.8
15	8a	74.6	104	5.7	6.1	1.0	29.2	0.8	67.0	4.9	2.5
16	19c-b	73.1	97.6	5.2	5.8	1.1	35.8	1.0	66.4	3.9	2.1
17	6a	75.3	99.7	5.6	6.4	1.1	28.3	0.9	68.3	6.3	2.9
18	7c-b	69.6	98.3	6.0	5.6	1.1	34.8	1.1	67.6	4.1	2.1
19	3a	76.3	100	5.5	6.7	1.1	28.6	0.8	70.4	5.9	2.7
20	25a	73.0	100	5.8	6.6	1.1	32.7	0.9	68.6	5.6	2.9
21	1b	71.1	97.8	5.9	5.2	1.1	32.2	1.1	67.4	4.7	2.5
22	14b	72.1	98.6	6.0	5.5	1.2	33.8	1.2	68.4	4.6	2.3
23	20b	71.5	96.6	5.2	5.7	1.1	32.0	1.0	68.7	4.7	2.4
24	22b	72.7	97.2	6.3	5.4	1.1	31.8	1.1	71.3	4.7	2.6
25	8b	70.8	96.4	5.2	5.1	1.1	34.4	1.1	71.7	4.0	2.5
26	19b	70.0	98.7	5.7	5.4	1.2	30.8	1.1	71.2	4.4	2.4

27	21b	67.7	96.0	5.7	5.4	1.1	32.4	1.0	66.5	4.2	2.8
28	24b	71.1	98.1	5.3	5.5	1.3	30.6	1.0	68.2	4.4	2.7
29	26b	69.1	98.7	5.4	5.3	1.2	31.4	1.0	69.2	3.9	2.5
30	2b	67.7	93.4	5.4	6.0	1.2	34.4	1.2	70.2	4.4	2.0
31	7b	69.8	101	5.2	5.1	1.2	32.5	1.0	68.9	4.3	2.2
32	6b	71.8	100	5.5	5.1	1.1	33.7	1.1	71.1	5.1	2.2
33	5b	67.8	95.4	5.7	5.0	1.1	31.7	1.1	71.1	4.0	2.4
34	10b	71.5	100	5.1	4.9	1.1	31.0	1.0	61.9	3.9	2.3
35	3b	68.3	94.2	6.1	5.4	1.1	31.3	1.0	70.2	5.1	2.1
36	17b	72.2	100	5.2	5.2	1.1	31.7	1.0	68.4	4.8	2.3
37	12b	69.4	97.0	5.3	5.0	1.2	32.3	1.0	69.1	4.7	2.8
38	18b	69.4	95.3	5.9	5.7	1.2	34.0	1.0	70.0	4.1	1.9
39	12a	74.9	102	5.2	6.9	1.1	30.2	0.9	62.7	5.9	3.1
40	1a	72.7	100	4.8	6.6	1.1	29.1	0.9	60.4	5.1	2.8
41	1c-b	74.0	96.1	5.2	6.4	1.3	32.2	1.0	73.5	4.3	2.4
42	25c-b	71.3	96.6	4.9	5.2	1.1	34.6	1.1	66.1	4.9	2.4
43	28a	73.2	98.1	5.5	6.3	1.0	29.6	0.8	66.4	6.5	3.7
44	16c-b	72.3	95.3	5.8	5.4	1.2	34.6	1.1	65.6	5.1	2.2
45	7a	81.1	100	5.8	6.5	1.2	28.2	0.9	69.5	6.4	4.0
46	13c	91.9	103	5.5	6.1	1.0	27.8	0.9	58.0	5.1	2.5
47	19c	74.9	96.4	5.2	5.6	1.1	26.5	0.9	64.7	5.6	4.0
48	20c	73.9	103	6.1	6.6	1.1	31.1	0.9	74.1	6.5	2.4
Mean		72.8	98.4	5.6	5.8	1.1	31.5	1.0	67.9	5.0	2.6
Min		67.7	93.4	4.8	4.9	1.0	26.5	0.8	58.0	3.9	1.9
Max		91.9	104	6.3	6.9	1.3	35.8	1.2	74.1	7.3	4.0
SEM		2.7	2.6	0.5	0.3	0.1	1.6	0.1	3.1	0.5	0.3
CV (%)		29.6	21.3	14.2	4.5	1.5	25.5	1.4	41.8	17.7	13.2

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers

Appendix 4: Mean performance of F4 progeny for ten quantitative traits at NaSAARI, 2013 second rain season

ENTRY	Name	DF	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	66.6	97.6	6.3	6.3	0.9	34.1	0.9	66.5	4.6	0.9
2	15a	64.8	96.4	4.9	7.7	0.9	25.0	0.7	63.8	5.2	1.4
3	8c-b	66.2	97.7	5.7	6.9	1.0	35.6	0.8	74.7	6.0	0.9
4	13c-b	64.3	96.7	5.5	6.2	0.9	32.3	0.8	65.4	4.5	0.2
5	22c-b	65.5	97.6	6.5	6.2	1.0	33.2	0.9	69.4	5.0	0.9
6	14c	67.2	97.7	5.5	8.1	0.9	36.2	0.8	72.3	6.9	0.5
7	23a	64.6	97.0	5.6	7.5	1.0	26.7	0.6	70.6	5.6	1.1
8	4c-b	64.8	99.7	5.9	5.7	1.0	26.1	0.7	65.7	4.5	1.3
9	18c-b	64.4	95.6	6.7	6.1	1.0	28.9	0.7	71.2	4.4	1.0
10	18a	67.1	96.0	5.6	7.6	0.9	29.6	0.7	67.2	5.6	2.1
11	2c-b	66.6	96.0	5.8	6.5	1.0	32.3	0.8	63.3	4.5	1.2
12	13a	64.3	96.3	6.1	5.8	1.0	26.2	0.7	72.8	5.0	1.3
13	9a	65.5	97.7	5.4	7.2	0.9	27.9	0.7	64.8	5.1	1.5
14	22a	68.3	97.3	6.5	7.5	0.8	25.8	0.7	66.4	6.2	1.5
15	8a	66.8	95.7	5.0	7.4	1.0	28.9	0.6	67.7	4.5	1.5
16	19c-b	65.1	96.0	6.3	6.3	1.1	35.4	0.8	71.9	4.5	1.1
17	6a	66.8	97.3	6.5	7.8	0.9	29.6	0.7	73.1	5.8	1.3
18	7c-b	65.8	96.0	6.4	6.3	1.1	35.2	0.8	71.1	4.9	1.2
19	3a	67.3	99.4	5.5	7.7	1.0	28.3	0.7	67.6	5.3	2.5
20	25a	65.8	98.7	5.5	7.2	1.0	27.1	0.6	72.4	6.0	1.2
21	1b	65.7	98.0	6.6	6.3	1.0	31.5	0.8	73.2	5.6	0.9
22	14b	64.3	96.7	6.1	6.0	1.0	35.2	0.9	69.8	4.9	1.3
23	20b	64.7	96.4	5.8	6.2	1.0	30.6	0.9	65.4	5.1	1.1
24	22b	63.2	99.6	4.8	5.1	1.0	26.6	0.7	63.5	3.9	0.6
25	8b	63.2	98.7	5.8	6.1	1.0	33.1	0.8	68.8	4.1	1.5
26	19b	65.2	99.0	6.1	5.7	1.0	28.6	0.8	78.4	6.2	1.0

27	21b	65.0	95.7	6.4	5.9	1.1	34.6	0.8	68.5	5.5	0.8
28	24b	65.6	95.7	5.9	5.5	1.0	27.5	0.7	61.6	4.6	0.8
29	26b	66.5	96.0	6.7	6.3	1.1	31.3	0.8	67.1	5.3	0.8
30	2b	65.2	99.7	6.3	5.8	1.1	29.9	0.8	64.8	5.3	1.0
31	7b	63.8	99.7	5.1	6.2	1.0	29.9	0.8	66.8	4.2	1.1
32	6b	65.2	97.0	6.5	5.7	1.0	33.6	0.8	74.7	4.7	1.4
33	5b	63.8	94.4	6.1	5.6	1.0	31.7	0.7	68.5	4.7	0.8
34	10b	66.4	98.7	5.4	6.5	1.0	32.4	0.8	68.3	5.2	0.9
35	3b	63.5	97.0	5.4	5.6	1.0	31.0	0.8	65.5	4.4	1.2
36	17b	66.1	97.3	5.9	5.9	1.0	30.6	0.8	67.0	4.2	0.9
37	12b	64.2	98.4	6.0	6.1	1.0	32.5	0.8	70.8	5.4	1.0
38	18b	65.9	99.3	5.4	5.8	1.0	26.0	0.8	69.8	5.0	1.0
39	12a	65.5	97.4	4.7	7.6	0.9	27.6	0.7	64.5	4.7	1.8
40	1a	64.2	96.7	6.0	7.8	1.1	28.3	0.7	67.3	4.9	1.5
41	1c-b	67.2	97.0	5.5	6.7	1.0	29.7	0.7	74.7	4.9	1.4
42	25c-b	65.7	97.6	5.5	6.4	1.0	31.0	0.7	62.7	5.1	0.4
43	28a	66.3	94.3	5.4	7.7	1.0	27.9	0.7	66.2	4.6	1.0
44	16c-b	65.1	96.0	5.8	5.7	1.0	26.6	0.7	63.6	4.9	0.6
45	7a	67.7	96.0	5.9	7.5	1.0	28.7	0.7	69.3	5.1	1.5
46	13c	65.6	96.7	6.6	7.0	1.1	35.0	0.8	68.2	4.6	0.7
47	19c	67.3	94.6	5.8	7.4	0.9	33.1	0.8	68.5	6.6	1.5
48	20c	67.5	96.0	6.3	7.6	1.0	30.7	0.7	73.0	7.0	1.3
Mean		65.6	97.1	5.9	6.6	1.0	30.4	0.8	68.5	5.1	1.1
Min		63.2	94.3	4.7	5.1	0.8	25.0	0.6	61.6	3.9	0.2
Max		68.3	99.7	6.7	8.1	1.1	36.2	0.9	78.4	7.0	2.5
SEM		0.9	1.4	0.4	0.3	0.0	2.3	0.0	3.4	0.6	0.3
CV (%)		3.4	6.3	9.7	3.0	0.5	52.4	0.8	49.8	18.4	22.5

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers

Appendix 5: Mean performance of F4 progeny for ten quantitative traits at MUARIK, 2013 second rain season

ENTRY	Name	DF	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	86.92	106.3	5.81	5.68	1.07	30.66	1.33	63.19	3.23	2.74
2	15a	86.43	111.3	5.72	4.83	1.10	30.17	1.21	63.36	8.34	3.26
3	8c-b	91.27	113.5	5.10	5.83	0.93	36.41	1.25	75.56	4.04	2.62
4	13c-b	75.98	98.8	5.45	5.84	1.07	33.58	1.20	66.15	2.84	2.51
5	22c-b	83.01	108.5	6.71	5.21	1.08	30.81	1.23	68.87	3.66	3.31
6	14c	93.98	114.1	6.51	4.84	1.04	28.06	1.21	65.00	5.29	2.84
7	23a	89.72	109.3	6.11	5.36	0.96	30.61	1.19	58.28	4.96	2.42
8	4c-b	83.55	107.5	6.44	5.53	1.03	30.89	1.31	63.72	3.31	2.87
9	18c-b	87.91	112.8	5.26	4.71	1.08	31.69	1.17	67.50	4.84	2.74
10	18a	88.85	103.7	5.75	5.00	1.05	31.43	1.31	71.70	6.40	3.02
11	2c-b	82.94	103.9	6.59	5.25	1.05	30.81	1.24	60.03	3.83	2.46
12	13a	88.40	106.8	4.75	5.31	1.13	31.35	1.27	70.41	3.86	2.16
13	9a	83.92	100.8 0	5.73	4.83	1.14	30.89	1.29	70.20	5.69	2.68
14	22a	85.82	112.9	6.16	4.76	1.02	29.51	1.37	53.15	4.32	2.59
15	8a	91.08	115.2	5.43	6.34	1.07	33.18	1.31	62.41	6.23	1.88
16	19c-b	82.81	110.1	5.29	2.62	1.07	31.16	1.27	59.43	6.09	2.73
17	6a	88.93	105.1	6.01	5.40	1.04	30.21	1.25	63.73	6.21	3.22
18	7c-b	80.62	102.9	5.43	4.99	1.10	32.97	1.32	68.36	3.10	2.09
19	3a	88.34	111.5	5.77	5.03	1.10	30.58	1.17	58.54	6.22	3.29
20	25a	86.71	107.6	5.85	4.91	1.05	33.18	1.19	64.50	6.38	4.52
21	1b	78.73	107.6	5.75	5.64	1.08	29.69	1.25	65.93	3.72	1.85
22	14b	76.57	106.0	5.38	5.30	1.09	33.24	1.31	71.26	3.11	2.72
23	20b	84.56	107.8	5.37	5.04	1.06	31.36	1.25	53.60	2.69	2.35
24	22b	77.00	98.80	5.87	4.76	1.08	32.60	1.29	71.09	2.81	2.67
25	8b	79.22	98.60	5.25	4.84	1.12	33.35	1.40	71.03	3.25	2.46

26	19b	79.44	98.90	6.51	5.49	1.14	30.97	1.26	64.31	3.38	2.52
27	21b	86.27	112.2	6.16	5.49	1.01	31.40	1.21	61.88	4.25	2.52
28	24b	81.24	110.2	5.73	4.74	1.15	32.99	1.27	65.60	2.69	3.24
29	26b	82.58	112.2	6.49	4.73	1.16	34.75	1.30	60.81	4.08	2.32
30	2b	74.9	96.5	5.7	5.1	1.0	33.5	1.3	74.9	3.1	2.3
31	7b	76.9	107.6	6.5	4.8	1.1	33.2	1.3	73.7	2.6	1.9
32	6b	78.6	98.6	6.2	5.0	0.9	31.6	1.4	73.4	4.5	2.4
33	5b	79.8	106.1	5.3	5.2	1.0	30.4	1.2	58.0	3.9	2.8
34	10b	82.5	114.2	5.5	5.6	1.0	35.2	1.3	60.4	3.5	2.9
35	3b	81.4	104.9	5.8	4.8	1.1	32.3	1.2	66.9	3.2	2.5
36	17b	84.3	106.5	5.7	4.8	1.1	30.2	1.2	57.5	3.1	2.4
37	12b	83.5	100.4	5.4	5.3	1.1	35.3	1.1	63.3	3.4	2.5
38	18b	82.3	103.7	5.8	5.1	1.2	34.9	1.4	68.0	3.1	2.2
39	12a	86.3	104.9	6.0	5.1	1.1	31.2	1.2	64.0	8.7	3.4
40	1a	85.4	98.7	5.2	5.3	1.1	33.2	1.1	66.9	6.6	2.9
41	1c-b	81.7	107.9	5.0	5.5	1.1	34.0	1.3	77.5	4.1	2.3
42	25c-b	83.0	102.0	5.4	5.1	1.1	32.7	1.2	66.8	2.6	4.2
43	28a	90.6	109.8	5.8	4.9	1.1	29.4	1.1	62.6	7.4	2.5
44	16c-b	80.4	97.8	5.8	5.4	1.0	33.7	1.2	71.0	3.9	1.9
45	7a	84.7	103.6	4.9	4.8	1.1	33.3	1.2	61.7	5.3	3.0
46	13c	83.3	101.9	5.6	5.2	1.1	32.0	1.2	61.8	4.4	1.6
47	19c	99.6	133.2	6.0	5.6	1.0	34.7	1.2	47.8	3.9	1.7
48	20c	95.3	116.0	6.4	4.4	1.1	29.5	1.1	64.3	5.1	2.5
Mean		84.3	106.9	5.8	5.1	1.1	32.1	1.2	65.0	4.4	2.6
Min		74.9	96.5	4.8	2.6	0.9	28.1	1.1	47.8	2.6	1.6
Max		99.6	133.2	6.7	6.3	1.2	36.4	1.4	77.5	8.7	4.5
SEM		3.4	5.3	0.5	0.4	0.0	1.5	0.1	5.1	0.8	0.5
CV (%)		40.4	79.5	12.6	8.4	0.7	21.3	1.1	37.8	46.2	33.0

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers

Appendix 6: Mean performance of F4 progeny for ten quantitative traits across locations, 2013 second rain season

ENTRY	Name	DF	DM	NF	FL	FW	FLL	FLW	PH	PTN	STN
1	24c-b	76.8	102.	6.1	6.0	1.0	32.4	1.1	64.9	3.9	1.8
2	15a	75.6	103	5.3	6.3	1.0	27.6	0.9	63.6	6.8	2.3
3	8c-b	78.7	105	5.4	6.3	1.0	36.0	1.0	75.2	5.0	1.8
4	13c-b	70.1	97.7	5.5	6.0	1.0	32.9	1.0	65.8	3.7	1.3
5	22c-b	74.2	103	6.6	5.7	1.0	32.0	1.1	69.1	4.3	2.1
6	14c	80.6	105	6.0	6.5	1.0	32.2	1.0	68.6	6.1	1.6
7	23a	77.2	103	5.9	6.4	1.0	28.6	0.9	64.4	5.3	1.8
8	4c-b	74.2	103	6.2	5.6	1.0	28.5	1.0	64.7	3.9	2.1
9	18c-b	76.1	104	6.0	5.4	1.0	30.3	1.0	69.4	4.6	1.9
10	18a	78.0	99.8	5.7	6.3	1.0	30.5	1.0	69.5	6.0	2.6
11	2c-b	74.8	100	6.2	5.9	1.0	31.5	1.0	61.7	4.2	1.8
12	13a	76.3	101	5.4	5.6	1.0	28.8	1.0	71.6	4.4	1.7
13	9a	74.7	99.3	5.6	6.0	1.0	29.4	1.0	67.5	5.4	2.1
14	22a	77.1	105	6.3	6.1	0.9	27.7	1.0	59.8	5.3	2.0
15	8a	78.9	105	5.2	6.9	1.0	31.0	1.0	65.1	5.4	1.7
16	19c-b	74.0	103	5.8	4.5	1.1	33.3	1.0	65.7	5.3	1.9
17	6a	77.8	101	6.2	6.6	1.0	29.9	1.0	68.4	6.0	2.2
18	7c-b	73.2	99.5	5.9	5.6	1.1	34.1	1.1	69.7	4.0	1.7
19	3a	77.8	105	5.6	6.3	1.0	29.5	0.9	63.1	5.8	2.9
20	25a	76.3	103	5.7	6.0	1.0	30.2	0.9	68.4	6.2	2.9
21	1b	72.2	102	6.2	5.9	1.1	30.6	1.0	69.6	4.7	1.4
22	14b	70.4	101	5.8	5.7	1.0	34.2	1.1	70.5	4.0	2.0
23	20b	74.6	102	5.6	5.6	1.0	31.0	1.1	59.5	3.9	1.7
24	22b	70.1	99.2	5.3	4.9	1.0	29.6	1.0	67.3	3.3	1.6
25	8b	71.2	98.6	5.5	5.5	1.1	33.2	1.1	69.9	3.7	2.0
26	19b	72.3	98.9	6.3	5.6	1.1	29.8	1.0	71.3	4.8	1.8

27	21b	75.6	103	6.3	5.7	1.0	33.0	1.0	65.2	4.9	1.6
28	24b	73.4	102	5.8	5.1	1.1	30.2	1.0	63.6	3.6	2.0
29	26b	74.5	104	6.6	5.5	1.1	33.0	1.1	64.0	4.7	1.5
30	2b	70.1	98.1	6.0	5.5	1.1	31.7	1.0	69.8	4.2	1.6
31	7b	70.4	103	5.8	5.5	1.0	31.5	1.0	70.3	3.4	1.5
32	6b	71.9	97.8	6.3	5.4	1.0	32.6	1.1	74.1	4.6	1.9
33	5b	71.8	100	5.7	5.4	1.0	31.0	0.9	63.3	4.3	1.8
34	10b	74.4	106	5.4	6.0	1.0	33.8	1.0	64.3	4.3	1.9
35	3b	72.4	100	5.6	5.2	1.0	31.6	1.0	66.2	3.8	1.8
36	17b	75.2	101	5.8	5.3	1.1	30.4	1.0	62.3	3.7	1.7
37	12b	73.8	99.4	5.7	5.7	1.1	33.9	0.9	67.0	4.4	1.7
38	18b	74.1	101	5.6	5.4	1.1	30.4	1.1	68.9	4.1	1.6
39	12a	75.9	101	5.4	6.4	1.0	29.4	1.0	64.2	6.7	2.6
40	1a	74.8	97.7	5.6	6.6	1.1	30.7	0.9	67.1	5.7	2.2
41	1c-b	74.4	102	5.3	6.1	1.0	31.8	1.0	76.1	4.5	1.8
42	25c-b	74.3	99.8	5.5	5.8	1.1	31.9	1.0	64.8	3.8	2.3
43	28a	78.4	102	5.6	6.3	1.0	28.6	0.9	64.4	6.0	1.7
44	16c-b	72.8	96.9	5.8	5.5	1.0	30.1	1.0	67.3	4.4	1.2
45	7a	76.2	99.8	5.4	6.1	1.0	31.0	0.9	65.5	5.2	2.3
46	13c	74.5	99.3	6.1	6.1	1.1	33.5	1.0	65.0	4.5	1.1
47	19c	83.4	113	5.9	6.5	1.0	33.9	1.0	58.1	5.2	1.6
48	20c	81.4	106	6.3	6.0	1.0	30.1	0.9	68.6	6.1	1.9
Mean		75.0	102.	6.0	5.8	1.0	31.0	1.0	66.7	5.0	2.0
Min		70.1	96.9	5.2	4.5	0.9	27.6	0.9	58.1	3.3	1.1
Max		83.4	113	6.6	6.9	1.1	36.0	1.1	76.1	6.8	2.9
SEM		2.2	3.4	0.4	0.5	0.0	1.6	0.1	3.5	0.8	0.3
CV (%)		20.0	34.3	6.0	12.1	0.4	25.8	1.0	5.4	37.0	14.5

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers

Appendix 7: Cluster 1 means of 10 quantitative traits of F3 interspecific millet progeny across two locations

Cluster 1	Name	race	DF	NF	FL	FW	FLL	FLW	PH	PTN	STN	DM
1	24c-b	<i>kigeziensis</i>	71.5	5.8	5.9	1.2	33.4	1.0	66.5	4.4	2.1	98.3
3	8c-b	<i>kigeziensis</i>	72.8	5.2	6.1	1.3	34.0	1.1	73.0	5.4	2.7	96.5
4	13c-b	<i>kigeziensis</i>	72.2	6.2	5.6	1.1	32.8	1.1	66.7	5.4	2.5	97.0
5	22c-b	<i>kigeziensis</i>	73.0	5.9	5.5	1.2	33.4	1.0	70.2	5.6	2.3	99.1
8	4c-b	<i>kigeziensis</i>	72.0	5.6	5.6	1.1	30.1	1.0	64.0	4.3	2.8	99.3
9	18c-b	<i>kigeziensis</i>	68.8	5.2	5.9	1.2	31.9	1.0	69.8	4.3	2.0	93.9
11	2c-b	<i>kigeziensis</i>	72.9	6.1	5.7	1.1	33.4	1.0	65.8	4.9	2.4	97.7
16	19c-b	<i>kigeziensis</i>	73.1	5.2	5.8	1.1	35.8	1.0	66.4	3.9	2.1	97.6
18	7c-b	<i>kigeziensis</i>	69.6	6.0	5.6	1.1	34.8	1.1	67.6	4.1	2.1	98.3
21	1b	<i>kigeziensis</i>	71.1	5.9	5.2	1.1	32.2	1.1	67.4	4.7	2.5	97.8
22	14b	<i>kigeziensis</i>	72.1	6.0	5.5	1.2	33.8	1.2	68.4	4.6	2.3	98.6
23	20b	<i>kigeziensis</i>	71.5	5.2	5.7	1.1	32.0	1.0	68.7	4.7	2.4	96.6
24	22b	<i>kigeziensis</i>	72.7	6.3	5.4	1.1	31.8	1.1	71.3	4.7	2.6	97.2
25	8b	<i>kigeziensis</i>	70.8	5.2	5.1	1.1	34.4	1.1	71.7	4.0	2.5	96.4
26	19b	<i>kigeziensis</i>	70.0	5.7	5.4	1.2	30.8	1.1	71.2	4.4	2.4	98.7
27	21b	<i>kigeziensis</i>	67.7	5.7	5.4	1.1	32.4	1.0	66.5	4.2	2.8	96.0
28	24b	<i>kigeziensis</i>	71.1	5.3	5.5	1.3	30.6	1.0	68.2	4.4	2.7	98.1
29	26b	<i>kigeziensis</i>	69.1	5.4	5.3	1.2	31.4	1.0	69.2	3.9	2.5	98.7
30	2b	<i>kigeziensis</i>	67.7	5.4	6.0	1.2	34.4	1.2	70.2	4.4	2.0	93.4
31	7b	<i>kigeziensis</i>	69.8	5.2	5.1	1.2	32.5	1.0	68.9	4.3	2.2	101.7
32	6b	<i>kigeziensis</i>	71.8	5.5	5.1	1.1	33.7	1.1	71.1	5.1	2.2	100.5
33	5b	<i>kigeziensis</i>	67.8	5.7	5.0	1.1	31.7	1.1	71.1	4.0	2.4	95.4
34	10b	<i>kigeziensis</i>	71.5	5.1	4.9	1.1	31.0	1.0	61.9	3.9	2.3	100.0
35	3b	<i>kigeziensis</i>	68.3	6.1	5.4	1.1	31.3	1.0	70.2	5.1	2.1	94.2
36	17b	<i>kigeziensis</i>	72.2	5.2	5.2	1.1	31.7	1.0	68.4	4.8	2.3	100.1
37	12b	<i>kigeziensis</i>	69.4	5.3	5.0	1.2	32.3	1.0	69.1	4.7	2.8	97.0
38	18b	<i>kigeziensis</i>	69.4	5.9	5.7	1.2	34.0	1.0	70.0	4.1	1.9	95.3

41	1c-b	kigeziensis	74.0	5.2	6.4	1.3	32.2	1.0	73.5	4.3	2.4	96.1
42	25c-b	kigeziensis	71.3	4.9	5.2	1.1	34.6	1.1	66.1	4.9	2.4	96.6
44	16c-b	kigeziensis	72.3	5.8	5.4	1.2	34.6	1.1	65.6	5.1	2.2	95.3
	Mean		70.9	5.6	5.5	1.2	32.8	1.0	68.6	4.6	2.4	97.4
	Min		67.7	4.9	4.9	1.1	30.1	1.0	61.9	3.9	1.9	93.4
	Max		74.0	6.3	6.4	1.3	35.8	1.2	73.5	5.6	2.8	101.7

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers,

Appendix 8: Cluster 2 means of 10 quantitative traits of F3 interspecific millet progeny across two locations

cluster 2	Name	Race	DF	NF	FL	FW	FLL	FLW	PH	PTN	STN	DM
2	15a	<i>africana</i>	72.9	5.7	6.5	1.1	31.0	0.9	65.0	5.6	2.9	99.1
6	14c	<i>africana</i>	80.8	5.2	6.5	1.1	34.0	1.0	66.9	4.8	3.7	102.6
7	23a	<i>africana</i>	72.9	6.3	6.2	1.0	28.2	0.8	70.0	5.0	3.4	98.7
10	18a	<i>africana</i>	73.6	5.7	6.9	1.0	29.0	0.9	66.0	5.8	3.7	98.0
12	13a	<i>africana</i>	71.4	5.6	6.6	1.1	30.8	1.0	66.4	7.3	3.2	95.5
13	9a	<i>africana</i>	80.3	5.7	6.0	1.1	29.3	0.9	68.4	6.3	3.0	101.6
14	22a	<i>africana</i>	74.5	5.6	6.6	1.0	27.4	0.9	66.6	6.0	2.8	99.4
15	8a	<i>africana</i>	74.6	5.7	6.1	1.0	29.2	0.8	67.0	4.9	2.5	104.2
17	6a	<i>africana</i>	75.3	5.6	6.4	1.1	28.3	0.9	68.3	6.3	2.9	99.7
19	3a	<i>africana</i>	76.3	5.5	6.7	1.1	28.6	0.8	70.4	5.9	2.7	100.1
20	25a	<i>africana</i>	73.0	5.8	6.6	1.1	32.7	0.9	68.6	5.6	2.9	100.4
39	12a	<i>africana</i>	74.9	5.2	6.9	1.1	30.2	0.9	62.7	5.9	3.1	102.2
40	1a	<i>africana</i>	72.7	4.8	6.6	1.1	29.1	0.9	60.4	5.1	2.8	100.1
43	28a	<i>africana</i>	73.2	5.5	6.3	1.0	29.6	0.8	66.4	6.5	3.7	98.1
45	7a	<i>africana</i>	81.1	5.8	6.5	1.2	28.2	0.9	69.5	6.4	4.0	100.9
47	19c	<i>africana</i>	74.9	5.2	5.6	1.1	26.5	0.9	64.7	5.6	4.0	96.4
48	20c	<i>africana</i>	73.9	6.1	6.6	1.1	31.1	0.9	74.1	6.5	2.4	103.0
	Mean		75.1	5.6	6.5	1.1	29.6	0.9	67.1	5.8	3.2	100.0
	Min		71.4	4.8	5.6	1.0	26.5	0.8	60.4	4.8	2.4	95.5

Max	81.1	6.3	6.9	1.2	34.0	1.0	74.1	7.3	4.0	104.2
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Appendix 9: Cluster 1 means of 10 quantitative traits of F4 interspecific millet progeny across two locations

Cluster 1	Name	race	DF	NF	FL	FW	FLL	FLW	PH	PTN	STN	DM
1	24c-b	<i>kigeziensis</i>	76.8	6.1	6.0	1.0	32.4	1.1	64.9	3.9	1.8	102.0
4	13c-b	<i>kigeziensis</i>	70.1	5.5	6.0	1.0	32.9	1.0	65.8	3.7	1.3	97.7
5	22c-b	<i>kigeziensis</i>	74.2	6.6	5.7	1.0	32.0	1.1	69.1	4.3	2.1	103.1
8	4c-b	<i>kigeziensis</i>	74.2	6.2	5.6	1.0	28.5	1.0	64.7	3.9	2.1	103.6
9	18c-b	<i>kigeziensis</i>	76.1	6.0	5.4	1.0	30.3	1.0	69.4	4.6	1.9	104.2
11	2c-b	<i>kigeziensis</i>	74.8	6.2	5.9	1.0	31.5	1.0	61.7	4.2	1.8	100.0
12	13a	<i>africana</i>	76.3	5.4	5.6	1.0	28.8	1.0	71.6	4.4	1.7	101.5
16	19c-b	<i>kigeziensis</i>	74.0	5.8	4.5	1.1	33.3	1.0	65.7	5.3	1.9	103.1
18	7c-b	<i>kigeziensis</i>	73.2	5.9	5.6	1.1	34.1	1.1	69.7	4.0	1.7	99.5
21	1b	<i>kigeziensis</i>	72.2	6.2	5.9	1.1	30.6	1.0	69.6	4.7	1.4	102.8
22	14b	<i>kigeziensis</i>	70.4	5.8	5.7	1.0	34.2	1.1	70.5	4.0	2.0	101.3
23	20b	<i>kigeziensis</i>	74.6	5.6	5.6	1.0	31.0	1.1	59.5	3.9	1.7	102.1
24	22b	<i>kigeziensis</i>	70.1	5.3	4.9	1.0	29.6	1.0	67.3	3.3	1.6	99.2
25	8b	<i>kigeziensis</i>	71.2	5.5	5.5	1.1	33.2	1.1	69.9	3.7	2.0	98.6
26	19b	<i>kigeziensis</i>	72.3	6.3	5.6	1.1	29.8	1.0	71.3	4.8	1.8	98.9
27	21b	<i>kigeziensis</i>	75.6	6.3	5.7	1.0	33.0	1.0	65.2	4.9	1.6	103.9
28	24b	<i>kigeziensis</i>	73.4	5.8	5.1	1.1	30.2	1.0	63.6	3.6	2.0	102.9
29	26b	<i>kigeziensis</i>	74.5	6.6	5.5	1.1	33.0	1.1	64.0	4.7	1.5	104.1
30	2b	<i>kigeziensis</i>	70.1	6.0	5.5	1.1	31.7	1.0	69.8	4.2	1.6	98.1
31	7b	<i>kigeziensis</i>	70.4	5.8	5.5	1.0	31.5	1.0	70.3	3.4	1.5	103.6
32	6b	<i>kigeziensis</i>	71.9	6.3	5.4	1.0	32.6	1.1	74.1	4.6	1.9	97.8
33	5b	<i>kigeziensis</i>	71.8	5.7	5.4	1.0	31.0	0.9	63.3	4.3	1.8	100.2
34	10b	<i>kigeziensis</i>	74.4	5.4	6.0	1.0	33.8	1.0	64.3	4.3	1.9	106.4
35	3b	<i>kigeziensis</i>	72.4	5.6	5.2	1.0	31.6	1.0	66.2	3.8	1.8	100.9
36	17b	<i>kigeziensis</i>	75.2	5.8	5.3	1.1	30.4	1.0	62.3	3.7	1.7	101.9
37	12b	<i>kigeziensis</i>	73.8	5.7	5.7	1.1	33.9	0.9	67.0	4.4	1.7	99.4

38	18b	<i>kigeziensis</i>	74.1	5.6	5.4	1.1	30.4	1.1	68.9	4.1	1.6	101.5
41	1c-b	<i>kigeziensis</i>	74.4	5.3	6.1	1.0	31.8	1.0	76.1	4.5	1.8	102.5
42	25c-b	<i>kigeziensis</i>	74.3	5.5	5.8	1.1	31.9	1.0	64.8	3.8	2.3	99.8
44	16c-b	<i>kigeziensis</i>	72.8	5.8	5.5	1.0	30.1	1.0	67.3	4.4	1.2	96.9
46	13c	<i>africana</i>	74.5	6.1	6.1	1.1	33.5	1.0	65.0	4.5	1.1	99.3
Mean			73.4	5.9	5.6	1.0	31.7	1.0	67.2	4.2	1.7	101.2
Min			70.1	5.3	4.5	1.0	28.5	0.9	59.5	3.3	1.1	96.9
Max			76.8	6.6	6.1	1.1	34.2	1.1	76.1	5.3	2.3	106.4

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers,

Appendix 10: Cluster 2 means of 10 quantitative traits of F4 interspecific millet progeny across two locations

Cluster 2	Name	race	DF	NF	FL	FW	FLL	FLW	PH	PTN	STN	DM
2	15a	<i>africana</i>	75.6	5.3	6.3	1.0	27.6	0.9	63.6	6.8	2.3	103.8
6	14c	<i>africana</i>	80.6	6.0	6.5	1.0	32.2	1.0	68.6	6.1	1.6	105.9
7	23a	<i>africana</i>	77.2	5.9	6.4	1.0	28.6	0.9	64.4	5.3	1.8	103.1
10	18a	<i>africana</i>	78.0	5.7	6.3	1.0	30.5	1.0	69.5	6.0	2.6	99.8
13	9a	<i>africana</i>	74.7	5.6	6.0	1.0	29.4	1.0	67.5	5.4	2.1	99.3
14	22a	<i>africana</i>	77.1	6.3	6.1	0.9	27.7	1.0	59.8	5.3	2.0	105.1
15	8a	<i>africana</i>	78.9	5.2	6.9	1.0	31.0	1.0	65.1	5.4	1.7	105.4
17	19c-b	<i>kigeziensis</i>	77.8	6.2	6.6	1.0	29.9	1.0	68.4	6.0	2.2	101.2
19	3a	<i>africana</i>	77.8	5.6	6.3	1.0	29.5	0.9	63.1	5.8	2.9	105.4
20	25a	<i>africana</i>	76.3	5.7	6.0	1.0	30.2	0.9	68.4	6.2	2.9	103.1
39	12a	<i>africana</i>	75.9	5.4	6.4	1.0	29.4	1.0	64.2	6.7	2.6	101.1
40	1a	<i>africana</i>	74.8	5.6	6.6	1.1	30.7	0.9	67.1	5.7	2.2	97.7
43	28a	<i>africana</i>	78.4	5.6	6.3	1.0	28.6	0.9	64.4	6.0	1.7	102.0
45	7a	<i>africana</i>	76.2	5.4	6.1	1.0	31.0	0.9	65.5	5.2	2.3	99.8
48	20c	<i>africana</i>	81.4	6.3	6.0	1.0	30.1	0.9	68.6	6.1	1.9	106.0
Mean			77.4	5.7	6.3	1.0	29.8	0.9	65.9	5.8	2.2	102.6
Min			74.7	5.2	6.0	0.9	27.6	0.9	59.8	5.2	1.6	97.7

Max 81.4 6.3 6.9 1.1 32.2 1.0 69.5 6.8 2.9 106.0

DF= Days to 50% flowering, DM= Days to 50% maturity, NF= Number of fingers per main ear, FL=Length of longest finger, FW= Width of longest finger, FLL= Flag leaf length, FLW= Flag leaf width, PH= Plant height, PTN= Primary tillers, STN= Secondary tillers,

Appendix 11: Reaction of the F3 interspecific progeny of finger millet to Leaf blast disease

Name	42 DAP	49 DAP	56 DAP	Mean score
19c-b	1.4	1.7	2	1.7
19c	1.6	1.7	2.2	1.8
13a	1.7	1.8	2.2	1.9
20b	1.2	2	2.5	1.9
22c-b	1.3	2.1	2.2	1.9
24b	1.5	1.9	2.2	1.9
24c-b	1.5	1.8	2.5	1.9
2b	1.6	1.9	2.3	1.9
6b	1.4	1.9	2.5	1.9
4c-b	1.8	1.9	2.2	2.0
2c-b	1.9	1.9	2.2	2.0
1c-b	1.8	1.8	2.4	2.0
22a	1.9	2.0	2.1	2.0
8c-b	1.8	2.1	2.1	2.0
20c	1.6	1.9	2.5	2.0
28a	2.0	2.0	2.1	2.0
6a	1.7	2.0	2.4	2.0
10b	1.7	1.9	2.5	2.0
22b	1.8	2.0	2.4	2.1
1b	1.9	1.9	2.4	2.1
14c	1.9	2.0	2.4	2.1
8b	2.1	2.1	2.1	2.1
15a	1.9	2.2	2.2	2.1
21b	2.1	2.1	2.0	2.1

25c-b	1.8	2.3	2.3	2.1
5b	1.6	2.3	2.5	2.1
18b	1.7	1.8	2.5	2.1
13c-b	2.0	2.1	2.3	2.1
23a	2.0	2.1	2.6	2.2
19b	2.0	2.2	2.3	2.2
25a	1.8	2.3	2.5	2.2
3a	1.9	2.0	2.7	2.2
7a	2.1	2.2	2.3	2.2
14b	1.7	2.1	2.6	2.2
12b	2.0	2.1	2.6	2.3
18a	2.0	2.3	2.5	2.3
3b	2.0	2.0	2.3	2.3
9a	1.9	2.5	2.5	2.3
17b	2	2.3	2.6	2.3
18c-b	2	2.3	2.6	2.3
1a	2	2.2	2.7	2.3
26b	1.8	2.2	2.8	2.3
7c-b	1.9	2.4	2.7	2.3
8a	2	2.2	2.7	2.3
12a	2.1	2.3	2.7	2.4
7b	1.9	2.1	2.6	2.4
16c-b	2.4	2.7	2.8	2.6
13c	2.4	2.9	3.0	2.8
PESE 1	1.7	2.1	2.4	2.1
Gulu E	1.8	2.1	2.8	2.2
SER 1	1.8	2	2.8	2.2
SER 3	1.7	2.2	2.6	2.2
OKIRING	2	2.2	2.7	2.3

SER 2	2.1	2.8	3.4	2.8
E11	1.9	3	3.4	2.8
KATFMI	2.8	3.4	3.6	3.3
Mean	1.8	2.1	2.6	2.2
SEM	0.1725	0.1713	0.2456	0.1694
LSD (5%)	0.48	0.48	0.69	0.48
CV	19.1	16.1	19.3	15.4

DAP= Days after planting

Appendix 12: Reaction of the F4 interspecific progeny of finger millet to the three forms blast disease

Name	Leaf blast (1-5 scale)					Neck blast (1-5 scale)		Head blast (1-5 scale)	
	42 DAP	49 DAP	56 DAP	Mean score		Mean score	Reaction	Mean score	Reaction
10b	2.1	2.1	2.3	2.2	MR	1.5	R	2.2	MR
12a	2.0	2.5	2.7	2.4	MR	1.1	R	2.4	MR
12b	2.2	2.1	2.3	2.2	MR	1.2	R	2.2	MR
13a	2.2	2.1	2.1	2.2	MR	1.0	R	2.2	MR
13c	2.3	2.2	2.4	2.3	MR	1.2	R	2.3	MR
13c-b	2.0	2.4	2.5	2.3	MR	1.3	R	2.3	MR
14b	2.4	2.6	2.1	2.4	MR	1.1	R	2.4	MR
14c	2.5	2.5	2.4	2.5	S	1.5	R	2.5	S
15a	2.2	2.2	2.3	2.2	MR	1.1	R	2.2	MR
16c-b	2.1	2.4	2.3	2.3	MR	1.1	R	2.3	MR
17b	2.0	2.2	2.4	2.2	MR	1.3	R	2.2	MR
18a	2.1	2.3	2.2	2.2	MR	1.8	R	2.2	MR
18B	1.9	2.1	1.8	1.9	R	1.5	R	1.9	R
18c-b	2.1	2.2	2.3	2.2	MR	1.1	R	2.2	MR
19b	1.9	2.1	1.6	1.9	R	1.4	R	1.9	R
19c	2.4	2.4	2.4	2.4	MR	1.1	R	2.4	MR
19c-b	2.0	2.3	2.3	2.2	MR	1.3	R	2.2	MR

1a	2.1	2.3	2.5	2.3	MR	1.4	R	2.3	MR
1b	2.1	2.0	2.2	2.1	MR	1.2	R	2.1	MR
1c-b	2.3	2.6	2.3	2.4	MR	1.2	R	2.4	MR
20b	2.3	2.2	2.2	2.3	MR	1.2	R	2.3	MR
20c	2.3	2.2	2.8	2.5	S	1.3	R	2.5	S
21b	2.2	2.4	2.4	2.3	MR	1.3	R	2.3	MR
22a	1.9	2.4	2.5	2.3	MR	1.0	R	2.3	MR
22b	2.2	2.3	2.2	2.2	MR	1.3	R	2.2	MR
22c-b	2.3	2.7	2.4	2.5	S	1.4	R	2.5	S
23a	2.0	2.5	2.9	2.5	S	1.4	R	2.5	S
24b	2.3	2.3	2.4	2.3	MR	1.2	R	2.3	MR
24c-b	2.4	2.2	2.1	2.2	MR	1.3	R	2.2	MR
25a	2.1	2.1	2.3	1.8	R	1.3	R	1.8	R
25c-b	2.0	2.1	2.0	1.9	R	1.3	R	1.9	R
26b	2.3	2.4	2.4	2.4	MR	1.2	R	2.4	MR
28a	2.2	2.9	3.0	2.7	S	1.4	R	2.7	S
2b	2.4	2.2	2.4	2.3	MR	1.1	R	2.3	MR
2c-b	2.3	2.2	2.0	2.2	MR	1.3	R	2.2	MR
3a	2.2	2.3	2.4	2.3	MR	1.1	R	2.3	MR
3b	2.5	2.3	2.2	2.3	MR	1.2	R	2.3	MR
4c-b	2.3	2.1	2.2	2.2	MR	1.4	R	2.2	MR
5b	2.3	2.7	2.5	2.5	S	1.3	R	2.5	S
6a	2.1	2.5	2.4	2.4	MR	1.2	R	2.4	MR
6b	2.0	2.2	2.2	2.1	MR	1.1	R	2.1	MR
7a	2.3	2.3	2.2	2.3	MR	1.4	R	2.3	MR
7b	2.2	2.0	2.2	1.9	R	1.1	R	1.9	R
7c-b	2.1	2.4	2.3	2.3	MR	1.3	R	2.3	MR
8a	2.0	2.2	2.7	2.3	MR	1.3	R	2.3	MR
8b	2.1	2.1	2.3	2.2	MR	1.5	R	2.2	MR

8c-b	2.2	2.1	2.1	2.1	MR	1.4	R	2.1	MR
9a	2.0	2.4	2.3	2.2	MR	1.5	R	2.2	MR
E11	1.9	2.2	2.0	2.1	MR	1.4	R	2.1	MR
GULU E	2.1	2.2	2.4	2.2	MR	1.6	R	2.2	MR
KATFMI	2.1	3.2	2.6	2.6	S	2.9	R	2.6	S
OKIRING	2.1	2.3	2.7	2.4	MR	1.4	R	2.4	MR
PESE 1	2.2	2.2	2.3	2.3	MR	1.3	R	2.3	MR
SER 1	2.1	2.2	2.6	2.3	MR	1.7	R	2.3	MR
SER 2	2.0	3.0	3.1	2.7	S	1.9	R	2.7	S
SER 3	2.4	2.3	2.5	2.4	MR	1.3	R	2.4	MR
Mean	2.2	2.3	2.4	2.3		1.3		2.3	
Min	1.9	2.0	1.6	1.8		1.0		1.8	
Max	2.5	3.2	3.1	2.7		2.9		2.7	
SEM	0.122	0.132	0.177	0.110		0.144		0.110	
LSD (5%)	0.3	0.4	0.5	0.3		0.4		0.3	
CV	2.70	3.00	5.30	2.10		22.6		2.10	
DAP= Days after planting									