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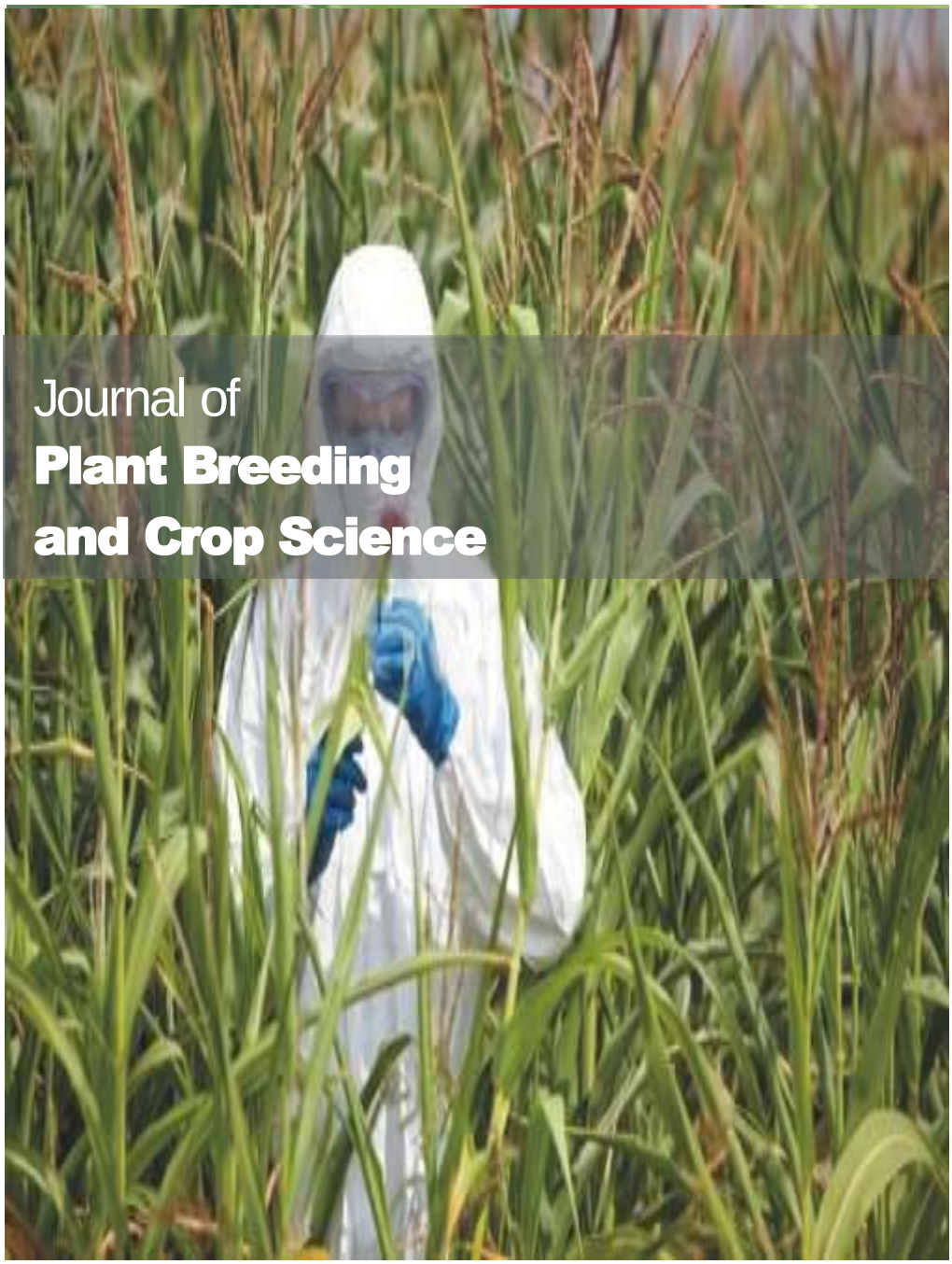

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Table of Content

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Full Length Research Paper

Allelic variability of oil palm inter-population progenies based on simple sequence repeats markers

Okoye Maxwell N.[1,2,4*], Uguru M. I.[2], Bakoumé C.[3] and Singh R.[4]

[1]Plant Breeding Division, Nigerian Institute for Oil Palm Research (NIFOR), P.M.B 1030 300001, Benin City, Edo State, Nigeria.
[2]Department of Crop Science, Faculty of Agriculture, University of Nigeria, Nsukka, Enugu State, Nigeria.
[3]Maxi Productivity Sarl, P. O. Box 2137 (or 24240), Douala, Cameroon.
[4]Advanced Biotechnology and Breeding Centre, Malaysian Palm Oil Board (MPOB), P. O. Box 10620, 50720 Kuala Lumpur, Malaysia.

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The genetic structure and variability was described among 52 oil palm inter-population crosses after two selection cycles using simple sequence repeats markers (SRR). The 10 sets of SSR markers covering 62.5% of the oil palm genome showed a high level of polymorphism (average number of alleles per locus = 6.7; unbiased expected heterozygosity = 0.655; G"st = 0.346) across the oil palm samples. On the basis of allelic variability indices, three genetically diverse progenies (P1, P2 and P5) with estimates higher than the overall mean values were identified. Analysis of molecular variance revealed that partitioning of variance was higher (82%) among palms within each progeny than among the progenies (18%). High pairwise fixation index (F_{ST} > 0.150) among progenies was evident, particularly between progeny P4 and progenies P1, P2 and P3. Crossing of selected palms from highly differentiated progenies could generate offsprings with more genetic variation. The mean Nei's standard genetic distance across progenies was 0.364. The lowest genetic distance was observed between progeny P2 and P5 (0.090) and the highest was found between progeny P1 and P4 (0.653). Based on the results, there is ample variation among the inter-population progenies for maximum exploitation of heterosis and further gains in future breeding programme.

Key words: *Elaeis guineensis* Jacq., microsatellite markers, NIFOR, reciprocal recurrent selection.

INTRODUCTION

Indigenous to West Africa but with widest occurrence in the South-Eastern States of Nigeria, oil palm (*Elaeis guineensis* Jacq.) is cultivated for palm oil and palm kernel oil extracted from the mesocarp and kernel, respectively (Ataga and Van der Vossen, 2007). Palm oil is the most preferred natural oil in the diets of Nigerians both as crude red palm oil and as refined oil (olein). Modest but steady progress has been made in the genetic improvement of the crop in the past eight decades, culminating in an increased average yield from 2.5 to 5.0 metric tonnes of fresh fruit bunch $ha^{-1}year^{-1}$ and 0.5 to 1.0 tonnes oil $ha^{-1}year^{-1}$ between 1930s and 1950s

*Corresponding author. E-mail: maxwellokoye@gmail.com. Tel: +234 703 297 0144.

to 20-25 metric tonnes of fresh fruit bunch ha^{-1} $year^{-1}$ and 3.5 to 4.0 tonnes oil $ha^{-1}year^{-1}$ to date (Okwuagwu et al., 2005). Even with this progress, there is still a huge discriminating and competitive demand on the yield and quality of palm oil for edible and non-edible industries. With an estimated 3 million hectares of land under cultivation, Nigeria's share of the global palm oil production is less than 2% with about 1.01 million metric tonnes of palm oil per annum (USDA, 2019). Although this level of production is below the domestic consumption of 1.34 million metric tonnes, the deficit in supply is complemented by an annual importation of about 325,000 metric tonnes. Consequently, continuous and systematic improvement for these traits of economic importance with a proportionate expansion of area under cultivation using improved genetic stock is highly desirable to meet industry demand and ensure a country-wide sufficiency of oils and fats.

The Nigerian Institute for Oil Palm Research (NIFOR) has continued to make advances in the improvement of bunch yield and oil quality of oil palm by the implementation of modified reciprocal recurrent selection (RRS) scheme. It was reported that the RRS scheme had increased oil yield by almost 18% per cycle compared to the base population (Okwuagwu et al., 2005; Durand-Gasselin et al., 2009). During each cycle of selection, the *dura* (D) and *tenera/pisifera* (T/P) base populations are kept separate and outstanding *dura* and *tenera* palms are identified through the performance of D × T and D × P progenies. These inter-population crosses of the base population are essential in the comparative trials of the breeding programme because it represents the evaluation units to identify the best crosses for prospective inter-population hybrid production. Additionally, it is one of the main sources of parents for the development of new populations exploitable in subsequent recombination cycles of the breeding programme (Falconer, 1989). However, frequent hybridization and selection among few parents in the RRS scheme tend to affect the effective population size, allele variability and genetic structure of the populations which risks long-term genetic progress in the scheme (Cao, 1995). For rapid and continued progress in oil palm breeding, the potential variability of the populations must be considered because genetic variability is required to achieve genetic gains.

Genetic variability can be estimated through the application of different molecular techniques and to date a series of different genetic markers have been explored and developed (Powell et al., 1996). Molecular genetic markers, especially Simple Sequence Repeats (SSRs) provide an important method of assessing genetic variability and have been widely employed in a variety of plant species including oil palm (Powell et al., 1996; Bakoumé, 2016). The preference for SSR markers is associated with their high information content, co-dominance, abundance in the genome, reproducibility and and PCR based detection (Powell et al., 1996).

This study is a subset of a larger programme designed to describe the genetic structure and variability among NIFOR oil palm breeding populations using molecular markers. The present paper aims at estimating the available genetic variability and population structure within and between five inter-population progenies of the NIFOR oil palm main breeding programme with SSR markers. Results obtained from this study would be exploited in the selection of new parent palms for the breeding programme as well as for the production of commercial planting material.

MATERIALS AND METHODS

Fifty-two individual palms from five divergent *dura* x *tenera* inter-population crosses in the comparative trials of NIFOR oil palm main breeding programme, referred to as P1 to P5 were evaluated. The *dura* (female parent) population is characterized by consistent high yield of heavy bunches and good bunch composition traits while the *tenera* (male parent) population has a high bunch number with excellent oil-to-mesocarp ratio. The genetic backgrounds of the parent palms were *dura* from Ecuador, Calabar, and Ufuma, with the *tenera* mainly from Umuabi open pollinated genetic collections (Okwuagwu, 1985). The experimental site is located at Benin City, Nigeria; 06°312 N latitude and 05°402 E longitude and at an altitude of 149.4 m.a.s.l. The annual rainfall range from 1595 to 1958 mm and a mean annual temperature of 31.8 to 32.0°C. The number of evaluated palms in each cross ranged from 8 to 13 individuals after hybrid validation of the progenies.

Total genomic DNA was extracted from lyophilized leaf tissues from an unopened spear leaf of individual palms following the protocol described by Doyle and Doyle (1990) with minor modifications. This protocol was originally designed for relatively large-scale DNA isolation but was scaled down to suit the present study. The amount of DNA needed for the SSR reaction is very small, only about 25 ng for a single reaction of a total volume of 10 µl. The PCR conditions using M13-tailed primers described by Ting et al. (2013) was used for the amplification of 10 SSR loci/primer pairs (mEgCIR0793, sMg00156, sEg00154, sMo00102, sMg00016, mEgCIR3519, mEgCIR0790, sEg00151, sMg00179, and sMg00087) developed for oil palm (Billotte et al., 2005; Singh et al., 2008). The detection of amplification products was carried out with an automated capillary DNA genetic analyzer (ABI 3739, Applied Biosystems, USA) at the Genomics unit of Advanced Biotechnology and Breeding Centre (ABBC), Malaysian Palm Oil Board (MPOB) Malaysia. Allele calls and sizing was performed using the software GeneMapper® version 4.1 (Applied Biosystems, USA).

Marker informativeness was evaluated based on the standardized genetic differentiation measure (G"st; Hedrick 2005) after correction for small population size as described by Peakall and Smouse (2006; 2012). In addition, estimates of population genetic variation such as average number of alleles (Ao), effective number of alleles (Ae), number of private alleles (PA) - number of alleles unique to a particular population, Shannon information index (I), observed heterozygosity (Ho), unbiased expected heterozygosity (uHe), and fixation index (F_{ST}) were computed for each progeny across the 10 SSR loci. The proportion of genetic variability components within and between the inter-population progenies was determined by analysis of molecular variance (AMOVA). Pairwise (Wright, 1978) and genetic distance values among progenies based on unbiased Nei's standard genetic distance (Nei 1978) were estimated to provide information of the relatedness among the progenies. All calculations were facilitated

Table 1. Characteristics and allelic diversity in SSR loci evaluated in 52 oil palm inter-population crosses.

SSR loci	Linkage group	Ta(°C)	SSR repeat	Expected fragment size (bp)	Accession number	Ao	Ho	uHe	G"st
mEgCIR0793	2	56	(GA)15	149	AJ578545	6	0.481	0.685	0.635
sMg00156	4	50	(CT)15	237	Pr010615888*	7	0.808	0.720	0.187
sEg00154	6	57	(CAG)5	238	EY410356**	5	0.596	0.696	0.381
sMo00102	7	53	(AG)11	235	Pr010615939*	6	0.731	0.702	0.366
sMg00016	9	52	(GA)13	274	Pr010615861*	5	0.381	0.533	0.528
mEgCIR3519	10	52	(GA)15(GT)8	236	AJ578672	9	0.372	0.482	0.081
mEgCIR0790	12	52	(GA)19	215	AJ578544	7	0.404	0.504	0.197
sEg00151	13	57	(CAG)8	219	EY411661**	6	0.667	0.725	0.329
sMg00179	14	54	(AAAAG)6	214	Pr010615893*	7	0.731	0.681	0.180
sMg00087	15	58	(AG)19AA(AG)	212	Pr010615880*	9	0.683	0.825	0.541
Mean						**6.7**	**0.585**	**0.655**	**0.346**

Ta = annealing temperature; Ao = number of different alleles; Ho = observed heterozygosity; uHe = unbiased expected heterozygosity; G"st = Hedrick's standardized Gst, corrected when population size is small; *Probe Unique Identifiers (PUIDs) of NCBI Probe Database; **Accession numbers of NCBI GenBank

using GenAlEx version 6.5 software (Peakall and Smouse, 2006; 2012).

RESULTS AND DISCUSSION

Genetic variation is fundamental for populations to be able to face the present environmental changes and to ensure long term response to selection for traits of economic interest. In this study, we have examined levels of allelic variability and population structure within and among five inter-population progenies of oil palm, using SSR markers. Table 1 gives the synopsis of the 10 SSR markers including the basic genetic diversity parameters estimated. The marker informativeness (G"st) value for all the scored markers in this study ranged from 0.081 to 0.635. Six markers namely, mEgCIR0793, sEg00154, sMo00102, sMg00016, sEg00151 and sMg00087 revealed high G"st values (>0.250) which provided sufficient discrimination to assess genetic variation within and between the progenies. The number of different alleles across the 10 SSR markers varied from 5 (sEg00154 and sMg00016) to 9 (mEgCIR3519 and sMg00087) with a mean value of 6.7 alleles per locus (Table 1).

The observed heterozygosity (Ho) values ranged from 0.372 (mEgCIR3519) to 0.808 (sMg00156) with an overall average of 0.585. The unbiased expected heterozygosity (uHe) showed slightly higher values than Ho with values ranging from 0.482 (mEgCIR3519) to 0.825 (sMg00087) and a mean value of 0.655. The high mean uHe value suggests a high expected heterosis effect upon which oil palm yield depends. The high allelic variation and genetic diversity across the 10 SSRs were relatively higher than those reported by Putri et al. (2017; Ao = 3.0; He = 0.543) for MTG oil palm commercial variety from Socfindo, Indonesia. However, the extent of SSR diversity in the current study (He = 0.655) was lower than that reported by Augustina et al. (2013) among 85 oil palm *pisifera* accessions from SA Indonesia (Ao = 8.2; He = 0.70). This variability could be explained by differences in the number, origin of genotypes and the number of SSR markers used.

Results of the allelic patterns across the progenies revealed the presence of 19 different alleles varying from 3.2 (Progeny P4) to 4.4 (Progeny P2) with a mean value of 3.8 alleles per locus (Figure 1).

The highest number of effective alleles (Ae = 2.733) was exhibited by Progeny P2 while Progeny P3 showed the lowest value (Ae = 2.341) with an average of 2.509. The average Ao (3.8) and Ae (2.509) revealed per locus was lower than 5.0 and 3.3 alleles from a previous study on natural oil palm collections from 10 African countries maintained at MPOB (Malaysia) and three breeding materials (Bakoumé et al., 2015), but higher than 2.0 and 1.627 reported on 30 individual clones of BTC A-group collection of PT

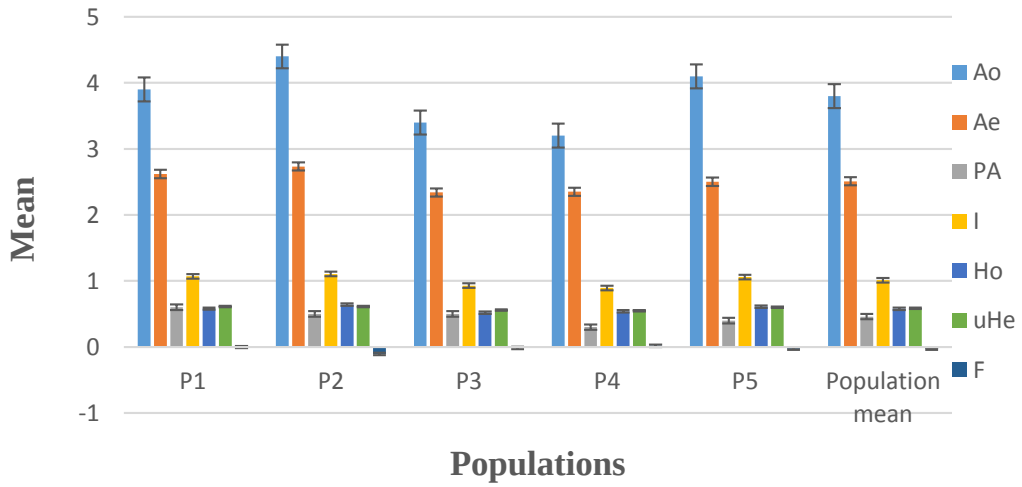

Figure 1. Mean allelic patterns across inter-population progenies; Ao = number of different alleles; Ae = number of effective alleles; PA = private alleles; I = Shannon's Information Index; Ho = observed heterozygosity; He = unbiased expected heterozygosity; F = inbreeding coefficient.

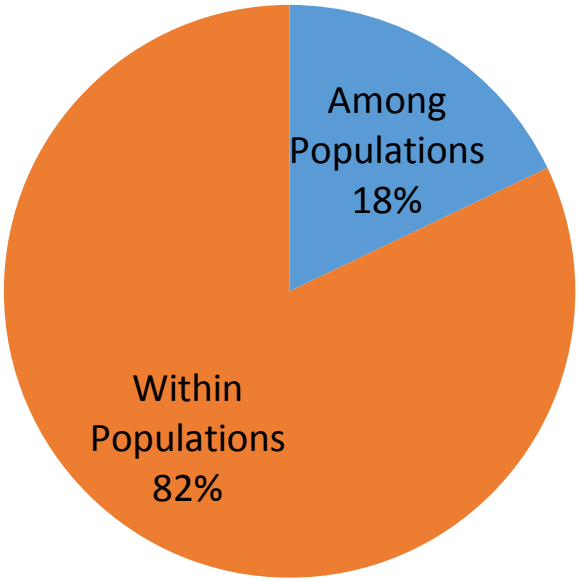

Figure 2. Pie chart of molecular variance estimated by AMOVA.

Socfindo (Putri et al., 2018). It is possible that the lower number of alleles observed among the progenies is a consequence of selection pressure on the parents of the progenies. Several studies have shown a general tendency of allele loss or reduction in the number of alleles after several cycles of selection (Cochard et al., 2009). Private alleles (PA) were identified among the progenies evaluated (Figure 1). The progenies with the most private alleles were P1 (0.6), P2 (0.5), and P3 (0.5) respectively. Progenies with private alleles can be used as sources of parents in the breeding programme to broaden the genetic base of the breeding population as well as development of more adapted variety. Progeny P4 recorded the least Shannon's index (I = 0.894) whereas P2 revealed the highest (I = 1.105). The mean observed (Ho) and unbiased expected (uHe) heterozygosities across the progenies were 0.578 and 0.590 respectively, implying that the progenies are highly heterozygous regardless of the two generations of selection by the parents. The uHe values ranged from 0.55 (P4) to 0.61 (P1 and P2). Meanwhile, Ho was lowest for P3 (0.52) while the highest was for P2 (0.64). The uHe values obtained in these progenies were high compared to those obtained from Ulu Remis Deli (He = 0.493; Bakoumé et al., 2007) and *E. oleifera* (He = 0.221; Maizura et al., 2017). However, the values were lower than those reported for oil palm germplasm from Owerri (He = 0.745; Bakoumé et al., 2007). Mean F-value (inbreeding coefficient) was low and negative (-0.027), implying excess of heterozygosity due to heterotic selection in the inter-population crosses. An excess of heterozygosity suggests the impact of selection, which favours heterozygous individuals. The negative F-values for most of the populations showed the prevalence of outcrossing, whereas the positive value in P4 indicated some level of inbreeding. Considering the high Ho and uHe values in most of the populations (P1, P2 and P5), the presence of private alleles unique to a specific population may explain the excess of heterozygosity. Figure 2 represents the components of genetic variance of the oil palm inter-population progenies estimated by AMOVA.

The analysis of molecular variance showed that 82% of the total genetic variations were due to differences within populations, while 18% were due to genetic variation among populations. The maximum percentage of variation (82%) present was among palms within

Table 2. Pairwise F_{ST} (upper diagonal) and unbiased Nei's standard genetic distance (below diagonal) between the 5 populations.

Population	P1	P2	P3	P4	P5
P1	0.000	0.063	0.121	0.167	0.090
P2	0.200	0.000	0.053	0.155	0.029
P3	0.430	0.147	0.000	0.175	0.056
P4	0.653	0.563	0.620	0.000	0.123
P5	0.321	0.090	0.155	0.402	0.000

populations, while the remaining 18% of the total variation was partitioned among populations. Permutation tests suggest that the total genetic differentiation among populations (*PhiPT*) was significant (0.179; p = 0.001) which indicates that differences among progenies are significant. This high level of intra-population diversity and low but significant genetic differentiation among oil palm progenies is in agreement with previous reports on oil palm (Bakoumé et al., 2007; Allou et al., 2008; Maizura et al., 2017), and consistent with outbreeding perennial species maintaining most of their variation within populations (Hamrick et al., 1992).

Genetic differentiation estimated by pairwise F_{ST} values among progenies were in the range of 0.029 to 0.179 (Table 2; upper diagonal). Progeny P4 was highly differentiated from P1, P2 and P3 with F_{ST} values above 0.150. According to Wright (1978), F_{ST} values between 0.15 and 0.25 indicate a high level of inter-population divergence. This high genetic relationship between individual palms of different progenies will enhance selection of parents for the establishment of crossing programmes to maximize the probability of finding transgressive hybrids in any of the following crosses; P4 x P1, P4 x P2 and P4 x P3. The unbiased Nei's standard genetic distance values ranged from 0.090 (P2 vs P5) to 0.653 (P1 vs P4) with an average distance of 0.364 (Table 2; lower diagonal). Considering the wide range of distance between the progenies and the assumption that progenies with the greatest distance is associated with inter-population heterotic potential, it may be reasonable to infer that crossing of the most distant progenies (P1 vs P4) with the other progenies will lead to the development of superior hybrids.

Conclusion

The results suggest that the inter-population progenies showed considerably high levels of allelic variation that will ensure continued progress in subsequent selection cycles of the breeding programme. Since high degree of genetic variation was observed among palms within the progenies, more palms should be sampled for a better insight on the genetic structure within and between the inter-population progenies. Within the framework of genetic differentiation and genetic distance of the inter-population hybridization programme, crossing of the genotype P4 with P1, P2 and P3 could offer a possible alternative for the maximum exploitation of heterosis and maintenance of genetic variation requisite for further gains in future breeding programme. The crossing between P1 and P3 may be acceptable for some gain in heterosis, although this gain will likely be lower than the crossing between P4 and P3.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Potential of ten wild diploid cotton species for the improvement of fiber fineness of upland cotton through interspecific hybridization

N'Guessan Olivier KONAN[1,2*], Jean Pierre BAUDOIN[2] and Guy MERGEAI[2]

[1]Agroforestry Unit, Jean Lorougnon, Guédé University, BP 150, Cote D'ivoire.
[2]Laboratory of Tropical Agroecology, Gembloux Agro-Bio Tech, Liège University, 2 passage des Déportés, B-5030 Gembloux, Belgium.

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Cotton is the highest source of natural fiber in textile industry worldwide. With the modern spinning technologies, the demand for cotton fiber with higher quality has increased, making the genetic improvement of fiber quality one of the main challenges for cotton breeders. In cotton breeding, wild species are important source of several desirable genes for genetic improvement of the main cultivated cotton *Gossypium hirsutum* L (Upland cotton). Besides length and strength, fineness is one of the most important criteria associated with cotton fiber quality. In this study, ten wild diploid species of cotton were investigated for their fiber fineness and potential to improve fiber fineness of *G. hirsutum* L. The method was measuring of ribbon width after caustic swelling. The results showed the potential of four wild species (*G. longicalyx* Hutch. & Lee, *G. anomalum* Wawra & Peyr., *G. thurberi* Todaro and *G. stocksii* Mast.) to significantly improve the fiber fineness of upland cotton in a hybrid configuration. Among them, *G. longicalyx* stood out for its exceptional fiber fineness, and its remarkable impact on reducing the fiber fineness of *G. hirsutum* L. The wild species highlighted in this study constitute an interesting genetic resource for the development of upland cotton varieties with improved fiber fineness.

Key words: Cotton, fiber fineness, *Gossypium* spp, hybrid, plant breeding, tetraploid species, wild diploid species.

INTRODUCTION

Cotton fiber is the major commercial product from cotton and the most widely used natural fiber in the world's textile industry (Ayubov et al., 2018). This important fiber crop belongs to the genus *Gossypium* which includes 46 diploid (2n = 2× = 26) and 7 tetraploid (2n = 4× = 52) species (Fang et al., 2017). All the diploid *Gossypium* species originated from a common ancestor and diversified into eight genome groups from A to G, and K (Wu et al., 2018). All tetraploid cotton species are allotetraploid and have a genome designated by AD; they come from a natural hybridization event between an A-genome species and a D-genome species, followed by a doubling of the chromosome number 1 to 2 million years ago (Wendel and Grover, 2015; Fang et al., 2017).

*Corresponding author. E-mail: nguessanolivier@yahoo.fr. Tel: +225 05742598.

Among the 53 *Gossypium* species, only four species including two diploids (*G. arboreum* L and *G. herbaceum* L) and two tetraploids (*G. hirsutum* L and *G. barbadense* L) are cultivated for their spinnable fibre (Gallagher et al., 2017; Wang et al., 2018; Ijaz et al., 2019). The remaining 46 species are wild.

G. hirsutum L, which is also known as Upland cotton, Long Staple cotton or Mexican cotton, is extensively cultivated due to its wide adaptability to the environment, high production, and better yield potential. It fulfils over 90 % of the output of global cotton fiber yield (Shim et al., 2018; Konan and Mergeai, 2020). *G. barbadense* L, otherwise known as Sea Island cotton, Pima cotton or Egyptian cotton, is known for excellent fiber quality with long, strong, and fine fibers (Avci et al., 2013). It contributes to 8% of the global cotton production (Shim et al., 2018). The cultivated diploid species provide approximately 2% of the world's cotton and are cultivated in the more traditional growing areas of India, Pakistan, China, Bangladesh and Iran (Kulkarni et al., 2009, Wendel et al., 2010; Shim et al., 2018).

Based on genetic hybridization properties, *Gossypium* species are grouped into the primary, secondary and tertiary gene pools. Both the cultivated (*G. hirsutum* L and *G. barbadense* L) and wild allotetraploids (*G. tomentosum* Nuttall ex Seemann*, G. mustelinum* Miers ex Watt and *G. darwinii* Watt) comprise the primary gene pool of cotton. The secondary gene pool includes the diploids having the A, B, D and F genomes, whereas the tertiary gene pool is composed of species with C, E, G and K genomes (Campbell et al., 2010).

Previously, cotton breeders primarily emphasized yield and agronomic characteristics, but with the recent development of high-speed spinning technologies, the demand for cotton fiber with higher quality has increased, making the improvement of fiber quality highly crucial in Upland cotton (Islam et al., 2016; Shang et al., 2016; Ayubov et al., 2018). Faced with this existing demand and the dynamics of modern textile industry, the perpetual need of genetic improvement in fiber quality is one of the main challenges for cotton breeders today. Biologically, cotton fibers are single-celled trichomes that grow from the epidermal cell layer of the ovule in a boll (Miao et al., 2017; Ayubov et al., 2018; Ijaz et al., 2019). Besides the length and the strength, the fineness is one of the most important criteria associated to cotton fiber quality (Bradow and Davidonis, 2000; Konan and Mergeai, 2020).The fineness of mature fiber is critical for fiber processing. It influences the fabric lustre, dye appearance, fabric stiffness, spinning performance, and yarn strength (Rodgers and Thibodeaux, 2012). The better the fineness of cotton, the more would be the number of fibers per cross-section. This would result in higher yarn strength, which improves spinning efficiency and yarn evenness (Ahmad et al. 2003; Islam et al., 2016).

Cotton fiber fineness can be expressed as the perimeter, diameter or ribbon width (RW), cross sectional area, and standard fiber weight (Rodgers and Thibodeaux, 2012). The indirect methods used for its measurements are Advanced Fibre Information System (AFIS), Fibre Maturity Tester (FMT), and Near Infrared (NIR) spectroscopy, Vibroscope, High Volume Instrument (HVI) for micronaire etc; the most common direct measurements of fiber fineness include cross-sectional image analysis and ribbon width measurement after caustic swelling (Rodgers and Thibodeaux, 2012). The most effective way to improve cotton fiber fineness is through breeding (Nacoulima and Mergeai, 2014; Islam et al., 2016).

Previous progress in the improvement of fiber quality of upland cotton has been mainly achieved using the genetic diversity present in the primary gene pool of cotton (especially *G. barbadense* L), but currently, this available diversity has been exhaustively utilized (Gotmare et al., 2000; Ayubov et al., 2018). Accordingly, it has become a necessity to exploit useful genes of wild species from the two other gene pools. Indeed, in cotton breeding, wild species constitute an important resource with several useful traits which can be introgressed into the main cultivated species for improvement (Konan and Mergeai, 2020). The objective of the present study is to detect donor parents for fiber fineness by determining the fiber fineness of a collection of wild diploid species using ribbon width measurement and evaluating their potential to improve fiber fineness of upland cotton through interspecific hybridization.

MATERIALS AND METHODS

Plant material

The plant material included plants from the living cotton collection of the Laboratory of Tropical Agro ecology of Gembloux Agro-Bio Tech (Liège University, Belgium). It was composed of eleven diploid cotton species, their bi-species hybrid with *G. hirsutum*L, one cultivar of the tetraploid species *G. barbadense* L, four cultivars of the tetraploid species *G. hirsutum* L and fifteen second back-cross (BC2) progenies of the HTL tri-species hybrid (*G. hirsutum* L × *G. thurberi* Todaro)² × *G. longicalyx* Hutch. & Lee (Table 1). The crossing scheme used to generate the bi-species hybrid and the BC2 progenies of the HTL tri-species hybrid are presented in Figures 1 and 2, respectively. The crossing procedures used are presented in detail by Konan et al. (2007) and Konan and Mergeai (2020). The plants were maintained in a ventilated greenhouse where the growing conditions during capsule maturation period were 55-60% relative humidity and 35-26°C day-night air temperatures. The plants were grown in 5 L pots filled with a 3:2:1 (v:v:v) sterile mixture of compost, sand and peat. Cotton fibers were harvested at full maturity and used for the analysis of their fineness.

Fiber fineness analysis

Fiber fineness analysis was conducted on all the genotypes studied. For this analysis, the fibers were combed and a tuft of parallel fibers was cut from the seed. Their free points were also cut and the median region was placed on a slide and covered with a cover glass.

Table 1. Presentation of the genotype, genome and status of the plant material used in the study.

Genotype	Genome	Status (distribution)
G. anomalum Wawra & Peyr.	B_1B_1	Wild diploid species (Africa)
G. sturtianum (R.Br.) J. H. Willis	C_1C_1	Wild diploid species (Australia)
G. armourianum Kearney	$D_{2\text{-}1}D_{2\text{-}1}$	Wild diploid species (America)
G. harknessii Brandegee	$D_{2\text{-}2}D_{2\text{-}2}$	Wild diploid species (America)
G. aridum (Rose &Standl.) Skovst.	D_4D_4	Wild diploid species (America)
G. raimondii Ulbr.	D_5D_5	Wild diploid species (America)
G. stocksii Mast.	E_1E_1	Wild diploid species (Arabia)
G. areysianum Deflers	E_3E_3	Wild diploid species (Arabia)
G. thurberi Todaro	D_1D_1	Wild diploid species (America)
G. longicalyx Hutch. & Lee	F_1F_1	Wild diploid species (Africa)
G. arboretum L.	A_2A_2	Cultivated diploid species (Indo-Burma, China and Arab)
G. hirsutum L. (cv. C2)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. NC8)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. 98M-2983)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. hirsutum L. (cv. 11240-RNR)	$(A_hA_hD_hD_h)$	Cultivated tetraploid species
G. barbadense L. (cv. 353)	$(A_bA_bD_bD_b)$	Cultivated tetraploid species
(*G. hirsutum* cv. C2 × *G. arboreum*)²	$2(A_hD_hA_2)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. anomalum*)²	$2(A_hD_hB_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. sturtianum*)²	$2(A_hD_hC_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. australe*)²	$2(A_hD_hC_3)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. harknessii*)²	$2(A_hD_hD_{2\text{-}2})$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. aridum*)²	$2(A_hD_hD_4)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. raimondii*)²	$2(A_hD_hD_5)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. stocksii*)²	$2(A_hD_hE_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. NC8 × *G. areysianum*)²	$2(A_hD_hE_3)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)²	$2(A_hD_hD_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. longicalyx*)²	$2(A_hD_hF_1)$	Bi-species hexaploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)² x *G. longicalyx*	$A_hF_1D_hD_1$	Tri-species tretraploid hybrid
(*G. hirsutum* cv. C2 × *G. thurberi*)² x *G. longicalyx* BC2	$A_hF_1D_hD_1$	Tri-species tretraploid BC2 hybrid

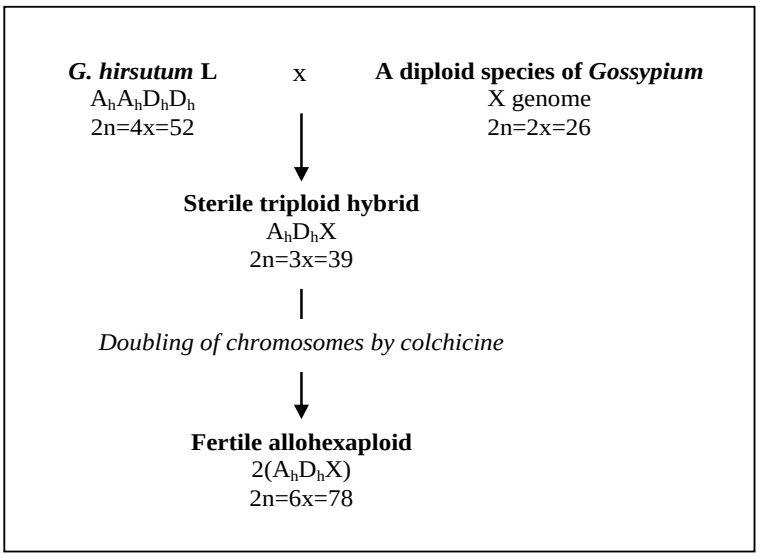

Figure 1. Development scheme of the bi-species hexaploid hybrids. "X" represents a diploid genome (A, B, C, D, E, F, G or K).

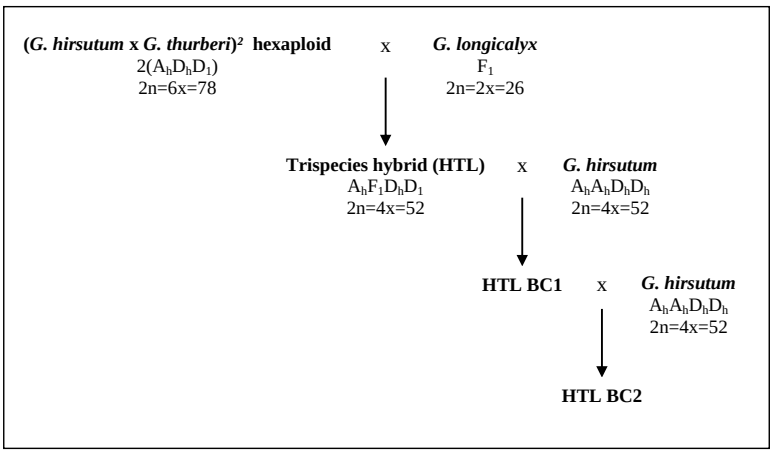

Figure 2. Development scheme of the tri-species BC2 hybrids.

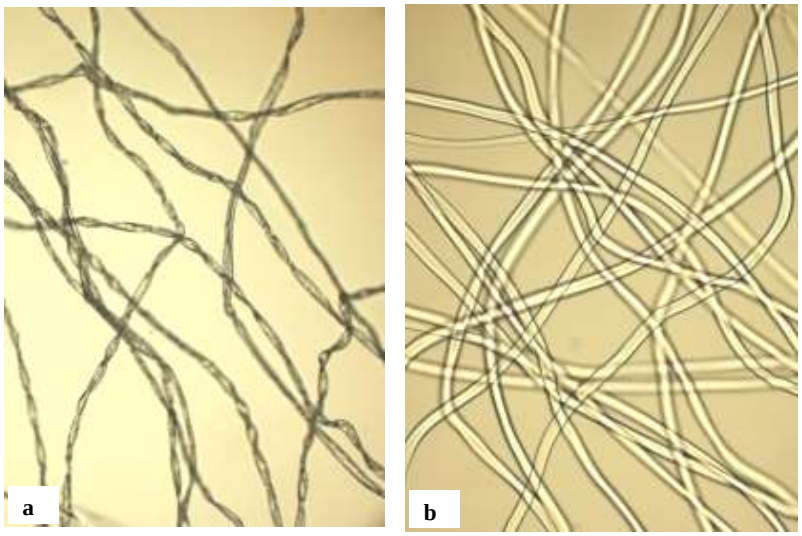

Figure 3. Swelling of cotton fibers after a treatment with 18% NaOH solution: (a) appearance of the fibers before treatment; (b) fibers swollen after treatment (x 200).

One or two drops of 18% NaOH solution was allowed to penetrate into the fibers by capillarity. The NaOH solution swells the fibers (Figure 3). The diameter of at least 100 fibers was then measured with the software NIS-Elements BR 2.30 (Nikon, Japan) using the Nikon Eclipse E800 microscope (Nikon, Tokyo, Japan) equipped with a digital JVC KY-F 58E camera (JVC, Yokohama, Japan). The ribbon width was determined by dividing the mean of the diameters measured by the 1.3 Summers coefficient (Roehrich, 1947; Nacoulima et al., 2016; Konan and Mergeai, 2020).

Statistical analysis

All the data collected were subjected to the analysis of variance (ANOVA) using the software Statistica 7.1 (Stat Soft, France). The least significant difference (LSD) was used to establish the differences between means at P=0.05.

RESULTS AND DISCUSSION

Analysis of fiber fineness of studied diploid and tetraploid cotton species

The results of the analysis of fiber fineness for the studied diploid and tetraploid cotton species are presented in Table 2. The ribbon width of the ten wild diploid species varied from 5.940 µm (*G. longicalyx* Hutch. & Lee) to 15.533 µm (*G. thurberi* Todaro), while that of the cultivated species ranged from 17.765 µm (*G. hirsutum* L cv. C2) to 24.374 µm (*G. arboretum* L). All the wild diploid species had finer fibers than the cultivated species. Their fibers were even finer than the Sea Island cotton (*G. barbadense* L), which is known for its fine

Table 2. Ribbon width of the diploid and tetraploid cotton species studied.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
G. anomalum	104	6.128 ±0.210	3.738	9.138	A
G. sturtianum	71	10.907 ±0.255	6.877	18.700	D
G. armourianum	102	13.967 ±0.212	7.769	20.438	F
G. harknessii	104	7.772 ±0.210	4.662	12.369	B
G. aridum	100	11.013 ±0.215	7.123	15.931	D
G. raimondii	110	8.570 ±0.205	5.592	11.585	C
G. stocksii	101	11.706 ±0.213	6.069	14.562	E
G. areysianum	102	13.786 ±0.212	7.685	20.085	F
G. thurberi	83	15.533 ±0.235	9.054	21.938	G
G. longicalyx	113	5.940 ±0.202	4.254	8.862	A
G. arboreum	107	24.374 ±0.207	16.338	37.308	K
G. hirsutum (cv. C2)	107	17.765 ±0.207	12.092	24.369	H
G. hirsutum (cv. NC8)	116	18.294 ±0.199	13.885	24.169	H
G. hirsutum (cv. 98M)	114	19.445 ±0.201	13.885	25.785	I
G. hirsutum (cv. 11240)	112	20.036 ±0.203	13.423	25.015	J
G. barbadense (cv. 353)	110	19.117 ±0.205	12.938	26.638	I

fibers (Avci et al., 2013; Ijaz et al., 2019). Regarding the LSD grouping, the finest fibers among the studied wild diploid species were given by *G. longicalyx* Hutch. & Lee (5.940 µm) and *G. anomalum* Wawra & Peyr.(6.128 µm), followed by *G. harknessii* Brandegee (7.772 µm) and *G. raimondii* Ulbr.(8.570 µm). The other wild diploid species presented values of ribbon width ranging from 10.907 to 15.533 10 µm. The very low ribbon width exhibited by the African wild diploid species *G. longicalyx* Hutch. & Lee underlines its potential to improve fiber fineness (Demol et al., 1978; Nacoulima et al., 2016; Konan et al., 2020). The results also highlighted another African wild species, *G. anomalum* Wawra & Peyr., which presented good fiber fineness close to that of *G. longicalyx* Hutch. & Lee, with no significant difference. The good fiber fineness of *G. anomalum* Wawra & Peyr. has also been reported by Mehetre (2010). The American wild species *G. harknessii* showed finer fiber than *G. raimondii* Ulbr, but it is rarely cited as a good source of fiber fineness like *G. raimondii* Ulbr (Gotmare et al., 2000; Islam et al., 2016).*G. harknessii* Brandegee is most often cited for its resistance to Verticillium wilt and Fusarium wilt, and as source of cytoplasmic male sterility and fertility restorer (Ano et al., 1982; Gotmare et al., 2000).

Among the cultivated species, the Upland cotton varieties *G. hirsutum* L (cv. C2) and *G. hirsutum* L (cv. NC8) had the finest fibers with 17.765 and 18.294 µm ribbon width respectively; while *G. barbadense* L presented a ribbon width of 19.117 µm. Although *G. barbadense* L is recognized as having finer fiber than Upland cotton (Avci et al., 2013), the present results showed finer fibers for these two varieties of *G. hirsutum* L. Actually, several varieties of upland cotton resulting from breeding programs for fiber quality have gained in fiber fineness comparable to that of *G. barbadense* L; this is the case for these two varieties of *G. hirsutum* L (cv. C2 and cv. NC8) in the present study.

Of the results presented in Table 2, the cultivated diploid species *G. arboreum* L had the highest ribbon width value. This result showed that not all diploid species produce fine fibers, even if all the other (wild) diploid species studied had finer fibers than the tetraploid cotton studied. It again stresses that wild diploid species can be a source of desirable genes for the genetic improvement of cultivated cotton (Konan and Mergeai, 2020).

Analysis of fiber fineness of the bi-species hexaploid hybrids

To evaluate the influence of the studied diploid genomes on the fiber fineness of upland cotton, hybrids including each of these genomes and genome of *G. hirsutum* L cv C2 or cv NC8 were examined for their fiber fineness. The results of this analysis are shown in Table 3. The mean values of ribbon width of the different hybrid ranged from 12.526 to 26.072 µm. The bi-species hexaploid hybrid (*G. hirsutum* L cv. C2 × *G. longicalyx* Hutch. & Lee)² showed the finest fibers with a mean value of ribbon width of 12.526 µm. It was followed by (*G. hirsutum* L cv. C2 × *G. anomalum* Wawra&Peyr)² with on average 15.833 µm of ribbon width, and then (*G. hirsutum* L cv. C2 × *G. thurberi* Todaro)² and (*G. hirsutum* L cv. NC8 x *G. stocksii* Mast.)² with mean value of 16.835 and 16.852 µm of ribbon width, respectively. The highest value of ribbon width

Table 3. Ribbon width of the bi-species hexaploid and tri-species hybrids studied.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
(*G. hirsutum* cv. C2 × *G. arboreum*)²	100	22.306 ±0.199	15.615	27.646	H
(*G. hirsutum* cv. C2 × *G. anomalum*)²	110	15.833 ±0.190	11.331	20.523	B
(*G. hirsutum* cv. C2 × *G. sturtianum*)²	106	19.499 ±0.193	12.538	26.338	F
(*G. hirsutum* cv. NC8 × *G. australe*)²	112	26.072 ±0.188	19.877	33.046	J
(*G. hirsutum* cv. C2 × *G. harknessii*)²	116	20.204 ±0.185	14.415	25.446	G
(*G. hirsutum* cv. NC8 × *G. aridum*)²	104	18.183 ±0.195	14.462	21.915	D
(*G. hirsutum* cv. C2 × *G. raimondii*)²	104	18.853 ±0.195	14.415	22.077	E
(*G. hirsutum* cv. NC8 × *G. stocksii*)²	103	16.852 ±0.196	12.069	20.977	C
(*G. hirsutum* cv. NC8 × *G. areysianum*)²	107	22.937 ±0.192	16.500	28.438	I
(*G. hirsutum* cv. C2 × *G. thurberi*)²	117	16.835 ±0.184	12.215	23.208	C
(*G. hirsutum* cv. C2 × *G. longicalyx*)²	122	12.526 ±0.180	8.946	16.008	A
(*G. hirsutum* cv. C2 × *G. thurberi*)²x *G. longicalyx* (HTL)	120	12.649 ±0.182	10.008	15.277	A

was presented by the bi-species hybrid (*G. hirsutum* L cv. NC8 × *G. austral* F.Muell.)². As for the diploid species where *G. longicalyx* Hutch. & Lee and *G. anomalum* Wawra & Peyr had the smallest ribbon width, it was the hexaploid hybrids which contained genomes of *G. longicalyx* Hutch. & Lee or *G. anomalum* Wawra&Peyr which showed the smallest ribbon width. However, the hexaploid hybrid including *G. longicalyx* produced significantly finer fibers than the hybrid including *G. anomalum* Wawra & Peyr. This result indicates the greater impact of the F_1 genome of *G. longicalyx* Hutch. & Lee in the improvement of fiber fineness of upland cotton than the B_1 genome of *G. anomalum* Wawra & Peyr. The results also showed that the D_1 genome of *G. thurberi* Todaroand E_1 genome of *G. stocksii* Mast.reduced the fiber fineness of *G. hirsutum* L as well, but not as much as *G. longicalyx* Hutch. & Lee and *G. anomalum* Wawra & Peyr.

Apart from the four wild diploid species *G. longicalyx* Hutch.& Lee, *G. anomalum* Wawra & Peyr, *G. thurberi* Todaro and *G. stocksii* Mast, all the other diploid species did not bring an interesting improvement in fiber fineness of *G. hirsutum*L. Even some wild diploid species such as *G. harknessii* Brandegee (genome E3) and *G. raimondii*Ulbr. (genome D5) which had good fiber fineness (ribbon width <10 µm) could not reduce the ribbon width of *G. hirsutum* L when combined to it in bi-species hybrids. These results suggest that the genes that control the fineness of the fibers in the different wild diploid species did not have the same action when they are confronted with the genome of upland cotton in a hybrid configuration. The diameter of the cotton fiber is primarily a genetic trait and the genetic mechanisms of fiber traits are complex (Matic-Leigh and Cauthen, 1994; Bradow and Davidonis, 2000; Zhang et al., 2013; Islam et al., 2016). According to Ijaz et al. (2019), cotton fiber quality traits are controlled by multiple genes (polygenic inheritance) with different mechanisms and complex genetic architecture. For instance, in the past decades, studies on cotton fiber quality traits on *G. hirsutum* L and *G. barbadense* L found a significant association between SSRs and fiber quality traits and identified 70 stable loci for target traits including 30 for fiber length, 27 for fiber strength, and 13 for fiber fineness (Zeng et al., 2009; Cai et al., 2014). Later, several studies, on cotton fiber quality traits that focused on both *G. hirsutum*L and *G. hirsutum* L×*G. barbadense*L populations, have mapped fiber QTLs in large genomic regions that may include hundreds or thousands of genes (Said et al., 2013; Fang et al., 2014; Shang et al., 2015; Tang et al., 2015; Tan et al., 2015; Ma et al., 2017, 2018; Ijaz et al., 2019). QTLs are chromosomal regions which contribute cumulatively to a trait with varying percentages of phenotypic variance from each QTL (Said et al., 2015). According to Ijaz et al. (2019),the number of fiber quality trait QTLs over the chromosomes of the cotton genome is not identical, and QTLs associated with cotton fiber quality obtained from Cotton QTL database (http://www.cottonqtldb. org) are distributed unevenly across the 26 chromosomes of the cotton genome.

Analysis of fiber fineness of the tri-species hybrid and its BC2 progenies

The HTL tri-species hybrid (*G. hirsutum* L × *G. thurberi* Todaro)² × *G. longicalyx* Hutch. & Lee (Konan et al., 2007) with a ribbon width of 12.65 µm (Table 3) had the same fiber fineness as *G. hirsutum*L × *G. longiclayx* Hutch. & Lee² hexaploid hybrid (P>0.05).To check the behavior of the genes of *G. longicalyx* Hutch. & Lee responsible for the fiber fineness in the advanced progenies of the tri-species hybrid, HTL/BC2 plants were examined for the fineness of their fibers. The results of

Table 4. Ribbon width of the BC2 progenies of the HTL tri-species hybrid.

Genotype	Number of fiber analysed	Ribbon widh (µm) ± standard deviation	Min	Max	LSD grouping
HTLBC2#1	102	15.332 ±0.171	10.262	20.977	C
HTLBC2#3	110	14.906 ±0.165	10.331	19.554	BC
HTLBC2#9	110	17.388 ±0.165	10.877	21.754	I
HTLBC2#11	102	14.650 ±0.171	11.331	18.292	B
HTLBC2#14	101	16.842 ±0.172	13.692	20.523	GH
HTLBC2#15	100	16.519 ±0.173	12.008	23.838	FG
HTLBC2#17	101	16.931 ±0.172	11.331	21.385	GHI
HTLBC2#18	103	15.977 ±0.171	12.538	20.415	DE
HTLBC2#5	116	13.922 ±0.161	10.723	17.154	A
HTLBC2#6	121	16.356 ±0.157	11.808	20.692	EF
HTLBC2#7	111	13.473 ±0.164	8.038	16.654	A
HTLBC2#10	112	15.876 ±0.164	12.008	22.077	D
HTLBC2#13	122	15.328 ±0.157	9.885	20.523	C
HTLBC2#16	117	17.024 ±0.160	13.400	20.962	HI
HTLBC2#20	109	16.757 ±0.166	10.238	23.154	FGH

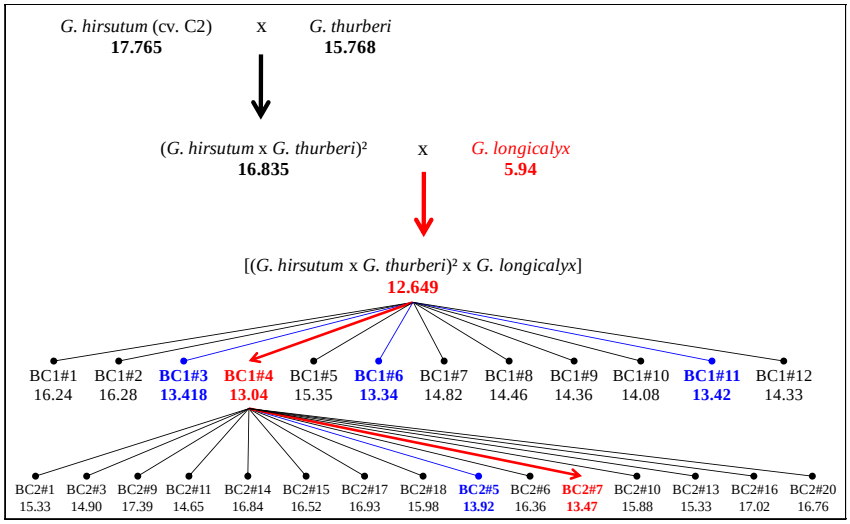

Figure 4. Ribbon width (µm) of parental species and the BC1 and BC2 progenies of the HTL tri-species hybrid. Ribbon width values of the BC1 plants come from the study of Konan et al. (2020).

this analysis are presented in Table 4. The ribbon width of the BC2 plants varied from 13,473 to 17,388 µm. The finest fibers were presented by BC2#7 and BC2#5 with 13.473 µm and 13.922 respectively, while the other BC2 plants had a ribbon width varying from 14.650 to 17.388 µm. These results show the presence of fiber fineness segregation among BC2 plants. Konan and Mergeai (2020), working on twelve BC1 progenies of the tri-species hybrid HTL, reported ribbon width ranging from 13.039 to 16.276 µm with four BC1 plants having the lowest ribbon width (13.039 – 13.416 µm). This fiber fineness segregation among the HTL/BC plants may be due to the segregation of *G. longicalyx* alleles among the BC plants. This suggests the differential presence or absence of this diploid species chromosomes and/or chromosome recombinants as shown by Konan and Mergeai (2020) with genomic *in situ* hybridization (GISH) analysis. The persistence of the outstanding fiber fineness of *G. longicalyx* Hutch. & Lee, in the bi-species hybrid with *G. hirsutum* L, in the HTL tri-species hybrid and in the HTL/BC1 and BC2 derivative plants demonstrates the inheritance of this trait through the crossing scheme (Figure 4). Hence, this finding brings out the good donor status of *G. longicalyx* Hutch. & Lee

for fiber fineness.In addition, according to Demol et al. (1978), the fibers of *G. longicalyx* Hutch. & Lee have exceptional fiber strength and a high molecular weight. Such finer and stronger fibers than those of *G. barbadense* L would undoubtedly be much appreciated by spinners. These results therefore make *G. longicalyx* Hutch. & Lee an interesting source that deserves more attention from breeders for the improvement of cotton fiber quality

Conclusion

The results obtained in the present study show the potential of four wild cotton diploid species (*G. longicalyx* Hutch. & Lee, *G. anomalum* Wawra & Peyr., *G. thurberi* Todaro and *G. stocksii* Mast.) to significantly improve the fineness of the fibers of upland cotton in a hybrid configuration. However, among these wild species, *G. longicalyx* Hutch. & Lee stood out for its exceptional fiber fineness, and its remarkable impact on improving the fiber fineness of *G. hirsutum* L. This wild African diploid species seems to be a good donor for the introgression of this useful trait into upland cotton. In view of the results of this study, the species *G. longicalyx*, and to a lesser extent the three other highlighted wild species, constitute interesting genetic resources for the development of cotton varieties with outstanding fiber fineness.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Establishment of an early selection method (criteria) for breeding in cowpea (*Vigna unguiculata*)

Avosa Oside Millicent[1]*, Orawu Martin[2], Ongom Obia Patrick[1], Dramadri Onziga Isaac[1], Rutayisire Amandin[1], Osundwa Cynthia[1], Paul Gibson[1] and Edema Richard[1]

[1]Makerere Regional Centre of Crop Improvement, CAES, Makerere University P. O. Box 7062, Kampala, Uganda.
[2]National Semi-Arid Resources Research Institute (NaSARRI), P. O. Box 56, Soroti Uganda.

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Populations with high genetic variability are targeted by breeders as they create opportunity for selection and genetic improvement. To achieve this, multiple populations are created, but resources are often scarce. This calls for identification of populations with the desired traits at early generation. The study was carried out at MUARIK in seasons 2017A and 2017B on 135 F2 and 40 F3 cowpea populations respectively together with 25 parental lines aimed at: Determining best performing populations for yield, resistance to scab, virus and flower thrip based on usefulness criterion and selection index methods. Usefulness criterion computed for yield identified NE 36 x 2392 as the best population. Usefulness criterion computed for yield and its components identified NE 5 x Sanzi as the best population. WC 48A x 2392 was identified as the best population using selection index values that included resistance to virus, thrips, scab, yield and its component and when only yield and its components were fitted in the model. Variability and high yield performance was maintained in the forty best populations identified and therefore amendable for future improvement. No differences were shown among the methods used for selection hence can be adapted for breeding in cowpea.

Key words: Selection index, scab, thrip and virus resistance, usefulness criteria, yield.

INTRODUCTION

Cowpea (*Vigna unguiculata*) occupies an economically important position in production compared to other legume crops in Uganda particularly in the eastern and northern regions where it is a dominant source of protein and household income for the resource poor subsistence farmers (Verlag et al*.,* 2006; Mundua, 2010). Despite its importance, cowpea productivity levels are generally low averaging 300-500 kg/ha yet its yield potential can be between 1500 and 3000 kg/ha as reported elsewhere (Gbaye and Holloway, 2011). The low productivity is attributed to the fact that cowpea varieties that are preferred and commonly grown by farmers are highly affected by pests, scab and viral diseases andpests (Mundua, 2010). Therefore, varietal improvement to increase the potential yield of locally adapted and farmer preferred cowpea varieties, which requires introgression of desirable traits from the elite lines and or other exotic germplasm into the farmer preferred local varieties is needed. It should be kept in mind that the development of elite lines requires the generation of populations with high

*Corresponding author. E-mail: milicentavosa@gmail.com or milicentavosa@yahoo.com.

genetic variability and judicious selection of promising lines in the most efficient manner possible (Monteagudo et al., 2019).

Population development highly depends on the inheritance of the traits. For traits such as yield, disease, and pest resistance, which are quantitatively inherited, adequate evaluation and selection could be achieved by generating larger populations (Bijma et al., 2007). Therefore, the cowpea breeding program at Makerere University generated multiple populations by crossing farmers' preferred cowpea cultivars with cowpea lines that have high yielding potential, thrip, scab, and viral diseases resistance background. This being done amidst scarce resources, it becomes a challenge to handle such huge populations from generation to generation.

Nevertheless, analysis of genetic attributes can be done in an early generation to identify desirable segregants, thus reducing the population size in later generations (Bhadru and Navale, 2012a). Early selection may start at F2 (Bernardo, 2003; Simic et al., 2003) or in later generations with emphasis put on populations with high mean performance and adequate genetic variance. It is worth mentioning that the most promising novelties for increasing the rate of genetic gain without greatly increasing program size appear to be related to reducing breeding cycle time. This is likely to be implemented by parental selection on non-inbred progeny, rapid generation advance, and genomic selection (Cobb et al., 2019). These are complex and expensive processes and so techniques that require less resource allocation should be considered. Usefulness criterion and selection index are the inexpensive early selection methods suggested for obtaining prospect lines in a breeding population (Bernado, 2010; Simic et al., 2003).

Usefulness criterion (UC) is a selection method that predicts the gain (response to selection) that can be obtained from a population when a selection pressure is imposed, thereby reducing the selection cycles. Additionally, this method allows suitable amount of genetic variability to be maintained in the population when used as it combines the information of the mean performance and genetic variance of a population to obtain prospect lines (Bernado, 2010; Simic et al., 2003). The variability maintained permits flexibility and survival of individuals in a population in the face of changing environmental circumstances (Hallauer, 2010).

Selection can be done by looking at one trait at a time from one generation to the other or by simultaneously selecting the attributes that are in consideration by creating a selection index (Bernado, 2010). However, single-trait selection becomes highly questionable and unreliable to choose for the traits that are highly correlated like yield and yield-related traits. Therefore, simultaneous selection of traits becomes better as it increases the chance of success in breeding programs and helps in choosing of populations with multiple characters put into consideration (Rodrigues et al., 2017).

Studies have been conducted using selection index as a discriminative function in selection of best genotypes in cowpea (Jost et al., 2013; Khanpara et al., 2016; Sivakumar et al., 2017). Other studies have been conducted in maize using both selection index and usefulness criteria (Nizeyimana, 2013). No research has been conducted using both usefulness selection criteria (UC) and base selection index (BSI) on cowpea for early generation selection of promising populations. Therefore, this study exploits the two selection criteria; base index selection, and usefulness criteria to select the best F2 segregating population for advancement.

MATERIALS AND METHODS

The study was conducted at MUARIK (32°36'24"E, 0°27'60"N) during seasons 2017A and 2017B on populations that were developed by Makerere University Cowpea Breeding Program in 2016A. The parents used in the development of the crosses were earlier characterized by Makerere cowpea breeding program for resistance to diseases (virus and scab) and thrips infestation including other traits like cream colored cowpea genotypes with intermediate grain yield (Table 1).

During Season 2017A study, a total of 135 F_2 populations and 25 parental lines were planted in an alpha lattice design of 5 blocks x 32 plots with two replicates. Each plot consisted of 32 cowpea plants

Season 2017B study comprised of the 24 parental lines and forty best populations selected from season 2017A evaluation. Within each population were the 8 best lines selected from the 64 evaluated plants in season 2017A thus a total of 320 lines. The experiment was set up in an alpha lattice design consisting of 10 blocks and 40 plots with two replications. Each block consisted of four populations (32 lines) and 8 parents planted alongside them.

Data were collected on agronomic parameters notably: number of pods per plant, number of pods per peduncle, seed weight and grain yield from each individual plant. Data on scab were collected on plot basis at vegetative and podding stage at a scale of 1-5 (Afutu et al., 2016a) and at vegetative and senescence stage for virus at a scale of 1-5 (Mbeyagala et al., 2014). Data on thrips was taken 35 days after planting at weekly intervals for three weeks at a scale of 1-9 **(Jackai and Singh, 1988).**

Data analysis

Analysis of variance for the average performances of the thrip damage scores, AUDPC for virus and scab on leaf severity, scab on pod, yield and yield components per plot were analyzed using linear mixed model (ReML: Restricted maximum Likelihood, Genstat 18) approach following alpha lattice design model. The following linear models were used:

ANOVA for 2017A

$$Y_{ijk} = \mu + R_i + B/R_J + G + e_{ijk}$$

ANOVA for 2017B

$$Y_{ijk} = \mu + R_i + B/R_J + Pop_k + P_l + Pop/L_m + PvsCrosses_{lj} + e_{ijk}$$

Where;R_i = the replication effect, B/R_j = the block within replication effect, Pop_k = population effect, $Pop\ /\ L$ = line effect, and P_i = the

Table 1. Cowpea parental lines used in the development of bi-parental populations.

S/N	Parent	Seed color	Strength of the genotype
1	2392	Brown	Resistant to virus disease
2	3306	Cream	Intermediate grain yield
3	Ayiyi	Cream	High podding and desired growth architecture
4	Danila	Black	Drought tolerant
5	Eberlat*NE51	Mottle	High grain yield
6	IT 889	Mottle	Virus resistant and high grain yield
7	KVU 27-1	Brown	Resistant to scab disease and intermediate grain yield
8	MU 15	Brown	Resistant to virus and intermediate in grain yield
9	MU 20B	Black	Resistant to scab and intermediate grain yield
10	MU 9	Brown	High grain yield
11	NE 21	Cream	Intermediate grain yield
12	NE36	Mottle	Resistant to virus and scab, and intermediate grain yield
13	NE 48	Brown	Resistant to virus and high grain yield
14	NE 5	Cream	Resistant scab and intermediate grain yield
15	NE 55	Cream	Intermediate grain yield
16	Sanzi	Mottle	Resistant to flower thrips
17	Secow 2w	Cream	Resistant to virus and most genotypically diverse
18	Secow 4w	Cream	Virus resistant
19	Secow 5T	Brown	Virus and Scab resistant
20	VCR 1432	Mottle	Flower thrip resistant
21	WC 27	Cream	Virus resistant
22	WC 48A	Brown	Scab resistant and high grain yield
23	WC 63	Mottle	Resistant to Virus and scab, and high grain yield
24	WC 64	Mottle	Resistant to scab and rust, and high grain yield
25	WC 66	Mottle	Resistant to virus and high grain yield

parental effect, $PvsPop$= parent versus population/crosses effect.

Further analysis to identify populations combining high genetic variance and mean performance for yield and yield components was conducted using usefulness criterion. The usefulness value (expected genetic gain) of each F_2 was computed based on the usefulness formula and the standardized selection differential (k_i). An assumption was made for selecting at least 20% of the best populations with a selection differential (k_i) of 1.40. The phenotypic variance for yield and yield components among the 64 plants for each population (σ^2_{F2}) and the parents $\left(\sigma^2_{p1} and\ \sigma^2_{p2}\right)$ was calculated using the variance function. The information on phenotypic variance for each population and the parents was used to calculate broad sense heritability (H^2). Broad sense heritability among F_2 families within a population was calculated using Equation 1 as presented by Hanson et al. (1956):

$$H^2 = \left\{\sigma^2_{F2} - (\sigma^2_{P1} + \sigma^2_{P2})/2\right\} \Big/ \sigma^2_{F2} \quad (1)$$

The variance components for the F_3 40 best selected cowpea populations were calculated as follows:

Genotypic variance;

$$\sigma^2_g F_3 = \frac{MSgenotype - MSerror}{r}$$

Phenotypic variance;

$$\sigma^2_p F_3 = \sigma^2_g + MSerror$$

Heritability estimates for the F3 best selected populations was calculated as per Equation 2

$$H^2 = \frac{\sigma^2_g F_3}{\sigma^2_p F_3} \quad (2)$$

The genetic gain of each population was calculated using Equation 3 as described by Johnson et al. (1955):

$$G = k_i * \left(\sqrt{\sigma^2_{Phenotype}}\right) * H^2 \quad (3)$$

Usefulness for each population was then calculated using Equation 4 as described by Bernado (2010):

$$U = \mu + G \quad (4)$$

Where; H^2 is the heritability of each trait, σ^2_{F2} is the phenotypic variance for each trait in F2 population, σ^2_{P1} and σ^2_{P2} is the variance for the first and second parents respectively, $\sigma^2_g F_3$ is the genotypic variance of the $F_{2:3}$ populations, $\sigma^2_p F_3$ is the phenotypic variance of the $F_{2:3}$ populations, G is the gain from selection, (k_i) is the selection differential, U is the usefulness of the population, and μ is the mean population for the trait.

Table 2. Assigned weights for the traits used in the formation of selection index for the parental lines and F_2 populations.

Trait	Weight assigned	Rationale
Grain yield	5	Ultimate goal of breeders and farmers
Pod No.[1]	3	Highly correlated with yield
Ped No.[2]	2	Highly correlated with yield
Virus	-2	Selection of resistant population to virus
Thrips	-3	Selection of resistant population to thrips
Scab on leaves	-2	Selection of resistant population to scab
Scab on pod	-1	Selection of resistant population to pod scab

[1]Number of pods per plant; [2]Number of peduncles per plant.

Table 3. Analysis of variance for thrip damage, virus and scab severity and yield and its components among cowpea genotypes evaluated during 2017A season.

SOV[1]	Virus Audpc[2]	Scab on leaf Audpc[2]	Scab on pod	Thrips	Ped No.[3]	Pod No.[4]	Yield
Genotype	51.32***	31.62*	0.36***	1.58[ns]	25.67***	9.59***	338481.6***
Lee[5]	32.48	26.13	0.19	1.36	16.25	40.34	162731.6
SED[7]	5.70	5.11	0.44	1.69	4.03	6.35	403.4

[1]Source of variation, [2]Area under disease progress curve, [3]Number of peduncles, [4]Number of pods, [5]Lattice effective error, [6]Coefficient of variation.

Usefulness value for both grain yield and yield components (number of peduncles and pods) were computed for 135 populations evaluated in season 2017A. A selection index of grain weight, number of pods and peduncles was calculated, and the values were used to generate within population variances and means of each population. Usefulness value for grain yield was calculated for the forty best selected populations evaluated in 2017B.

Index values for each of the 135 populations and 25 parents evaluated in season 2017A were calculated in an Excel spreadsheet using the average means of the traits. Relative weights were assigned to the traits according to their relative contribution in the final product or desired genetic gain where traits with much contribution were given much weights (Table 2). The following formula was used to calculate the index values.

$$I = \sum b_i \, x_i \quad (4)$$

Where b_i is the weight of the trait (i) and x_i is the phenotypic value of the trait (i) (Bernado, 2010).

Analysis of variance was carried out to test the difference in the methods used using R version 3.4.1 and a boxplot generated. A t-test was also conducted to compare the two methods of selection using the means of the 30 best selected populations by the following formula (Amirtage and Berry, 1994)

$$t = \frac{\bar{x}_1 - \bar{x}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \quad (5)$$

Spearman rank correlation was carried out to determine the relationship between the two methods used in selection.

Further analysis to determine the realized heritability the realized genetic gain obtained from the selection from the 40 selected plants evaluated in 2017B was carried out using Equation 6 as presented by Rédei (2008)

$$Realized\ heritability\ (Rh) = \frac{Responce\ to\ Selection}{Selection\ Differential} \quad (6)$$

Where; *Response to Selection (R) = Avg. of the 1s^t Gen - Avg. of the 2nd Gen*and

$$Selection\ Differential\ (s) = Avg\ of\ the\ 1st\ Gen - Avg\ of\ the\ selected\ popolations$$

$Avg\ of\ the\ 1st\ Gen$ = Average mean of the 135 evaluated populations in season 2017A, $Avg\ of\ the\ 2nd\ Gen$ = Average mean of the forty populations evaluated in season 2017B and $Avg\ of\ the\ selected\ popolations$ = the mean of the selected forty populations evaluated in 2017A

RESULTS

Performance of cowpea genotypes evaluated in season 2017A for biotic stresses, yield and yield components

The populations tested differed significantly (P<0.001) for reaction to virus disease and scab on pod, number of pods, peduncles and grain yield except for severity for scab on leaves which was significant at P<0.05 and thrips infestation which was not significant (Table 3).

Determination of the usefulness value of cowpea populations for yield and yield components

Usefulness values for grain yield ranged from 1.93 to 72.39 (Table 4 and Appendix 1) and between -1.64 and 10.8 for yield and yield components (Table 5, Appendix 2). The highest genetic variance of 576.04 was recorded for NE 36 x 2392 for grain yield, and 24.04 for NE 5 x Sanzifor yield and its components (Table 5). Fourteen populations that ranked top and seven populations that

Table 4. Estimated usefulness value (U) of 21 representative populations for grain yield (I=0.2, k=1.4).

Population	Vpop[1]	VP1[2]	VP2[3]	Vg[4]	H[5]	Gs[6]	μ[7]	U[8]
NE 36 X 2392	695.63	100.80	138.39	576.04	0.83	30.58	41.81	72.39
Danila X NE 48	361.32	48.72	69.78	302.08	0.84	22.25	43.41	65.66
SECOW 5T X Ayiyi	483.79	44.50	67.27	427.90	0.88	27.24	34.72	61.96
NE 5 X Sanzi	342.00	55.78	26.58	300.82	0.88	22.77	38.26	61.03
Ayiyi X WC 66	430.43	67.27	34.81	379.40	0.88	25.60	34.78	60.38
SECOW 5T X 3306	477.08	44.50	59.24	425.21	0.89	27.25	33.07	60.32
NE 5 X 2392	340.92	55.78	138.39	243.83	0.72	18.49	41.51	60.00
Danila X VCR 1432	228.20	48.72	52.20	177.74	0.78	16.47	42.45	58.92
Danila X KVU271	412.67	48.72	78.27	349.17	0.85	24.06	34.75	58.81
WC 48 X WC 27	409.89	72.17	65.31	341.15	0.83	23.59	35.10	58.69
Ayiyi X 2392	414.02	67.27	138.39	311.19	0.75	21.41	35.03	56.44
NE 21 X WC 48	232.92	42.01	72.17	175.83	0.75	16.13	39.87	56.00
WC 63 X NE 48	335.07	47.39	69.78	276.49	0.83	21.15	34.68	55.83
WC 48 X 2392	471.34	72.17	138.39	366.06	0.78	23.61	31.65	55.26
MU 20B X 2392	76.76	30.74	138.39	-7.81	-0.10	-1.25	13.84	12.59
WC 27 X Sanzi	55.62	65.31	26.58	9.68	0.17	1.82	9.17	10.99
Sanzi X 2392	64.05	26.58	138.39	-18.44	-0.29	-3.23	14.20	10.97
Eberlat*NE 51 X MU 20B	66.01	100.00	30.74	0.63	0.01	0.11	9.839	9.95
MU 20B X SECOW 5T	34.37	30.74	44.50	-3.26	-0.09	-0.78	7.231	6.45
WC 66 X 2392	46.94	34.81	138.39	-39.67	-0.85	-8.11	11.32	3.21
WC 63 X 2392	47.18	47.39	138.39	-45.71	-0.97	-9.32	11.25	1.93

[1]Population variance, [2]Variance for the 1st Parent, [3]Variance for the 2nd parent, [4]Genetic variance, [5]Expected genetic gain, [6]Broad sense heritability value, [7]Population mean for grain yield, number of pods and peduncles, [8]Usefulness Value, K: Standardized selection differential.

Table 5. Usefulness value (U) of *21 representative populations* for yield and yield components.

Population	Vpop[1]	VP1[2]	VP2[3]	Vg[4]	H[5]	Gs[6]	μ[7]	U[8]
NE 5 X Sanzi	25.63	2.05	1.12	24.04	0.94	6.65	4.15	10.80
Ayiyi X 2392	25.51	2.49	1.99	23.26	0.91	6.45	3.11	9.56
NE 36 X 2392	22.13	1.53	1.99	20.37	0.92	6.06	3.33	9.39
Danila X NE 48	9.19	1.71	3.04	6.82	0.74	3.15	3.16	6.31
NE 21 X NE 55	13.68	1.43	3.80	11.07	0.81	4.19	1.35	5.53
MU 20B X NE 36	12.42	2.28	1.53	10.51	0.85	4.18	1.36	5.53
WC 48A X WC 27	12.28	4.31	1.31	9.47	0.77	3.78	1.62	5.40
MU 20B X WC 27	10.53	2.28	1.31	8.73	0.83	3.77	1.34	5.11
2392 X Eberlat*NE 51	10.95	1.99	4.67	7.62	0.70	3.23	1.80	5.02
SECOW 5T X Ayiyi	11.66	2.78	2.49	9.02	0.77	3.70	1.33	5.02
KVU 271 X WC 27	9.19	1.38	1.31	7.84	0.85	3.62	1.37	4.99
MU 9 X NE 55	11.55	1.17	5.09	8.41	0.73	3.47	1.49	4.95
Ayiyi X WC 66	11.25	2.49	0.86	9.58	0.85	4.00	0.92	4.92
Danila X KVU 271	9.24	1.71	1.38	7.70	0.83	3.55	1.00	4.55
WC 48A X MU 9	2.45	4.31	1.17	-0.29	-0.12	-0.26	-0.98	-1.24
NE 48 X Ayiyi	3.18	3.04	2.49	0.41	0.13	0.32	-1.66	-1.34
WC 63 X 2392	1.81	1.36	1.99	0.14	0.08	0.14	-1.77	-1.63
Eberlat*NE 51 X NE 48	2.20	4.67	3.04	-1.65	-0.75	-1.56	-0.19	-1.75
WC 64 X NE 55	1.62	1.19	3.80	-0.87	-0.54	-0.96	-1.75	-2.71
MU 9 X NE 36	1.10	1.17	1.53	-0.25	-0.23	-0.34	-2.49	-2.82
MU 20B X SECOW 5T	1.23	2.28	2.78	-1.30	-1.06	-1.64	-2.72	-4.36

[1]Population variance, [2]Variance for the 1st Parent, [3]Variance for the 2nd parent, [4]Genetic variance, [5]Expected genetic gain, [6]Broad sense heritability

Table 6. Estimated Base Selection Index values (BSI) for the 21 representative populations.

Genotype	Virus	Thrips	Scab-a[1]	Scab-b[2]	Ped No.[3]	Pod No.[4]	Yield	BSI-a[5]	BSI-b[6]
WC 48A X 2392	-0.33	-3.97	-3.3	-1.56	6.01	9.74	19.70	35.45	44.61
NE 5 X Sanzi	-3.93	-6.12	-2.87	-1.51	8.11	10.52	9.67	28.31	42.74
Danila X NE 48	-1.23	-2.67	-2.44	-1.54	4.61	6.54	13.16	24.31	32.18
NE 36 X 2392	0.82	-4.69	-2.53	-0.93	4.38	8.03	10.7	23.10	30.43
Danila X VCR 1432	0.01	-6.35	0.53	-1.56	3.29	5.34	11.55	20.19	27.55
NE 5 X 2392	-3.40	1.35	-2.86	-1.22	1.42	3.34	14.47	19.23	25.35
NE 55	-4.81	-3.31	-2.48	-0.32	2.15	4.72	7.49	14.37	25.28
Ayiyi X 2392	-3.40	1.81	-1.2	-1.59	5.87	5.90	7.68	19.44	23.81
SECOW 5T X Ayiyi	0.87	-0.58	-2.86	-1.49	4.45	6.31	7.58	18.34	22.39
MU 20B X NE 36	-4.73	-1.12	-0.32	-1.51	3.56	4.93	4.92	13.41	21.09
WC 48A	-0.32	0.77	-2.93	-1.54	2.19	2.71	10.36	15.26	19.28
2392 X Eberlat*NE 51	2.00	-7.84	-1.20	0.34	4.38	7.59	-0.32	11.65	18.35
Danila X NE 5	-3.80	0.70	-2.43	-0.88	1.96	2.59	6.68	11.23	17.63
3306 X Ayiyi	-1.71	0.00	-1.20	-1.53	1.51	2.78	8.68	12.97	17.41
MU 20B	1.02	3.96	2.24	1.55	-2.55	-4.37	-6.31	-13.23	-22.00
MU 9 X NE 36	3.39	4.69	0.04	0.91	-3.88	-4.89	-7.07	-15.84	-24.86
MU 9	0.46	2.70	1.54	2.79	-3.53	-5.66	-8.25	-17.44	-24.93
WC 63 X 2392	2.27	1.59	7.04	2.13	-1.72	-3.34	-7.22	-12.28	-25.32
MU 20B X NE 55	0.12	1.72	6.97	2.15	-3.00	-3.95	-7.74	-14.70	-25.65
NE 21	1.13	3.26	5.74	2.18	-2.99	-4.29	-7.71	-14.98	-27.30
MU 20B X SECOW 5T	3.13	6.61	7.45	-0.31	-3.81	-5.69	-9.33	-18.82	-35.71

[1]Scab on leaf, [2]Scab on pod, [3]Number of peduncles, [4]Number of pods, [5]Base Selection Index for yield and its components, [6]Base Selection Index for Grain Yield.

Table 7. Correlation (r) values obtained from the association between the selections criteria (Usefulness criterion, Base index Selection Index and Mean performance).

Correlation	UC-1[1]	UC-2[2]	BSI-1[3]	BSI-2[4]	Mean yield
UC-1[1]	1.00				
UC-2[2]	0.76***	1.00			
BSI-1[3]	0.74***	0.88***	1.00		
BSI-2[4]	0.71***	0.84***	0.94***	1.00	
Mean yield	0.82***	0.80***	0.93***	0.87***	1.00

***: P<0.001, [1]UC considering grain yield, [2]UC considering grain yield, pods and peduncles, [3]BSI for grain yield, number, [4]BSI for grain yield, pods and peduncles, resistance to scab on leaf, pod, virus and thrips,

had the least usefulness values were selected as a representative to show the usefulness values of the populations for grain yield (Table 4) and grain yield and its components (Table 5).

Development of selection index for yield and agronomic traits and selection of best populations

The computed indices were based on the weighted mean values of the traits regarded as important and populations with higher selection index value were considered to be the best. WC 48A x 2392 (44.61) ranked first in the selection index for yield, yield components, thrip damage, scab and virus severity, while MU 20B x SEC 5T ranked last (Table 6 and Appendix 3). The same population (WC 48A x 2392) ranked first with a BSI value of 35.71 for the selection index value created for grain yield, number of pods and peduncles (Table 6 and Appendix 3). Fourteen populations that ranked top and seven populations that had the base selection index values were selected as a representative to show the usefulness values of the populations for grain yield (Table 6).

Comparison of the three selection criteria (usefulness criterion, base index selection and mean performance) for determining the best F_2 populations

Using the spearman rank correlation, the result revealed that there was a strong positive correlation (P< 0.001) in the comparison of each selection criteria to the other (Table 7).

Table 8. Comparison of various selection criteria using t-values.

Selection criteria	t-Value	Populations in common
UC[1] Yield Vs. UCYield and yield components	0.19[ns]	20
UC[1] Yield Vs. BSI[2] for Yield and its components	-0.09[ns]	20
UC[1] Yield Vs. BSI[2] for 7Traits[3]	0.63[ns]	16
UC[1] Yield Vs. Mean Yield	1.31[ns]	19
UC[1] Yield and its components Vs. BSI[2] Yieldand its components	0.10[ns]	22
UC[2] Yield and its components Vs. BSI[2] for 7Traits[3]	0.81[ns]	22
UC[2] Yield and its components Vs. Mean Yield	1.47[ns]	21
BSI[2] for Yield and yield components Vs. BSI[2] for 7 Traits[3]	-0.70[ns]	25
BSI[2] for Yield and yield components Vs. Mean Yield	1.36[ns]	24
BSI[2] for 7Traits[3] compared to Mean Yield	0.67[ns]	20

ns: not significant, [1]Usefulness Criteria, [2]Base selection index, [3]Grain yield, number of pods and peduncles, resistance to thrips, virus, scab on leaf and pod.

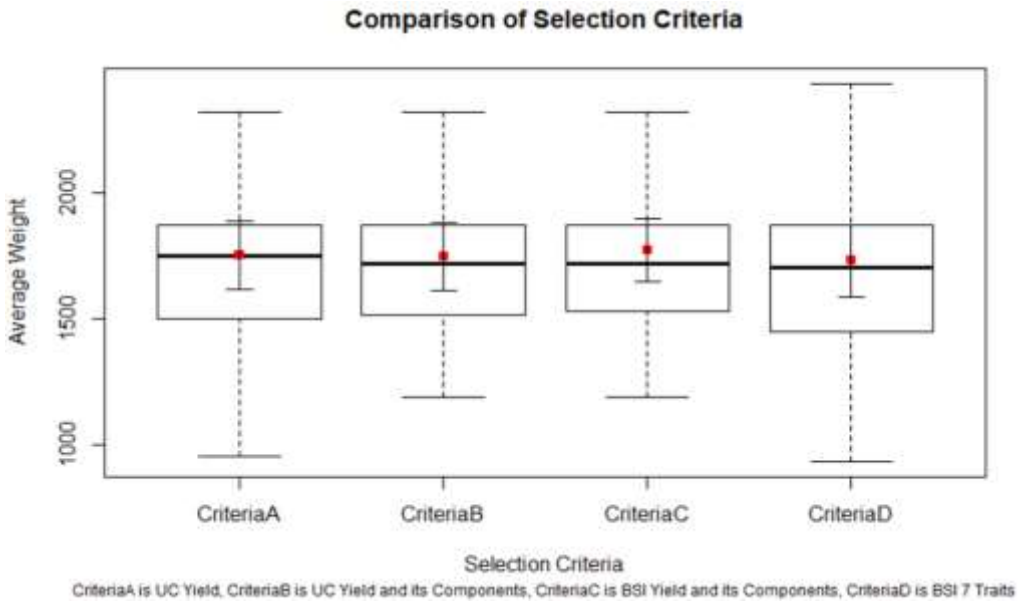

Figure 1. A boxplot showing differences among criteria used in the selection of the best populations.

There were no significant differences (P>0.05) observed for the mean yield of the top ranked populations in the different criteria used in the selection (Table 8 and Figure 1).

Selection of the best F_2 populations

A total of 40 cowpea populations were selected by choosing populations that occured in common when the 30 best populations were ranked in the 5 different selection criteria. Also populations that occurred among the 30 best in only one selection criterion and not in others but had unique capabilities such as disease resistance were selected for instance WC 27 x VCR 1432 (Table 9).

Eight plants that had high mean for grain yield were selected within each population and advanced for evaluation. The 320 lines selected were advanced to determine the effectiveness of the selection methods and populations.

Performances of the cowpea parents and F_3 cowpea as evaluated for virus and scab disease severity, thrips damage, yield and yield componentsin single site in season 2017B

The parents performed significantly different (P<0.001) for all the traits assessed except for their reaction to thrip (Table 10). Similarly, significant differences were

Table 9. Best populations selected from the methods usefulness criteria and base selection index.

Population	Yield (kg/ha)	Rank				
		BSI -1[1]	BSI -2[2]	UC-1[3]	UC-2[4]	Yield (kg/ha)
2392 x Ebelat*NE 51	1187	13	10	99	9	73
2392 x NE 5	1515	25	35	50	31	32
2392 x Sanzi	1202	37	19	56	15	70
3306 x Ayiyi	1947	11	12	18	35	7
3306 x Ebelat*NE 51	1334	21	22	52	28	52
Ayiyi x 2392	1863	6	7	11	2	11
Ayiyi x WC 66	1796	14	28	5	13	13
Danila x Ebelat*NE 51	1532	20	15	19	18	29
Danila x KVU 27-1	1867	16	14	9	14	10
Danila x NE 48	2326	3	3	2	4	3
Danila x NE 5	1778	15	11	45	24	15
Danila x NE 55	1311	91	94	23	97	50
Danila x VCR 1432	2190	5	5	8	25	4
KVU 27-1 x WC 27	1752	26	44	15	11	17
MU 15 x Ebelat*NE 51	1415	24	27	36	40	42
MU 15 x WC 64	1445	38	18	34	21	37
MU 20B x NE 36	1630	9	9	76	6	20
MU 20B x WC 27	1594	23	21	19	8	23
MU 9 x NE 55	1612	18	33	27	12	21
NE 21 x MU 20B	1399	42	72	17	29	44
NE 21 x NE 55	1517	29	27	38	5	31
NE 21 x WC 48A	1784	12	29	12	36	14
NE 36 x 2392	2118	4	4	1	3	5
NE 5 x 2392	2436	7	6	7	16	2
NE 5 x Sanzi	2031	2	2	4	1	6
NE 5 x WC 64	1531	58	25	48	83	30
NE 55 x MU 20B	1554	17	17	24	49	28
NE 55 x MU 9	1458	39	41	22	39	35
NE 55 x NE 5	1359	46	36	32	17	47
SECOW 2W x Ebelat*NE51	1685	10	31	30	20	19
SECOW 5T x 3306	1754	30	32	6	22	16
SECOW 5T x Ayiyi	1854	8	8	3	10	12
WC 27 x VCR 1432	935	34	16	101	51	104
WC 48A x 2392	2878	1	1	14	19	1
WC 48A x WC 27	1874	22	30	10	7	8
WC 48A x WC 66	1389	49	61	26	37	45
WC 63 x MU 9	1564	45	54	21	23	26
WC 63 x NE 48	1875	19	20	13	26	9
WC 64 x 3306	1601	28	13	28	41	22
WC 64 x SECOW 4W	1425	61	63	25	27	39
Total		29	28	28	29	26

[1]Base selection index comprising traits virus, scab on leaves, thrips damage, scab on pod incidence, grain yield, pods and peduncles, [2]Base selection index comprising traits grain yield pods and peduncles, [3]Usefulness criteria for grain yield, [4]Usefulness criteria for grain yield, pods and peduncles.

observed in the performance of the populations for all traits evaluated (Table 10). Significant differences ($P<0.001$) were also observed in the performance of the cowpea lines within a population for all the traits except for the reaction to thrip, number of peduncles and pods per plant (Table 10). When the performances of the parents were compared to the populations, we observed significant differences in their reaction scab disease

Table 10. Mean squares of cowpea parents and F_3 populations for virus and scab disease severity, thrips damage, yield and yield components for the season 2017B.

SOV[1]	Virus	Thrips	Scab	DF[2]	Ped No.[3]	Pod No.[4]	100 SW[5]	Yield (kg/ha)
Parents	0.23*	2.47^{ns}	0.22***	20.84***	147.20***	281.20***	10.21***	617057***
Populations	0.11***	4.40*	0.29***	27.61***	79.52*	214.93***	16.87***	1810374***
Population/Lines	0.15***	2.44^{ns}	0.15***	17.31***	40.43^{ns}	89.61^{ns}	4.93***	486252***
Par Vs. Crosses[6]	0.11^{ns}	5.58^{ns}	2.11***	66.16**	358.57**	738.30**	3.77^{ns}	341471^{ns}
Residual	0.13	2.82	0.1	9.33	46.12	108.39	1.82	299577
CV[7]	17.69	39.77	18.85	4.93	27.23	28.31	13.64	32.86
SED[8]	0.361	1.68	0.316	3.05	7.11	10.41	1.82	547

***, **, *: Significant at p<0.001, p<0.01 and p<0.5, ns: not significant, [1]Source of variation, [2]Days to 50% flowering, [3]Number of peduncles per plant, [4]Number of pods, [5]weight of 100 seeds, [6]Perfomances of parents as compared to the populations, [7]Coefficient of variation, [8]Standard error of the difference.

(P<0.001), number of days to 50% flowering and number of peduncles and pods per plant at P<0.01 (Table 10).

Mean performance of the cowpea parents, F3 populations and lines evaluated for virus and scab disease severity, thrips damage, yield and yield components in 2017B

The parents reacted differently to the various diseases and pests with their means ranging from 1.6 to 2.5 for virus, 3.2 to 5.9 for thrip and 1.6 to 2.4 for scab (Table 11). In terms of days to 50% flowering, it was observed that the parent Sanzi flowered earlier at 58 days than the rest (Table 11). In terms of yield, NE 48 recorded the highest yield of 2560 kg/ha while the lowest yield was recorded by SECOW 4W (Table 11).

The mean performance of the 19 cowpea lines selected as a representative of the 320 cowpea lines evaluated are presented in Table 12. The mean performance of the cowpea lines for virus disease ranged from 1.2 to 3.0, for thrip damage, ranged from 1.0 to 7.4, and for scab disease ranged from 1.0 to 3.0. The cowpea lines took 51 to 73 days to attain 50% flowering. Line NE 21 x MU 20B/1 registered the highest grain yield of 3533 kg/ha while line Danila x KVU 27-1/7 had the lowest yield of 77 kg/ha (Table 12).

Comparing the performance of parents to the crosses, the results showed that the crosses were better performers than their parents as they recorded the lowest mean scores for scab disease and early flowering time. However, the parents on the other hand performed better than the crosses in terms of the number of peduncles, pods per plant and, consequently had high yield (Table 13).

The populations' mean scores ranged from 1.7 to 2.4 for virus disease, 1.9 to 6.6 for thrip damage and 1.4 to 2.2 for scab disease. The days to 50% flowering ranged from 53 to 68 days. Danila x Ebelat*NE 51 recorded the lowest grain yield of 785 kg/ha and population WC 63 x NE 48 recorded the highest grain yield of 2475 kg/ha (Table 14).

Determination of the effectiveness of the selection methods and populations

Usefulness value of the $F_{2:3}$ populations and the genetic gain (Response to Selection)

Usefulness values obtained in the individual populations ranged from 351.1 to 1277.2 (Table 4). The highest genetic variance (427180.5) and genetic gain (855.7) were recorded on KVU 271 x WC 27 (695.63-Table 15). Thirteen populations had a negative genetic variance which meant there is zero genetic variance in them but due to the high mean that existed on those populations, they still recorded a high usefulness value.

Generally, high realized heritability (Rh) and genetic gain (Gs) were obtained for yield and its components when the realized genetic gain was calculated for the whole 40 populations evaluated (Table 16).

DISCUSSION

There was significant level of variability among the cowpea populations and parents for diseases such as virus and scab, number of pods per plant, grain yield and number of pods per plant assessed and these findings are in agreement with the results obtained in previous studies (Bhadru and Navale, 2012b; Idahosa et al.,2010).This suggests that there was high level of genetic variability among the cowpea genotypes for traits measured which could be utilized to maximize genetic gain for these traits through improved selection.

The large variability that was observed within the populations for yield and yield components made it possible to identify the best populations using the usefulness criteria. Populations with larger genetic

Table 11. Mean performance of cowpea parents evaluated for virus and scab disease severity, thrips damage, yield and yield components in season 2017B.

Parent	Virus	Thrips	Scab	DF[1]	Ped No.[2]	Pod No.[3]	100 SW[4] (g)	Yield (kg/ha)
2392	1.6	3.5	1.7	63	23	32	13.5	1957
3306	1.8	4.3	1.7	62	27	38	11.8	1809
AYIYI	1.9	4.2	1.7	61	27	39	16.3	1886
DANILA	1.9	4.7	1.7	63	25	37	14.8	1139
EBELAT*NE 51	2.2	4.8	2.1	60	42	55	13.3	1198
KVU 271	2.0	3.5	1.8	66	27	26	13.2	1361
MU 15	2.5	5.1	1.7	64	22	33	14.1	1965
MU 20B	2.2	5.5	2.1	66	32	47	13.5	2090
MU 9	2.1	4.1	1.7	63	25	37	12.7	1790
NE 21	2.0	3.9	1.9	64	25	35	12.9	1133
NE 36	2.0	4.6	1.6	66	26	43	17.3	1857
NE 48	1.9	3.6	1.9	62	21	33	14.5	2560
NE 5	1.9	4.2	1.7	62	38	52	12.9	1433
NE 55	2.0	3.3	1.6	64	29	42	13.0	2156
SANZI	2.2	5.5	1.9	58	29	40	12.7	1541
SECOW 2W	2.5	5.1	2.3	61	29	42	13.5	1317
SECOW 4W	1.8	5.9	2.0	63	22	32	12.0	965
SECOW 5T	1.8	4.2	1.9	61	20	28	14.5	1982
VCR 1432	2.4	5.0	2.4	63	25	29	15.0	1174
WC 27	2.0	4.5	1.6	66	23	32	12.3	1850
WC 48A	2.1	4.9	1.8	65	26	37	12.6	1415
WC 63	1.9	3.7	1.6	63	25	35	13.5	2006
WC 64	2.3	5.5	1.8	60	29	44	12.5	2125
WC 66	2.3	4.9	2.4	59	25	34	14.7	2136
LSD	0.5	1.9	0.5	6	11	17	2.2	657

[1]Days to 50% flowering, [2]Number of peduncles, [3]Number of pods, [4]Weight of 100 seeds.

Table 12. Mean performance of the $F_{2:3}$ cowpea lines evaluated for virus and scab severity, thrips damage, yield and yield components in 2017B.

Lines	Virus	Thrips	Scab	DF[1]	Ped No.[2]	Pod No.[3]	100 SW[4] (g)	Yield (kg/ha)
Danila X Ebelat*NE51/6	2.2	4.8	2.2	67	17	19	12.5	443
Danila X KVU 27-1/7	2.0	3.9	2.5	69	7	24	5.0	77
Danila X VCR 1432/5	2.2	5.2	1.7	67	17	23	12.5	885
Danila X VCR 1432/7	1.5	5.6	1.0	59	23	29	20.0	1787
KVU 27-1 X WC 27/8	2.0	3.9	2.5	65	53	65	13.0	613
MU 15 X Ebelat*NE 51/1	3.0	1.0	2.5	55	24	30	16.0	1170
NE 21 X MU 20B/1	1.5	6.8	1.5	67	29	47	15.0	3533
NE 21 X NE 55/2	2.0	4.8	1.5	55	30	31	11.0	993
NE 5 X 2392/7	1.2	4.3	1.5	58	28	45	14.5	1795
NE 55 X MU 9/3	2.5	3.5	1.5	51	25	31	16.0	2046
NE 55 X NE 5/6	1.5	3.1	2.0	65	52	80	13.0	1653
NE 55 X NE 5/7	2.0	5.1	3.0	65	16	25	9.0	130
SECOW 2W X Ebelat*NE51/1	2.2	5.2	3.0	65	26	36	11.0	1208
SECOW 5T X 3306/3	1.8	5.5	1.5	64	20	30	16.5	2070
SECOW 5T X Ayiyi/4	2.2	5.4	1.5	63	29	22	15.5	1199
WC 48A X 2392/7	2.0	2.0	1.0	58	24	31	15.7	2114
WC 48A X WC 66/1	2.5	3.9	1.5	73	40	64	13.0	1587
WC 48A X WC 66/2	2.2	3.8	2.0	66	14	27	9.0	589

Table 12. Contd.

WC 64 X SECOW 4W/8	2.3	7.4	1.8	59	35	53	11.5	2316
LSD	0.7	1.2	0.6	7	12	17	4.0	1091.16

[1]Days to 50% flowering, [2]Number of peduncles, [3]Number of pods, [4]Weight of 100 seeds.

Table 13. Comparison of the parents' performance to the $F_{2:3}$ generation cowpea crosses evaluated for virus and scab disease severity, thrip damage, yield and yield components in season 2017B.

Parents vs. crosses	Virus	Thrips	Scab	DF[1]	Ped No.[2]	Pod No.[3]	100 SW[4] (g)	Yield (kg/ha)
Parents	2.0	4.2	1.7	62	26	37	13.3	1672
Crosses	2.0	4.4	1.8	63	28	39	13.5	1726
LSD	0.07	0.3	0.07	1	1	2	0.4	124.6

[1]Days to 50% flowering, [2]Number of peduncles, [3]Number of pods, [4]Weight of 100 seeds.

Table 14. Mean performance of the $F_{2:3}$ generation cowpea populations evaluated for virus and scab disease severity, thrip damage, yield and yield components in season 2017B.

Population	Virus	Thrips	Scab	DF[1]	Ped No.[2]	Pod No.[3]	100 SW[4] (g)	Yield (kg/ha)
2392 X EBELAT*NE 51	2.1	4.2	1.7	63	24	37	12.2	1540.0
2392 X NE 5	2.1	5.4	1.6	57	23	30	13.2	1762.0
2392 X SANZI	2.1	3.1	1.5	53	26	41	10.1	1076.0
3306 X AYIYI	1.8	4.0	1.7	65	25	34	13.7	1615.0
3306 X EBELAT*NE 51	2.1	4.5	1.6	60	30	46	12.8	1511.0
AYIYI X 2392	1.8	4.3	1.7	65	27	40	12.9	1272.0
AYIYI X WC 66	2.0	4.2	1.6	57	27	41	15.3	2244.0
DANILA X EBELAT*NE51	2.4	4.9	2.2	64	24	26	10.7	785.0
DANILA X KVU 271	2.0	4.1	1.7	65	25	34	14.3	1401.0
DANILA X NE 48	2.3	3.9	1.7	65	24	31	14.3	1374.0
DANILA X NE 5	2.1	3.7	1.8	61	26	35	13.2	1317.0
DANILA X NE 55	2.2	3.5	1.7	59	30	40	13.0	1746.0
DANILA X VCR 1432	1.9	4.9	1.8	63	30	41	15.1	1731.0
KVU 271 X WC 27	2.3	2.9	1.6	60	30	40	14.5	1617.0
MU 15 X EBELAT*NE51	2.2	3.2	2.1	60	25	38	12.5	1365.0
MU 15 X WC 27	2.1	4.9	1.5	63	23	34	11.4	1678.0
MU 20B X NE 36	1.8	4.1	1.5	64	26	39	12.4	2022.0
MU 20B X WC 27	2.3	4.6	1.6	63	23	34	13.9	1625.0
MU 9 X NE 55	2.0	5.3	1.5	66	27	39	13.9	2088.0
NE 21 X MU 20B	1.8	3.7	1.6	68	29	39	12.6	1740.0
NE 21 X NE 55	2.0	5.0	1.6	61	25	34	13.9	1511.0
NE 21 X WC 48A	2.1	4.3	1.6	62	25	36	13.7	1607.0
NE 36 X 2392	2.1	4.3	1.4	62	28	43	12.8	2278.0
NE 5 X 2392	1.9	4.1	1.7	60	26	38	15.3	1450.0
NE 5 X SANZI	2.2	4.6	1.7	60	24	30	12.5	1288.0
NE 5 X WC 64	2.1	5.0	1.5	63	25	37	13.8	2002.0
NE 55 X MU 20B	2.1	3.0	2.0	63	26	35	12.2	1254.0
NE 55 X MU 9	2.3	3.7	1.7	58	26	35	14.7	1556.0
NE 55 X NE 5	1.7	3.8	1.7	64	37	58	13.4	1943.0
SECOW 2W X EBELAT*NE 51	2.0	3.6	2.0	64	28	38	12.1	1551.0
SECOW 5T X 3306	2.0	4.6	1.5	64	25	38	15.1	2203.0

Table 14. Contd.

SECOW 5T X AYIYI	2.1	3.9	1.8	61	23	32	14.7	1761.0
WC 27 X VCR 1432	1.8	4.5	1.4	63	22	31	12.0	1265.0
WC 48A X 2392	2.2	3.9	1.6	57	21	30	13.3	1725.0
WC 48A X WC 27	2.1	4.7	1.7	65	26	39	12.9	2178.0
WC 48A X WC 66	2.4	4.5	1.8	65	25	34	12.7	1152.0
WC 63 X MU 9	1.9	4.4	1.6	64	28	40	13.2	2451.0
WC 63 X NE 48	1.7	3.8	1.5	60	21	30	16.2	2475.0
WC 64 X 3306	2.0	2.5	1.7	61	26	34	14.1	1598.0
WC 64 X SECOW 4W	2.0	6.6	1.6	59	31	43	12.8	1943.0
LSD	0.3	1.2	0.3	2	5	7	1.5	476.5

variances gave high genetic gain and eventually high usefulness value. Populations such as NE 36 x 2392, Danila x NE 48, SECOW 5T x Ayiyi, NE 5 x Sanzi, Ayiyi x WC 66, SECOW 5T x 3306, NE 5 x 2392 showed high genetic gain for grain yield and its components (number of pods and peduncles). This could be due to the high heritability values for yield and yield components that existed in the same populations. In fact, genetic gain (response to selection) depends on the breeding value of the parents used in population development, and it is the deviation of the progeny mean performance from the population mean (Falconer, 1989). The NE 36 x 2392 population was ranked first by the usefulness criterion based on its grain yield as it had a high genetic variance and a genetic gain. The same population ranked third in the usefulness value, based on its yield and yield components (number of pods and peduncles). This may suggest that the high correlation between the three traits namely yield and number of pods (r=0.76), yield and number of peduncles (r=0.75) contributed to the high genetic gain as considered by the usefulness criteria combining yield and its components. These results are consistent with the findings of Singh (2005), who observed that secondary traits showed moderate to high correlation with yield and a higher heritability than yield per se, and as such it can be a good selection criterion in breeding for yield improvement. Some populations like NE 21 x MU 20B and Danila x NE 5 that ranked highly in the usefulness criterion but low in the base selection index and the mean yield (yield perse)indicated the greater role of genetic variance in the populations because as much as the mean yields for the same populations were low, consideration of the genetic variance in those populations improved their ranks. Similar results were reported by Nizeyimana (2013) who evaluated some maize hybrids and found out that some populations improved in their ranks when both genetic variance and means of the populations were considered.

Selection for traits that are highly expressed phenotypically such as plant height, vigor and days to flowering become easier when using visual selection. However, visual rating is said to be unreliable for quantitative traits such as yield and yield components, yet they are highly targeted by breeders (Hallauer, 2010). This calls for selection of individual trait with consideration of how much a trait contributes to the final product. The response of individual traits in the final product largely depends on how each trait has been weighted and selected in the reference population. Several studies suggest that selection based on multi trait index is more convenient in predicting the best genotypes than relying on direct selection (Oliveira et al., 2017; Rodrigues et al., 2017). This was observed in some populations, when visual selection was used for traits such as average yield, they ranked almost the last but when multiple trait selection was used they ranked among the top most populations. For instance, 2392 x Ebelat*NE 51 ranked 73rd in the visual selection and 99th in the usefulness value for grain yield alone yet it ranked 9th in both usefulness value (combining yield and its component) and base selection index for disease and yield components and 13 in the base index selection for yield and its components. Such results show that when traits of importance are put into consideration then potential populations could be identified and strengthened for multiple traits. These results are in accordance to Nizeyimana (2013) who evaluated some maize hybrids and reported that some populations such as E99, E80, E87, E74 and E93 ranked as the best populations when the contributions of AD, SD, ASI, resistance to Turcicum Leaf Blight and Maize Streak Virus, in the inbreds and hybrids, along with yield and 100-kernel weight in the hybrids were put into consideration.

Comparison of the selection criteria used in the selection of the best F_2 populations

The non-significant differences observed when comparing the selection criteria suggest that the criteria are equally the same for selecting the best populations.

Table 15. Estimated usefulness value (U) of the $F_{2:3}$ populations for grain yield (I=0.2, k=1.4).

Population	Vg[1]	Vp[2]	Sqrt Vp[3]	Heritability	K[4]	Gs[5]	Mean	UC[6]
2392 X NE5	-101364	156764	395.9	0.00	1.4	0.0	476.7	476.7
2392 X Sanzi	7854	95623	309.2	0.08	1.4	35.6	315.5	351.1
2392XEbelat*NE51	140917	274398	523.8	0.51	1.4	376.6	474.8	851.4
3306 x Eberlat*NE 51	-184944	401336	633.5	0.00	1.4	0.0	450.4	450.4
3306x Ayiyi	28028	238867	488.7	0.12	1.4	80.3	376.9	457.2
3306xAyiyi	51204	130215	360.9	0.39	1.4	198.7	485.5	684.2
Ayiyi x WC 66	-15296	258013	507.9	0.00	1.4	0.0	643.7	643.7
DANILA X EBELAT*NE51	187600	347427	589.4	0.54	1.4	445.6	212.8	658.4
DANILA X KVU 271	15847	155308	394.1	0.10	1.4	56.3	354.9	411.2
DANILA X NE 48	241398	569926	754.9	0.42	1.4	447.7	416.2	863.9
DANILA X NE 5	78375	448410	669.6	0.17	1.4	163.9	360.8	524.7
DANILA X NE 55	39911	74545	273.0	0.54	1.4	204.6	514.5	719.1
DANILA X VCR 1432	147028	1178742	1085.7	0.12	1.4	189.6	376.6	566.2
KVU 271 X WC 27	427181	488484	698.9	0.87	1.4	855.7	342.1	1197.8
MU 15 X EBELAT*NE 51	-5239	262399	512.2	0.00	1.4	0.0	409.9	409.9
MU 15 X WC 27	-56718	290489	539.0	0.00	1.4	0.0	503.0	503.0
MU 20B X NE 36	147108	291270	539.7	0.51	1.4	381.6	606.5	988.1
MU 20B X WC 27	-111726	192581	438.8	0.00	1.4	0.0	487.1	487.1
MU 9 X NE 55	264726	319990	565.7	0.83	1.4	655.2	598.9	1254.1
NE 21 X MU 20B	140347	425319	652.2	0.33	1.4	301.3	388.5	689.8
NE 21 X NE 55	-7971	148024	384.7	0.00	1.4	0.0	416.8	416.8
NE 21 X WC 48A	157733	269448	519.1	0.59	1.4	425.4	472.3	897.7
NE 36 X 2392	-143273	739223	859.8	0.00	1.4	0.0	550.7	550.7
NE 5 X 2392	-75872	302744	550.2	0.00	1.4	0.0	397.0	397.0
NE 5 X SANZI	75793	343627	586.2	0.22	1.4	181.0	331.4	512.4
NE 5 X WC 64	55282	172233	415.0	0.32	1.4	186.5	590.8	777.3
NE 55 X MU 20B	205186	575073	758.3	0.36	1.4	378.8	358.6	737.4
NE 55 X MU 9	-28946	139676	373.7	0.00	1.4	0.0	432.6	432.6
NE 55 X NE 5	-343980	1671895	1293.0	0.00	1.4	0.0	415.6	415.6
SECOW 2W X EBELAT*NE51	41970	134809	367.2	0.31	1.4	160.0	465.3	625.3
SECOW 5T X 3306	267965	339228	582.4	0.79	1.4	644.1	633.1	1277.2
SECOW 5T X AYIYI	370453	677603	823.2	0.55	1.4	630.0	519.0	1149.0
WC 27 X VCR 1432	425390	546809	739.5	0.78	1.4	805.4	364.9	1170.3
WC 48A X 2392	267785	669679	818.3	0.40	1.4	458.1	517.4	975.5
WC 48A X WC 27	103043	189075	434.8	0.54	1.4	331.8	653.1	984.9
WC 48A X WC 66	145721	364505	603.7	0.40	1.4	337.9	321.9	659.8
WC 63 X MU 9	245986	712114	843.9	0.35	1.4	408.1	617.9	1026.0
WC 63 X NE 48	-6745	247423	497.4	0.00	1.4	0.0	699.6	699.6
WC 64 X 3306	46897	132517	364.0	0.35	1.4	180.4	479.5	659.9
WC 64 X SECOW 4W	-21678	323174	568.5	0.00	1.4	0.0	556.5	556.5

[1]Genetic variance, [2]Phenotypic variance, [3]Square root of the phenotypic variance, [4]Selection intensity, [5]Genetic gain, [6]Usefulness criteria.

This further approved that the best populations with high mean selected in one selection criterion was most likely the ones selected in the other selection criteria and so, any method can be used to select the populations depending on the breeder's objective. If the breeder's main concern is to select populations with high variation and mean yield, then usefulness criteria becomes the best to handle such a selection. Some of the best populations selected in one selection criteria could be similar to the others selected in the different selection criteria, but the ranking of the populations may differ in the different selection criteria. In fact, the strong positive correlations that existed among the selection criteria suggested that the populations that had high usefulness values are more likely to have high base selection index values. For this case, 16 populations happened to be in

Table 16. Realized heritability and estimated genetic gain obtained from selection.

Parameter	Virus	Thrip	Scab	Ped No.[1]	Pod No.[2]	Grain yield
Average 2017A (Uo)	4.7	5.5	3.4	14	20	1214
Average Selected Pop	4.7	5.5	3.4	34	53	1683
Average 2017B (Up)	2.0	4.0	1.7	26	37	1662
Response to Selection (R)	-2.7	-1.5	-1.7	12	17	447
Selection differential (s)	-	-	-	20	33	469
Realized heritability (Rh)	-	-	-	0.62	0.51	0.95
Selection intensity (k)	-	-	-	1.4	1.4	1.4
Genetic variance (Vg)	-	-	-	16.7	53.3	755399
Phenotypic variance (Vp)	-	-	-	62.8	161.7	1054976
Genetic Gain (Gs)	-	-	-	6.9	9.0	1372

[1]Number of peduncles, [2]Number of pods.

common among the 30 ranked best in each method. For instance, WC 48A x 2392 population ranked 1st in the base index selection criteria but 14 and 19 in the usefulness criteria for grain yield and yield components and thus ended up being among the 30 best populations in both methods. The high ranking of the populations 2392 x Ebelat*NE 51 and WC 27 x VCR 1432 in the BSI for diseases, pests and yield yet low rankings in the UC and yield, suggested that there was the level of disease and pest resistance in the respective population. Therefore, this further emphasizes the need for selection in reference to the breeder's objective. If resistance to diseases and pest is a major concern to the breeder then BSI that comprises the diseases, pests and yield could be used.

Yield potential of cowpea parents and the selected $F_{2:3}$ lines for identification of transgressive segregants

In determining yield potential, valuable traits such as resistance to diseases, insect pest and other agronomic traits as well as the physiology of the crop were equally important. The parents had better performance than the populations in reaction to scab disease as well as the number of days to flowering. On the other hand, the crosses performed better than their parents in the number of peduncles per plant with a difference of 4% (2 peduncles per plant). This suggested the presence of transgressive segregants as evidently seen in the lines KVU 27-1 x WC27/8 (53 peduncles and 65 pods per plant) and NE 55 x NE5/6 (52 peduncles and 80 pods per plant). These lines outperformed the best parents WC 27 (23 peduncles and 31 pods) and NE 5 (37 peduncles and 52 pods). Similar results have been reported elsewhere by Shivakumar et al. (2013) and Kurer (2007). Line NE 21 x MU 20B/1 had high yield performance which probably was as a result of its better performance for some of the yield related component traits such as pod length and number of seeds per pod. This was probably due to the fact that, line NE 21 x MU 20B/1 showed moderate resistance to virus and scab disease infection. Danila x KVU 27-1/7 gave lower yields due to the poor vigor and consistent attack by pests and diseases. WC 63 x NE 48 was the best population in Kabanyolo in terms of grain yield as it had longer pods, which created space for many seeds per pod. This could be attributed to the fact that parents that resulted in its formation performed equally as good in the same location as its parents WC 63 and NE 48 gave yields of 2006 and 2560 kg/ha, respectively. These two parents played a vital role in generating some crosses that inherited their potential as they were known to be high grain yielders and also resistant to both scab and virus disease (Mbeyagala et al., 2014; Afutu et al., 2016b).

High usefulness values were observed in the forty populations that were advanced due to the high predicted genetic gain that was due to the high genetic variance maintained in the populations. This is an indication that the methods worked to select the best populations and that the populations selected were the best. Though some populations had zero genetic gain due to the negative genetic variance observed in them they still had a high mean which guaranteed a high usefulness value for them (Bernado, 2010). Highest magnitude of response to selection and selection differential was recordedfor virus and scab diseases, thrip damage, number of peduncles and pods per plant and yield at harvest on the selected $F_{2:3}$ populations suggesting progress in achievement andeffectiveness of selection for these traits. The selected $F_{2:3}$ populations recorded high realized heritability for characters yield, number of peduncles and pods per plants suggesting the value of these characters in selection programme and the achievement made after selection. The realized genetic gain obtained in the $F_{2:3}$ lines for number of pods, number of peduncles and grain yield at harvest further magnified the importance of selection of such characters in advanced breeding. Similar results were obtained by Bhadru and Navale (2012b).

Conclusion

This study has shown the existence of cowpea populations with substantial genetic variability for traits namely flower thrips, virus and scab resistance, and high yielding potential; which are therefore promising for the advancement of the populations to the next generation that could result in developing superior lines. The selection criteria, that is, the usefulness criterion and base selection index were able to identify the best segregating populations with desired traits (high yields, resistant to virus, scab and flower thrips) for further improvement in future breeding programs. The usefulness criterion revealed that the selection of the best populations should be based on high mean and high genetic variance. Selection index on the other hand proved that populations that are ranked low based on only their yield performance could be highly ranked when several traits were considered including disease and pest resistance which are among key traits in a population like WC 27 x VCR 1432.

When the usefulness criterion and selection index methods were compared, the results indicated no statistical difference. Some of the best populations selected within one criterion were also the best populations selected in another method, suggesting that either of the methods can be used depending on the goal of the breeder. If variability is a prerequisite by the breeder, usefulness criterion is the preferred selection criterion. However, if multiple traits need to be selected at once, then selection index is much preferred. Generally, the approach of using genetic gain and selection index is not only necessary for identifying promising genotypes to increase the efficiency but also useful in the selection of parents used for creation of future crosses.

The results from this study showed the effectiveness of early generation selection while breeding for yield and other agronomic parameters in cowpea.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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APPENDIX

Table 1. Estimated Usefulness value (U) of the evaluated populations for grain yield (I=0.2, k=1.4).

Population	VPop	VP1	VP2	V_G	H	Gs	μ	U
NE 36 X 2392	695.63	100.80	138.39	576.04	0.83	30.58	41.81	72.39
Danila X NE 48	361.32	48.72	69.78	302.08	0.84	22.25	43.41	65.66
SECOW 5T X Ayiyi	483.79	44.50	67.27	427.90	0.88	27.24	34.72	61.96
NE 5 X Sanzi	342.00	55.78	26.58	300.82	0.88	22.77	38.26	61.03
Ayiyi X WC 66	430.43	67.27	34.81	379.40	0.88	25.60	34.78	60.38
SECOW 5T X 3306	477.08	44.50	59.24	425.21	0.89	27.25	33.07	60.32
NE 5 X 2392	340.92	55.78	138.39	243.83	0.72	18.49	41.51	60.00
Danila X VCR 1432	228.20	48.72	52.20	177.74	0.78	16.47	42.45	58.92
Danila X KVU271	412.67	48.72	78.27	349.17	0.85	24.06	34.75	58.81
WC 48 X WC 27	409.89	72.17	65.31	341.15	0.83	23.59	35.1	58.69
Ayiyi X 2392	414.02	67.27	138.39	311.19	0.75	21.41	35.03	56.44
NE 21 X WC 48	232.92	42.01	72.17	175.83	0.75	16.13	39.87	56.00
WC 63 X NE 48	335.07	47.39	69.78	276.49	0.83	21.15	34.68	55.83
WC 48 X 2392	471.34	72.17	138.39	366.06	0.78	23.61	31.65	55.26
KVU 271X WC 27	276.48	78.27	65.31	204.68	0.74	17.23	32.85	50.08
MU 20B X MU 15	275.70	30.74	56.38	232.14	0.84	19.57	30.48	50.05
NE 21 X MU 20B	362.60	42.01	30.74	326.23	0.90	23.98	25.53	49.51
3306 X Ayiyi	218.61	59.24	67.27	155.35	0.71	14.71	34.54	49.25
Danila X Eberlat*NE 51	329.43	48.72	100.00	255.07	0.77	19.67	28.93	48.60
MU 20B X WC 27	279.01	30.74	65.31	230.99	0.83	19.36	28.98	48.34
WC 63 X MU 9	229.79	47.39	40.23	185.98	0.81	17.18	29.98	47.16
NE 55 X MU 9	286.43	62.40	40.23	235.12	0.82	19.45	27.38	46.83
Danila X NE 55	182.61	48.72	62.40	127.05	0.70	13.16	33.31	46.47
NE 55 X MU 20B	233.22	62.40	30.74	186.65	0.80	17.11	29.19	46.30
WC 64 X SECOW 4W	260.28	42.77	58.87	209.46	0.80	18.18	27.7	45.88
WC 48 X WC 66	343.36	72.17	69.00	272.78	0.79	20.61	25.25	45.86
MU 9 X NE 55	406.85	40.23	62.40	355.54	0.87	24.68	20.97	45.65
WC 64 X 3306	211.92	42.77	59.24	160.91	0.76	15.48	30.02	45.50
SECOW 5T X SECOW 4W	243.42	44.50	58.87	191.73	0.79	17.20	28.16	45.36
SECOW 2W X Eberlat*NE 51	339.76	78.61	100.00	250.46	0.74	19.02	25.78	44.80
NE 55 X WC 63	217.62	62.40	47.39	162.73	0.75	15.44	28.37	43.81
NE 55 X NE 5	240.86	62.40	55.78	181.77	0.75	16.40	27.22	43.62
WC 63 X SECOW 4W	178.17	47.39	58.87	125.04	0.70	13.11	29.41	42.52
MU 15 X WC 64	218.83	56.38	42.77	169.25	0.77	16.02	25.42	41.44
Ayiyi X SECOW 2W	323.26	67.27	78.61	250.32	0.77	19.49	21.92	41.41
MU 15 X Eberlat*NE 51	234.21	56.38	100.00	156.02	0.67	14.27	27	41.27
Ayiyi X IT889	193.89	67.27	82.56	118.97	0.61	11.96	29.3	41.26
NE 21 X NE 55	409.82	42.01	62.40	357.62	0.87	24.73	16.28	41.01
MU 9 X NE 5	137.94	40.23	55.78	89.94	0.65	10.72	30.22	40.94
WC 66 X MU 9	234.73	34.81	40.23	197.21	0.84	18.02	22.81	40.83
NE 55 X WC 48	198.09	62.40	72.17	130.80	0.66	13.01	27.11	40.12
NE 55 X Danila	187.10	62.40	48.72	131.54	0.70	13.46	26.63	40.09
WC 66 X Danila	170.12	34.81	48.72	128.35	0.75	13.78	26.27	40.05
SECOW 2W X Sanzi	210.61	78.61	26.58	158.02	0.75	15.24	24.72	39.96
Danila X NE 5	205.89	48.72	55.78	153.64	0.75	14.99	24.29	39.28
MU 15 X Ayiyi	160.65	56.38	67.27	98.82	0.62	10.92	28.22	39.14
NE 21 X NE 5	140.13	42.01	55.78	91.23	0.65	10.79	28.16	38.95
NE 5 X WC 64	154.62	55.78	83.48	84.99	0.55	9.57	28.76	38.33
Ayiyi X Danila	217.91	67.27	48.72	159.92	0.73	15.17	23.1	38.27

Table 1. Contd.

2392 X NE 5	228.05	138.39	55.78	130.96	0.57	12.14	25.78	37.92
WC 64 X WC 27	116.79	42.77	65.31	62.75	0.54	8.13	29.1	37.23
3306 X Eberlat*NE 51	201.81	59.24	100.00	122.20	0.61	12.04	25	37.04
NE 21 X Ayiyi	148.03	42.01	67.27	93.40	0.63	10.75	26.17	36.92
Eberlat*NE 51 X KVU 271	195.28	100.00	78.27	106.14	0.54	10.63	26.03	36.66
MU 20B X 3306	140.28	30.74	59.24	95.28	0.68	11.26	25.25	36.51
2392 X Sanzi	223.45	138.39	26.58	140.97	0.63	13.20	22.63	35.83
IT889 X WC 27	178.69	82.56	65.31	104.75	0.59	10.97	24.38	35.35
3306 X NE 5	152.59	59.24	55.78	95.08	0.62	10.78	24.32	35.10
WC 63 X NE 36	189.79	47.39	100.80	115.69	0.61	11.76	23.02	34.78
IT889 X SECOW 2W	183.19	82.56	78.61	102.61	0.56	10.61	24.16	34.77
NE 55 X Sanzi	174.95	62.40	26.58	130.46	0.75	13.81	20.31	34.12
NE 5 X MU 9	164.17	55.78	40.23	116.16	0.71	12.69	21.33	34.02
NE 48 X SECOW 5T	164.45	69.78	44.50	107.31	0.65	11.72	22.24	33.96
VCR1432 X WC 27	176.47	52.20	65.31	117.71	0.67	12.41	21.46	33.87
3306 X MU 9	170.42	59.24	40.23	120.68	0.71	12.94	20.7	33.64
MU 9 X NE 48	143.68	40.23	69.78	88.68	0.62	10.36	23.08	33.44
MU 20B X NE 55	173.18	30.74	62.40	126.60	0.73	13.47	19.56	33.03
WC 66 X NE 5	105.48	34.81	55.78	60.19	0.57	8.20	24.48	32.68
SECOW 2W X SECOW 4W	152.32	78.61	58.87	83.58	0.55	9.48	23.08	32.56
Danila X WC 48	130.26	48.72	72.17	69.81	0.54	8.56	23.76	32.32
NE 5 X 3306	136.40	55.78	59.24	78.90	0.58	9.46	22.02	31.48
WC 64 X SECOW 5T	135.63	42.77	44.50	92.00	0.68	11.06	20.38	31.44
NE 36 X Eberlat*NE 51	168.30	100.80	100.00	67.90	0.40	7.33	23.98	31.31
NE 5 X KVU271	126.57	55.78	78.27	59.54	0.47	7.41	23.55	30.96
SECOW 4W X MU 20B	109.02	58.87	30.74	64.21	0.59	8.61	21.56	30.17
MU 20B X NE 36	331.01	30.74	100.80	265.24	0.80	0.00	29.8	29.80
SECOW 5T X Eberlat*NE 51	154.29	44.50	100.00	82.04	0.53	9.25	19.89	29.14
WC 48 X SECOW 2W	164.87	72.17	78.61	89.48	0.54	9.76	19.37	29.13
KVU 271 X NE 21	139.24	78.27	42.01	79.10	0.57	9.38	19.55	28.93
Eberlat*NE 51 X 2392	211.54	100.00	138.39	92.35	0.44	8.89	19.89	28.78
WC 64 X NE 36	112.11	42.77	100.80	40.32	0.36	5.33	23.38	28.71
NE 5 X IT889	189.67	55.78	82.56	120.50	0.64	12.25	16.43	28.68
MU 15 X MU 20B	134.56	56.38	30.74	90.99	0.68	10.98	17.39	28.37
3306 X WC 66	136.15	59.24	34.81	89.13	0.65	10.69	17.45	28.14
MU 20B X NE 21	113.88	30.74	42.01	77.50	0.68	10.17	17.96	28.13
Eberlat*NE 51 X Ayiyi	129.89	100.00	67.27	46.26	0.36	5.68	22.12	27.80
2392 X NE 21	172.04	138.39	42.01	81.84	0.48	8.74	18.89	27.63
SECOW 4W X MU 9	128.06	58.87	40.23	78.51	0.61	9.71	17.87	27.58
WC 48 X NE 48	163.43	72.17	69.78	92.45	0.57	10.12	16.33	26.45
WC 66 X NE 55	155.64	34.81	62.40	107.03	0.69	12.01	14.44	26.45
WC 48 X IT889	118.93	72.17	82.56	41.56	0.35	5.34	21	26.34
2392 X WC 48	146.44	138.39	72.17	41.16	0.28	4.76	21.56	26.32
WC 48 X MU 9	96.73	72.17	40.23	40.53	0.42	5.77	20.34	26.11
Sanzi X WC 27	94.13	26.58	65.31	48.19	0.51	6.95	19.09	26.04
NE 48 X Ayiyi	138.46	69.78	67.27	69.94	0.51	8.32	16.96	25.28
KVU 271X 2392	144.02	78.27	138.39	35.68	0.25	4.16	19.93	24.09
Eberlat*NE 51 X MU 15	142.88	100.00	56.38	64.69	0.45	7.58	16.38	23.96
IT889 X 2392	202.81	82.56	138.39	92.34	0.46	9.08	14.69	23.77
2392 X Eberlat*NE 51	129.06	138.39	100.00	9.87	0.08	1.22	22.53	23.75
NE 55 X SECOW 2W	124.46	62.40	78.61	53.95	0.43	6.77	16.9	23.67
WC 27 X VCR1432	101.30	65.31	52.20	42.55	0.42	5.92	17.53	23.45

Table 1. Contd.

Sanzi X NE 36	195.05	26.58	100.80	131.36	0.67	0.00	23.29	23.29
WC 27 X WC 63	62.92	65.31	47.39	6.57	0.10	1.16	21.43	22.59
WC 27 X WC 48	95.63	65.31	72.17	26.89	0.28	3.85	18.64	22.49
SECOW 5T X 2392	108.85	44.50	138.39	17.41	0.16	2.34	20.15	22.49
NE 21 X MU 9	85.92	42.01	40.23	44.80	0.52	6.77	15.61	22.38
WC 64 X 2392	120.72	42.77	138.39	30.14	0.25	3.84	18.49	22.33
2392 X WC 63	139.15	138.39	47.39	46.26	0.33	5.49	16.69	22.18
WC 27 X IT889	143.35	65.31	82.56	69.42	0.48	8.12	14.05	22.17
WC 64 X NE 21	84.59	42.77	42.01	42.20	0.50	6.42	15.41	21.83
Danila X 2392	128.95	48.72	138.39	35.39	0.27	4.36	17.33	21.69
WC 64 X NE 5	132.64	42.77	55.78	83.37	0.63	10.13	11.21	21.34
WC 27 X MU 20B	90.54	65.31	30.74	42.52	0.47	6.26	14.52	20.78
Sanzi X NE 21	65.24	26.58	42.01	30.95	0.47	5.36	14.94	20.30
Eberlat*NE 51 X WC 27	104.07	100.00	75.49	16.32	0.16	2.24	17.76	20.00
Ayiyi X MU 9	92.65	67.27	40.23	38.91	0.42	5.66	14.18	19.84
Eberlat*NE 51 X NE 48	82.59	100.00	69.78	-2.30	-0.03	-0.35	19.67	19.32
KVU 271 X NE 55	82.01	78.27	62.40	11.67	0.14	1.80	15.84	17.64
WC 64 X NE 55	40.15	42.77	62.40	-12.43	-0.31	-2.75	19.86	17.11
MU 9 X MU 20B	67.26	40.23	30.74	31.77	0.47	5.42	11.56	16.98
SECOW 4W X VCR1432	91.31	58.87	52.20	35.77	0.39	5.24	11.61	16.85
MU 9 X NE 36	32.64	40.23	100.80	-37.87	-1.16	0.00	16.75	16.75
VCR1432 X 2392	87.39	52.20	138.39	-7.91	-0.09	-1.18	17.27	16.09
VCR1432 X WC 66	56.96	52.20	34.81	13.46	0.24	2.50	13.39	15.89
KVU 271 X NE 36	192.24	78.27	100.80	102.70	0.53	0.00	15.81	15.81
NE 55 X NE 36	110.20	62.40	100.80	28.60	0.26	3.81	11.53	15.34
NE 21 x Eberlat*NE 51	77.56	42.01	100.00	6.55	0.08	1.04	13.8	14.84
WC 27 X Eberlat*NE 51	72.19	65.31	100.00	-10.46	-0.14	-1.72	16.07	14.35
MU 20B X 2392	76.76	30.74	138.39	-7.81	-0.10	-1.25	13.84	12.59
WC 27 X Sanzi	55.62	65.31	26.58	9.68	0.17	1.82	9.174	10.99
Sanzi X 2392	64.05	26.58	138.39	-18.44	-0.29	-3.23	14.2	10.97
Eberlat*NE 51 X MU 20B	66.01	100.00	30.74	0.63	0.01	0.11	9.839	9.95
MU 20B X SECOW 5T	34.37	30.74	44.50	-3.26	-0.09	-0.78	7.231	6.45
WC 66 X 2392	46.94	34.81	138.39	-39.67	-0.85	-8.11	11.315	3.21
WC 63 X 2392	47.18	47.39	138.39	-45.71	-0.97	-9.32	11.25	1.93

Table 2. Estimated usefulness value (U) of the evaluated *populations* for yield and yield components.

Population	Vpop	VP1	VP2	Vg	H	Gs	μ	U
NE 5 X Sanzi	25.63	2.05	1.12	24.04	0.94	6.65	4.15	10.80
Ayiyi X 2392	25.51	2.49	1.99	23.26	0.91	6.45	3.11	9.56
NE 36 X 2392	22.13	1.53	1.99	20.37	0.92	6.06	3.33	9.39
Danila X NE 48	9.19	1.71	3.04	6.82	0.74	3.15	3.16	6.31
NE 21 X NE 55	13.68	1.43	3.80	11.07	0.81	4.19	1.35	5.53
MU 20B X NE 36	12.42	2.28	1.53	10.51	0.85	4.18	1.36	5.53
WC 48A X WC 27	12.28	4.31	1.31	9.47	0.77	3.78	1.62	5.40
MU 20B X WC 27	10.53	2.28	1.31	8.73	0.83	3.77	1.34	5.11
2392 X Eberlat*NE 51	10.95	1.99	4.67	7.62	0.70	3.23	1.80	5.02
SECOW 5T X Ayiyi	11.66	2.78	2.49	9.02	0.77	3.70	1.33	5.02
KVU 271 X WC 27	9.19	1.38	1.31	7.84	0.85	3.62	1.37	4.99

Table 2. Contd.

MU 9 X NE 55	11.55	1.17	5.09	8.41	0.73	3.47	1.49	4.95
Ayiyi X WC 66	11.25	2.49	0.86	9.58	0.85	4.00	0.92	4.92
Danila X KVU 271	9.24	1.71	1.38	7.70	0.83	3.55	1.00	4.55
2392 X Sanzi	9.83	1.99	1.12	8.28	0.84	3.70	0.77	4.47
NE 5 X 2392	7.98	2.05	1.99	5.96	0.75	2.95	1.49	4.44
NE 55 X NE 5	11.62	3.80	2.05	8.70	0.75	3.57	0.74	4.32
Danila X Eberlat*NE 51	10.24	1.71	4.67	7.06	0.69	3.09	1.22	4.31
WC 48A X 2392	14.94	4.31	1.99	11.79	0.79	4.27	-0.06	4.21
SECOW 2W X Eberlat*NE 51	7.43	1.34	4.67	4.42	0.60	2.27	1.93	4.20
MU 15 X WC 64	8.48	2.14	1.19	6.82	0.80	3.28	0.86	4.14
SECOW 5T X 3306	10.14	2.78	2.28	7.61	0.75	3.35	0.61	3.95
WC 63 X MU 9	6.81	1.36	1.17	5.55	0.81	2.98	0.84	3.82
Danila X NE 5	5.73	1.71	2.05	3.85	0.67	2.25	1.36	3.61
Danila X VCR 1432	7.93	1.71	2.21	5.97	0.75	2.97	0.64	3.60
WC 63 X NE 48	6.71	1.36	3.04	4.51	0.67	2.44	1.13	3.57
WC 64 X SECOW 4W	7.70	1.19	1.98	6.11	0.79	3.08	0.46	3.55
3306 X Eberlat*NE 51	8.07	2.28	4.67	4.60	0.57	2.27	1.25	3.52
NE 21 X MU 20B	10.73	1.43	2.28	8.87	0.83	3.79	-0.38	3.41
WC 63 X SECOW 4W	6.22	1.36	1.98	4.55	0.73	2.55	0.80	3.35
2392 X NE 5	6.58	1.99	2.05	4.56	0.69	2.49	0.83	3.31
NE 5 X KVU 271	6.04	2.05	1.38	4.32	0.72	2.46	0.83	3.29
Ayiyi X IT 889	5.26	2.49	1.61	3.21	0.61	1.96	1.32	3.28
3306 X Ayiyi	5.38	2.28	2.49	3.00	0.56	1.81	1.45	3.26
VCR1432 X WC 27	7.66	2.21	1.31	5.90	0.77	2.98	0.27	3.26
NE 21 X WC 48A	4.83	1.43	4.31	1.96	0.41	1.25	1.98	3.23
WC 48A X WC 66	8.44	4.31	0.86	5.86	0.69	2.82	0.38	3.20
WC 66 X MU 9	6.59	0.86	1.17	5.58	0.85	3.04	0.11	3.15
NE 55 X MU 9	7.61	3.80	1.17	5.13	0.67	2.60	0.49	3.10
MU 15 X Eberlat*NE 51	6.65	2.14	4.67	3.24	0.49	1.76	1.31	3.07
WC 64 X 3306	5.46	1.19	2.28	3.73	0.68	2.23	0.83	3.06
SECOW 2W X SECOW 4W	6.40	1.34	1.98	4.74	0.74	2.62	0.34	2.96
Eberlat*NE 51 X Ayiyi	7.84	4.67	2.49	4.26	0.54	2.13	0.80	2.93
2392 X NE 21	7.44	1.99	1.43	5.73	0.77	2.94	-0.03	2.91
Sanzi X NE 36	4.74	1.12	1.53	3.41	0.72	2.20	0.70	2.90
NE 55 X Danila	5.68	3.80	1.71	2.93	0.52	1.72	1.12	2.84
Eberlat*NE 51 X KVU 271	6.84	4.67	1.38	3.82	0.56	2.04	0.72	2.76
Eberlat*NE 51 X 2392	7.80	4.67	1.99	4.47	0.57	2.24	0.41	2.65
NE 55 X MU 20B	5.14	3.80	2.28	2.10	0.41	1.30	1.35	2.65
Ayiyi X SECOW 2W	7.64	2.49	1.34	5.72	0.75	2.90	-0.32	2.57
WC 27 X VCR1432	5.00	1.31	2.21	3.24	0.65	2.03	0.49	2.52
WC 64 X WC 27	3.31	1.19	1.31	2.06	0.62	1.59	0.87	2.45
SECOW 5T X SECOW 4W	6.08	2.78	1.98	3.70	0.61	2.10	0.29	2.39
WC 64 X NE 36	4.38	1.19	1.53	3.02	0.69	2.02	0.33	2.35
WC 64 X 2392	5.39	1.19	1.99	3.80	0.71	2.29	0.05	2.35
IT 889 X SECOW 2W	5.65	1.61	1.34	4.18	0.74	2.46	-0.21	2.25
SECOW 2W X Sanzi	5.88	1.34	1.12	4.65	0.79	2.68	-0.57	2.11
WC 66 X Danila	4.41	0.86	1.71	3.13	0.71	2.08	-0.02	2.06
MU 20B X 3306	4.49	2.28	2.28	2.21	0.49	1.46	0.55	2.01
NE 36 X Eberlat*NE 51	5.37	1.53	4.67	2.27	0.42	1.37	0.63	2.00
NE 21 X Ayiyi	4.79	1.43	2.49	2.83	0.59	1.81	0.15	1.96
NE 5 X MU 9	5.46	2.05	1.17	3.84	0.70	2.30	-0.35	1.95
IT 889 X WC 27	5.71	1.61	1.31	4.25	0.74	2.49	-0.56	1.93

Table 2. Contd.

NE 55 X WC 63	3.78	3.80	1.36	1.21	0.32	0.87	1.05	1.92
Ayiyi X Danila	5.58	2.49	1.71	3.48	0.62	2.06	-0.15	1.92
Sanzi X WC 27	4.54	1.12	1.31	3.32	0.73	2.19	-0.35	1.83
Danila X 2392	4.89	1.71	1.99	3.04	0.62	1.92	-0.18	1.74
SECOW 5T X 2392	4.68	2.78	1.99	2.30	0.49	1.49	0.24	1.72
SECOW 4W X VCR1432	4.93	1.98	2.21	2.83	0.57	1.79	-0.29	1.50
KVU 271 X 2392	4.44	1.38	1.99	2.75	0.62	1.83	-0.35	1.48
3306 X WC 66	5.08	2.28	0.86	3.51	0.69	2.18	-0.73	1.45
Eberlat*NE 51 X MU 15	6.91	4.67	2.14	3.50	0.51	1.87	-0.47	1.40
WC 48A X SECOW 2W	5.89	4.31	1.34	3.07	0.52	1.77	-0.39	1.38
MU 9 X NE 48	3.79	1.17	3.04	1.68	0.44	1.21	0.15	1.36
MU 9 X NE 5	4.26	1.17	2.05	2.65	0.62	1.80	-0.45	1.34
3306 X MU 9	4.67	2.28	1.17	2.94	0.63	1.91	-0.59	1.32
MU 15 X Ayiyi	3.11	2.14	2.49	0.79	0.25	0.63	0.67	1.30
WC 64 X NE 5	4.33	1.19	2.05	2.71	0.63	1.82	-0.65	1.17
NE 5 X 3306	3.77	2.05	2.28	1.60	0.43	1.16	-0.04	1.12
WC 63 X NE 36	3.60	1.36	1.53	2.15	0.60	1.59	-0.48	1.11
WC 48A X NE 48	5.54	4.31	3.04	1.87	0.34	1.11	-0.04	1.07
KVU 271 X NE 21	3.83	1.38	1.43	2.42	0.63	1.73	-0.68	1.05
NE 5 X WC 64	2.95	2.05	1.19	1.33	0.45	1.08	-0.10	0.99
NE 55 X Sanzi	4.65	3.80	1.12	2.19	0.47	1.42	-0.47	0.95
WC 64 X SECOW 5T	3.37	1.19	2.78	1.39	0.41	1.06	-0.16	0.90
KVU 271 X NE 36	4.72	1.38	1.53	3.27	0.69	2.10	-1.24	0.87
IT 889 X 2392	5.43	1.61	1.99	3.64	0.67	2.18	-1.34	0.84
Danila X WC 48A	3.90	1.71	4.31	0.89	0.23	0.63	0.11	0.74
MU 20B X NE 21	4.34	2.28	1.43	2.48	0.57	1.67	-0.92	0.74
WC 27 X Sanzi	3.87	1.31	1.12	2.66	0.69	1.89	-1.27	0.62
MU 20B X MU 15	3.48	2.28	2.14	1.27	0.36	0.95	-0.38	0.57
3306 X NE 5	4.15	2.28	2.05	1.99	0.48	1.37	-0.80	0.57
NE 5 X IT 889	5.02	2.05	1.61	3.20	0.64	2.00	-1.55	0.45
Eberlat*NE 51 X WC 27	3.56	4.67	1.31	0.58	0.16	0.43	0.01	0.44
NE 55 X WC 48A	4.16	3.80	4.31	0.11	0.03	0.07	0.33	0.40
SECOW 4W X MU 20B	3.22	1.98	2.28	1.09	0.34	0.85	-0.48	0.37
Danila X NE 55	4.99	1.71	3.80	2.24	0.45	1.40	-1.10	0.31
NE 55 X NE 36	3.60	3.80	1.53	0.94	0.26	0.69	-0.42	0.27
MU 15 X MU 20B	3.32	2.14	2.28	1.10	0.33	0.85	-0.61	0.24
WC 27 X WC 48A	4.07	1.31	4.31	1.27	0.31	0.88	-0.66	0.22
WC 27 X IT 889	3.59	1.31	1.61	2.13	0.59	1.58	-1.37	0.21
2392 X WC 63	3.26	1.99	1.36	1.58	0.49	1.23	-1.07	0.16
SECOW 5T X Eberlat*NE 51	4.26	2.78	4.67	0.53	0.13	0.36	-0.21	0.15
WC 27 X WC 63	2.27	1.31	1.36	0.94	0.41	0.87	-0.76	0.11
WC 66 X 2392	2.62	0.86	4.80	-0.21	-0.08	-0.17	0.26	0.09
SECOW 4W X MU 9	3.49	1.98	1.17	1.91	0.55	1.43	-1.35	0.08
Eberlat*NE 51 X MU 20B	5.77	4.67	2.28	2.29	0.40	1.34	-1.41	-0.07
Sanzi X 2392	2.53	1.12	1.99	0.97	0.39	0.86	-0.94	-0.08
WC 66 X NE 5	3.32	0.86	2.05	1.87	0.56	1.43	-1.53	-0.10
NE 55 X SECOW 2W	3.74	3.80	1.34	1.17	0.31	0.85	-0.96	-0.12
WC 64 X NE 21	3.03	1.19	1.43	1.72	0.57	1.38	-1.51	-0.13
WC 27 X Eberlat*NE 51	3.71	1.31	4.67	0.72	0.19	0.52	-0.70	-0.18
NE 21 X MU 9	2.42	1.43	1.17	1.12	0.46	1.01	-1.22	-0.22
VCR1432 X WC 66	2.44	2.21	0.86	0.90	0.37	0.81	-1.07	-0.26
WC 48A X IT 889	2.96	4.31	1.61	0.01	0.00	0.00	-0.35	-0.35

Table 2. Contd.

VCR1432 X 2392	2.32	2.21	1.99	0.22	0.10	0.20	-0.56	-0.36
NE 48 X SECOW 5T	3.04	3.04	2.78	0.13	0.04	0.11	-0.53	-0.42
Sanzi X NE 21	1.88	1.12	1.43	0.61	0.32	0.62	-1.08	-0.46
2392 X WC 48A	2.78	1.99	4.31	-0.37	-0.13	-0.31	-0.29	-0.60
WC 27 X MU 20B	2.88	1.31	2.28	1.08	0.38	0.89	-1.51	-0.62
WC 66 X NE 55	2.41	0.86	3.80	0.08	0.03	0.07	-0.74	-0.66
NE 21 x Eberlat*NE 51	4.09	1.43	4.67	1.05	0.26	0.72	-1.55	-0.82
Ayiyi X MU 9	2.53	2.49	1.17	0.69	0.27	0.61	-1.46	-0.85
NE 21 X NE 5	1.58	1.43	2.05	-0.16	-0.10	-0.18	-0.74	-0.92
MU 9 X MU 20B	2.79	1.17	2.28	1.07	0.38	0.89	-1.83	-0.94
KVU 271 X NE 55	2.86	1.38	3.80	0.27	0.09	0.22	-1.23	-1.00
MU 20B X NE 55	3.59	2.28	3.80	0.55	0.15	0.40	-1.48	-1.08
MU 20B X 2392	2.53	2.28	1.99	0.39	0.16	0.35	-1.48	-1.13
WC 48A X MU 9	2.45	4.31	1.17	-0.29	-0.12	-0.26	-0.98	-1.24
NE 48 X Ayiyi	3.18	3.04	2.49	0.41	0.13	0.32	-1.66	-1.34
WC 63 X 2392	1.81	1.36	1.99	0.14	0.08	0.14	-1.77	-1.63
Eberlat*NE 51 X NE 48	2.20	4.67	3.04	-1.65	-0.75	-1.56	-0.19	-1.75
WC 64 X NE 55	1.62	1.19	3.80	-0.87	-0.54	-0.96	-1.75	-2.71
MU 9 X NE 36	1.10	1.17	1.53	-0.25	-0.23	-0.34	-2.49	-2.82
MU 20B X SECOW 5T	1.23	2.28	2.78	-1.30	-1.06	-1.64	-2.72	-4.36

Table 3. Estimated base selection index values of the evaluated populations.

Genotype	Virus	Thrips	Scab-a[1]	Scab-b[2]	PedNo[3]	PodNo[4]	Yield	BSI-a[5]	BSI-b[6]
WC 48A X 2392	-0.33	-3.97	-3.30	-1.56	6.01	9.74	19.70	35.45	44.61
NE 5 X Sanzi	-3.93	-6.12	-2.87	-1.51	8.11	10.52	9.67	28.31	42.74
Danila X NE 48	-1.23	-2.67	-2.44	-1.54	4.61	6.54	13.16	24.31	32.18
NE 36 X 2392	0.82	-4.69	-2.53	-0.93	4.38	8.03	10.70	23.10	30.43
Danila X VCR 1432	0.01	-6.35	0.53	-1.56	3.29	5.34	11.55	20.19	27.55
NE 5 X 2392	-3.40	1.35	-2.86	-1.22	1.42	3.34	14.47	19.23	25.35
NE 55	-4.81	-3.31	-2.48	-0.32	2.15	4.72	7.49	14.37	25.28
Ayiyi X 2392	-3.40	1.81	-1.20	-1.59	5.87	5.90	7.68	19.44	23.81
SECOW 5T X Ayiyi	0.87	-0.58	-2.86	-1.49	4.45	6.31	7.58	18.34	22.39
MU 20B X NE 36	-4.73	-1.12	-0.32	-1.51	3.56	4.93	4.92	13.41	21.09
WC 48A	-0.32	0.77	-2.93	-1.54	2.19	2.71	10.36	15.26	19.28
2392 X Eberlat*NE 51	2.00	-7.84	-1.20	0.34	4.38	7.59	-0.32	11.65	18.35
Danila X NE 5	-3.80	0.70	-2.43	-0.88	1.96	2.59	6.68	11.23	17.63
3306 X Ayiyi	-1.71	0.00	-1.20	-1.53	1.51	2.78	8.68	12.97	17.41
WC 64 X 3306	-1.44	-5.13	-1.11	-0.89	1.54	1.90	4.58	8.02	16.58
Danila X KVU271	-1.44	-0.09	-1.54	-1.48	1.65	1.68	7.73	11.05	15.60
Danila X Eberlat*NE 51	-1.68	-2.85	0.46	-0.89	2.50	3.50	3.76	9.76	14.72
WC 27 X VCR 1432	-1.71	-6.03	0.04	-0.95	3.45	5.36	-3.30	5.50	14.16
2392	0.31	-3.13	-1.29	-0.87	-0.13	0.24	8.91	9.03	14.01
NE 55 X MU 20B	-1.00	0.37	-2.43	-0.11	2.85	3.91	4.02	10.78	13.97
MU 15 X WC 64	-0.36	-6.16	-1.20	-0.90	0.30	2.08	2.73	5.11	13.74
2392 X Sanzi	0.24	-6.04	-1.23	-1.53	2.13	3.15	-0.14	5.14	13.69
WC 63 X NE 48	-1.54	0.35	0.07	-1.54	0.87	2.01	7.82	10.70	13.36
MU 20B X WC 27	1.66	-4.25	-0.79	-0.88	1.49	2.68	4.50	8.67	12.92
3306 X Eberlat*NE 51	-2.69	-2.29	-0.85	2.72	3.30	4.94	1.42	9.66	12.77

Table 3. Contd.

NE 21 X Ayiyi	-1.54	-2.45	-2.10	-0.32	0.93	2.50	2.82	6.24	12.65
Sanzi X NE 36	-1.10	-1.97	-3.41	-0.87	1.10	1.77	2.36	5.23	12.58
NE 5 X WC 64	-0.33	-8.59	-0.77	-0.28	-0.46	-0.90	3.75	2.40	12.37
NE 21 X NE 55	-1.29	0.64	-2.58	-0.92	1.50	2.91	3.59	8.00	12.17
MU 15 X Eberlat*NE 51	1.59	-4.99	0.13	-0.32	2.53	3.61	2.38	8.52	12.10
Ayiyi X WC 66	-2.03	-0.56	3.15	-0.90	1.68	2.98	6.89	11.55	11.90
NE 21 X WC 48A	-1.83	2.22	0.10	0.33	2.21	3.33	6.75	12.29	11.46
WC 48A X WC 27	0.40	-1.60	-2.93	2.13	1.13	0.51	7.81	9.45	11.45
SECOW 2W X Eberlat*NE 51	-0.47	5.34	-1.65	-0.91	1.89	5.67	5.58	13.13	10.81
SECOW 5T X 3306	-1.77	-1.08	0.96	-0.95	0.16	0.33	6.39	6.88	9.72
MU 9 X NE 55	-1.23	1.16	1.86	-0.31	2.73	3.29	4.71	10.73	9.24
MU 15 X Ayiyi	-2.79	-0.98	0.61	-0.27	1.22	1.37	3.23	5.82	9.24
2392 X NE 5	2.27	-2.19	0.13	-0.90	1.76	3.11	3.60	8.47	9.16
NE 55 X NE 5	-1.10	-2.66	-0.69	-0.27	1.79	0.74	1.72	4.25	8.97
MU 20B X 3306	-2.35	-1.74	-0.33	-0.34	1.01	0.87	1.55	3.43	8.18
WC 66 X MU 9	-2.71	-1.69	-0.32	-0.95	0.00	0.51	1.69	2.20	7.87
WC 48A X NE 48	-3.38	0.68	-0.43	-0.33	1.14	1.17	1.55	3.86	7.32
NE 55 X Danila	-1.04	0.00	0.54	-0.29	1.34	2.12	2.39	5.85	6.64
NE 55 X MU 9	-0.68	0.68	-1.73	0.28	0.65	1.43	2.89	4.97	6.42
SECOW 5T X SECOW 4W	-0.34	-2.68	-0.86	0.89	0.42	-0.48	3.41	3.34	6.34
Ayiyi	-2.92	-1.64	0.12	0.30	-0.03	-0.20	2.24	2.01	6.14
WC 63 X SECOW 4W	0.21	0.86	-1.65	-0.30	0.25	0.47	4.19	4.91	5.78
KVU271 X WC 27	0.65	1.35	0.08	0.32	0.14	1.63	6.37	8.15	5.75
Eberlat*NE 51 X KVU271	-0.76	-5.00	-0.41	0.25	1.53	2.66	-4.37	-0.18	5.75
SECOW 2W X SECOW 4W	0.12	-2.20	1.43	-0.92	1.23	2.73	0.02	3.99	5.57
NE 55 X WC 63	-1.97	-2.72	2.63	0.91	0.56	0.90	2.40	3.86	5.01
NE 36 X Eberlat*NE 51	0.93	-0.94	0.02	0.25	1.60	2.84	0.72	5.17	4.92
NE 5 X KVU 271	-0.66	1.89	0.61	-1.49	1.66	2.10	1.04	4.81	4.46
Eberlat*NE 51 X Ayiyi	-0.76	4.06	0.09	0.30	2.39	3.78	1.98	8.15	4.45
WC 27 XWC 63	-1.67	-5.56	0.07	-0.90	-1.27	-1.66	-1.02	-3.94	4.12
NE 5 X MU 9	-0.43	-4.92	-1.61	0.91	-0.63	-0.75	-0.90	-2.28	3.78
2392 X NE 21	2.38	-2.03	-0.69	-0.32	0.17	1.20	1.33	2.69	3.36
WC 63 X MU 9	0.99	0.14	0.04	0.29	0.14	0.34	4.14	4.62	3.17
WC 66 X Danila	-2.84	2.22	-1.63	-0.88	-0.46	-0.64	1.09	-0.01	3.11
SECOW 2W X Sanzi	0.59	-0.85	0.50	0.30	0.75	2.21	0.67	3.63	3.10
VCR 1432 X WC 27	0.99	0.23	-1.66	-0.90	0.10	-0.21	1.65	1.54	2.88
NE 55 X WC 48A	-1.11	0.68	0.08	0.93	0.71	-0.16	2.72	3.27	2.69
WC 64 X WC 27	1.90	1.43	-0.78	-0.30	0.07	0.75	4.10	4.92	2.67
Danila X WC48 A	0.12	0.46	-1.54	-0.26	0.56	-0.16	0.62	1.01	2.24
WC 48A X WC 66	-2.79	2.97	0.02	1.47	0.57	1.23	2.07	3.87	2.19
Eberlat*NE 51 X NE 48	0.25	-1.00	-1.65	-0.31	0.53	0.10	-1.75	-1.13	1.58
WC 64 X SECOW 4W	-0.36	2.47	-1.66	-0.30	-0.56	-0.21	2.50	1.72	1.57
IT 889 X SECOW 2W	1.16	-1.89	0.07	0.29	-0.36	0.63	0.80	1.07	1.43
WC 27 X Eberlat*NE 51	2.38	1.33	-0.69	-0.27	-1.12	-0.69	5.87	4.06	1.32
Ayiyi X SECOW 2W	-1.88	-0.21	0.88	-0.32	0.31	-0.05	-0.54	-0.28	1.25
Ayiyi X IT 889	0.69	2.45	1.48	-0.90	0.52	-0.11	4.30	4.71	1.00
MU 9 X NE 48	-1.10	3.41	-0.31	-0.34	1.17	0.61	0.28	2.06	0.40
WC 64 X NE 36	0.35	0.77	0.61	-0.27	0.37	0.90	0.40	1.67	0.21
WC 63 X NE 36	-0.87	-0.21	-0.79	-0.32	-1.07	-1.45	0.53	-1.99	0.21
Eberlat*NE 51	-6.44	-8.40	4.39	3.05	-3.21	-3.75	-0.36	-7.32	0.08
WC 64 X 2392	1.21	-0.58	-2.60	0.35	0.27	0.67	-2.69	-1.75	-0.14

Table 3. Contd.

NE 21 X MU 20B	2.28	0.74	2.63	-0.36	0.90	1.72	2.19	4.82	-0.46
3306 X NE 5	-0.32	1.33	0.61	-0.27	0.22	-0.41	1.07	0.88	-0.47
MU 20B X NE 21	-1.77	0.74	-3.02	-0.28	-0.84	-1.44	-2.63	-4.91	-0.57
Eberlat*NE 51 X 2392	1.60	0.04	1.91	0.34	1.67	1.89	-0.25	3.31	-0.58
3306	0.68	-1.08	-1.23	-0.29	-1.40	-1.67	0.48	-2.59	-0.68
NE 5 X 3306	-0.32	0.77	-0.69	-0.27	-0.24	-0.53	-0.47	-1.25	-0.73
Sanzi	-0.77	-6.04	1.09	0.32	0.14	-0.77	-5.60	-6.23	-0.83
SECOW 5T X 2392	-1.20	0.90	1.33	0.35	1.27	1.00	-1.75	0.52	-0.86
NE 48	-1.04	2.80	-1.73	-0.90	-0.29	-0.60	-0.99	-1.88	-1.00
KVU 27-1 X NE 36	-1.44	-1.64	-0.78	-0.31	-1.17	-1.67	-2.40	-5.25	-1.08
WC 48A X IT 889	-0.58	1.57	0.44	-0.31	0.25	-1.03	0.40	-0.38	-1.50
MU 9 X NE 5	-1.35	1.24	-0.84	-0.29	-0.62	-1.18	-1.21	-3.01	-1.76
WC 64 X NE 5	-3.04	3.48	-2.93	0.35	-0.99	-1.30	-1.84	-4.12	-1.98
WC 64 X SECOW 5T	-0.34	0.68	3.04	-0.11	0.09	0.75	0.39	1.23	-2.04
WC 48A XSECOW 2W	0.58	2.29	-2.48	-0.93	0.40	-0.79	-2.19	-2.58	-2.05
WC 66 X NE 55	-0.70	-6.72	-0.76	0.91	-3.17	-4.10	-2.19	-9.46	-2.19
NE 55 X Sanzi	-0.01	-2.12	1.31	0.28	-0.49	-0.96	-1.28	-2.73	-2.19
3306 X WC 66	-1.44	-0.94	0.46	0.22	-0.15	-1.01	-2.79	-3.96	-2.27
KVU 27-1 X 2392	-0.62	1.76	-2.58	-0.31	-1.14	-1.46	-1.84	-4.44	-2.68
Sanzi X NE 21	-1.10	-2.89	-2.41	0.91	-1.38	-2.19	-5.19	-8.76	-3.27
Ayiyi X Danila	-0.66	1.89	-0.26	2.18	-0.02	-0.36	-0.02	-0.40	-3.55
SECOW 4W X VCR 1432	0.77	-1.79	0.01	-0.31	-1.11	2.68	-6.98	-5.41	-4.09
NE 21 X NE 5	-0.43	0.15	-1.20	0.34	-0.85	-0.62	-3.93	-5.40	-4.27
Sanzi X WC 27	-0.68	1.12	1.41	0.33	0.02	0.05	-2.30	-2.22	-4.39
WC 66 X 2392	2.17	1.34	-1.12	0.94	0.81	-0.26	-2.04	-1.48	-4.81
Danila X NE 55	2.61	1.82	-2.43	-0.27	-1.39	-3.17	1.15	-3.41	-5.15
SECOW 5T X Eberlat*NE 51	-0.36	2.47	-1.66	0.32	-1.33	-1.79	-1.49	-4.62	-5.38
KVU 27-1 X NE 21	-1.37	0.23	-0.35	-0.90	-2.62	-3.15	-2.01	-7.79	-5.38
2392 X WC 48A	3.80	-1.79	1.82	0.32	0.26	-1.03	-0.76	-1.52	-5.68
WC 48A X MU 9	1.26	1.16	-1.98	0.91	-1.56	-2.13	-1.53	-5.22	-6.57
WC 64	-0.89	1.02	-1.57	-0.87	-2.33	-4.02	-2.56	-8.91	-6.60
NE 48 X SECOW 5T	-1.04	-0.43	0.90	2.10	-2.00	-2.95	-0.30	-5.25	-6.79
WC 27 XWC 48A	1.78	2.13	-0.43	0.92	-0.32	-1.20	-0.92	-2.44	-6.84
3306 X MU 9	-0.33	-0.61	3.93	0.89	-0.58	-1.15	-1.27	-3.00	-6.87
VCR 1432 X WC 66	0.92	-3.21	1.91	-0.88	-0.96	-1.41	-5.79	-8.15	-6.90
KVU 27-1 X NE 55	0.93	-2.07	-0.67	0.25	-1.79	-2.43	-4.70	-8.92	-7.36
Eberlat*NE 51 X WC 27	3.96	0.15	1.04	1.57	0.72	1.71	-3.14	-0.71	-7.42
NE 5	-0.47	0.30	-0.33	-0.91	-2.09	-2.21	-4.64	-8.93	-7.54
KVU 27-1	1.41	1.20	-1.28	-0.31	-2.10	-2.82	-1.92	-6.84	-7.85
NE 55 X NE 36	-1.44	4.06	0.52	-1.49	-0.62	-0.94	-4.88	-6.44	-8.09
MU 20B X MU 15	2.14	-0.10	0.19	-0.26	-1.09	-2.10	-3.10	-6.29	-8.26
SECOW 4W	-0.92	2.13	0.01	0.31	-0.92	-2.53	-3.34	-6.79	-8.31
Eberlat*NE 51 X MU 20B	1.93	-0.85	3.58	-0.90	-1.54	-1.07	-1.95	-4.57	-8.32
VCR 1432 X 2392	7.68	-2.53	-2.54	0.92	-0.86	-0.70	-3.45	-5.01	-8.53
VCR 1432	-0.33	-2.99	3.57	1.55	-0.77	-1.45	-5.14	-7.36	-9.15
Sanzi X2392	3.04	-1.17	0.89	-0.34	-0.64	-0.94	-5.41	-6.99	-9.42
IT 889	0.25	0.04	-1.23	-0.31	-2.90	-4.05	-3.76	-10.71	-9.46
NE 48 X Ayiyi	0.68	1.49	-1.20	-0.90	-2.15	-3.74	-3.58	-9.46	-9.54
NE 55 X SECOW 2W	0.33	3.91	-0.32	0.37	-0.88	-1.30	-3.79	-5.97	-10.27
Danila X 2392	4.59	2.78	0.54	0.27	0.54	0.39	-3.29	-2.37	-10.55
2392 X WC 63	1.02	0.60	1.37	-0.29	-1.75	-2.36	-3.84	-7.95	-10.66
NE 21 X Eberlat*NE 51	0.92	2.71	0.04	-0.26	-1.17	-1.65	-4.59	-7.41	-10.82

Table 3. Contd.

MU 15 X MU 20B	2.00	2.93	-0.69	0.27	-1.67	-1.87	-2.90	-6.44	-10.95
SECOW 4W X MU 20B	0.48	5.26	2.78	0.95	-0.81	-0.99	-0.32	-2.12	-11.60
WC 27 X IT 889	1.81	1.58	-1.11	-0.26	-1.63	-2.85	-5.28	-9.76	-11.78
NE 21 X MU 9	1.93	1.26	-0.78	-0.11	-1.67	-3.15	-4.74	-9.55	-11.85
WC 66 X NE 5	-0.68	-0.01	2.19	0.94	-1.88	-2.98	-4.87	-9.72	-12.16
NE 5 X IT 889	-1.02	6.16	0.55	-0.90	-1.57	-2.75	-3.60	-7.92	-12.71
IT 889 X WC 27	3.35	2.93	3.51	0.88	-0.83	-1.63	0.34	-2.11	-12.79
SECOW 5T	1.47	-0.99	1.47	0.35	-2.24	-3.55	-5.04	-10.83	-13.13
WC 27	4.02	0.79	0.52	0.32	-2.75	-3.44	-2.05	-8.24	-13.88
WC 64 X NE 21	-0.22	4.52	0.12	0.29	-2.16	-2.68	-4.76	-9.61	-14.32
WC 27 X MU 20B	3.16	1.58	1.49	-0.90	-1.83	-3.14	-4.04	-9.01	-14.33
WC 66	1.93	2.94	-0.26	-0.27	-2.48	-4.32	-3.61	-10.41	-14.76
SECOW 2W	-1.88	0.78	3.58	0.91	-1.91	-3.61	-6.00	-11.52	-14.91
SECOW 4W X MU 9	1.34	3.35	0.98	-0.28	-1.92	-3.77	-4.03	-9.71	-15.09
MU 15	2.03	4.52	-1.67	1.55	-1.83	-3.40	-3.49	-8.72	-15.16
IT 889 X 2392	4.63	1.23	0.08	0.96	-1.41	-2.34	-5.10	-8.85	-15.75
WC 27 X Sanzi	2.71	-0.61	3.07	1.50	0.19	-1.02	-8.58	-9.41	-16.07
MU 9 X MU 20B	-1.34	4.98	0.61	0.32	-1.67	-2.98	-7.15	-11.80	-16.37
Eberlat*NE 51 X MU 15	1.60	2.42	2.24	1.52	-0.69	-0.43	-7.60	-8.71	-16.49
Danila	-1.59	1.57	3.51	2.72	-1.83	-2.90	-6.78	-11.51	-17.71
WC 63	1.81	4.05	0.61	-0.26	-3.12	-4.42	-4.56	-12.10	-18.30
WC 64 X NE 55	1.70	3.57	-0.69	0.94	-2.51	-3.43	-7.53	-13.47	-18.99
MU 20B X 2392	1.32	4.48	1.76	0.91	-2.56	-3.51	-5.74	-11.82	-20.29
Ayiyi X MU 9	2.51	5.39	1.37	0.90	-2.25	-3.30	-5.41	-10.96	-21.14
MU 20B	1.02	3.96	2.24	1.55	-2.55	-4.37	-6.31	-13.23	-22.00
MU 9 X NE 36	3.39	4.69	0.04	0.91	-3.88	-4.89	-7.07	-15.84	-24.86
MU 9	0.46	2.70	1.54	2.79	-3.53	-5.66	-8.25	-17.44	-24.93
WC 63 X 2392	2.27	1.59	7.04	2.13	-1.72	-3.34	-7.22	-12.28	-25.32
MU 20B X NE 55	0.12	1.72	6.97	2.15	-3.00	-3.95	-7.74	-14.70	-25.65
NE 21	1.13	3.26	5.74	2.18	-2.99	-4.29	-7.71	-14.98	-27.30
MU 20B X SECOW 5T	3.13	6.61	7.45	-0.31	-3.81	-5.69	-9.33	-18.82	-35.71

[1]Scab on leaf, [2]Scab on pod, [3]Number of peduncles, [4]Number of pods, [5]Base Selection Index for yield and its components, [6]Base Selection Index for Grain Yield.

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Harnessing genotype-by-environment interaction to determine adaptability of advanced cowpea lines to multiple environments in Uganda

Francis Abiriga[1], Patrick O. Ongom[2,4*], Patrick R. Rubaihayo[1], Richard Edema[1,2], Paul T. Gibson[2], Isaac Dramadri[2] and Martin Orawu[3]

[1]College of Agricultural and Environmental Sciences, Department of Agricultural Production, P. O. Box 7062, Makerere University, Kampala, Uganda.
[2]Makerere University Regional Centre for Crop Improvement (MaRCCI), Uganda.
[3]National Semi-arid Resources Research Institute (NaSARRI), P. O. Box 56, Soroti, Uganda.
[4]International Institute of Tropical Agriculture (IITA), Kano, Nigeria.

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This study was conducted to determine the yield stability of advanced cowpea lines in diverse agro-ecological zones of Uganda in order to facilitate documentation requirements for national performance trials (NPT). Thirty cowpea genotypes were evaluated against six checks in three localities, over three growing seasons, making a total of 9 unique environments. The trials were laid in a 6x6 alpha lattice design with three replications and grain yield was the principal trait measured. Single-site and multi-location data were summarized using analysis of variance. Further analysis of stability was visualized using the genotype and genotype by environment interaction (GGE) biplot and the additive main effect and multiplicative interaction (AMMI) models. ANOVA depicted highly significant differences among the genotypes, locations, seasons and GEI for grain yield. Based on AMMI analysis, environmental effect accounted for the most variation (84.7%) in the phenotype followed by GE (9.45%) and genotypes (4.45%), alluding to the complex inheritance of grain yield in cowpea. The polygon view and the average environment coordination view of the GGE biplot revealed Ayiyi as the wining genotype in the major mega environment and the most stable and high yielding across environments respectively. The genotypes Ayiyi, WC64 and ALEGIxACC2 yielded higher than the checks and were very stable. The other genotypes G36 (WC 36), G3 (ACC12xSECOW3B), G32 (WC16), and G14 (MU9) did not outperform the checks but displayed high yield stability and the mean yields were above the overall average. These genotypes were considered desirable for advancement to National Performance Trial for potential release as new improved cowpea cultivars.

Key words: Cowpea (*Vigna unguiculata* L. Walp), additive main effect and multiplicative interaction (AMMI), genotype and genotype by environment interaction (GGE), stability, grain yield.

INTRODUCTION

Cowpea (*Vignaunguiculata* L. Walp) is an annual,herbaceous legume that belongs to the Fabaceae family. It ranks fourth among the most important legume crops after beans, groundnuts and soybean (Mwale et al., 2017) and it is an important source of food for most people in the sub-Saharan region which is consumed in form of vegetable and grain. Farmers in eastern and northern Uganda start harvesting cowpea vegetables

three weeks after planting, thus making it one of the best food security crops (Orawu et al., 2013). Cowpea provides high quality fodder for livestock and is a good protein supplement for small scale farming communities with high nutritive values of 24.8% protein, 1.9% fat, 6.3% fiber and 63.6% carbohydrate (Mwale et al., 2017). Unlike beans and other legumes, cowpea is a multi-purpose crop, providing the farmer with not only grains, but also a wide range of other products.

According to FAOSTAT (2015), the world production statistics of cowpea stands at 4.46 million metric tons with Sub-Saharan Africa producing over 95% of the world cowpea (4.24 million metric tons). Asia is the second largest producer with only 3% of the world production (0.13 million metric tons). Nigeria is the leading producer of cowpea in the world with 2.46 million metric tons. In the case of Uganda, production of cowpea stood at 12,929 tons from 26,354 hectares in 2016 with an average yield of 0.49 kg/ha (FAOSTAT, 2016), with the northern and eastern parts of the country accounting for most of the production.

The production of cowpea is greatly affected by both biotic and abiotic stresses (Mwale et al., 2017). Yield attained in farmer's field fluctuates and, in most cases, averages of less than 500 kg/ha can be attained compared to the yield potential of the crop estimated at 1,500 kg/ha. The development and deployment of improved varieties remains the ultimate strategy to curb these challenges. However, genetic improvement of quantitative traits is challenging because their expressions are modified by the environment (Yan et al., 2010). Selection of complex traits like grain yield in a breeding program is effective at advanced generations when the lines have become homozygous and replicated trials are possible. At this stage, replicated and multi-location trials becomes handy in assessing consistency in performance of genetic materials that are destined for advanced testing and possible release. Yield stability studies provide useful information on the adaptability of potentially high yielding lines in vast agro-ecological zones and help breeders to make recommendations about genotypes that are widely or specifically adapted (Asio et al., 2005). The data for making such decisions are often complex and requires rigorous analysis with advanced statistical models, including AMMI and GGE to discover and summarize consistent patterns in the experimental trial data sets. The GGE biplot and the AMMI models have been widely applied in the analysis of GxE by several workers in a wide range of crops: Crossa et al. (1997) in wheat; Yan and Rajcan (2002) in soybean; Yan and Tinker (2005) in wheat; Yan and Tinker (2006) IN wheat; Ding and Tier (2008) in *Pinus radiata*; Yan et al. (2010) in oat; Farshadfar et al. (2013) in chicken pea; Rad et al. (2013) in wheat. The present study utilized 36 cowpea lines, previously tested and selected in the breeding program for various attributes including yield potential, to assess their adaptation and stability to diverse agro-ecological zones in Uganda. The study utilized eight unique environments which involved a combination of three locations and three growing seasons, using grain yield measurement as a parameter to evaluate stability and adaptability of the 30 lines in comparison to six locally adapted check varieties. Specifically, this was meant to ascertain if any of the 30 lines were broadly adapted and outperformed the six local checks in terms of grain yield. The study identified potential cowpea lines for further test at NPT and release, and in addition, provided insights into how GxE can be exploited by breeders to identify high yielding, stable and adapted varieties.

MATERIALS AND METHODS

Experimental sites and their geographic characteristics

The study was conducted in three diverse regions of Uganda and these included Arua (Abi-ZARDI) in West Nile, Serere (NaSARRI) in Eastern and Makerere University Agricultural Research Institute, Kabanyolo (MUARIK) in Central for three consecutive seasons (2017A, 2017B and 2018A). The soil characteristics of the study sites are sandy clay loam for MUARK, sandy clay loam for Arua and black clay for Serere (Sserumaga et al., 2015). The first season trials (2017A and 2018A) were sown in the month of March of the respective years, while the 2017B season trials were sown in August 2017. Details of the experimental sites and their geographic characteristics are given in Table 1, while the seasonal rainfall data are provided in Table 2.

Experimental design, field management and data collection

The experimental trials were laid out in alpha-lattice design of six blocks with six genotypes per block and replicated three times. Each replication measured 30 m long and 27 m wide, thus totaling an area of 810 m^2. Plot dimension measured 3 m by 2 m. The seeds were sown at a spacing of 0.75 m between rows and 0.25 m within plants. This formed five rows and eight plants per row and resulted in a total of 40 plants per plot. Inter-plot distance was 1.5 m, while inter-replication distance was 2.0 m.

The plants were sprayed twice with chemicals, first at seedling stage to protect against aphids using cypermethrin (10% EC) at the rate of 2.5 g per hectare and the second application was at50% flowering stage with non-systemic insecticide; lambda-cyhalothrin (2.5 EC) at the rate of 2.5 g per hectare to protect against thrips and pod borers. No fertilizers were applied since the soils are generally fertile.

The following data were collected; Number of primary branches per plant (NB) estimated as an average from 5 plants per plot; days to 95% maturity (MAT95%) determined by counting the number of days from sowing to the date at which about 95% of the pods were mature.

Number of pods per plant (NPP) estimated as the average of

*Corresponding author. E-mail P.Ongom@cgiar.org.

Table 1. Experimental sites and their geographic and soil characteristics.

Location	Latitude	Longitude	Altitude (m.a.s.l)	Average annual temperature (°C)	Average annual rainfall (mm)	Soil type
MUARIK	0º28'N	32º37'E	1200	21.5	1150	Sandy clay loam
AbiZARDI	3º4.58'N	30º56'E,	1206	24	1250	Sandy clay loam
NaSARRI	1º35'N	33º35'E	1140	26.5	1415	Black clay

Source: Sserumaga et al. (2015).

Table 2. Seasonal rainfall data (mm) for 2017A, 2017B and 2018B collected from three agro ecological zones in Uganda.

Station	2017A					
	Mar	Apr	May	Jun	Jul	Mean
MUARIK	207.1	171	140	43.4	123	683.7
NaSARRI	44.5	181	195	81.2	98.8	600.6
AbiZARDI	71.1	69.7	128	147	243	658.6
			2017B			
	Aug	Sep	Oct	Nov	Dec	Mean
MUARIK	50.7	147	88.4	204	27.4	517.2
NaSARRI	79.8	153	168	98	0	498.5
AbiZARDI	238.7	223	213	165	0	840.1
			2018A			
	Mar	April	May	June	Jul	Mean
MUARIK	133	204	147	77	69	630
NaSARRI	105	208	187	107	112	719
AbiZARDI	79	119	117	130	167	612

Source: Uganda Bureau of statistics (2018).

number of pods of five plants selected randomly in a given plot; number of seeds per pod (NSP) estimated as the average of the total number of seeds from five plants; hundred seed weight (100SW) determined as the weight in grams of 100 seeds randomly sampled from each plant and averaged for five plants; grain yield per plot (GY/PLOT) where all plants in a plot were harvested and bulked to determine the yield per plot in grams after drying the seeds to an estimated moisture content of 12%; grain yield per plant (GY/P) determined as the average weight of five randomly selected plants harvested from each plot expressed in grams and grain yield per hectare (GY/HA) determined as the total yield of a given genotype in kilograms per hectors.

Plant genetic materials

Thirty cowpea lines that included land races from local farmers in Uganda, breeding lines and released varieties from National Agricultural Research Organization (NARO) in Uganda and varieties from Ghana and International Institute for Tropical Agriculture (IITA) were used for this study. The details of the genotypes are provided in Table 3.

Statistical analysis

Analysis of variance

Analysis of variance (ANOVA) was performed for grain yield using statistical package, Genstat 18th edition to detect differences among the genotypes and F-test at 0.05 and 0.001 probability levels to detect the significance of the differences among the genotype means (Moore et al., 2015a). Genotypes were considered as fixed factors while location, season and blocking were considered as random factors. The analysis process involved single site analysis to obtain single site means. The best linear unbiased predictors (BLUPS) were then used to obtain multi-location means and multi-location analysis of variance using general ANOVA. Pooled analysis of variance was then conducted across seasons to test for the effect of seasons. The stability of genotypes over time (across seasons) and over space (across locations) was determined from the analysis of variance by testing the level of significance of the mean square value of season (MS_Y) and location ($MS_{L)}$ respectively (Beavis, 2015). MSY and MSL values enabled determination of temporary/spatial stability. Since the (MS_Y) and MS_L are often inflated by experimental error, the actual variance due to season/location was obtained by equating the MS_Y or MS_L to the mean square error (MS_e). In order to do this, GxE was decomposed into its components as presented in the model according to Moore et al. (2015b)

$G \times L_{(locations)} + G \times S_{(seasons)} + G \times SL_{(seasons \times locations)}$

Linear model for single site analysis

$$\mathbf{Y_{ijk}} = \mu + G_i + R_j + B/R_{(k)} + e_{ijk}$$

Linear model for across location analysis:

Table 3. List of 36 Cowpea genotypes used in the study.

Genotype	Genotype code	Origin	Genotype type
ACC12 * SECOW 5T	G2	NARO, Uganda	Breeding line
ACC 2 * SECOW 2W	G3	NARO, Uganda	Breeding line
IT 889	G4	IITA	Breeding line
IT 2841 * BROWN	G5	IITA	Breeding line
ALEGI * SECOW 5T	G6	NARO, Uganda	Breeding line
EBELAT * NE 51	G8	NARO, Uganda	Breeding line
AYIYI	G10	Ghana	Breeding line
NAROCOWPEAS 3	G11	NARO, Uganda	Breeding line
F2588T2E	G12	Ghana	Breeding line
NE 39 * SECOW 4W	G13	NARO, Uganda	Breeding line
SECOW 4W * SECOW 5T	G18	NARO, Uganda	Breeding line
ACC12 X SECOW 3B	G23	NARO, Uganda	Breeding line
ALEGI X ACC2	G28	NARO, Uganda	Breeding line
Sunshine 2S	G9	Uganda	Land race
WC 68A	G19	West Central Uganda	Land race
WC 16	G20	West Central Uganda	Land race
WC 37	G21	West Central Uganda	Land race
NE 55	G22	North Eastern Uganda	Land race
NE 23	G25	North Eastern, Uganda	Land race
NE 37	G30	North Eastern, Uganda	Land race
CP 1	G31	Uganda	Land race
WC 36	G32	West Central, Uganda	Land race
NE 15	G33	North Eastern, Uganda	Land race
NE 20	G35	North Eastern, Uganda	Land race
NE 55	G36	North Eastern Uganda	Land race
NE 48	G1	North Eastern Uganda	Landrace
MU 9	G14	Unknown	Landrace
MU 9A	G15	Uganda	Landrace
WC 63	G24	West Central Uganda	Landrace
2392	G34	Uganda	Landrace
SECOW 5T	G16	NARO, Uganda	Released Variety
SECOW 4W	G17	NARO, Uganda	Released Variety
SECOW 1T	G26	NARO, Uganda	Released Variety
NAROCOWPEA1	G27	NARO, Uganda	Released variety
NAROCOWPEA4	G29	NARO, Uganda	Released variety
ASONTEM	G7	Ghana	Variety

$$Y_{ijkl} = \mu + L_i + Y_j + LY_{(ij)} + Rep(E)_k + B(Rep.L.Y) + G_l + GL_{(il)} + GY_{(lj)} + GLY_{(lij)} + e_{ijlk}$$

Where *:* Y_{ijkl}= observation of i[th] genotype in l[th] location, and season j, in replication k, μ = general mean, G_l= effect of genotype l, L_i= effect of location i, Y_j = effect of season j, $LY_{(ij)}$ = interaction between location and season (effect of environment) $Rep(E)_k$ = effect of rep k in location i and season j, $B(Rep.L.Y)$= blocking effect, $GLY_{(lij)}$ = interaction of genotype l with location i and in season j, e_{ijlk} = residual error of genotype l in environment (*ij*), replication k.

GGE biplot analysis

The linear model for the biplot analysis based on singular value decomposition of the first two principal components described by Yan and Rajcan (2002) is presented thus;

$$Y_{ij} - \mu - \beta_j = \sum \lambda_j \varepsilon_{i(l)} \eta_{lj} + \in_{ij} \quad (1)$$

Where: Y_{ij}= is the observed mean performance of genotype i in environment j, (*i =1,2…n), (j=1,2…m)*, μ = grand mean, β_j = main effect of environment *j* (μ + β_j), ë$_l$= *SV* of the *l*[th]PC, the square of singular value is the sum of squares explained by $PC_l$where; *l* = 1,2…k. with k ≤ min (m, n) and for a two-dimensional biplot, k = 2. $\varepsilon_{i(l)}$ = eigen vector of genotype i for PC_l, η_{lj} = eigen vector for environment j for PC_l, ε_{ij}= residual associated with genotype i in environment j. PC1 and PC2 eigen vectors cannot be plotted

directly to construct a meaningful biplot before the singular values are partitioned into the genotype and environment eigenvectors (Yan and Tinker, 2006). In order to visualize the MET data, singular value partitioning (SVP) was partitioned into the genotype and environment eigen vectors as follows:

$$Y_{ij} - \mu - \beta_j = \sum G_{il} E_{jl} + \epsilon_{ij}$$

Where G_{il} and E_{jl} are the PC_l scores for genotype i and environment j respectively (Yan and Tinker, 2006). In a biplot, genotype i is displayed by a point defined by all the G_{il} values and environment j is displayed by a point defined by all the E_{jl} values where i = 1 and 2 for a two dimensional biplot (Yan and Tinker, 2006). Singular value was thus implemented by,

$$G_{il} = \lambda_l^{fl} \varepsilon_{il} \text{ and } E_{ij} = \lambda_l^{1-fl} \eta_{lj} \quad (2)$$

Where;*fl*= partition factor for PC *l* and is usually between 0 and 1. The partition factor influences the kind of interpretation we can give to a biplot. To analyze the relationship between the trials, genotypes and the environments, the GGE biplot was generated using the formula presented as:

$$Y_{ij} - \mu - \beta_j = G_{i1} E_{j1} + G_{i2} E_{j2} + \epsilon_{ij} \quad (3)$$

The polygon view was constructed using the environment standardized GGE model presented as;

$$\frac{Y_{ij} - \mu - \beta_j}{sj} = \sum \lambda_l G_{il} E_{jl} + \epsilon_{ij} \quad (4)$$

The GGE biplot based on genotype scaling was used for the evaluation of genotypes because the relative importance of the PC_1 and PC_2 is fully reflected by the location of the genotypes in the GGE biplot (Yan and Tinker, 2006). Symmetrical scaling: *fl=0.5*. $G_{il} = \lambda_l^{0.5} \varepsilon_{il}$ and $E_{jl} = \lambda_l^{0.5} \eta ij$ was used to visualize the relative importance of both the genotype variation and environment variation for both PC_1 and PC_2. The GGE biplots were generated using the R software version 3.5.0, while AMMI stability values were generated using Genstat 18th edition software.

AMMI analysis

The AMMI model as described by Akter et al. (2014) is presented below.

$$Y_{ijk} = \mu + G_i + E_j + \sum \lambda_k \alpha_{(ik)} \gamma_{jk} + d_{ij} + e_{ijk}$$

Where, μ = the grand mean. G_i = the genotype deviations from the grand mean. E_j= the environment deviations from the grand mean. λ_k = k^{th} eigen value. $\alpha_{(ik)}$= principal component score for the i^{th} genotype for the k^{th} principal component axis. γ_{jk} = principal component score for the j^{th} environment for the k^{th} PC axis. d_{ij}= residual GEI not explained by model. e_{ijk}= residual model. The AMMI stability values (ASV) were determined from the described expression below (Lin et al., 1986):

$$\text{ASV} = \sqrt{\frac{IPCA1SS}{IPCA2SS}(IPCA1SCORE)^2 + (IPCA2SCORE)^2}$$

Where: ss = the sum of squares, IPCA1 and IPCA2 = the first and second interaction principal component axes respectively. The average stability value (ASV) could be considered as the distance from zero in a two-dimensional scatter plot of IPCA 1 scores against IPCA2 scores. The genotypes were evaluated for both cultivar superiority and static stability. The more the IPCA scores approximates zero, the more stable or adapted the genotype is over all environments tested. Genotypes with smaller stability values were considered to be more stable. The AMMI analysis of variance was generated using Genstat 18th edition software and the GxE effect was further partitioned into the first and second interaction principal component axis and GxE residual.

RESULTS

Agronomic attributes of the genotypes

The mean agronomic attributes of the 36 genotypes determined over two seasons (2017A and 2017B) in the three locations are presented in Table 4. The genotypes ACC2xSECOW2W, ALEGIxACC2, NAROCOWPEA1, SECOW2W, NAROCOWPEA3, Ayiyi, NAROCOWPEA4 and WC64 had higher 100 seed weight and superior grain yield per plant. These genotypes also exhibited higher number of pods per plant, number of seeds per plant and higher number of branches per plant.

Variances and summary statistics for major phenological traits among 36 cowpea genotypes assessed across three locations in two seasons (2017A and 2017B) are presented in Table 5. All the traits were significantly influenced by the location effect at P<0.001 except the weight of 100 seeds that was not significantly affected at P< 0.05. The phenological traits exhibited moderate to high heritability (H) values ranging from 0.67 for MAT to 0.91 for GY/P (Table 5). The results for genotypic coefficient of variation (GCV) ranged from 3.38% to 13.33% with maturity date recording the lowest GCV and grain yield per plant recording the highest GCV at 13.33%. The number of pods per plant attained GCV of 13.21% followed by the weight of 100 seeds (11.9%) and number of seeds per pod (10.0%).

Multi-location analysis of variance

The results of the combined analysis of variance for grain yield among 36 cowpea genotypes evaluated across three locations in three seasons are presented in Table 6. There were highly significant differences (P<0.001) observed among genotypes, locations and seasons for grain yield and thus the three main sources of variation (G, E and GxE) greatly influenced grain yield in cowpea. The genotype x season, genotype x location and the genotype x location x season (GxE) interactions were highly significant (P<0.001). Grain yield in cowpea was greatly affected by the season and location effect and the season/location (GxE) interaction effect. Of the three main effects (genotype, location and season), the

Table 4. Mean phenological attributes of 36 cowpea lines determined for two seasons across three locations in 2017A and 2017B.

Genotype	Genotype code	MAT	NB	NPP	NSP	SW	GY/P
2392	G1	77	4.5	19.9	11.1	10.5	36.7
ACC 2 * SECOW 2W	G2	72.8	5.1	23.5	12.1	12	42.9
ACC12 x SECOW 3B	G3	71.7	5	27	12.6	12.9	47
ACC12 x SECOW 5T	G4	74.1	5	26.8	11.7	12	46.6
Alegi * SECOW 5T	G5	73.7	4.6	27.9	13.2	13	47.5
ALEGI x ACC2	G6	74.5	4.9	31.4	14.1	14.7	52.9
Asontem	G7	75.9	4.4	22.8	11	11.8	40.1
Ayiyi	G8	75.4	5.3	32.8	14.5	15.2	53.4
CP 1	G9	76.5	4.7	22	10	12.7	42.5
Ebelat * NE 51	G10	71.8	5	28.9	12.4	14.5	49.7
F2588T2E	G11	74.2	4.6	23	10.9	11.2	37.4
IT 2841 * BROWN	G12	77.5	4.7	26.6	11.1	12.9	44.1
IT 889	G13	72.2	4.7	28.5	12.6	14.5	49
MU 9	G14	75.5	4.8	29.5	12.5	14.6	49
MU 9A	G15	73.7	4.8	26.6	11.6	13.4	44.5
NAROCOWPEA1	G16	73.7	5.5	32.2	13.4	16.9	57
NAROCOWPEA3	G17	74.9	5.3	31.6	13.4	16.1	54.9
NAROCOWPEA4	G18	72.9	5.4	31.9	14.3	15.9	53.6
NE 15	G19	69.6	4.6	23.8	11.4	12.3	41.2
NE 20	G20	71.6	4.3	22.5	10.7	11	37.1
NE 23	G21	72.5	4.7	28.9	12.4	12.3	39.6
NE 37	G22	75.5	4.5	25.2	10.9	12	35.2
NE 39 * SECOW 4W	G23	80.0	4.5	24.7	12	13.4	40.2
NE 48	G24	73.7	4.4	26.2	13.3	13.9	44.8
NE 55	G25	75.3	4.3	22.8	11.2	12	38.2
Secow 1T	G26	72.7	4.5	24.2	12.6	12.5	41.9
Secow 4W	G27	74.7	5	30.9	13.7	14.6	52.6
SECOW 4W * SECOW 5T	G28	78	4.8	26.9	12.4	13	46.3
Secow 5T	G29	80.0	4.5	27.8	12	12.9	46
Sunshine 2S	G30	71.3	4.7	25.1	12.1	12.7	41
WC 16	G31	75	4.4	22.4	11.3	12	37.9
WC 36	G32	74.7	4.9	27.4	12	13.2	44.8
WC 37	G33	72.2	4.7	25.6	11.5	12.3	42.2
WC 63	G34	74.9	4.8	28.2	11.7	12.7	47.4
WC 68A	G35	80.1	4.8	29.7	12.7	12.3	52
WC64	G36	75.6	5	27.1	12.6	12.8	46.5

MAT=days to maturity, NB= number of branches, NPP= number of pods per plant, NSP=number of seeds per pod, SW= weight of 100 seeds, GY/P= grain yield per plant.

greatest contribution to the variation in cowpea yield was due to the seasonal effect (52.3%), followed by the locality (25.1%) and the genotype main effect had the lowest contribution to cowpea grain yield (8.5%).

AMMI analysis of variance

The additive main effect and multiplicative interaction (AMMI) analysis of variance for 36 cowpea lines evaluated across three locations in three seasons is presented in Table 7. The results showed that there was highly significant ($P<0.001$) main effect of genotype, environment and GxE effect. The GxE interaction term was further partitioned into the first and second principal components which were both highly significant at $P<0.001$. The AMMI analysis showed that all the treatments (E+G+GE) accounted for 98.6% of the total variation in cowpea grain yield, while error only accounted for 1.24%. The total sum of squares was then

Table 5. Heritability, variances and summary statistics for major phenological traits among 36 cowpea genotypes assessed across three locations in two seasons (2017A and 2017B).

Statistics	MAT	NB	NPP	NSP	SW	GY/P
BSH (genotype mean basis)	0.90	0.67	0.86	0.76	0.85	0.91
σ2g	6.37	0.14	12.47	1.48	2.44	36.18
σ2GxL	2.55	0.29	8.15	1.86	1.64	12.89
σ2 L	6.47	0.06	8.66	1.62	0.02	13.76
σ2e	2.85	0.17	5.71	1.41	1.42	16.33
GM	74.6	4.77	26.7	12.2	13.1	45.11
LSD	1.75	0.43	2.79	1.22	1.19	3.94
CV	2.26	8.60	8.94	9.74	9.07	8.96
P (G)	0.00	0.00	0.00	0.00	0.00	0.00
P(GXL)	0.00	0.00	0.00	0.00	0.00	0.00
P(L)	0.00	0.00	0.00	0.00	0.67	0.00
GCV	3.38	7.79	13.21	10.00	11.9	13.33

BSH = Broad sense heritability, σ^2g =genotypic variance, σ^2GxL =genotype location variance, σ^2 L= location variance, σ^2e =error variance, GM=grant mean, LSD =least significance difference, MAT = days to maturity, NB= number of branches, NPP= number of pods per plant, NSP=number of seeds per pod, SW= weight of 100 seeds, GY/P= grain yield per plant. GCV= genotypic coefficient of variation, P(G), P (GxE), and P(L) = significance of genotype, GxE, and location at P<0.05.

Table 6. ANOVA for multi-location evaluation of 36 cowpea genotypes for grain yield (kg/ha)

Source of variation	d.f	SS	MS	Explained SS
Total	863	748,091,291		100
Location	2	185,139,090	92,569,545***	24.7
Season	2	386,077,104	193,038,552***	51.6
Location x Season	3	63,041,021	21,013,674***	8.4
(Location/Season/Rep)	16	463,406	28,963*	0.1
Genotype	35	33,293,680	951,248***	4.5
Genotype x location	70	21,846,777	312,097***	2.9
Genotype x Season	70	26,146,239	373,518***	3.5
Genotype x location x Season	105	22,722,080	216,401***	3
Pooled error	560	9,361,894	16,718***	1.3

d.f = degrees of freedom, MS = mean square, SS= sum of squares, *, **, *** = significant at P<0.05, 0.01, 0.001 respectively.

Table 7. Additive Main effect and Multiplicative Interaction (AMMI) analysis of variance for yield of 36 cowpea genotypes across three locations for three seasons (kg/ha)

Source	d.f	S.S.	M.S.	Explained	%GxE
Total	863	748,091,291	866,850***		
Treatments (G+E+GE)	287	738,265,992	2,572,355***	98.6	
Genotypes	35	33,293,680	951,248***	4.45	
Environments (E)	7	634,257,215	90,608,174***	84.7	
Block	16	463,406	28,963ns	0.061	
Interactions (GxE)	245	70,715,096	288,633***	9.452	
IPCA 1	41	22,081,952	538,584***		31.2
IPCA 2	39	14,555,779	373,225***		20.58
Residuals	165	34,077,366	206,529		48.18
Error	560	9,361,894	16,718	1.25	

d.f = degrees of freedom, M.S = mean square, S.S= sum of squares, *, **, *** = significant at P<0.05, 0.01, 0.001.

Table 8. Environment means and IPCA Scores for grain yield for 36 cowpea genotypes in Uganda.

Environment	Mean (kg/ha)	Variance	IPCAe1	IPCAe2
ARUA2017A	2671	175123	-18.2018	19.2375
ARUA2018A	1010	173490	13.75941	-29.1266
MUARIK 2017A	2483	247623	-38.6323	-8.946
MUARIK 2017B	2800	168864	6.09907	-17.2794
MUARIK2018A	871	66918	7.83788	0.68376
SERERE2017A	877	96922	-4.85107	4.64067
SERERE2017B	1651	83178	16.68372	7.9908
SERERE2018A	550	51751	17.30501	22.79924

IPCAe1/IPCAe2 the first and second environment interaction principal components.

Table 9. Mean yield performance of 36 cowpea genotypes evaluated across locations in three seasons of 2017A, 2017B and 2018A.

Location	Season			
	2017A	2017B	2018A	Total
ARUA	2670	-	1010	1840
MUARIK	2482	2800	870	2051
SERERE	876	1650	550	1025
Mean	2009	2225	810	1682

Yield data is not presented for the location ARUA in season 2017B as it was affected by combination of factors, especially dry spell and destruction by animals.

partitioned into the main effects where, the greatest contribution to the variation in cowpea grain yield was by the environment (E) which accounted for 84.7% of the total variation. This was followed by the interactions (GE), with 9.45% of the variation, while the genotypes only accounted for 4.45% of the total variation in cowpea grain yield. The blocking effect explained 0.061% of the total variation in cowpea yield and was barely significant. GxE was partitioned into its first and second interaction principal components (IPCA1 and IPCA2), where IPCA1 accounted for 31.2% of the total GxE, IPCA2 accounted for 20.58% and the residual accounted for 48.18% of the total GxE effect. The first two IPCAs were therefore sufficient to justify the AMMI model.

Environmental IPCA scores and variances for 36 cowpea genotypes evaluated in three seasons across three locations

The results for the environmental IPCA scores and variances for 36 cowpea genotypes evaluated over three seasons across three locations are presented in Table 8. The first environment linear interaction terms (IPCA1 scores) were able to discriminate between the environments with Kabanyolo (MUARIK 2017A) having the highest IPCA1 score of -38.63, followed by ARUA 2017A, that recorded an IPCA1 score of -18.2 and the least interactive environment was observed with Serere 2017A (IPCA1 score of -4.85).

The environment variance ranged from 247,623 to 51,751, where Kabanyolo (MUARIK2017A) registered the highest and Serere 2018A recorded the least variation among the genotypes. MUARIK 2017A and ARUA 2017A contributed the greatest variation among cowpea genotypes and were the most favorable environments for testing the genotypes. According to the AMMI analysis, the order of discriminating ability of the environments based on their variances was MUARIK 2017A (247,623), ARUA2017A (175,123) and Serere 2018A (51,751). With respect to the mean yield of environments, the AMMI analysis showed that, MUARIK, season 2017B had an average mean yield of 2,800 kg/ha compared to ARUA, season 2017A which recorded an average mean yield of 2671 kg/ha. Serere, in season 2018A was the least representative and discriminatory environment since it had the lowest average mean yield of 550 kg/ha.

The results of the grand season/locality and overall grand mean for 36 cowpea genotypes are presented in Table 9. The overall mean yield of cowpea genotypes across localities and seasons was 1,682 kg/ha. With

respect to localities, the highest mean yield of cowpea genotypes was observed in Kabanyolo (MUARIK) with 2,051 kg/ha, followed by ARUA with 1,840 kg/ha and Serere had the least mean yield of 1,025 kg/ha.The estimates of the season mean yields revealed that, season 2017B registered the highest mean yield of cowpea at 2,225 kg/ha and the worst season was 2018A with a mean yield of 810 kg/ha across locations. The trials in season 2017B at Arua were completely destroyed by stray animals and therefore it was omitted in the analysis. The average yield for season 2017B was thus obtained from two localities.

Genotypic IPCA scores and variances for 36 cowpea genotypes evaluated in three seasons across three locations

The results for the genotype IPCA scores are presented in Table 10. Based on IPCA scores, the first linear interaction term (IPCA1 scores) were both negative and positive and ranged from -18.2 to 17.4 with WC68A registering the highest IPCA1 score and NE15 registering the lowest IPCA1 score. Since IPCA scores are absolute values, the lowest IPCA1 score was 0.8. Seventeen of the genotypes recorded negative IPCA1 scores, while 19 had positive IPCA1 scores. The genotypes with the negative IPCA1 scores were the higher yielders and included among others, WC64 (-13.8), NAROCOWPEA3 (-12.3), NAROCOWPEA4 (-11.6), NAROCOWPEA1 (-10.2), Ayiyi (-9.6), WC36 (-8.8) and ALEGIxACC2 (-3.4). The genotypes with positive IPCA1 scores were lower yielders and had the highest variation in yield and included 2392 (17.4), NE55 (14), Asontem (10.3), NE37 (9.7), CP1 (9.5) and F2588T2E (8.8). The most interactive and therefore unstable cowpea genotypes were WC68A (IPCA1 score = -18.2) followed by 2392 (IPCA1 = 17) and NE55 (IPCA1 score = 14). The least interactive and therefore, most stable genotype was NE15 (IPCA1 score = 0.8) followed by MU9 (IPCA1 score = 1.3) and SECOW 1T (2.0).

The ranking of genotypes based on cultivar superiority coefficients revealed that the genotypes with the lowest cultivar stability values were Ayiyi, WC64, ALEGIxACC2, ACC12 x SECOW 3B, NAROCOWPEA1, ACC12XSECOW3B, NAROCOWPEA3, WC36 and were the most stable genotypes. The genotypes NE15, F2588T2E, CP1, SECOW 1T, NE55 and 2392 had the highest cultivar stability values and were the most unstable as well as low yielding. Based on the cultivar superiority coefficients, the genotype Ayiyi was ranked first in both stability and yield performance and this was followed by WC64, ALEGIxACC2, ACC12 x SECOW 3B, NAROCOWPEA1, ACC12XSECOW3B, NAROCOWPEA3 and WC36, while the genotype NE15 ranked least in both cultivar superiority and mean yield followed by F2588T2E, CP1, SECOW 1T, NE55 and 2392.

The genotypes Ayiyi, WC64 and ALEGIxACC2 also ranked above the checks in both cultivar superiority coefficient and yield performance.

On the basis of mean yield of the genotypes across the three locations and three seasons, it was observed that the mean yield ranged from 1,206 to 2,069 kg/ha with an overall grand mean of 1,682 kg/ha. Fourteen of the thirty-six genotypes performed above the mean and among others included Ayiyi, WC64, ALEGIxACC2, ACC12 x SECOW 3B, NAROCOWPEA1, ACC12XSECOW3B, NAROCOWPEA3 and WC36. Twelve of the genotypes performed below average and among others including NE15, F2588T2E, CP1, SECOW 1T, NE55, and 2392. The AMMI analysis revealed that, the genotype Ayiyi had the highest mean yield (2,067 kg/ha) followed by WC64 (1,978 kg/ha) and ALEGIxACC2 (1,921 kg/ha), and the same genotypes had the lowest stability values. The genotypes G8 (Ayiyi), G36 (WC64) and G6 (ALEGIXACC2) all ranked above the checks in both mean yield and stability. The general trend in IPCA scores, cultivar stability coefficients and mean yield of cowpea genotypes was that, where the genotype IPCA scores were negative, their cultivar superiority coefficients were very low but such genotypes registered the highest mean yields.

GGE biplot analysis

Best genotypes and cross over interactions

The ‘which-won-where’ pattern of the GGE biplot was constructed by joining the vertices of the genotypes that were furthest from the biplot origin and the results are presented in Figure 1. The genotypes G8, G36, G6, G1, G11, G19 and G35 were positioned on the vertices of the polygon and showed to have the longest vectors and being the most responsive genotypes. The line joining the vertices is a measure of the Euclidian distance between the genotypes when SVP = 1. The joining of these lines resulted into the formation of a polygon within which all the other 29 genotypes fell. The equality line was then drawn between the lines joining two genotypes from the origin of the biplot. This is a line on which the performance of two genotypes was the same in all environments. The equality line between the genotypes G36 (WC64) and G35 (WC68A) indicated that, genotype G36 was better in the environments MA and AA, and thus the ranking of the genotypes in this mega environment was as follows: G36 > G17 > G35; whereas genotype G8 was better in the environments MAA, MB, SA and AAA. The overall order of ranking of the best genotypes in all environments was as follows: G8 (Ayiyi) > G36 (WC64) > G6 (ALEGI*ACC2) > G16 (NAROCOWPEA1) > G3 (ACC12*SECOW3B) > G17 (NAROCOWPEA3). The genotypes G25, G9 and G11 were located on the line that connected G1 and G19. The ranking of the poorest genotypes in all environments was G1 > G25 > G26 > G9

Table 10. AMMI IPCA scores and genotype superiority for genotype mean yield (kg/ha).

Genotype	Superiority	Means	Rank	IPCAg1	IPCAg2
Ayiyi	61200	2069	1	-9.6	-17.9
WC64	85047	1980	2	-13.8	-8.4
ALEGI x ACC2	93253	1921	3	-3.4	-18.8
NAROCOWPEA1	110630	1891	4	-10.2	-0.4
ACC12 x SECOW 3B	121371	1863	5	3.1	-11.3
NAROCOWPEA3	141432	1871	6	-12.3	6.4
WC 36	164377	1767	7	-8.8	-5.9
SECOW 4W * SECOW 5T	181173	1773	8	4.5	1.1
NE 23	200636	1786	9	3.2	3.5
MU 9	202195	1741	10	1.3	-4.5
NAROCOWPEA4	203379	1735	11	-11.6	0.8
WC 16	225353	1703	12	8.2	-9.6
NE 37	248806	1731	13	9.7	3.1
Secow 4W	251711	1684	14	-12.3	9.5
MU 9A	252133	1675	15	2.9	7.1
IT 889	262172	1602	16	-4.9	3.1
WC 63	286872	1577	17	-4.7	-2.2
Ebalet * NE 51	308686	1574	18	-8.1	2.7
Alegi * SECOW 5T	309535	1518	19	-2.4	-5.8
Sunshine 2S	313475	1562	20	6.8	-7.0
ACC12 x SECOW 5T	324920	1564	21	12.7	-4.8
ACC 2 * SECOW 2W	327535	1521	22	-2.2	3.8
IT 2841 * BROWN	356400	1492	23	3.5	-1.1
WC 37	369051	1524	24	-6.5	-3.9
NE 48	373567	1470	25	-3.2	-4.6
NE 39 * SECOW 4W	393394	1484	26	7.2	3.6
Asontem	417392	1441	27	10.3	-4.8
WC 68A	422950	1496	28	-18.2	12.9
Secow 5T	431447	1448	29	3.6	11.9
NE 20	433986	1429	30	4.1	8.5
2392	453825	1498	31	17.4	-0.8
NE 55	491225	1409	32	14.0	1.0
Secow 1T	500809	1430	33	2.0	11.6
CP 1	534352	1327	34	9.5	-0.5
F2588T2E	560577	1342	35	8.8	13.0
NE 15	648444	1206	36	-0.8	8.7

> G11 > G19.

The equality line divided the polygon into four sectors. The first sector consisted of the environments MAA, AAA, MB and SA, while the second sector consisted of environments AA and MA, the third environment with SB and the fourth environment with SAA were categorized as minor environments. The genotype, G8 performed best in the first sector (MAA, AAA, MB and SA), while G16 was the best genotype in the environment sector formed by AA and MA, but genotype G31 was only best in the environment SB. The change in the ranking of the genotypes in each environment or group of environments depicted the presence of cross over interaction, suggesting that the genotype G16 was specifically adapted to environments AA and MA, while genotype G31 was specifically adapted to environment SB. The genotype G16 could be thought of as being specifically adapted to season A, since MA and AA are 'season A' environments while the genotype G8 was widely adapted since it performed best in both seasons A and B. G19 was the poorest genotype in all environments followed by G1, G9 and G25 since they positioned on the vertices of the biplot on the negative side of the origin.

Mean yield performance and stability of genotypes

The average-environment coordination view (AECV)

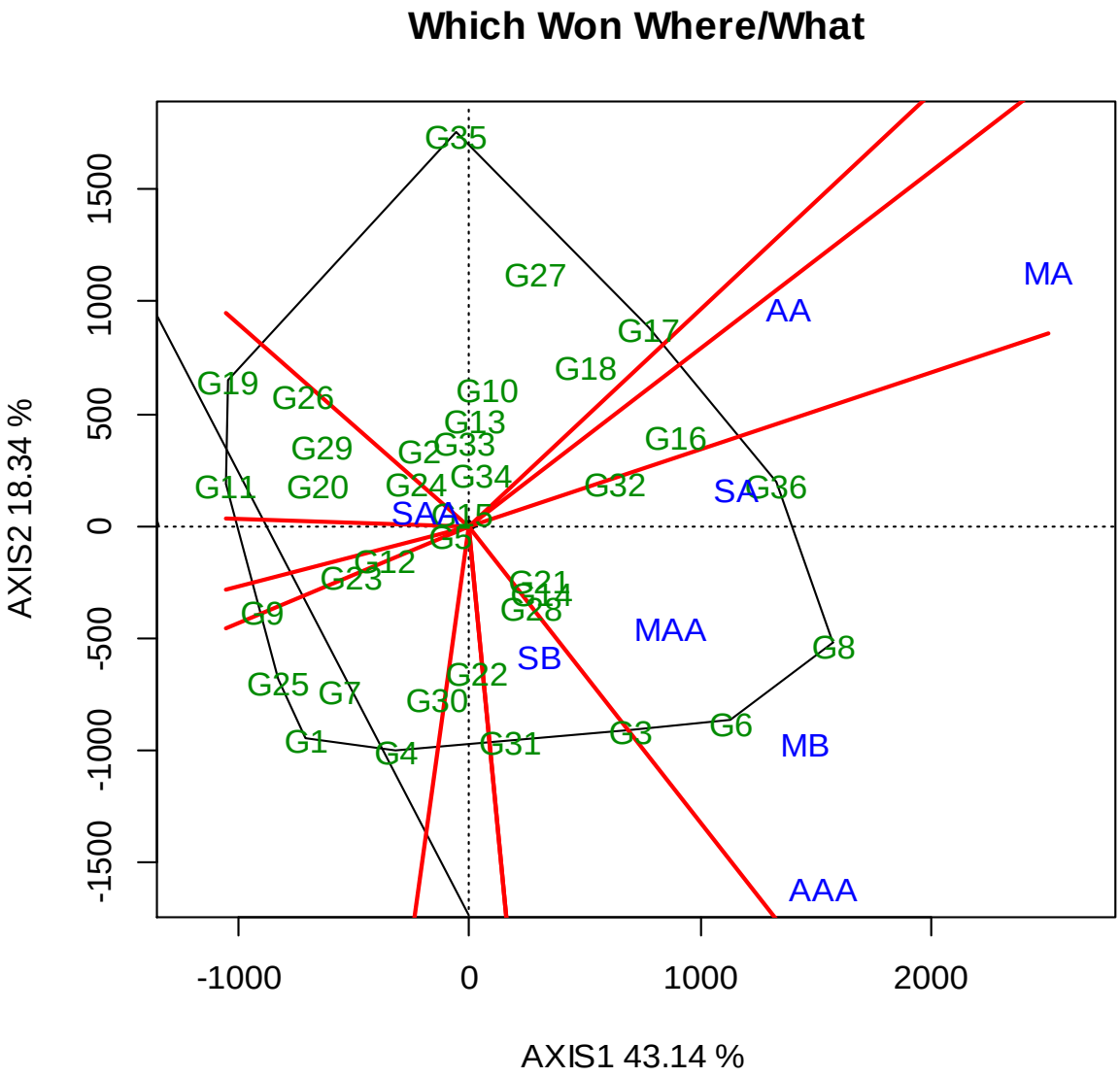

Figure 1. The "which-won-where" polygon view of the GGE biplot. PC1=43.14%, PC2=18.34% Total=61.5%, Scaling=0, Tester-centered G+GE, SVP=GH column-metric preserving. AA=Arua season 2017A, MA= MUARIK season 2017A, SA= Serere season 2017A, MB = MUARIK season 2017B, SB= Serere season 2017B, MAA= MUARIK season 2018A, SAA= Serere season 2018A, AAA= Arua season 2018A.

showing mean performance and stability of 36 genotypes across eight environments is presented in Figure 2. The AECV biplot was used to rank genotypes by their mean performance and stability. In this biplot, the x-axis is the performance line and it passes through the origin of the biplot with an arrow indicating the positive end of the axis and ranked genotypes according to their mean performance. The y-axis also passes through the origin of the biplot and is perpendicular to the x-axis and measured the stability of the genotypes. The projection of genotypes onto the AEC abscissa (x-axis) represented the main effect of the genotypes. The AEC_a ranked the genotypes according to their mean performance. The ranking of genotypes onto the AEC_a was highly correlated to the genotype main effect. Therefore, the AEC_a approximated the contribution of each genotype to the main effect of the genotypes and the AEC ordinate (Y-axis) expressed the genotype's contribution to the GxE and thus, it represented genotypic stability.

Based on the magnitude of variation (GxE) across environments, the genotypes with longer markers had higher variation than those with shorter markers. Therefore, the genotype G35 had the longest projection to the AEC_a and the greatest contribution to the GxE. Based on the magnitude of the projections to the AEC_a, the genotypes ranked as; G35, G5, G4, G17 and G27 in order of their contribution to the interaction of yield with environments.

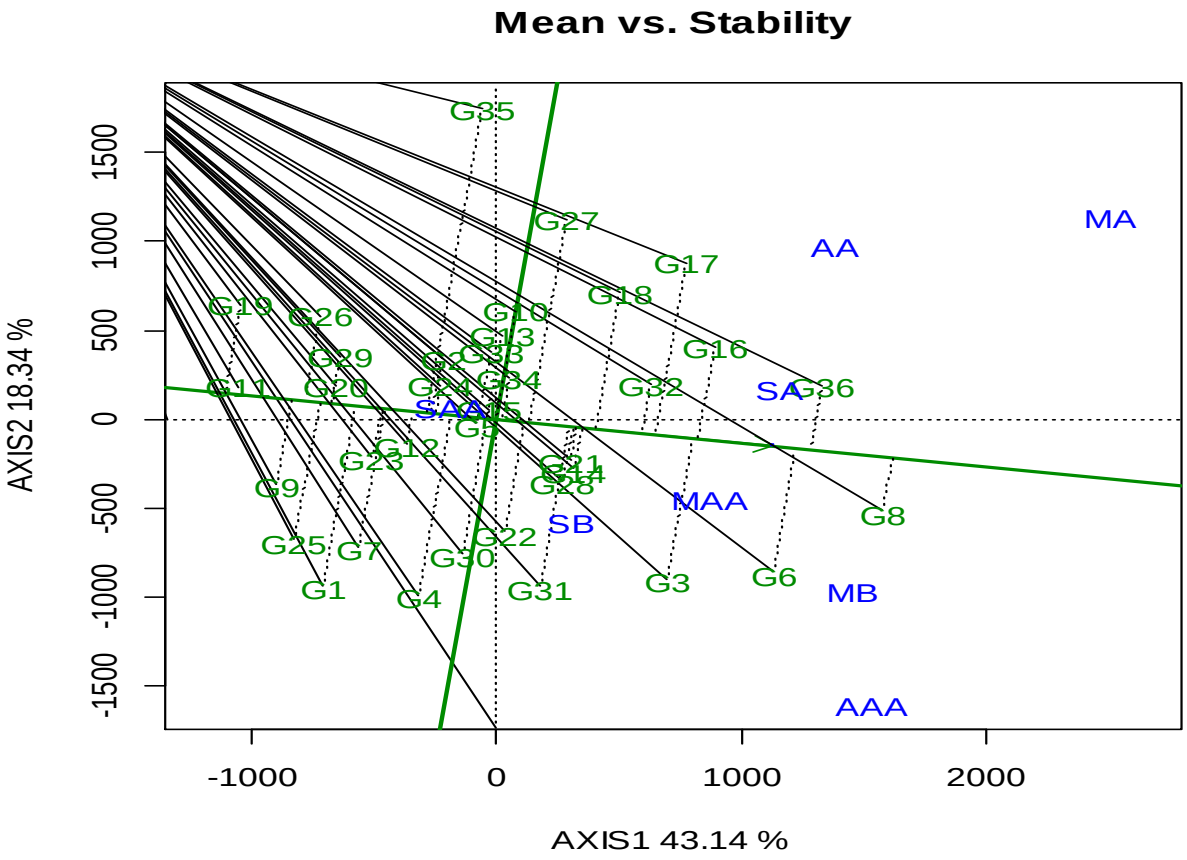

Figure 2. The average-environment-coordination view showing mean performance and stability of 36 genotypes across eight environments. AA=Arua season 2017A, MA= MUARIK season 2017A, SA= Serere season 2017A, MB = MUARIK season 2017B, SB= Serere season 2017B, MAA= MUARIK season 2018A, SAA= Serere season 2018A, AAA= Arua season 2018A.

The genotype G8 (Ayiyi) had a short projection to the AEC_a and thus contributed less to the GxE. However, the genotype G8 (Ayiyi) was the furthest from the origin of the biplot in the positive direction of the AEC_a and hence had the greatest contribution to the genotype main effect. On the other hand, the genotype G19 was the furthest from the origin of the biplot in the negative direction of the AEC_a, implying that it contributed least to the genotype main effect.

The most stable and high yielding genotype was one furthest to the positive side of the performance line and with the shortest marker. Based on both mean performance and stability, the genotype G8 (Ayiyi) was the most stable and high yielding. This was followed by the genotypes G36 (WC64), G6 (ALEGIxACC2), G16 (NAROCOWPEA1), G3 (ACC12xSECOW3B), G17 (NAROCOWPEA3), G32 (WC36), G14 (MU9) and G18 (NAROCOWPEA4). The genotypes G8 (Ayiyi), G36 (WC64), and G6 (ALEGIXACC2) were all ranked above the checks in both mean yield and stability. Genotypes G34, G15, G24, and G33 were considered as average yielders because the genotypes at the origin of the biplothave average stability and performance. Genotypes close to the performance line were considered more stable than those furthest from it. The genotype G11 (F2588T2E) was on the AEC ordinate and very stable across localities but furthest from the ideal genotype or situated on the negative side of the AEC ordinate implying least mean performance. Such a genotype may therefore not be more desirable compared to, for example, genotype G5 (ALEGIxSECOW5T) which was off the AEC ordinate but close to the ideal genotype.

Ranking of genotypes relative to an ideal genotype

Figure 3 shows the GGE biplot that was used to rank genotypes by their mean performance and stability relative to an ideal genotype in a number of environments. In this biplot, the x-axis is referred to as the average tester coordinate (ATC) x-axis or the performance axis and the y- axis is the stability axis (ATC) y-axis. An ideal genotype is one that has both high yield capacity and high stability. Based on these principles,

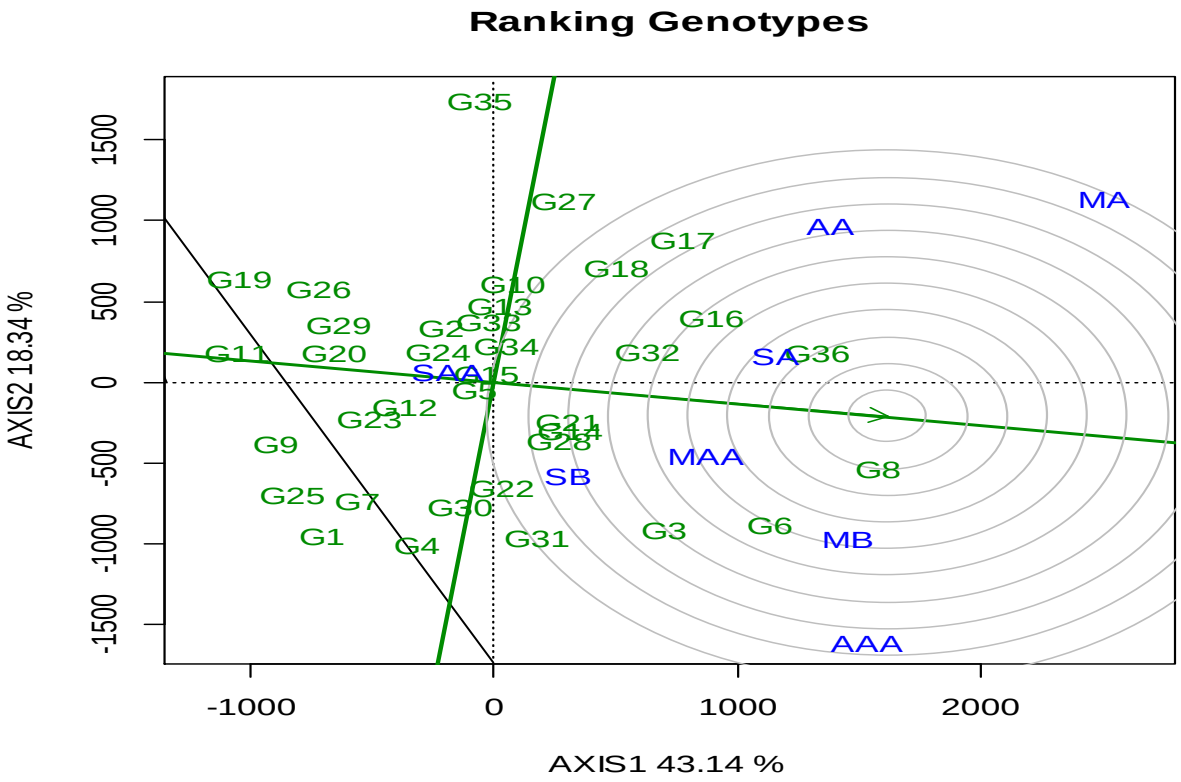

Figure 3. The comparison biplot (AEC) for ranking genotypes relative to an ideal genotype. AA=Arua season 2017A, MA= MUARIK season 2017A, SA= Serere season 2017A, MB = MUARIK season 2017B, SB= Serere season 2017B, MAA= MUARIK season 2018A, SAA= Serere season 2018A, AAA=Arua season 2018A.

there was no ideal genotype but the genotype G8 (Ayiyi) approximated the ideal genotype since it fell closest to the smallest inner circle, and the desirable genotypes were G36 (WC 36), G6 (ALEGXACC2), G16 (NARO COWPEA1), G3 (ACC12xSECOW3B), G17 (NAROCOWPEA 3), G32 (WC16), G18 (NAROCOWPEA4) and G14 (MU9).

DISCUSSION

In this study, the significant differences observed among the genotypes were expected since these were diverse collections from all parts of Uganda, International Institute for Tropical Agriculture (IITA) Nigeria, National Agricultural Research Organization (NARO) and Ghana with diverse genetic backgrounds. Rubaihayo and Rusoke (1994) collected germplasm from all over Uganda, breeding lines from international programs, for instance the CGIAR centers and found highly significant differences among the lines. The presence of GxE in cowpea has also been reported by Asio et al. (2005) and Santos et al. (2015). From the present study, season effect contributed 52.3% of the total variation observed in cowpea yield, followed by localities that contributed 25.1%. Agbahoungba et al. (2016), in a trial involving 72 genotypes of cowpea tested in the same locations in the 2015/2016 seasons obtained similar results of the effect of GxE on cowpea grain yield. In this study, the season effect on grain yield was therefore, more profound than the location effect and this is contrary to the finding of Dehghani et al. (2008) and Agbahoungba et al. (2016) who observed a more profound effect of location than seasons. The AMMI analysis result showed that a large environmental sum of squares explained the diversity in the environmental conditions to which the genotypes were subjected as well as the inconsistent performance of the genotypes across those environments. This also explained the rank changes in the performance of the genotypes. The environmental effect was generally larger than the genotype main effect and the GxE effect but the most important sources of variations were those due to genotype and GxE. The trends observed in this study were very similar to the findings of other workers (Rad et al., 2013; Orawu et al., 2017), who observed higher contribution of environmental effect and lower contribution of genotype effect to the total variation in yield.

A further understanding of the genotypes was enhanced with the construction of the polygon view of the

GGE biplot and was a useful tool for identifying the presence of cross over interaction, comparison of pairs of genotypes, identification of specifically adapted genotypes and elucidation of the best or poorest genotypes in each environment or groups of environments. In this biplot, genotypes G8, G36, G6, G1, G11, G19 and G35 were positioned on the vertices of the polygon and showed to have the longest vectors and being the most responsive genotypes. Some of the genotypes in this study responded well when grown in the first season and others in the second season of each year, with the overall performance of the genotypes being better in the second season. According to Orawu et al. (2017), mega-environment differentiation may be due to variations in weather pattern or soil types resulting in differences in the performances of crops. Yan and Tinker (2005) noted that test environments were dynamic factors that fluctuate considerably between years or seasons. The genotype cross-over interaction was also detected in this study because the ranking of the genotypes changed.

In this study, the AMMI analysis revealed that G8 (Ayiyi) had the highest mean yield (2,067 kg/ha) followed by G36 (WC64) (1,978 kg/ha) and G6 (ALEGIxACC2) (1,921 kg/ha) and the lowest stability values. These genotypes were considered to exhibit static stability or type I stability. Static stability is only useful to the breeder if it is associated with high yield. Accordingly, genotypes with the lowest stability values are the most stable.

In order to identify the most stable and high yielding genotype (widely adapted genotype), the average environment coordination view of the GGE biplot was used. The AEC was constructed using the mean performance of genotypes and their stability values. The AEC was genotype-metric preserving and consisted of both the stability and performance axes. In the biplot constructed, it showed that the genotype G11 (F2588T2E) was on the AEC ordinate and very stable across locations but furthest from the ideal genotype (from the center of the concentric circle or on the negative side of the AEC ordinate) implying least mean performance. Such a genotype might not be desirable compared to the genotype G5 (ALEGIxSECOW5T) which was off the AEC ordinate but closer to the ideal genotype. It was acknowledged that the genotype G11 (F2588T2E) was only consistent in its poor performance. Yan and Tinker (2006) used the average coordination view to evaluate Ontario winter wheat in Canada and were able to identify the most consistent genotypes, the discriminatory and representative environments.

Conclusion

Overall, the analyses in this study found grain yield in cowpea to be greatly influenced by the main effects of genotypes, environment and the interaction between the genotype and the environment. The GGE biplot and the AMMI stability values were congruent in ranking the genotypes based on their mean yield and stability and complimented each other in determining the mean performance and stability of genotypes. The general trend in IPCA scores, cultivar stability coefficients and mean yield of cowpea genotypes was that, where the genotype IPCA scores were negative, their cultivar superiority coefficients were very low, but such genotypes registered the highest mean yields. The change in the ranking of the genotypes in each environment or group of environments depicted the presence of cross over interaction, suggesting specific adaptation of some genotypes to some environments.

The AMMI analysis also revealed that the genotype Ayiyi had the highest mean yield (2,067 kg/ha), contributed less to the GxE but had the greatest contribution to the genotype main effect. This was followed by WC64 (1,978 kg/ha) and ALEGIxACC2 (1,921 kg/ha) and the best stability values and ranked above the checks in both mean grain yield performance and stability and were superior to all local varieties.

The genotypes Ayiyi, WC64, ALEGIxACC2 ranked above the checks and other local varieties in both mean grain yield and stability. Therefore, they could be advanced to the national performance trials. The GGE and the AMMI biplots should be used concurrently to help understand the mean performance and stability of genotypes since the two complement each other. None of the three locations showed mega environment associations. Genotype interactions showed some differing responses to the two rainy seasons but additional years of data will be needed to determine if different genotypes should be recommended for the two different seasons.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Selection of drought tolerant genotypes in groundnut (*Arachis hypogaea* L.) using indices

Ousmane Sanogo[1,2*], Pangirayi B. Tongoona[1], Kwadwo Ofori[1] and Haile Desmae[2]

[1]West Africa Centre for Crop Improvement, University of Ghana, P. M. B. 30, Legon, Accra, Ghana.
[2]International Crop Research Institute for the Semi-Arid Tropics, BP 320 Bamako, Mali.

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A study was carried out to evaluate the effect of drought stress on pod yield and other traits of groundnut genotypes to select the ten best performing genotypes using indices. Ninety six genotypes including 90 $F_{2:3}$ progenies, 4 parents and 2 checks were planted under well-watered (WW) and water-stressed (WS) conditions at the International Crops Research Institute for the Semi-Arid Tropics ICRISAT, Mali. Six selection indices including mean productivity (MP), tolerance (TOL), geometric mean productivity (GMP), stress tolerance index (STI), drought tolerance index (DTI) and reduction (%) (RED) were used. The indices were adjusted based on pod yield under WW and WS conditions. High DTI, STI, MP, and GMP values under both well-watered and water-stressed conditions were more effective in identifying high yielding cultivars under water limited conditions. Based on these indices, the $F_{2:3}$ progenies ICGV-IS 13012F2-B1-297, ICGV-IS 13012F2-B1-40, ICGV-IS 13005F2-B1-46, ICGV-IS 13005F2-B1-252, ICGV-IS 13012F2-B1-29, ICGV-IS 13005F2-B1-205, ICGV-IS 13005F2-B1-287, ICGV-IS 13012F2-B1-525, ICGV-IS 13012F2-B1-576 and ICGV-IS 13005F2-B1-91 were identified as the most drought tolerant genotypes with high yield stability in the well-watered and drought stress conditions. The indices STI, MP and GMP were positively correlated with pod yield under WW and WS conditions and breeding for drought tolerance.

Key words: Groundnut, breeding, selection indices, drought stress.

INTRODUCTION

In the Sahel region, yield in groundnut is low and about 1000 kg /ha (FAOSTAT, 2015). The historical trend in groundnut production revealed that grain yield is highly affected by drought events (Debrah and Waliyar, 1998). These authors argued that drought occurs in Mali once every three years, while groundnut is the first legume crop grown in Mali with 71% of the overall legume production. However, the rain-fed groundnut production and quality are seriously challenged by drought stress. This calls for more research on groundnut concerning the climate change and its unpredictable and irregular rainfall patterns in the Sahelian region. The groundnut crop exhibits low heritability for yield and drought tolerance. Lack of effective field selection approaches limit development of resistant groundnut genotypes to environmental stress. Many selection indices are used to identify high yield genotypes under stress conditions in durum wheat (Talebi et al., 2009; Karimizadeh et al.,

*Corresponding author. E-mail: ouzbi777@gmail.com.

2011), maize (Jafari et al., 2009), mungbean (Fernandez, 1992) wheat (Sio-Se et al., 2006; Anwar et al., 2011), rice (Raman et al., 2012); and groundnut (Nautiyal et al., 2002) crops. These authors use a mathematical relation between stress- and optimum conditions to identify drought tolerant and susceptible genotypes. In the selection of Mungbean (*Vigna radiata* (L.)Wilczek) lines, Fernandez (1992) classified genotypes according to their performance in moisture stress and non-stress environments to four groups: genotypes with similar good performance in both environments (Group A); genotypes with good performance only in non-stress environments (Group B) or stressful environments (Group C); and genotypes with weak performance in both environments (Group D). According to Talebi et al. (2009) selection based on a combination of indices may provide a more useful criterion for improving drought resistance of crop but study of correlation coefficients is useful in finding the degree of overall linear association between any two attributes. A better approach than a correlation analysis such as Principal Component Analysis (PCA) is needed to identify the superior genotypes for both stress and non-stress environments (Porch, 2006; Talebi et al., 2009; Jafari et al., 2009; Allahdou, 2012). Information on selection of groundnut genotypes under different drought stress conditions could be relevant in Mali. This could be used to understand the genetic variation of the crop and to identify the drought tolerant cultivars. The present study aimed to assess the selection criteria for identifying drought tolerance in groundnut genotypes and to select the top 10 high yielding genotypes tolerant to drought stress using indices.

MATERIALS AND METHODS

Ninety six groundnut genotypes were evaluated under drought stress and full irrigation conditions (Table 1). These genotypes were part of an on-going breeding program focused on selection of drought tolerant lines. Forty five 45 $F_{2:3}$ progenies from each two of the populations (ICGX-IS 13005 and ICGV-IS 13012) were evaluated along with their 4 parental lines (ICIAR 19BT, ICGV 91317, ICGV 87378 and ICGS 44) and two local checks (Fleur11 and 47-10).

Experimental conditions

The groundnut populations were established at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Samanko (12°54'N and 8°4'W, 330 m above the sea) in Mali rain-free period in November 2014 to March 2015. The Samanko soil was a Ferric Lixisol clay loam with a pH of 4.5 and deficient in organic matter and total nitrogen with low fertility. Ninety-six genotypes were evaluated in Split plot where subplots (genotypes) were arranged in 9 × 11 alpha (0.1) lattices with two replications in dry season. An experimental plot consisted of a 4 m long single row, with spacing 0.2 m × 0.60 m. The irrigation water management was applied as followed: the water-stressed (WS) block, full irrigation was provided till 50 days after sowing (DAS). At 50 DAS, drought stress was imposed for 14 days and irrigation was resumed at the 15th day to bring the soil up to saturation. Then, drought stress was imposed for 10 days, followed by irrigation up to saturation. After that, drought stress was imposed for 7 days followed by irrigation up to harvest. This technique was supposed to mimic the end-of-season drought since water was withheld during the critical stage of the reproductive phase. The well-watered (WW) block received full irrigation throughout the life cycle of the crop (from sowing to harvesting period). Plants were irrigated one to two times per week with 20 mm of water until end-of-season (pod filling to pod maturity) at seven day interval depending on the prevailing weather conditions. Except for the different irrigation treatments; all field management practices were uniform for both the well-watered and water-stressed experiments. Basal fertilizer of 100 kg ha^{-1} Simple Super phosphate was applied before hand-planting with one seed per hill. Standard cultural practices, including hand planting, hand weeding while the first as early as 16-20 days after sowing (DAS) were followed. The average ambient temperature during the trial period (November-March) was 26.07°C, with a standard deviation STDEV= 9.55%. The average relative humidity within the same period was 27.17%, with a standard deviation STDEV of 16.56%.

Data collection

Data recorded on plot basis were number of days to 50% plants flowering [PF], pod yield [PY] (kg.ha^{-1}) was determined from pod harvested from 15 plants in the middle of the plot after air drying to constant weight for two weeks, 100 – Sound seed weight [HSW] (g): the weight of 100 – kernels for each plant was recorded and shelling percentage [SP] (%) was recorded as the weight of seeds in 50pods/weight of 50 pods) × 100.

Statistical analysis

The analysis of variance (ANOVA) was performed using PROC GLM in SAS (SAS Institute, 2009). PROC CORR in SAS was used for correlation analysis of the selection indices. The PCA biplot was performed using XLSTAT software under Microsoft Windows. In order to apply indices, drought resistance was calculated using the following mathematical relationships:

(i) Mean productivity (MP) = (Ys+Yp)/2 (Hossain et al., 1990)
(ii) Tolerance (TOL) = (Yp-Ys) (Hossain et al., 1990)
(iii) Geometric mean productivity (GMP) = $\sqrt{(Ys \times Yp)}$ (Fernadez,1992)
(iv) Stress tolerance index (STI) = $(Yp)(Ys)/(\bar{Y}p)^2$ (Fernadez, 1992)
(v) Drought tolerance index (DTI) = Ys/Yp (Nautiyal et al., 2002)
(vi) Reduction (%) (RED) = (Yp-Ys)/Yp (Choukan et al., 2006)

Where Yp is the yield of cultivar under optimum (well-watered) environment, Ys is the yield of cultivar stress (water stress) environment, $\bar{Y}p$ is the mean yields of all cultivars under optimum condition.

RESULTS AND DISCUSSION

Mean squares from the ANOVA across well-watered and water stressed conditions for various traits

Results from the analysis of variance (ANOVA) for pod yield and other traits across environments revealed highly significant ($P<0.001$ and $P<0.05$) difference for PY among genotypes under well-watered condition while, the mean squares for genotypes were significant ($P<0.05$) for HSW (Table 2). Under water-stressed environment,

Table 1. List of 90 $F_{2:3}$ genotypes plus their 4 parents and 2 two checks.

S/N	Genotypes	Pedigree	S/N	Genotypes	Pedigree
1	ICGX-IS 13005F2-B1-106	ICGV 91317 /ICGV87378	46	ICGX-IS 13012F2-B1-105	ICIAR 19 BT / ICGS 44
2	ICGX-IS 13005F2-B1-11	ICGV 91317 /ICGV87378	47	ICGX-IS 13012F2-B1-114	ICIAR 19 BT / ICGS 44
3	ICGX-IS 1300F2-B1-12	ICGV 91317 /ICGV87378	48	ICGX-IS 13012F2-B1-115	ICIAR 19 BT / ICGS 44
4	ICGX-IS 13005F2-B1-132	ICGV 91317 /ICGV87378	49	ICGX-IS 13012F2-B1-130	ICIAR 19 BT / ICGS 44
5	ICGX-IS 13005F2-B1-14	ICGV 91317 /ICGV87378	50	ICGX-IS 13012F2-B1-140	ICIAR 19 BT / ICGS 44
6	ICGX-IS 13005F2-B1-167	ICGV 91317 /ICGV87378	51	ICGX-IS 13012F2-B1-15	ICIAR 19 BT / ICGS 44
7	ICGX-IS 13005F2-B1-171	ICGV 91317 /ICGV87378	52	ICGX-IS 13012F2-B1-156	ICIAR 19 BT / ICGS 44
8	ICGX-IS 13005F2-B1-182	ICGV 91317 /ICGV87378	53	ICGX-IS 13012F2-B1-20	ICIAR 19 BT / ICGS 44
9	ICGX-IS 13005F2-B1-185	ICGV 91317 /ICGV87378	54	ICGX-IS 13012F2-B1-207	ICIAR 19 BT / ICGS 44
10	ICGX-IS 1300F2-B1-187	ICGV 91317 /ICGV87378	55	ICGX-IS 13012F2-B1-24	ICIAR 19 BT / ICGS 44
11	ICGX-IS 13005F2-B1-189	ICGV 91317 /ICGV87378	56	ICGX-IS 13012F2-B1-268	ICIAR 19 BT / ICGS 44
12	ICGX-IS 13005F2-B1-19	ICGV 91317 /ICGV87378	57	ICGX-IS 13012F2-B1-276	ICIAR 19 BT / ICGS 44
13	ICGX-IS 13005F2-B1-198	ICGV 91317 /ICGV87378	58	ICGX-IS 13012F2-B1-281	ICIAR 19 BT / ICGS 44
14	ICGX-IS 13005F2-B1-205	ICGV 91317 /ICGV87378	59	ICGX-IS 13012F2-B1-29	ICIAR 19 BT / ICGS 44
15	ICGX-IS 13005F2-B1-222	ICGV 91317 /ICGV87378	60	ICGX-IS 13012F2-B1-297	ICIAR 19 BT / ICGS 44
16	ICGX-IS 13005F2-B1-252	ICGV 91317 /ICGV87378	61	ICGX-IS 13012F2-B1-312	ICIAR 19 BT / ICGS 44
17	ICGX-IS 13005F2-B1-262	ICGV 91317 /ICGV87378	62	ICGX-IS 13012F2-B1-319	ICIAR 19 BT / ICGS 44
18	ICGX-IS 13005F2-B1-287	ICGV 91317 /ICGV87378	63	ICGX-IS 13012F2-B1-381	ICIAR 19 BT / ICGS 44
19	ICGX-IS 13005F2-B1-301	ICGV 91317 /ICGV87378	64	ICGX-IS 13012F2-B1-40	ICIAR 19 BT / ICGS 44
20	ICGX-IS 13005F2-B1-359	ICGV 91317 /ICGV87378	65	ICGX-IS 13012F2-B1-431	ICIAR 19 BT / ICGS 44
21	ICGX-IS 13005F2-B1-37	ICGV 91317 /ICGV87378	66	ICGX-IS 13012F2-B1-475	ICIAR 19 BT / ICGS 44
22	ICGX-IS 13005F2-B1-381	ICGV 91317 /ICGV87378	67	ICGX-IS 13012F2-B1-491	ICIAR 19 BT / ICGS 44
23	ICGX-IS 13005F2-B1-388	ICGV 91317 /ICGV87378	68	ICGX-IS 13012F2-B1-50	ICIAR 19 BT / ICGS 44
24	ICGX-IS 13005F2-B1-40	ICGV 91317 /ICGV87378	69	ICGX-IS 13012F2-B1-518	ICIAR 19 BT / ICGS 44
25	ICGX-IS 13005F2-B1-404	ICGV 91317 /ICGV87378	70	ICGX-IS 13012F2-B1-520	ICIAR 19 BT / ICGS 44
26	ICGX-IS 13005F2-B1-411	ICGV 91317 /ICGV87378	71	ICGX-IS 13012F2-B1-525	ICIAR 19 BT / ICGS 44
27	ICGX-IS 13005F2-B1-425	ICGV 91317 /ICGV87378	72	ICGX-IS 13012F2-B1-528	ICIAR 19 BT / ICGS 44
28	ICGX-IS 13005F2-B1-450	ICGV 91317 /ICGV87378	73	ICGX-IS 13012F2-B1-534	ICIAR 19 BT / ICGS 44
29	ICGX-IS 13005F2-B1-46	ICGV 91317 /ICGV87378	74	ICGX-IS 13012F2-B1-537	ICIAR 19 BT / ICGS 44
30	ICGX-IS 13005F2-B1-470	ICGV 91317 /ICGV87378	75	ICGX-IS 13012F2-B1-554	ICIAR 19 BT / ICGS 44
31	ICGX-IS 13005F2-B1-481	ICGV 91317 /ICGV87378	76	ICGX-IS 13012F2-B1-561	ICIAR 19 BT / ICGS 44
32	ICGX-IS 13005F2-B1-488	ICGV 91317 /ICGV87378	77	ICGX-IS 13012F2-B1-562	ICIAR 19 BT / ICGS 44
33	ICGX-IS 13005F2-B1-49	ICGV 91317 /ICGV87378	78	ICGX-IS 13012F2-B1-563	ICIAR 19 BT / ICGS 44
34	ICGX-IS 13005F2-B1-494	ICGV 91317 /ICGV87378	79	ICGX-IS 13012F2-B1-566	ICIAR 19 BT / ICGS 44
35	ICGX-IS 13005F2-B1-498	ICGV 91317 /ICGV87378	80	ICGX-IS 13012F2-B1-571	ICIAR 19 BT / ICGS 44
36	ICGX-IS 13005F2-B1-5	ICGV 91317 /ICGV87378	81	ICGX-IS 13012F2-B1-576	ICIAR 19 BT / ICGS 44
37	ICGX-IS 13005F2-B1-50	ICGV 91317 /ICGV87378	82	ICGX-IS 13012F2-B1-586	ICIAR 19 BT / ICGS 44
38	ICGX-IS 13005F2-B1-559	ICGV 91317 /ICGV87378	83	ICGX-IS 13012F2-B1-600	ICIAR 19 BT / ICGS 44
39	ICGX-IS 13005F2-B1-586	ICGV 91317 /ICGV87378	84	ICGX-IS 13012F2-B1-62	ICIAR 19 BT / ICGS 44
40	ICGX-IS 13005F2-B1-591	ICGV 91317 /ICGV87378	85	ICGX-IS 13012F2-B1-69	ICIAR 19 BT / ICGS 44
41	ICGX-IS 13005F2-B1-65	ICGV 91317 /ICGV87378	86	ICGX-IS 13012F2-B1-75	ICIAR 19 BT / ICGS 44
42	ICGX-IS 13005F2-B1-85	ICGV 91317 /ICGV87378	87	ICGX-IS 13012F2-B1-78	ICIAR 19 BT / ICGS 44
43	ICGX-IS 13005F2-B1-90	ICGV 91317 /ICGV87378	88	ICGX-IS 13012F2-B1-84	ICIAR 19 BT / ICGS 44
44	ICGX-IS 13005F2-B1-91	ICGV 91317 /ICGV87378	89	ICGX-IS 13012F2-B1-93	ICIAR 19 BT / ICGS 44
45	ICGX-IS 13005F2-B1-93	ICGV 91317 /ICGV87378	90	ICGX-IS 13012F2-B1-98	ICIAR 19 BT / ICGS 44
91	[§]Fleur 11				
92	[§]47-10				
93	[¥]ICGS 44				
94	[¥]ICGV 87378				
95	[¥]ICGV 91317				
96	[¥]ICIAR 19BT				

[§] Local cultivars used as checks, [¥] parental lines used as introduced checks.

Table 2. Effect of irrigation treatment on studying the drought and yield traits.

Water management	50%DF	SCMR1	SCMR2	PY	SLA1	SLA2	HSW	SP
	days			Kg.ha^{-1}	cm^2 g^{-1}	cm^2 g^{-1}	g	(%)
Water-stressed	29.13	38.77	35.87	2103.87	216.26	206.84	32.22	60.86
Well-watered	28.77	42.37	41.10	1318.20	227.44	201.43	34.15	63.59
SE±	0.12	0.13	0.25	0.26	2.98	3.66	0.39	0.61
R^2	0.58	0.81	0.72	0.82	0.64	0.51	0.59	0.61
CV (%)	5.44	4.47	8.77	22.13	17.96	24.83	15.28	13.47
Mean	28.95	40.57	38.49	1711.03	221.85	204.14	33.19	62.23
Probability	***	***	***	***	***	***	***	***

***p<0.0001. PY= pod yield (kg ha^{-1}), 50%DF= Day to 50% flowering (days), SCMR1=SPAD meter reading at 60DAS, SCMR2=SPAD meter reading at 80DAS, SLA1= Specific leaf area (cm^2 g^{-1}) at 60DAS, SLA2=Specific leaf area (cm^2 g^{-1}) at 80DAS, HWS=hundred seed weight (g), SP=Shelling percentage (%)

Table 3. The Mean Squares of drought and yield traits of 90 F3 groundnut genotypes, 4 parental lines and 2 checks (Fleur 11 and 47-10) grown under well-watered and water-stressed condition in Mali 2015.

Traits	Well-watered condition						Water-stressed condition					
	Rep	Block (Rep)	Genotype	Error	Mean	CV (%)	Rep	Block (Rep)	Genotype	Error	Mean	CV (%)
¥df	1	2	95	93			1	2	95	93		
50%DF	0.002	0.13	1.73	1.32	28.77	3.99	3.04	1.14	4.33	3.72	29.13	6.62
SCMR1	1.73	3.87	7.55***	3.19	42.37	4.21	0.22	0.55	6.71***	3.44	38.77	4.78
SCMR2	26.66	15.85	12.84	9.27	41.10	7.41	19.00*	0.84	17.96	13.66	35.87	10.30
PY	6.18	0.97	39.12***	13.82	18.93	19.64	6.14	13.51	17.65***	9.60	11.87	26.10
SLA1	203.30	1677.18	2804.24***	1207.44	227.44	15.28	312.40	5518.25	2467.76	1882.06	216.26	20.06
SLA2	1394.84	186.33	2597.89	2927.72	201.43	26.86	1190.84	999.40	2639.19	2294.57	206.84	23.16
HSW	35.97	6.70	29.81*	19.67	34.15	12.99	110.75*	6.34	32.07	32.60	32.22	17.72
SP	0.77	9.78	63.66	78.42	63.59	13.93	19.94	40.92	140.23***	63.99	60.86	13.14

¥df= degree of freedom. PY= pod yield (kg ha^{-1}), 50%DF= Day to 50% flowering (days), SCMR1=SPAD chlorophyll meter reading at 60DAS, SCMR2=SPAD chlorophyll meter reading at 80DAS, SLA1= Specific leaf area (cm^2 g^{-1}) at 60DAS, SLA2=Specific leaf area (cm^2 g^{-1}) at 80DAS, HWS=hundred seed weight (g), SP=Shelling percentage (%)*p<0.05; **p<0.01; ***p<0.001 respectively.

mean squares genotypes were highly significant (P<0.001) for PY and SP traits. Combined analysis showed highly significant differences (P<0.01) for all traits (Table 3). Under water-stressed conditions, reductions in values were observed for the entire yield and yield components traits such as hundred seed weight, shelling percentage and pod yield. The overall genotype mean performance for 100-seed weight, shelling percentage and pod yield were lower under drought stress conditions than those under well-watered-conditions. Thus, significant reductions (P<0.001) in performance of traits were found for these traits both environments. Yp and Ys were the yield of cultivar under optimum environment and the yield of cultivar under stress environment, respectively.

In this study, results showed that the greater the TOL value, the larger the yield reduction under stress conditions and the higher the drought sensitivity (Table 4). Based on TOL index, the genotypes ICGX-IS 13005F2-B1-198 (1744.44 and 1644.45 kg/ha) and ICGX-IS 13005F2B1-494 (1388.89 and 1288.89 kg/ha) with low values were considered as tolerant genotypes but mostly with low values of pod yield in both environments. Thus, TOL favours genotypes with good yield under stress. These findings were in line with the work of Jafari et al. (2009) and Fernandez (1992) who reported that TOL index failed to select maize genotypes with proper yield under stress and non-stress environments. TOL index was closer to the RED since they identified tolerant genotypes but not always the top performers under well-watered condition.

The highest Stress tolerance (STI) indices were recorded for genotypes ICGX-IS 13012F2-B1-297 (2866.67 and 2155.56 kg/ha), ICGX-IS 13012F2-B1-525 (3200.00 and 1766.67 kg/ha) and ICGX-IS 13005F2-B1-46 (2900.00 and 1933.34 kg/ha) with high values (1.27 to 1.40). They were considered as tolerant genotypes with high yield stability under both conditions (Table 4). On the

Table 4. Estimates of drought stress tolerance attributes from the potential yield (Yp) and the stress yield (Ys) data for 96 groundnut genotypes evaluated in off-season at ICRISAT Samanko, Mali.

S/N	Genotype	Pod Yield (kg ha^{-1})		RED	Drought tolerance indices¥				
		Yp	Ys		MP	TOL	STI	GMP	DTI
1	ICGX-IS 13005F2-B1-106	1433.33 (89)	877.78 (88)	38.76 (60)	1155.56 (90)	555.55 (67)	0.28 (89)	1121.67 (89)	0.61 (60)
2	ICGX-IS 13005F2-B1-11	1511.12 (87)	1022.23 (76)	32.35 (37)	1266.67 (86)	488.89 (74)	0.35 (84)	1242.86 (84)	0.68 (37)
3	ICGX-IS 13005F2-B1-12	1600.00 (81)	633.33 (94)	60.42 (92)	1116.67 (92)	966.67 (24)	0.23 (94)	1006.64 (94)	0.40 (92)
4	ICGX-IS 13005F2-B1-132	2600.00 (17)	1722.23 (11)	33.76 (42)	2161.11 (10)	877.78 (36)	1.01 (10)	2116.08 (10)	0.66 (42)
5	ICGX-IS 13005F2-B1-14	2866.67 (7)	1155.56 (68)	59.69 (90)	2011.11 (20)	1711.12 (4)	0.75 (33)	1820.05 (33)	0.40 (90)
6	ICGX-IS 13005F2-B1-167	2100.00 (50)	1511.11 (31)	28.04 (28)	1805.56 (38)	588.89 (61)	0.72 (36)	1781.38 (36)	0.72 (28)
7	ICGX-IS 13005F2-B1-171	1577.78 (82)	1322.23 (47)	16.20 (8)	1450.00 (72)	255.56 (91)	0.47 (69)	1444.36 (69)	0.84 (8)
8	ICGX-IS 13005F2-B1-182	1988.89 (57)	933.34 (83)	53.07 (84)	1461.11 (70)	1055.56 (18)	0.42 (74)	1362.46 (74)	0.47 (84)
9	ICGX-IS 13005F2-B1-185	1988.89 (58)	1466.67 (36)	26.26 (24)	1727.78 (49)	522.23 (71)	0.66 (46)	1707.93 (46)	0.74 (24)
10	ICGX-IS 13005F2-B1-187	2311.12 (30)	1633.34 (14)	29.33 (32)	1972.23 (23)	677.78 (51)	0.85 (17)	1942.89 (17)	0.71 (32)
11	ICGX-IS 13005F2-B1-189	1855.56 (65)	988.89 (79)	46.71 (78)	1422.22 (73)	866.67 (38)	0.41 (75)	1354.60 (75)	0.53 (78)
12	ICGX-IS 13005F2-B1-19	2611.11 (16)	1511.11 (30)	42.13 (68)	2061.11 (16)	1100.00 (17)	0.89 (15)	1986.37 (15)	0.58 (68)
13	ICGX-IS 13005F2-B1-198	1744.44 (71)	1644.45 (13)	5.73 (1)	1694.44 (52)	100.00 (96)	0.65 (47)	1693.70 (47)	0.94 (1)
14	ICGX-IS 13005F2-B1-205	2377.78 (24)	1800.00 (6)	24.30 (17)	2088.89 (12)	577.78 (66)	0.97 (11)	2068.81 (11)	0.76 (17)
15	ICGX-IS 13005F2-B1-222	2244.45 (33)	1588.89 (19)	29.21 (31)	1916.67 (28)	655.56 (54)	0.81 (24)	1888.43 (24)	0.71 (31)
16	ICGX-IS 13005F2-B1-252	2844.45 (9)	1855.56 (4)	34.77 (45)	2350.00 (6)	988.89 (21)	1.19 (5)	2297.40 (5)	0.65 (45)
17	ICGX-IS 13005F2-B1-262	2411.11 (21)	1455.56 (37)	39.63 (63)	1933.33 (27)	955.56 (27)	0.79 (28)	1873.37 (28)	0.60 (63)
18	ICGX-IS 13005F2-B1-287	2233.33 (38)	1800.00 (7)	19.40 (12)	2016.67 (19)	433.33 (78)	0.91 (13)	2004.99 (13)	0.81 (12)
19	ICGX-IS 13005F2-B1-301	2133.33 (47)	1544.45 (27)	27.60 (27)	1838.89 (35)	588.89 (62)	0.74 (34)	1815.16 (34)	0.72 (27)
20	ICGX-IS 13005F2-B1-359	1422.22 (90)	900.00 (86)	36.72 (52)	1161.11 (89)	522.22 (72)	0.29 (88)	1131.37 (88)	0.63 (52)
21	ICGX-IS 13005F2-B1-37	2188.89 (39)	1000.00 (77)	54.31 (86)	1594.44 (63)	1188.89 (14)	0.49 (65)	1479.49 (65)	0.46 (86)
22	ICGX-IS 13005F2-B1-381	2766.67 (11)	1233.33 (60)	55.42 (88)	2000.00 (21)	1533.34 (6)	0.77 (30)	1847.22 (30)	0.45 (88)
23	ICGX-IS 13005F2-B1-388	1922.22 (63)	1022.23 (75)	46.82 (79)	1472.22 (69)	900.00 (35)	0.44 (70)	1401.76 (70)	0.53 (79)
24	ICGX-IS 13005F2-B1-40	2166.67 (42)	1411.11 (43)	34.87 (46)	1788.89 (39)	755.56 (43)	0.69 (40)	1748.54 (40)	0.65 (46)
25	ICGX-IS 13005F2-B1-404	1422.22 (91)	611.11 (95)	57.03 (89)	1016.67 (95)	811.11 (40)	0.20 (96)	932.27 (96)	0.43 (89)
26	ICGX-IS 13005F2-B1-411	2233.34 (37)	1266.67 (58)	43.28 (70)	1750.00 (47)	966.67 (23)	0.64 (49)	1681.93 (49)	0.57 (70)
27	ICGX-IS 13005F2-B1-425	1966.67 (60)	1555.56 (24)	20.90 (13)	1761.11 (45)	411.11 (79)	0.69 (39)	1749.07 (39)	0.79 (13)
28	ICGX-IS 13005F2-B1-450	2144.45 (43)	1555.56 (23)	27.46 (26)	1850.00 (33)	588.89 (60)	0.75 (32)	1826.42 (32)	0.73 (26)
29	ICGX-IS 13005F2-B1-46	2900.00 (4)	1933.34 (3)	33.33 (40)	2416.67 (4)	966.67 (26)	1.27 (3)	2367.84 (3)	0.67 (40)
30	ICGX-IS 13005F2-B1-470	2133.34 (46)	1422.22 (41)	33.33 (41)	1777.78 (40)	711.12 (48)	0.69 (41)	1741.86 (41)	0.67 (41)
31	ICGX-IS 13005F2-B1-481	1644.45 (76)	1066.67 (72)	35.14 (48)	1355.56 (79)	577.78 (64)	0.40 (79)	1324.41 (79)	0.65 (48)
32	ICGX-IS 13005F2-B1-488	2811.11 (10)	1322.22 (48)	52.96 (83)	2066.67 (15)	1488.89 (7)	0.84 (21)	1927.93 (21)	0.47 (83)
33	ICGX-IS 13005F2-B1-49	2244.45 (34)	1655.56 (12)	26.24 (23)	1950.00 (25)	588.89 (59)	0.84 (22)	1927.64 (22)	0.74 (23)
34	ICGX-IS 13005F2-B1-494	1388.89 (93)	1288.89 (53)	7.20 (2)	1338.89 (81)	100.00 (95)	0.40 (77)	1337.96 (77)	0.93 (2)
35	ICGX-IS 13005F2-B1-498	1455.56 (88)	1277.78 (55)	12.21 (4)	1366.67 (77)	177.78 (93)	0.42 (72)	1363.77 (72)	0.88 (4)
36	ICGX-IS 13005F2-B1-5	2144.45 (44)	1177.78 (64)	45.08 (75)	1661.11 (54)	966.67 (25)	0.57 (57)	1589.24 (57)	0.55 (75)
37	ICGX-IS 13005F2-B1-50	1688.89 (73)	933.34 (84)	44.74 (73)	1311.11 (83)	755.56 (44)	0.36 (83)	1255.51 (83)	0.55 (73)
38	ICGX-IS 13005F2-B1-559	1655.56 (74)	966.67 (81)	41.61 (66)	1311.11 (84)	688.89 (49)	0.36 (81)	1265.06 (81)	0.58 (66)
39	ICGX-IS 13005F2-B1-586	2244.45 (35)	1300.00 (50)	42.08 (67)	1772.22 (42)	944.45 (30)	0.66 (45)	1708.15 (45)	0.58 (67)
40	ICGX-IS 13005F2-B1-591	2877.78 (5)	1311.11 (49)	54.44 (87)	2094.44 (11)	1566.67 (5)	0.85 (18)	1942.44 (18)	0.46 (87)
41	ICGX-IS 13005F2-B1-65	2144.45 (45)	1622.22 (17)	24.35 (18)	1883.33 (31)	522.23 (70)	0.79 (29)	1865.14 (29)	0.76 (18)
42	ICGX-IS 13005F2-B1-85	2344.45 (25)	1211.11 (62)	48.34 (80)	1777.78 (41)	1133.34 (16)	0.64 (48)	1685.05 (48)	0.52 (80)
43	ICGX-IS 13005F2-B1-90	2044.45 (53)	1277.78 (56)	37.50 (57)	1661.11 (55)	766.67 (42)	0.59 (53)	1616.27 (53)	0.62 (57)
44	ICGX-IS 13005F2-B1-91	3088.89 (3)	1744.45 (10)	43.53 (71)	2416.67 (5)	1344.45 (11)	1.22 (4)	2321.29 (4)	0.56 (71)
45	ICGX-IS 13005F2-B1-93	2344.45 (26)	933.33 (85)	60.19 (91)	1638.89 (57)	1411.12 (10)	0.49 (66)	1479.24 (66)	0.40 (91)
46	ICGX-IS 13012F2-B1-105	2166.67 (41)	1544.45 (26)	28.72 (30)	1855.56 (32)	622.23 (56)	0.76 (31)	1829.29 (31)	0.71 (30)
47	ICGX-IS 13012F2-B1-114	2644.45 (15)	1500.00 (32)	43.28 (69)	2072.22 (13)	1144.45 (15)	0.90 (14)	1991.65 (14)	0.57 (69)
48	ICGX-IS 13012F2-B1-115	1955.56 (61)	1577.78 (21)	19.32 (11)	1766.67 (44)	377.78 (82)	0.70 (38)	1756.54 (38)	0.81 (11)
49	ICGX-IS 13012F2-B1-130	2700.00 (13)	1377.78 (45)	48.97 (81)	2038.89 (17)	1322.23 (12)	0.84 (20)	1928.73 (20)	0.51 (81)

Table 4. Contd.

50	ICGX-IS 13012F2-B1-140	2022.22 (54)	1277.78 (54)	36.81 (53)	1650.00 (56)	744.44 (45)	0.58 (55)	1607.47 (55)	0.63 (53)
51	ICGX-IS 13012F2-B1-15	2266.67 (31)	1366.67 (46)	39.71 (64)	1816.67 (37)	900.00 (34)	0.70 (37)	1760.05 (37)	0.60 (64)
52	ICGX-IS 13012F2-B1-156	1622.22 (79)	1422.22 (42)	12.33 (5)	1522.22 (66)	200.00 (92)	0.52 (63)	1518.93 (63)	0.88 (5)
53	ICGX-IS 13012F2-B1-20	1311.11 (94)	900.00 (87)	31.36 (36)	1105.56 (93)	411.11 (80)	0.27 (92)	1086.28 (92)	0.69 (36)
54	ICGX-IS 13012F2-B1-207	1766.67 (67)	1388.89 (44)	21.38 (14)	1577.78 (64)	377.78 (83)	0.55 (60)	1566.43 (60)	0.79 (14)
55	ICGX-IS 13012F2-B1-24	1622.23 (78)	1044.45 (74)	35.62 (49)	1333.34 (82)	577.78 (65)	0.38 (80)	1301.66 (80)	0.64 (49)
56	ICGX-IS 13012F2-B1-268	2244.45 (36)	1200.00 (63)	46.53 (77)	1722.22 (50)	1044.45 (20)	0.61 (51)	1641.14 (51)	0.53 (77)
57	ICGX-IS 13012F2-B1-276	1777.78 (66)	1044.45 (73)	41.25 (65)	1411.11 (75)	733.34 (46)	0.42 (73)	1362.64 (73)	0.59 (65)
58	ICGX-IS 13012F2-B1-281	1266.67 (95)	822.23 (90)	35.09 (47)	1044.45 (94)	444.44 (77)	0.24 (93)	1020.53 (93)	0.65 (47)
59	ICGX-IS 13012F2-B1-29	2877.78 (6)	1822.23 (5)	36.68 (51)	2350.00 (7)	1055.55 (19)	1.18 (6)	2289.97 (6)	0.63 (51)
60	ICGX-IS 13012F2-B1-297	2866.67 (8)	2155.56 (1)	24.81 (20)	2511.11 (2)	711.12 (47)	1.40 (1)	2485.81 (1)	0.75 (20)
61	ICGX-IS 13012F2-B1-312	2405.56 (22)	1466.67 (35)	39.03 (62)	1936.11 (26)	938.89 (31)	0.80 (27)	1878.34 (27)	0.61 (62)
62	ICGX-IS 13012F2-B1-319	2744.45 (12)	944.45 (82)	65.59 (93)	1844.45 (34)	1800.00 (2)	0.59 (54)	1609.96 (54)	0.34 (93)
63	ICGX-IS 13012F2-B1-381	1933.34 (62)	1266.67 (59)	34.48 (44)	1600.00 (62)	666.67 (53)	0.55 (61)	1564.89 (61)	0.66 (44)
64	ICGX-IS 13012F2-B1-40	2344.45 (27)	2000.00 (2)	14.69 (6)	2172.22 (9)	344.45 (87)	1.06 (7)	2165.38 (7)	0.85 (6)
65	ICGX-IS 13012F2-B1-431	2077.78 (52)	1133.33 (69)	45.45 (76)	1605.56 (59)	944.45 (29)	0.53 (62)	1534.54 (62)	0.55 (76)
66	ICGX-IS 13012F2-B1-475	1566.67 (83)	777.78 (92)	50.35 (82)	1172.22 (88)	788.89 (41)	0.28 (91)	1103.87 (91)	0.50 (82)
67	ICGX-IS 13012F2-B1-491	1411.11 (92)	877.78 (89)	37.80 (58)	1144.45 (91)	533.33 (69)	0.28 (90)	1112.94 (90)	0.62 (58)
68	ICGX-IS 13012F2-B1-50	2333.34 (28)	577.78 (96)	75.24 (96)	1455.56 (71)	1755.56 (3)	0.30 (87)	1161.10 (87)	0.25 (96)
69	ICGX-IS 13012F2-B1-518	1911.11 (64)	1288.89 (52)	32.56 (38)	1600.00 (61)	622.22 (57)	0.56 (59)	1569.46 (59)	0.67 (38)
70	ICGX-IS 13012F2-B1-520	1555.56 (84)	977.78 (80)	37.14 (55)	1266.67 (87)	577.78 (63)	0.34 (85)	1233.28 (85)	0.63 (55)
71	ICGX-IS 13012F2-B1-525	3200.00 (2)	1766.67 (8)	44.79 (74)	2483.34 (3)	1433.33 (9)	1.28 (2)	2377.68 (2)	0.55 (74)
72	ICGX-IS 13012F2-B1-528	1655.56 (75)	1300.00 (51)	21.48 (15)	1477.78 (68)	355.56 (86)	0.49 (68)	1467.05 (68)	0.79 (15)
73	ICGX-IS 13012F2-B1-534	2333.34 (29)	1066.67 (71)	54.29 (85)	1700.00 (51)	1266.67 (13)	0.56 (58)	1577.62 (58)	0.46 (85)
74	ICGX-IS 13012F2-B1-537	1766.67 (68)	1444.45 (38)	18.24 (9)	1605.56 (60)	322.22 (89)	0.58 (56)	1597.45 (56)	0.82 (9)
75	ICGX-IS 13012F2-B1-554	2466.67 (20)	1511.12 (29)	38.74 (59)	1988.89 (22)	955.55 (28)	0.84 (19)	1930.65 (19)	0.61 (59)
76	ICGX-IS 13012F2-B1-561	1522.23 (86)	1166.67 (67)	23.36 (16)	1344.45 (80)	355.56 (85)	0.40 (78)	1332.64 (78)	0.77 (16)
77	ICGX-IS 13012F2-B1-562	1744.45 (70)	1588.89 (20)	8.92 (3)	1666.67 (53)	155.56 (94)	0.63 (50)	1664.85 (50)	0.91 (3)
78	ICGX-IS 13012F2-B1-563	1133.33 (96)	788.89 (91)	30.39 (34)	961.11 (96)	344.45 (88)	0.20 (95)	945.55 (95)	0.70 (34)
79	ICGX-IS 13012F2-B1-566	1644.45 (77)	1177.78 (65)	28.38 (29)	1411.11 (74)	466.67 (75)	0.44 (71)	1391.69 (71)	0.72 (29)
80	ICGX-IS 13012F2-B1-571	2000.00 (55)	1633.33 (16)	18.33 (10)	1816.67 (36)	366.67 (84)	0.74 (35)	1807.39 (35)	0.82 (10)
81	ICGX-IS 13012F2-B1-576	2666.67 (14)	1755.56 (9)	34.17 (43)	2211.11 (8)	911.11 (33)	1.06 (8)	2163.67 (8)	0.66 (43)
82	ICGX-IS 13012F2-B1-586	2177.78 (40)	1633.33 (15)	25.00 (21)	1905.56 (30)	544.45 (68)	0.80 (25)	1886.01 (25)	0.75 (21)
83	ICGX-IS 13012F2-B1-600	3833.34 (1)	1211.11 (61)	68.41 (95)	2522.22 (1)	2622.23 (1)	1.05 (9)	2154.67 (9)	0.32 (95)
84	ICGX-IS 13012F2-B1-62	1544.45 (85)	1166.67 (66)	24.46 (19)	1355.56 (78)	377.78 (81)	0.41 (76)	1342.33 (76)	0.76 (19)
85	ICGX-IS 13012F2-B1-69	2000.00 (56)	1488.89 (33)	25.56 (22)	1744.45 (48)	511.11 (73)	0.67 (44)	1725.62 (44)	0.74 (22)
86	ICGX-IS 13012F2-B1-75	2111.12 (49)	1422.23 (40)	32.63 (39)	1766.67 (43)	688.89 (50)	0.68 (42)	1732.77 (42)	0.67 (39)
87	ICGX-IS 13012F2-B1-78	1755.56 (69)	1488.89 (34)	15.19 (7)	1622.22 (58)	266.67 (90)	0.59 (52)	1616.73 (52)	0.85 (7)
88	ICGX-IS 13012F2-B1-84	1722.22 (72)	1266.67 (57)	26.45 (25)	1494.45 (67)	455.55 (76)	0.49 (67)	1476.98 (67)	0.74 (25)
89	ICGX-IS 13012F2-B1-93	1977.78 (59)	1111.11 (70)	43.82 (72)	1544.45 (65)	866.67 (37)	0.50 (64)	1482.41 (64)	0.56 (72)
90	ICGX-IS 13012F2-B1-98	2533.34 (18)	1600.00 (18)	36.84 (54)	2066.67 (14)	933.34 (32)	0.92 (12)	2013.29 (12)	0.63 (54)
91	Fleur 11	2122.23 (48)	688.89 (93)	67.54 (94)	1405.56 (76)	1433.34 (8)	0.33 (86)	1209.12 (86)	0.32 (94)
92	47-10	2244.45 (32)	1577.78 (22)	29.70 (33)	1911.11 (29)	666.67 (52)	0.80 (26)	1881.82 (26)	0.70 (33)
93	ICGS 44	1600.00 (80)	1000.00 (78)	37.50 (56)	1300.00 (85)	600.00 (58)	0.36 (82)	1264.91 (82)	0.63 (56)
94	ICGV 87378	2400.00 (23)	1544.44 (28)	35.65 (50)	1972.22 (24)	855.56 (39)	0.84 (23)	1925.27 (23)	0.64 (50)
95	ICGV 91317	2522.22 (19)	1544.45 (25)	38.77 (61)	2033.33 (18)	977.78 (22)	0.88 (16)	1973.68 (16)	0.61 (61)
96	ICIART 19BT	2077.78 (51)	1433.34 (39)	31.02 (35)	1755.56 (46)	644.45 (55)	0.67 (43)	1725.73 (43)	0.69 (35)

[¥]Yp = yield under normal condition, Ys = yield under drought condition, RED= reduction in yield, MP= mean productivity, TOL = tolerance index, STI = stress tolerance index, GMP = geometric mean productivity, DTI = drought tolerance index. The numbers in parentheses indicate the genotype ranks for each index.

contrary, the genotypes ICGX-IS 13005F2-B1-404 (1422.22 and 611.11 kg/ha), ICGX-IS 13012F2-B1-563 (1133.33 and 788.89 kg/ha) and ICGX-IS 13005F2-B1-12 (1600.00 and 633.33 kg/ha) were reported as susceptible to stress and they showed the lowest values (0.20 to0.23) of STI. Results revealed that STI indices were closer to

Table 5. Correlation coefficients between Yp, Ys and drought tolerance indices in 90 F3 progenies and six checks of groundnut evaluated under well water and water stress conditions at ICRISAT Samanko, 2015.

	Yp	Ys	RED	MP	TOL	STI	GMP	DTI
Yp	1.00							
Ys	0.55***	1.00						
RED	0.39***	-0.55***	1.00					
MP	0.92***	0.81***	0.02	1.00				
TOL	0.75***	-0.17	0.88***	0.44***	1.00			
STI	0.85***	0.88***	-0.11	0.98***	0.30**	1.00		
GMP	0.84***	0.90***	-0.13	0.99***	0.28**	0.99***	1.00	
DTI	-0.40***	0.55***	-1.00***	-0.02	-0.88***	0.11	0.13	1.00

, * = significant at 1% and 0.1% of probability level; Yp = yield under irrigated conditions, Ys = yield under drought-stressed, Red = percentage reduction, MP = Mean productivity, TOL = tolerance index, STI = stress tolerance index, GMP = Geometric mean productivity, DTI = drought tolerance index.

GMP and MP in the ranking.

For the Drought tolerance index (DTI), the highest values were recorded for genotypes ICGX–IS 13005F2B1-198, (1744.44 and 1644.45 kg/ha), ICGX-IS 13005F2B1-494 (1388.89 and 1288.89 kg/ha) and ICGX-IS 13012F2-B1-562 (1744.45 and 1588.89 kg/ha), with high value (0.91 to 0.94) were found as tolerant genotypes (Table 4) while the genotypes ICGX-IS 13012F2-B1-50 (2333.34 and 577.78 kg/ha), ICGX-IS 13012F2-B1-600 (3833.34 and 688.89 kg/ha) and Fleur 11 (2122.23 and 688.89 kg/ha) were considered as susceptible to drought with low value (0.25 to 0.32). Results showed that DTI indices were similar to reduction percentage (RED %), but the higher the DTI, the smaller the (RED) in pod yields. The MP, STI and GMP indices were closer in the ranking, and they favored the identification of tolerant genotypes with stable yield under non-stress and stress environments. The highest STI indices were recorded for genotypes ICGX-IS 13012F2-B1-297 (2866.67 and 2155.56 kg/ha), ICGX-IS 13012F2-B1-525 (3200.00 and 1766.67 kg/ha) and ICGX-IS 13005F2-B1-46 (2900.00 and 1933.34 kg/ha) with high values (1.27 to 1.40). They were considered as tolerant genotypes with high yield stability under both conditions. The use of the STI index was encouraged by Fernandez (1992) who argue that a high STI value indicate a high tolerance to stress. Sio-Se et al. (2006) agreed that these GMP, MP and STI are reliable indices in identifying stable genotypes in wheat. The RED revealed the percent loss of pod yield; and it also provided information about high performing genotypes in yield. But care should be taken when using this index since it might not always give good indication of stable and tolerant genotypes. The current study identified drought tolerant with high yielding genotypes after removing some poor genotypes with good RED indices as low RED values of a genotype could be due to less yield under optimal condition. The RED and DTI indices were opposite such that the higher the DTI, the lower the RED in pod yield. Based on DTI index, genotypes ICGX–IS 13005F2B1-198, (1744.44 and 1644.45 kg/ha), ICGX-IS 13005F2B1-494 (1388.89 and 1288.89 kg/ha) and ICGX-IS 13012F2-B1-562 (1744.45 and 1588.89 kg/ha), with high values (0.91 to 0.94) were found as tolerant and stable genotypes. This is in agreement with the work of Nautiyal et al. (2002) for groundnut. In this study, parental lines performed less than most of their offspring. The high performing parents were ICGV 87378, ICIAR 19BT and ICGV 91317, respectively. Despite large variability among the progenies, they showed the top 10 high yielding genotypes tolerant to drought. Yield loss in groundnut due to drought ranges from 44% to 85%. In our knowledge, this is the first attempt to provide genetic information and yield loss in breeding for drought tolerant groundnut varieties in Mali.

Correlation of pod yield and drought tolerance indices

Highly significant (P<0.001) and positive correlations were found between yield under well-watered conditions (Yp) and the other five indices (Ys, RED, MP, TOL, STI, GMP, and DTI). Similarly, yield under drought stress conditions (Ys) was highly significant (P<0.001) and associated with all the selection indices except TOL (Table 5). Selection Indices including GMP, MP and STI were highly significant (P<0.001) and positively correlated with each other and to both well-watered (Yp) condition and water-stressed (Ys) condition. The observed relations were consistent with those reported by Fernandez (1992) on mungbean, Jafari et al. (2009) on maize; Talebi et al. (2009) and Allahdou (2012) on tritipyrum.

Principal component analysis of indices and traits

The PCA analysis showed eight axes (Prin or PCA) with

Table 6. Principal component analysis for potential yield (Yp), stress yield (Ys) and drought tolerance indices in $90F_{2:3}$ progenies and six checks of groundnut evaluated under well water and water stress conditions at ICRISAT Samanko, 2015.

Principal component	Prin1	Prin2	Prin3	Prin4	Prin5	Prin6	Prin7	Prin8
Yp	0.30	0.41	0.29	-0.20	0.00	0.16	-0.77	0.00
Ys	-0.16	0.49	-0.40	-0.41	0.01	0.57	0.28	0.00
RED	0.46	-0.13	-0.30	-0.03	0.82	0.00	0.00	0.00
MP	0.13	0.51	0.02	-0.33	0.00	-0.74	0.26	0.00
TOL	0.47	0.09	0.64	0.08	-0.01	0.30	0.51	0.00
STI	-0.46	0.13	0.32	0.04	0.40	0.00	0.00	0.71
GMP	0.06	0.52	-0.22	0.82	0.00	0.00	0.00	0.00
DTI	-0.46	0.13	0.32	0.04	0.40	0.00	0.00	-0.71
Eigenvalue	4.31	3.62	0.06	0.00	0.00	0.00	0.00	0.00
Proportion	0.54	0.45	0.01	0.00	0.00	0.00	0.00	0.00
Cumulative	0.54	0.99	1.00	1.00	1.00	1.00	1.00	1.00

Yp= yield under irrigated condition, Ys= yield under drought stressed condition, RED = percentage reduction, MP = Mean productivity, TOL = tolerance index, STI = stress tolerance index, GMP = Geometric mean productivity, DTI=drought tolerance index.

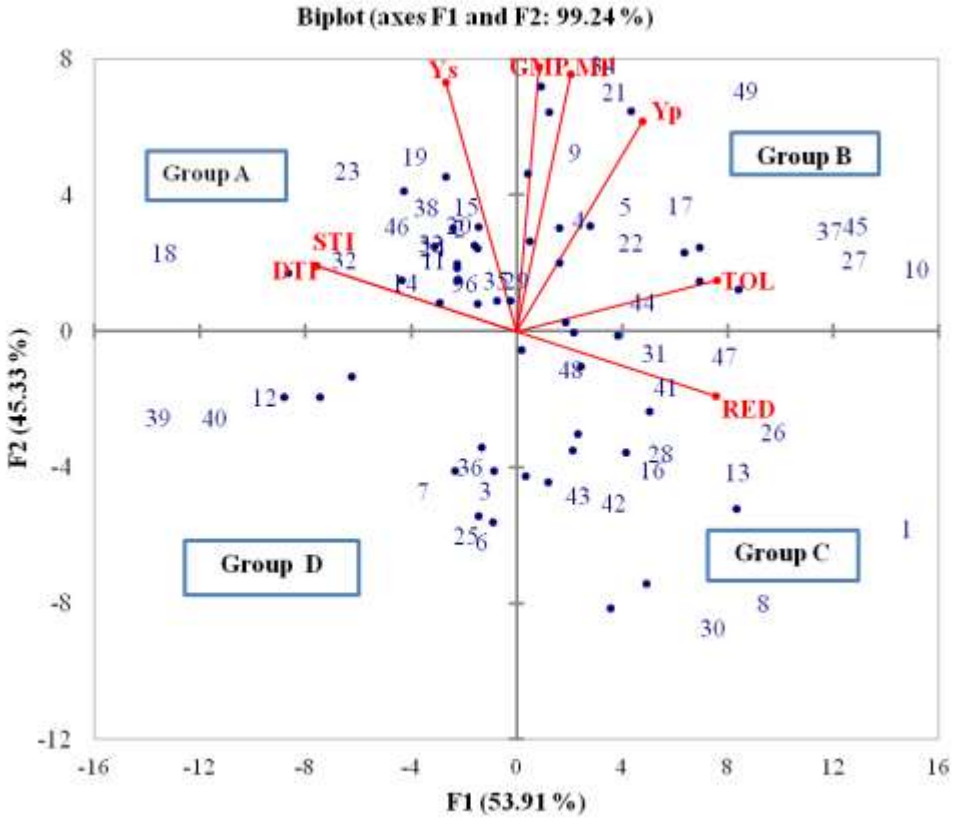

Figure 1. The Biplot diagram of principal components analysis of genotypes according to yield under well-watered and stress conditions and drought tolerance indices

their corresponding eigenvalues and the proportion of variation of each PCA (Table 6 and Figure 1). The results revealed that the first PCA explained 54% of the variation with PYWW, MP, STI, and GMP being significant (Table 6 and Figure 1). Thus, the first dimension (Prin1) can be named as the yield potential and drought tolerance. Genotypes that had high values of these indices were high yielding under both stressed and non-stressed conditions. The second PCA (Prin2) explained 45% of the total variability and correlated positively with RED and

TOL but had negative correlation with DTI and pod yield under stressed conditions (PYWS) (Table 6). Therefore, the second component can be named as a stress-tolerant dimension and it separates the stress tolerant genotypes from the non-tolerant ones. The Prin1 and the Prin2 (in bold) explained 99% of the total variation (Table 6). Variables making the most important contribution to each of the two (Prin1 and Prin2) components have their loading shown in underlined bold (loading >0.3 were considered most important). Hence, selection of genotypes that have high Prin1 and low Prin2 would result in genotypes good in both stressed and non-stressed conditions. Principal component analysis (PCA) provided the degree of importance of stress indices. Groundnut is a highly self-pollinated crop where pure line selection is needed; selection should be based on individual genotypes. Talebi et al. (2009) proposed PCA analysis as a better approach than the correlation analysis to identify individual superior genotypes for both stress and non-stress conditions. Results of PCA revealed that PC1 was associated positively with Yp, RED, TOL and negatively with STI and DTI, while PC2 was associated positively with Yp, Ys, MP and GMP. Talebi et al. (2009), Karimizadeh et al. (2011) and Allahdou (2012) obtained similar results in multivariate analysis of drought tolerance. Selection indices including high STI, DTI and low RED contributed to the largest variation in identifying thigh yielding genotypes tolerant to drought stress. The top 10 $F_{2:3}$ genotypes identified were ICGV-IS 13012F2-297-B1; ICGV-IS 13012F2-40-B1; ICGV-IS 13012F2-576-B1 from ICIAR 19BT/IGGS 44 and ICGV-IS 13005F2-46-B1; ICGV-IS 13005F2-252-B1; ICGV-IS 13012F2-29-B1; ICGV-IS 13005F2-205-B1; ICGV-IS 13005F2-287-B1; ICGV-IS 13012F2-525-B1 and ICGV-IS 13005F2-91-B1 from ICGV 91317/ICGV 87378. The pod yield ranged from 1744.5 kg/ha to 2155.6 kg/ha under drought-stressed conditions and under full irrigation conditions, pod yield ranged from 2233.3 kg/ha to 3200 kg/ha. These genotypes were the most tolerant with high yielding and stable yield in both environments in the current study conditions. In summary, the results from the selection indices could depend on the stress severity in reference to Blum (1996) arguing that under moderate stress conditions, potential yield greatly influences yield under stress conditions.

Conclusion

Low RED values and high DTI, STI, MP, and GMP values under both well-watered and water-stressed conditions were more effective in identifying high yielding cultivars under water limited conditions. Based on these indices, the $F_{2:3}$ progenies ICGV-IS 13012F2-B1-297, ICGV-IS 13012F2-B1-40, ICGV-IS 13005F2-B1-46, ICGV-IS 13005F2-B1-252, ICGV-IS 13012F2-B1-29, ICGV-IS 13005F2-B1-205, ICGV-IS 13005F2-B1-287, ICGV-IS 13012F2-B1-525, ICGV-IS 13012F2-B1-576 and, ICGV-IS 13005F2-B1-91 were identified as the most drought tolerant genotypes with high yield stability in the well-watered and drought stress conditions. The indices STI, MP and GMP were positively correlated with Yp and Ys, and they were useful for breeding for drought tolerance. Similarly, RED and DTI values that are highly significant and negatively correlated could be powerful in helping breeders to select tolerant genotypes with stable yield under contrasting stress environments. These indices, in combination with the STI, MP and GMP were of great importance for the selection of genotypes in this study. Crop breeders should consider the level of stress of the environments when studying an index.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Genetic variation among white lupin (*Lupinus albus* L.) landraces from Northwestern and Southern Ethiopia for agronomic traits and nutrient contents of grain

Chaltu Beyene

Crop and Horticulture Biodiversity Directorate, Ethiopian Biodiversity Institute, Addis Ababa, Ethiopia

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White lupin *(Lupinus albus L.)* is rich in quality protein, relatively tolerant to drought, soil salinity and acidity, increase the fertility of soils and can contribute to improved agricultural sustainability, food security and reduce malnutrition which has close associations with climate change. This study was conducted to assess genetic variability of white lupin genotypes for agronomic traits and nutrient contents of grain, and to estimate association of traits. Twenty-five genotypes of white lupin were evaluated for 29 quantitative traits in 5 x 5 simple lattice designs at Holeta Agricultural Research Center during 2018/2019. The variations of genotypes for yield and grain protein content ranged from 122 to 3206 kg ha^{-1} and 28.55 and 35.81%, respectively. The genotypes had 2763, 772.3 and 81.59 mg/kg of average phosphorus, calcium and iron contents of grain. The PCV and GCV coefficient of variations varied from 4.39 to 29.54% and 3.41 to 28%, respectively. Heritability in broad sense and genetic advance as percent of mean ranged from 42.07 to 88.94% and 5.34 to 53.98%, respectively. The estimates of GCV, PCV, H^2 and GAM were high to moderate. The research results showed the presence of variations among landraces of white lupin in Ethiopia and further evaluation of germplasm could be rewarding to improve the genetic resource in the country.

Key words: Genetic advance, genotypic, phenotypic, heritability, protein and mineral content

INTRODUCTION

White lupin (*Lupinus albus* L. (2n=50) originated from the North-East Mediterranean and is now distributed throughout the Mediterranean region and from the Azores Islands across North Africa to Ethiopia and Kenya (Vipin et al*.,* 2013). Lupin production is targeted for its grain used as snack, for preparation of local alcoholic drink (*Areke*), to soil fertility maintenance values in Ethiopia and livestock feed in Australia, Europe and America (Yeheyis et al., 2010); besides, it also has higher protein content 30-40% (Hofmanova et al., 2014). The seed has a higher level of essential amino acids and important dietary minerals (iron and potassium) compared with other legumes such as pea, and faba bean, which are useful as ingredients of functional or healthy food products (Annicchiarico et al., 2014). The crop is produced by smallholder subsistent farmers in Ethiopia by more than 90,000 farmers on 15,500 ha of land and 17,690 tons of grain yields where the crop is mainly

E-mail: chaltubeyene56@gmail.com.

Table 1. Description of white lupin landraces.

Landraces code	Collection area description			Altitude (m.a.s.l.)	Coordinate	
	Regional State	Zone	Woreda/District		Latitude	Longitude
9960	Amhara	Mirab Gojam	Dembecha	2129	10-34-04-N	37-28-01-E
9963	Amhara	Misrak Gojam	Gozamn	2432	10-22-36-N	37-44-26-E
24850	Amhara	Misrak Gojam	Goncha Siso Enese	2496	10-57-11-N	38-04-46-E
26634	Amhara	Misrak Gojam	Gozamen	2883	10-28-28-N	37-51-06-E
26635	Amhara	Misrak Gojam	Machakal	2793	10-36-25-N	37-41-51-E
26636	Amhara	Misrak Gojam	Senan	2975	10-03-54-N	37-46-41-E
29054	Amhara	Agew Awi	Dengla	2215	11-19-03-N	36-44-43-E
29056	Amhara	Agew Awi	Dangila	2201	11-21-40-N	36-46-06-E
29057	Amhara	Agew Awi	Dangila	2254	11-20-38-N	36-45-26-E
29251	SNNP	Gurage	Gumer	2933	07-59-20-N	38-05-10-E
105002	Amhara	Debub Gondar	Este	2420	11-37-00-N	38-01-00-E
105007	Amhara	Misrak Gojam	Guzamn	2430	10-18-00-N	37-47-00-E
225802	SNNP	Semen Omo	Dita Dermalo	2800	06-15-00-N	37-32-00-E
238999	Amhara	Mirab Gojam	Merawi	2050	11-25-09-N	37-09-54-E
239004	Amhara	Agew Awi	Dangela	2220	11-30-29-N	36-51-58-E
239005	Amhara	Agew Awi	Dangela	2360	11-10-22-N	36-52-10-E
239006	Amhara	Agew Awi	Dangela	2400	11-09-02-N	36-52-30-E
239012	Amhara	Semen Gondar	Gondar Zuria	1930	11-36-57-N	37-27-11-E
239014	Amhara	Semen Gondar	Gondar Zuria	1920	11-40-27-N	37-28-34-E
239027	Amhara	Mirab Gojam	Achefer	2060	11-23-41-N	36-57-10-E
239036	Amhara	Mirab Gojam	Achefer	2000	11-34-22-N	36-56-35-E
239051	Amhara	Mirab Gojam	Bure Wemberma	2120	10-42-45-N	37-07-33-E
239055	Amhara	Mirab Gojam	Dembecha	2160	10-33-26-N	37-31-01-E
239059	Amhara	Misrak Gojam	Guzamn	2420	10-18-35-N	37-44-07-E
239060	Amhara	Semen Gondar	Gondar Zuria	1900	11-42-54-N	37-30-29-E

Source: Ethiopian Biodiversity Institute (1979-2016).

tons of grain yields where the crop is mainly produced in the Amhara, Benesangul, SNNPR, Oromiya, and Tigray Regions of Ethiopia (CSA, 2015). However, Amhara Regional States is the largest producer and the production of lupin on 17,877.23 ha in the 2017/18 *Meher* season was 24629.42 tons with average yields of 1.378 t ha^{-1}. It had a 0.08% share of the total production of pulse crops (CSA, 2018).

In Ethiopia, about 500 white lupin genotypes have been collected and conserved at Ethiopia Biodiversity Conservation Institute (EBI, 1979-2016). In the previous studies on agromoropology conducted, the genotypes of white lupin indicated the presence of genetic diversity (Mulugeta et al., 2015; Hibistu, 2016). However, lack of information about the use of white lupin crop improvement in respect to climate change mitigation crops for goal of smart agriculture aims to reduce food insecurity problem. The information generated from agro-morphological and genetic characteristics of white lupin landraces was required to use the available genetic resource in the country and to give attention for importance of white lupin crops for utilization and essential to the current problem that comes with climate change. It was therefore important to conduct more studies on evaluation and characterization of white lupin landraces for improvement. The objective of this study was to assess the genetic variability of white lupin landraces as potential use of the crop for food security and nutrition, and present a possibility of exploiting its potential to tolerate various stresses aggravated by or resulting from climate change in Ethiopia.

MATERIALS AND METHODS

Germplasm collection

Twenty-five white lupin landraces collected from northwestern and southern parts of Ethiopia by Ethiopian Biodiversity Institute (EBI) were used in this study (Table 1).

Description of the study site

The landraces were evaluated at Holeta (09`N latitude and 38`29E longitude) during 2018/2019. Holeta is located at 2400 m above sea

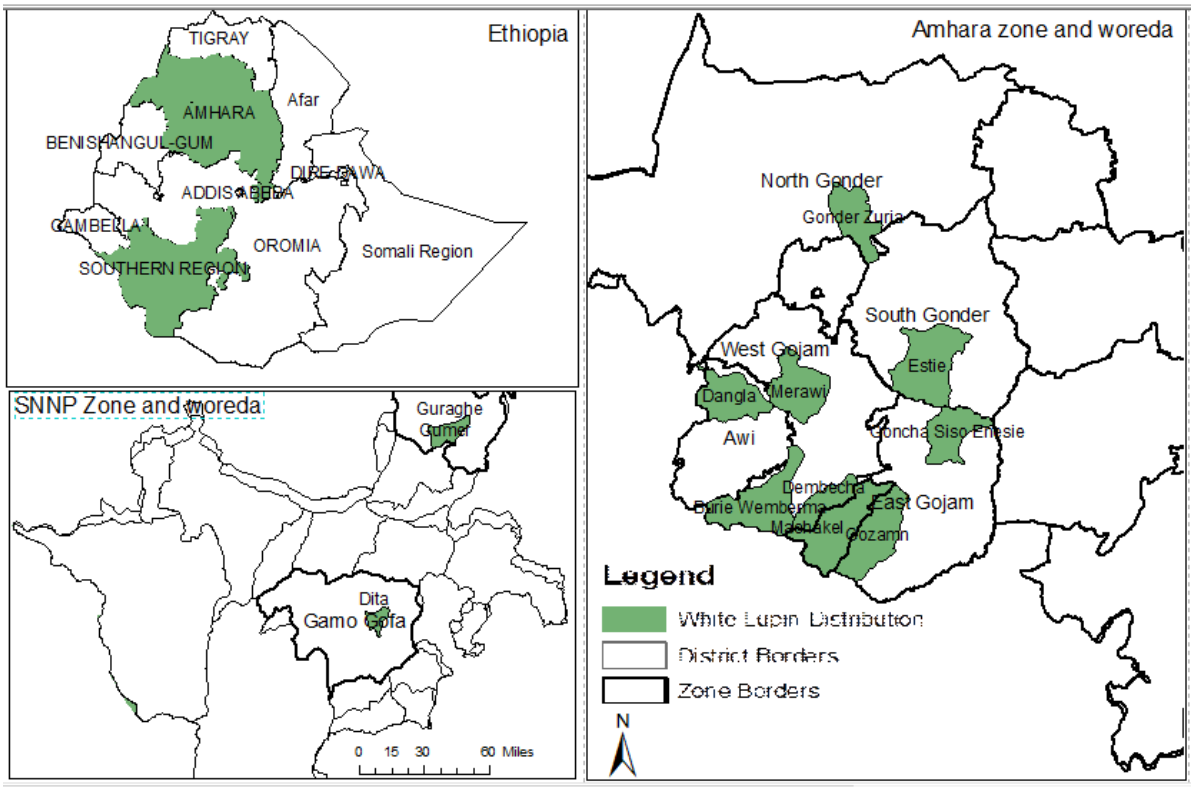

Figure 1. Indicated collection areas of white lupin in Ethiopia used for this study.

level (Figure 1) and receives 1100 mm of rainfall per annum and a mean relative humidity of 60.6%. Its soil is a predominantly *Nitosol* which is characterized by average organic matter (AOM) content of 1.8%, Nitrogen 0.17%, Phosphorous 4.55 ppm and Potassium 1.12 Meq/100 g of soil and pH 5.24.

Experimental genetic materials and design

The trial was laid down in a 5 x 5 simple lattice design. Each landraces was planted in one plot in each replication. Each plot consisted of one row and a total of 12 plants per row or per plot. The spacing between rows and plants was maintained at 0.75 and 0.25 m, respectively. The spacing between blocks and replications was 1.5 m.

Data collection

Grain yield was collected per plot and later converted to metric tons per hectare. Days to emergence, days to first flowering, days to 50% flowering, days to maturity and 100-seed weight were also determined on a plot basis. Height of lowest primary branch, plant height, petiole length, inflorescence length, number of branches per plant, stem thickness, leaf length, diameter of leaf, verticil number and number of leaflets per leaf, number of pods per plant, pod length, pod thickness, number of seeds per pod, seed length, seed width and seed weight per plant were recorded on plant basis. Protein and mineral composition of grains were estimated on plot basis. Protein and mineral content were estimated from 0.3 and 0.5 g respectively of grain using Kjeldahl method and Phosphorous was estimated by Magnesium Nitrate dry ashing Molybdenum blue method as the procedure established by Murphy and Riley (1962). Calcium, Potassium and Iron contents of grain were determined by Atomic Absorption Spectrometry.

Data analysis

Analysis of variance and mean comparison

The quantitative data were subjected to analysis of variance (ANOVA) for simple lattice (partially balanced or incomplete block) design (Gomez and Gomez, 1984) and computed with SAS statistical software (9.0) (SAS, 2004). In addition, the relative efficiency of square lattice to randomized complete block design (RCBD) was computed for each trait as:

$$\text{Relative efficiency of a square lattice (\%)} = \frac{\text{Mean square error in a square lattice design}}{\text{Mean square error in RCBD}} \times 100$$

The comparison of the mean performance of genotypes was done following the significance of mean squares using Duncan's Multiple Range (DMRT) at $P<0.05$. The traits that exhibited significant mean squares in general ANOVA were further subjected to genetic analyses.

Phenotypic and genotypic variances, heritability and genetic advance

The genotypic variance was estimated according to the method suggested by Burton and de Vane (1953).

i) For trait in which the efficiency of lattice design relative to RCBD was ≥100%

Table 2. Mean square from analysis of variance for some phenology traits.

Source of variation	DF	Days to 50% emergence	Days to first flowering	Days to 50% flowering	Days to maturity
Replication	1	1.445	0.605	0.18	214.25
Block with Replication	8	0.92	13.6488	2.6988	29.795
Treatment (Unadj.)	24	5.5208*	26.5521*	20.6029**	143.24*
Intra Block Error	16	1.6763	11.2238	5.0925	47.0012
RCBD Error	24	1.4242	12.0321	4.2946	41.2658
Total	49	3.4311	18.9107	12.1984	94.743
Efficiency relative to RCBD (%)		84.9615	101.21	84.3315	87.7973
CV (%)		12.27	4.271	2.76	3.72

*, **: Significant at 5 and 1%, respectively. DF= degree of freedom, Unadj.= Unadjusted, RCBD = randomized complete block design, and CV (%) = coefficient of variation in percent.

$$\sigma^2 g = \left(\frac{K+1}{kr}\right)(Msg - Mse)$$

ii) For trait in which the efficiency of lattice design relative to RCBD was <100%

$$\sigma^2 g = \frac{Msg - Mse}{r}$$

Where; $\sigma^2 g$ = genotypic variance, K = Number of plots in a block, *r* = Number of replications, Msg = genotype/treatment mean square, Mse = error mean square.

The phenotypic and genotypic variance was estimated (Burton and de Vane, 1953) as follows

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

Where, $\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = genotypic variance, $\sigma^2 e$ = Environmental variance.

$$PCV = \left[\frac{\sqrt{\sigma^2 p}}{\overline{X}}\right] x\ 100$$

$$GCV = \left[\frac{\sqrt{\sigma^2 g}}{\overline{X}}\right] x\ 100$$

Where; PCV = Phenotypic coefficient of variation, GCV = Genotypic coefficient of variation, $\overline{X}$ = Population mean of the trait evaluated. Low = 0 - 10%, Moderate = 10 – 20% and High = >20%. as indicated by Sivasubramaniah and Menon (1973).

Broad-sense heritability values were estimated using the formula adopted by Falconer and Mackay (1996) as follows:

$$H^2 = (\sigma^2 g/\sigma^2 p) \times 100$$

Where; H^2 = heritability in a broad sense, $\sigma^2 p$ = phenotypic variance, $\sigma^2 g$ = Genotypic variance.

As suggested by Robinson et al. (1949), heritability percentage was categorized Low = 0 - 30%, Moderate = 30 – 60%, and High = > 60%.

Genetic advance in the absolute unit (GA) and percent of the mean (GAM), assuming selection of superior 5% of the genotypes were estimated in accordance with the methods illustrated by Johnson et al. (1955) as:

$$GA = K\ x\sqrt{\sigma^2 p}\ x\ H^2$$

Where; GA = Genetic advance, K= selection intensity at 5% (K = 2.063) $\sqrt{\sigma^2 p}$ = Phenotypic standard deviation, H^2 = Heritability in the broad sense, genetic advance as percent of the mean was estimated as follows:

$$GAM = \left(\frac{GA}{\overline{X}}\right) x100$$

Where; GAM = Genetic advance as percent of mean, GA = Genetic advance, $\overline{X}$ = Populations mean for trait evaluated. as suggested by Johnson et al. (1955) as follows. Low = 0 - 10%, Moderate = 10 – 20, and High = >20

RESULTS and DISCUSSION

Analysis of variance and mean performance of genotypes

Phenological parameters

The twenty-five white lupin landraces showed significant differences for days to emergence, days to first flowering, days to maturity and highly significant differences for days to 50% of flowering (Table 2). Georgieva and Kosev (2016) reported significance difference of day to maturity by using 23 genotypes and stated that 10 genotypes fall under early maturity period in the range 92-95. Mulugeta et al. (2015) reported significant differences among 143 white lupin landraces from Ethiopian and one genotype from Germany for days to 50% flowering and days to 75% physiological maturity. Hibstu (2016) evaluated observed significant differences among 110 accessions of white lupin for days to 50% flowering and days to maturity at two locations. Georgieva et al. (2018) observed significance differences among 23 white lupin cultivars for days to flowering and maturity during the period 2014-2016 at the Institute of Forage Crops (Pleven). Obtaining of landraces that fall under the early maturity group might be more important in tackling the problems caused by climate change because early maturing landraces have a chance of escaping the terminal drought. The shortening of the length of growing duration is predicated as one of the future agriculture problems in Ethiopia (Evangelista et al., 2013; Hadgu et al., 2014; Kassie et al., 2014).

Table 3. Mean values of 25 white lupin landraces for phenology traits.

Landraces	Days to 50% emergence	Days to first flowering	Days to 50% flowering	Days to maturity
9960	11.00^{a-f}	80.50^{abc}	84.00^{abc}	187.50^{ab}
9963	9.25^{def}	76.50^{a-e}	80.00^{b-f}	182.00^{a-d}
24850	9.00^{def}	76.00^{a-e}	79.50^{b-f}	180.00^{a-d}
26634	8.50^{ef}	74.00^{b-e}	78.00^{d-g}	174.50^{b-e}
26635	8.50^{ef}	75.50^{b-e}	79.00^{c-g}	176.50^{b-e}
26636	8.50^{ef}	73.00^{cde}	77.00^{egf}	169.25^{cde}
29054	10.50^{a-f}	79.50^{abc}	82.75^{a-d}	186.50^{ab}
29056	11.00^{a-f}	79.75^{abc}	83.00^{a-d}	187.00^{ab}
29057	10.25^{b-f}	79.00^{a-d}	82.25^{a-e}	184.50^{a-d}
29251	8.00^{f}	70.00^{e}	74.00^{g}	163.00^{e}
105002	13.50^{a}	84.00^{a}	85.75^{a}	196.00^{a}
105007	9.50^{c-f}	77.50^{a-e}	80.00^{b-f}	182.50^{a-d}
225802	8.50^{ef}	71.00^{ed}	75.50^{gf}	168.00^{ed}
238999	12.00^{a-d}	81.00^{abc}	84.50^{abc}	190.50^{ab}
239004	10.50^{a-f}	79.00^{a-d}	82.50^{a-e}	185.75^{abc}
239005	10.25^{b-f}	78.75^{a-d}	80.75^{a-f}	184.00^{a-d}
239006	10.00^{b-f}	78.00^{a-e}	80.50^{a-f}	184.00^{a-d}
239012	12.75^{ab}	81.75^{ab}	84.75^{ab}	193.50^{a}
239014	13.00^{ab}	82.00^{ab}	85.00^{ab}	194.25^{a}
239027	11.50^{a-e}	81.00^{abc}	84.50^{abc}	189.50^{ab}
239036	12.50^{abc}	81.50^{ab}	84.75^{ab}	191.00^{ab}
239051	11.25^{a-e}	80.50^{abc}	84.00^{abc}	188.00^{ab}
239055	11.00^{a-f}	80.00^{abc}	84.00^{abc}	187.50^{ab}
239059	9.50^{c-f}	77.50^{a-e}	80.50^{a-f}	183.25^{a-d}
239060	13.50^{a}	84.00^{a}	85.00^{ab}	194.75^{a}

Mean values with a similar letter(s) in each column had non-significant differences at 5% probability level as tested by Duncan's Multiple Range Test (DMRT).

The variation of 25 white lupin landraces for days to 50% emergence was in the range between 8 and 13.5 days after sowing while the variation ranged from 70 to 84, 74 to 85.75 and 163 to 196 days after sowing for first flowering, 50% flowering and maturity, respectively. On average, the landrace took 10.55 days to reach 50% plant emergence, while landrace had an overall mean of 78.45, 81.66 and 184.13 days after sowing to set first flowering, attain 50% flowering and maturity, respectively (Table 3). The early days to 50% emergence, days to first flowering, days to 50% flowering and days to maturity were registered for 29251 while the delayed days to 50% emergence and days to first flowering registered for 239060 and 105002 while the delayed days to 50% flowering and days to maturity registered for 105002. However, this landrace had statistically non-significant differences with most of the other landraces for days to 50% emergence, days to first flowering, days to 50% flowering and days to maturity.

In lupin, germination can take from 5 to 15 days depending on soil temperature, moisture, and depth of sowing. The maximum emergence occurs between 10 and 20°C and for example, at 20°C lupin takes 4 to 4.5 days to emerge from a depth of 4 cm. A lupin plant was the flower for 4 to 8 weeks (Australia, 2011). In Old World lupins, flowering on the main inflorescence (primary flower set) starts 59-136 days from planting depending on species, landrace and the growth conditions (Buirchell and Cowling, 1998). Berger et al. (2017) evaluated wild and domesticated old world lupins and reported 70 days to flowering and 144 days to maturity. Mulugeta et al. (2015) reported 62.95 to 92.64 and 131 to 179 days to 50% flowering and days to 75% physiological maturity, respectively, for 143 white lupin landraces from Ethiopia and one genotype from Germany. Hibstu (2016) observed 57.71 to 86.46 and 149.08 to 215.21 days to 50% flowering and days to maturity, respectively, for 110 white lupin accessions evaluated at two locations in Ethiopia. Georgieva et al. (2018) finding also showed the early cultivars reached technical maturity on average about 129 to 134 days after sowing and the late ones at about 140-148 days after sowing. Dalaram (2017) suggested that the harvesting of white lupin is between 116 and 130 days after sowing. Other recent publications by Temesgen (2019) indicate that day to emergence starts from 6.67 after sowing to 15 days and start first

Table 4. Mean square from analysis of variance for growth traits.

Trait	Rep (1)	Block with Rep. (8)	Treatment (Unadj.) (24)	Intra Block Error (16)	RCBD Error (24)	Total (49)	Efficiency Relative to RCBD	CV (%)
HLPB	2.416	5.188	27.204**	4.074	4.445	15.551	101.83	7.78
PH	475.3	47.815	135.390*	32.184	37.393	94.320	104.77	7.03
PTL	0.058	0.2162	0.54201**	0.132	0.160	0.345	107.26	5.90
IFL	3.185	0.704	9.294*	2.1444	1.664	5.432	77.62	8.31
NBPP	3.38	0.563	0.877**	0.105	0.258	0.625	192.80	5.21
STY	0.045	0.028	0.179**	0.0426	0.0377	0.107	88.61	18.10
LL	5.882	2.225	3.434**	0.740	1.235	2.407	136.57	7.01
DL	0.718	0.4940	1.556ns	3.3835	2.4203	1.9623	71.534	20.53
VL	61.61	2.423	8.876*	2.595	2.538	6.848	97.79	8.59
NLPL	0.106	0.2013	0.286ns	0.2462	0.2312	0.2556	93.924	7.65

ns, * and**, non-significance, Significant at 5 and 1%, respectively. Rep = replication, RCBD = randomized complete block design, and CV (%) = coefficient of variation in percent. Numbers in parenthesis represent the degree of freedom for the respective source of variation. HLPB=Height lowest primary branch, PH=Plant height (cm), PTL=Petiole length, IFL=Inflorescence length, NBPP=Number of branches/plant, STY=Stem thickness, LL=Leaf length, DL=Diameter of the leaf, VN=Verticil number, and NLPL=Number of leaflets per leaf.

flowering 51 days after sowing to 108 late flowering genotypes. He also reports day to 50% flowerings and day to maturity range from 66 to121.5 and 170.33 to 223.33 respectively in two locations using 36 white lupin genotypes.

Growth traits

The results from ANOVA showed the presence of significant differences among white lupin landraces for plant height, inflorescence length, verticillated numbers. There was high significance for height lowest primary branch, petiole length, number of branches/plant, stem thickness and leaf length while non-significance for number of leaflets per leaf (Table 4) which implies presence of variability in growth traits for the crop useful for selection. Hibstu (2016) reported significant differences among 110 accessions of white lupin for plant height, inflorescence length, petiole length, number of branches/plant and stem thickness. Mulugeta et al. (2015) also reported significant difference among white lupin genotypes for growth characteristics. González-Andrés et al. (2007) reported significant differences for most of the growth traits of 31 accessions from Spanish Germplasm Collection except for the height of the lowest primary branch' and the leaflet number.

The mean values of landrace for height lowest primary branch ranged from 32.05 to 21.05 cm whereas it was in the range between 64.75 and 93.2, 5.1 and 7.2 and 0.83 and 2.43 cm for plant height, petiole length and stem thickness, respectively. The entire highest and lowest mean values for all growth traits registered for landrace 105002 and 29251, respectively. However, 8, 14 and 8 landraces for height lowest primary branch, plant height, and petiole length, respectively, had mean values non-significant differences from landraces 105002. Whereas 11 landrace for height lowest primary branch, and 7, 9 and 22 landraces for plant height, petiole length and stem thickness, respectively, had non-significant differences with mean values of 29251 (Table 5). Annual lupin species differ from each other by the shape of the cross-section of their stems and by size (Petrova, 2002). The plant height of various species ranges from 0.2-1.5 m (Australia, 2011). Hibstu (2016) observed 44.81 to 83.1 of plant height in 110 accessions of white lupin evaluated at two locations in 2011. Písaříková and Zralý (2009) observed plant height in the range between 75 to 100 cm white lupine genotypes.

The mean values of landraces ranged from 9.75 to 14.9 cm and 13.3 to 23.29 cm for leaf length and inflorescence length, respectively. The landraces had mean values for a number of branches per plant and verticil number in the range between 5.35 and 8.5 and 15.1 and 23.85, respectively. The highest mean values for leaf length, inflorescence length, number of branches per plant and verticil number were registered for landraces 105002 while all the lowest mean values for the traits were registered for landraces 29251. But 9, 1 and 4 landraces had mean values for leaf length, inflorescence length and verticil number, respectively, non-significant from mean values of 105002, and nine landraces for leaf length, 6, 14 and 13 landraces for inflorescence length, number of branches per plant and verticil number, respectively, had non-significant difference from mean values of 29251 (Table 5). Hibstu (2016) observed minimum and maximum values of 11.31 and 20.84 cm inflorescence length, respectively for 110 white lupin genotypes. Also, Georgieva et al. (2018) reported that there was a wide range of variations for growth traits of 23 white lupin genotypes. Kurlovich (2002) observed that white lupin had a height of 30 to 130. A similar result of 120 cm

Table 5. Mean values of 25 white lupin landraces for growth traits.

Acc. No.	HLPB	PH	PTL	IFL	NBPP	STY	LL	NV
9960	27.70^{a-h}	84.50^{a-e}	6.33^{a-h}	18.50^{b-e}	6.25^{c-h}	1.13^{bc}	12.85^{a-g}	19.38^{b-e}
9963	22.60^{ijk}	76.35^{c-h}	5.70^{e-i}	16.55^{b-h}	5.85^{f-j}	1.03^{c}	11.50^{d-i}	17.75^{c-f}
24850	21.98^{ijk}	75.70^{d-h}	5.70^{e-i}	16.45^{c-h}	5.80^{f-j}	1.02^{c}	11.28^{e-i}	17.18^{def}
26634	21.20^{k}	68.20^{fgh}	5.60^{ghi}	15.10^{e-h}	5.75^{g-j}	0.98^{c}	11.01^{f-i}	16.35^{ef}
26635	21.58^{jk}	71.75^{e-h}	5.68^{f-i}	15.45^{d-h}	5.80^{f-j}	0.99^{c}	11.01^{f-i}	16.78^{ef}
26636	21.20^{k}	66.95^{gh}	5.50^{hi}	14.55^{fgh}	5.55^{hij}	0.98^{c}	10.76^{ghi}	16.10^{ef}
29054	26.53^{c-i}	82.35^{a-e}	6.27^{b-h}	18.15^{b-e}	6.10^{c-j}	1.10^{bc}	12.38^{c-g}	18.53^{c-f}
29056	26.80^{b-i}	83.90^{a-e}	6.28^{b-h}	18.23^{b-e}	6.15^{c-i}	1.10^{bc}	12.72^{b-g}	19.15^{b-e}
29057	25.48^{e-k}	79.80^{a-g}	6.10^{c-h}	17.70^{b-f}	6.00^{d-j}	1.07^{c}	12.19^{d-g}	18.25^{c-f}
29251	21.05^{k}	64.75^{h}	5.10^{i}	13.30^{h}	5.35^{j}	0.83^{c}	9.75^{i}	15.10^{f}
105002	32.05^{a}	93.20^{a}	7.20^{a}	23.29^{a}	8.50^{a}	2.43^{a}	14.90^{a}	23.85^{a}
105007	23.03^{h-k}	77.95^{b-h}	5.90^{d-i}	16.95^{b-g}	5.90^{e-j}	1.03^{c}	11.51^{d-i}	17.90^{c-f}
225802	21.08^{k}	66.35^{gh}	5.45^{hi}	13.80^{gh}	5.40^{ij}	0.97^{c}	10.08^{hi}	16.00^{ef}
238999	29.74^{a-e}	88.75^{a-d}	6.53^{a-f}	19.10^{bc}	6.65^{b-e}	1.14^{bc}	13.09^{a-f}	19.90^{b-e}
239004	26.23^{d-j}	81.85^{a-f}	6.23^{b-h}	17.88^{b-f}	6.10^{c-j}	1.08^{c}	12.29^{c-g}	18.48^{c-f}
239005	25.35^{e-k}	79.38^{a-g}	6.08^{c-h}	17.38^{b-f}	5.95^{e-j}	1.05^{c}	11.98^{d-h}	18.10^{c-f}
239006	24.73^{f-k}	79.05^{b-g}	5.98^{d-i}	17.20^{b-g}	5.95^{e-j}	1.04 ^{c}	11.60^{d-i}	17.95^{c-f}
239012	30.50^{a-d}	89.55^{a-d}	6.75^{a-d}	19.40^{bc}	6.75^{bcd}	1.17^{bc}	13.43^{a-d}	21.12^{a-d}
239014	31.37^{abc}	89.80^{abc}	6.90^{abc}	19.50^{bc}	6.80^{bc}	1.22^{bc}	14.36^{abc}	21.59^{abc}
239027	29.12^{a-f}	88.20^{a-d}	6.50^{a-f}	18.85^{bcd}	6.55^{b-e}	1.14^{bc}	13.00^{a-f}	19.65^{b-e}
239036	30.05^{a-e}	88.95^{a-d}	6.58^{a-e}	19.10^{bc}	6.75^{bcd}	1.16^{bc}	13.28^{a-e}	20.95^{a-e}
239051	28.43^{a-f}	85.30^{a-e}	6.40^{a-g}	18.65^{b-e}	6.45^{c-g}	1.13^{bc}	12.89^{a-f}	19.40^{b-e}
239055	26.82^{b-i}	84.40^{a-e}	6.30^{b-h}	18.45^{b-e}	6.20^{c-h}	1.12^{bc}	12.82^{a-g}	19.18^{b-e}
239059	23.60^{g-k}	78.70^{b-g}	5.98^{d-i}	17.05^{b-g}	5.90^{e-j}	1.04^{c}	11.58^{d-i}	17.90^{c-f}
239060	31.59^{ab}	91.10^{ab}	7.05^{ab}	20.13^{b}	7.25^{b}	1.60^{b}	14.58^{ab}	22.60^{ab}

Mean values with a similar letter(s) in each column had non-significant differences at 5% probability level as tested by Duncan's Multiple Range Test (DMRT). HLPB (cm) = Height lowest primary branch, PH (cm) = Plant height, PTL (cm) = Petiole length, IFL (cm) Inflorescence length, NBPP= number of branch per plant, STY (cm) = Stem thickness, LL (cm) = Leaf length and NV= Verticil number.

height of white lupin genotypes was reported by Clark (2014). Similar results were also reported by Arab et al. (2014) white lupin genotypes height at green ripening was recorded in range 63 to 115. Also, Temesgen (2019) reports that plant height at flowering ranges from the shortest genotypes which were 56 in cm to the longest one which is 137.83 cm long.

Yield and yield component

Statistical analysis of the data revealed that pod length was significantly different and seed weight/plant, number of pods per plant, number of seeds per pod and grain yield showed highly significant. However, the landraces exhibited a non-significant difference, 100-seed weight, seed length, and seed width was present as shown in Table 6. Georgieva et al. (2018) reported significant and highly significant differences among white lupin genotypes for yield traits such as seed weight per plant, pod length and pod thickness using 23 white lupin genotypes. Also, Ehab et al. (2016) in seasonal differences observed significant differences for number of seed per pod. Hibstu (2016) also reported by using 110 accessions of white lupin results of yield and yield component showed significant deference for pod length at Haramaya in 2012.

The mean values of landrace for the number of pods per plant ranged from 24.85 to 48.10 whereas it was in the range between 5.91 and 7.61 and 1.14 and 2.25 cm for pod length and pod thickness, respectively. The entire highest and lowest mean values for all pod character traits were registered for landraces 105002 and 29251, respectively. However, 7, 17 and 5 landraces for the number of pod per plant, pod length and pod thickness respectively, had mean values non-significant differences from landrace 105002. Whereas 2 landraces for the number of pod per plant and 7 and 13 landraces for pod length and pod thickness, respectively, had non-significant differences with mean values of 29251 (Table 7). The result indicated that the significant difference between the landrace of white lupin depends on the pod characters' agronomic traits. This was important for the breeder to select good landrace for yield and other

Table 6. Mean square from analysis of variance for yield trait.

Trait	Rep (1)	Block with Rep. (8)	Treatment (Unadj.) (24)	Intra block Error (16)	RCBD error (24)	Total (49)	Efficiency relative to RCBD	CV (%)
NPPP	20.301	4.4843	73.41**	9.8100	8.0348	40.307	81.904	8.218
PL	0.0260	0.2701	0.3685*	0.1667	0.2012	0.2796	107.01	5.997
PT	0.0072	0.0165	0.087**	0.0123	0.0137	0.0494	102.54	8.702
NSPP	0.4881	0.1452	1.210**	0.1754	0.1653	0.6838	94.248	7.967
HSW	2.8513	0.7236	4.842ns	5.1761	3.6919	4.2383	71.327	7.614
SL	0.0069	0.0011	0.001ns	0.0012	0.0012	0.0014	97.321	4.203
SW	0.0004	0.0021	0.001ns	0.0018	0.0019	0.0015	100.97	4.508
SWPP	116.11	16.200	135.5**	21.772	19.915	78.490	91.469	10.47
GY	855027	103478	1389511**	96499	98825	746430	100.16	9.799

*, **: Significant at 5 and 1%, respectively. Rep = replication, RCBD = randomized complete block design, and CV (%) = coefficient of variation in percent. NPPP=Number of pods per plant, PL=Pod length, PT=Pod thickness, NSPP= Number of seeds per pod, HSW=100-seed weight, SL=Seed length, Seed width, SWPP=Seed weight/plant, GY=Grain yield.

Table 7. Mean values of 25 white lupin landraces for yield traits.

Landraces	NPPP (cm)	PL (cm)	PT (cm)	NSPP (cm)	SWPP (g)	GY (kg)
9960	39.85^{b-f}	6.99^{a-e}	1.28^{d-g}	5.35^{d-g}	48.48^{a-e}	3589.5^{b-f}
9963	34.55^{f-h}	6.50^{b-f}	1.20^{e-h}	4.80^{e-i}	39.16^{e-h}	2785.7^{g-j}
24850	34.30^{f-h}	6.47^{b-f}	1.18^{egh}	4.75^{f-i}	38.50^{e-h}	2765.0^{g-j}
26634	32.15^{ghi}	6.38^{c-f}	1.18^{egh}	4.45^{ghi}	36.34^{gh}	2469.6^{ij}
26635	33.38^{f-h}	6.39^{c-f}	1.18^{egh}	4.60^{ghi}	36.94^{fgh}	2737.1^{hij}
26636	31.35^{hij}	6.31^{def}	1.12^{gh}	4.40^{ghi}	33.34^{hi}	2395.8^{j}
29054	37.78^{c-h}	6.79^{a-f}	1.26^{d-g}	5.20^{d-h}	46.79^{b-g}	3427.5^{b-h}
29056	38.25^{c-h}	6.83^{a-f}	1.26 $^{d-g}$	5.30^{d-g}	47.10^{b-g}	3500.6^{b-g}
29057	36.39^{d-i}	6.73^{a-f}	1.25^{e-h}	5.00^{d-i}	44.10^{b-h}	3182.8^{d-i}
29251	24.85^{j}	5.91^{f}	1.14^{h}	4.10^{i}	24.57^{i}	530.0^{l}
105002	48.10^{a}	7.61^{a}	2.25^{e-h}	7.34^{a}	59.42^{a}	4374.6^{a}
105007	34.85^{f-h}	6.62^{a-f}	1.21^{e-h}	4.85^{e-i}	40.35^{d-h}	2874.9^{f-j}
225802	29.10^{ij}	6.14^{ef}	1.16^{gh}	4.18^{hi}	32.90^{hi}	1678.9^{k}
238999	44.07^{abc}	7.14^{a-d}	1.29^{bcd}	5.80^{b-e}	51.10^{a-d}	3783.5^{a-d}
239004	37.75^{c-h}	6.74^{a-f}	1.25^{e-h}	5.15^{d-h}	46.30^{b-g}	3264.7^{c-h}
239005	35.65^{d-i}	6.73^{a-f}	1.24^{e-h}	4.95^{d-i}	43.52^{c-h}	3020.5^{e-j}
239006	35.43^{e-i}	6.72^{a-f}	1.24^{e-h}	4.95^{d-i}	40.79^{d-h}	2986.5^{e-j}
239012	46.12^{ab}	7.34^{abc}	1.30^{abc}	5.93^{bcd}	54.31^{abc}	4018.6^{abc}
239014	46.33^{ab}	7.38^{abc}	1.31^{abc}	6.49^{abc}	54.83^{abc}	4065.7^{ab}
239027	43.18^{a-d}	7.14^{a-e}	1.29^{c-f}	5.70^{c-f}	50.90^{a-d}	3778.4^{a-d}
239036	44.50^{abc}	7.32^{abc}	1.30^{abc}	5.80^{b-e}	51.32^{a-d}	3800.9^{a-d}
239051	42.65^{a-e}	7.07^{a-e}	1.29^{c-f}	5.38^{d-g}	49.10^{a-e}	3647.2^{a-e}
239055	39.10^{b-g}	6.94^{a-e}	1.28^{d-g}	5.33^{d-g}	47.78^{b-f}	3543.3^{b-f}
239059	35.15^{e-i}	6.63^{a-f}	1.21^{e-h}	4.95^{d-i}	40.78^{d-h}	2942.0^{e-j}
239060	48.08^{a}	7.43^{ab}	1.31^{ab}	6.70^{ab}	55.27^{ab}	4092.6^{ab}

Mean values with a similar letter(s) in each column (trait) had non-significant differences at 5% probability level as tested by Duncan's Multiple Range Test (DMRT). NPPP=Number of pods per plant, PL=Pod length, PT=Pod thickness, NSPP= Number of seeds per pod, SWPP=Seed weight/plant, GY=Grain yield.

breeding purpose. Ehab et al. (2016) reported that the number of pods/plant and number of seeds/pod had an overall average of 22.8 and ranged from 15.2 to 30.5 and 4.4 to 4.3 number of seeds/pod respectively. Number of seed per pods 3 to 6 seeded, pod length 9 to 15 cm and pod thickness 1 to 2 cm wide was reported by Clark 2014) and El Bassam (2010). Also, Hibstu (2016) observed minimum and maximum values of 11.31 and

Table 8. Mean square from analysis of variance for nutritional contents.

Trait	Rep (1)	Block with Rep. (8)	Treatment (Unadj.) (24)	Intra block error (16)	RCBD error (24)	Total (49)	Efficiency relative to RCBD	CV (%)
Pr	0.6116	5.8524	7.7256*	2.8650	3.8608	5.6875	115.16	5.310
P	283188	16368	79105**	14780	15310	52023	100.34	4.400
Ca	199304	8345.6	28565***	2141.1	4209.3	20120	157.55	5.991
K	1322706	102449	77299ns	98179	99602	113640	100.06	5.518
Fe	128.96	21.691	339.91**	66.410	51.504	194.35	77.554	9.988

*, **: Significant at 5 and 1%, respectively. Rep = replication, RCBD = randomized complete block design, and CV (%) = coefficient of variation in percent. Pr=Protein, P=Phosphorus, Ca=Calcium, K=Potassium, Fe=Iron.

(20.84 cm inflorescence length, respectively, for 110 white lupin accessions. Similar results were also reported by Arab et al. (2014) pod length with minimum 3 and a maximum of 7 was recorded using 36 white lupin genotypes.

The mean values of landrace ranged from 4.1 to 7.34, 24.57 to 59.42 and 530.0 to 4374.6 for number of seed per pod, seed weight per plant and grain weight, respectively. The highest mean number of seed per pod, seed weight per plant and grain weight was registered for landrace 105002 while all the lowest mean values for the traits were registered for landrace 29251. But 2, 8 and 7 landraces had mean values for number of seed per pod, seed weight per plant and grain weight, respectively, non-significant from mean values of 105002, and 12, 2 landraces for number of seed per pod and seed weight per plant, had non-significant difference from mean values of 29251 (Table 7). Hibstu (2016) observed minimum and maximum values of 11.31 and 20.84 cm inflorescence length, respectively, for 110 white lupin accessions. The landrace that was superior in one of the yield components can be involved in a breeding program like 105002 for the number of pod per plant, pod length, pod thickness, number of seed per plant, seed weight per plant and grain weight respectively. In another study, Ehab et al. (2016) observes that the best seed yield per plant was produced by the Australian genotype 75B9.10 (38.3 g) closely followed by the landrace Fayed1 (38.2 g). Kurlovich (2002) observed pod length and number of seed per pod range from 1-2 to 7-16 cm and 3 to 6. Similar results were also reported by Clark (2014) who noted number of seeds per pod containing 3-7 seeds. Šariková et al. (2011) observed that grain yield ranged from 790 to 3940 kg/ha^{-1} in 2006–2008 trial seasons. Similarly, Gonzalez-Andre et al. (2007) reports during his findings, the lowest and highest values of mean grain yield per plant, number of pods per plant and number of seeds per pod was 26.6 g to 60.3g per plant, 17.5 to 45.6 pods per plant and 4.9 to 5.7 seeds per pod.

Protein and chemical composition of white lupin

Chemical composition of white lupin grain indicated that significant difference exist for protein, phosphorus, iron and very high significance for calcium contents of grain in Table 8. Yorgancilar and Bilgiçli (2014) and Sujak et al. (2006) reported significant differences among white lupin genotypes for protein content of grain. Tizazu and Emire (2010) evaluated grains from the market in northwestern Ethiopia and observed significant differences for protein and mineral contents among the sample grains.

The mean values of landrace for protein% ranged from 28.55 to 35.81 (mg/kg) whereas it was in the range between 2468.1 and 3423.2, 635.67 and 1043.72, 68.67 and 104.69 (mg/kg) for phosphorous, calcium and iron, respectively in Table 9. The entire highest and lowest mean values for all chemical composition traits registered for landraces 9960 and 105002, respectively. However, 13, 3 and 8 landraces for protein, phosphorous, calcium and iron respectively, had mean values of non-significant differences from landraces 9960; whereas 10 landraces for protein, and 14, 14 and 15 landraces for Phosphorous, Calcium and Iron, respectively, had non-significant differences with mean values of 105002 (Table 9). Martinez-Villaluenga et al. (2006), and Straková et al. (2006) observed the protein content of white lupin range from 32.9% to more than 36% (Sujak et al., 2006). The variation attributed in the protein content between species and cultivars as a result of the characteristics depended on growing conditions and soil types (Martínez-Villaluenga et al., 2006) which varies from 28 to 48% (Capraroa et al., 2008). The variation of white lupin protein content was important for crop improvement through the selection to alleviate the protein malnutrition problem due to climate change in Ethiopia.

Tizazu and Emire (2010) observed significant variations among white lupin landraces for phosphorus and calcium contents in the range between 979.8 and 2487.7 µg/g and 671.3 and 2490.2 µg/g, respectively using genotype of lupin (*L. albus*) seeds which were collected from the local markets of Dembecha and Debretabor in Amhara region (Northern part of Ethiopia). However, from both locations (Dembecha and Debretabor), they observed 2489, 125.1 and 825.6 µg/g, phosphorus, iron and calcium contents respectively. Paulos (2009) also reported 60.0 and 67.2 µg/g contents of Iron for Dangla and Tilili white lupin genotypes respectively. Zelalem and

Table 9. Mean values of 25 white lupin genotypes seed for nutritional contents.

Accession	Protein (%)	Phosphorous (mg/kg)	Calcium (mg/kg)	Iron (mg/kg)
9960	35.81^{a}	3423.2^{a}	1043.72^{a}	104.69^{a}
9963	32.70^{a-f}	2795.2^{cde}	758.08^{cd}	85.56^{a-e}
24850	30.59^{c-f}	2681.0^{c-f}	695.64^{cde}	70.79^{e}
26634	30.11^{c-f}	2636.7^{c-f}	687.06^{cde}	70.65^{e}
26635	29.29^{def}	2598.2^{efd}	666.69^{cde}	70.34^{e}
26636	30.03^{c-f}	2623.2^{c-f}	677.75^{cde}	70.41^{e}
29054	29.28^{def}	2530.7^{fd}	658.96^{de}	69.54^{e}
29056	32.08^{a-f}	2722.5^{c-f}	735.91^{cde}	74.31^{cde}
29057	32.28^{a-f}	2745.8^{c-f}	741.70^{cde}	82.70^{b-e}
29251	31.75^{a-f}	2706.0^{c-f}	720.75^{cde}	73.35^{ed}
105002	28.55^{f}	2468.1^{f}	635.67^{e}	68.67^{e}
105007	30.62^{c-f}	2684.0^{c-f}	716.49^{cde}	70.88^{e}
225802	29.13^{ef}	2483.9^{f}	647.04^{de}	68.99^{e}
238999	33.83^{abc}	2871.5^{bcd}	884.09^{b}	99.41^{ab}
239004	31.98^{a-f}	2721.2^{c-f}	734.27^{cde}	73.60^{ed}
239005	31.08^{b-f}	2703.5^{c-f}	719.25^{cde}	72.89^{ed}
239006	30.99^{c-f}	2694.5^{c-f}	719.03^{cde}	71.15^{e}
239012	34.09^{abc}	2894.7^{bcd}	949.80^{ab}	100.28^{ab}
239014	34.11^{abc}	2914.9^{bc}	963.58^{ab}	100.51^{ab}
239027	33.38^{a-d}	2862.0^{bcd}	777.41^{c}	93.44^{abc}
239036	33.87^{abc}	2892.3^{bcd}	900.50^{b}	100.13^{ab}
239051	32.85^{a-e}	2849.8^{bcd}	759.40^{cd}	91.42^{a-d}
239055	32.49^{a-f}	2790.8^{cde}	754.82^{cd}	84.38^{b-e}
239059	30.93^{c-f}	2689.3^{c-f}	718.52^{cde}	71.12^{e}
239060	35.18^{ab}	3095.2^{b}	1042.35^{a}	100.64^{ab}

Mean values with a similar letter(s) in each column (trait) had non-significant differences at 5% probability level as tested by Duncan's Multiple Range Test (DMRT).

Chandravanshi (2014) reported significant differences among white lupin genotype for calcium and iron in the range of 502 to 967 and 78 to 93 µg/g, respectively.

The mean value for phosphorus was higher than the other elements followed by calcium and iron was the least. The higher phosphorus in the white lupin landrace was probably due to the fact that phosphorus elements were highly mobile in the plant tissue and trans-located from old plant tissue to new plant tissue according to (Ishibashi et al., 2004). Highly fertilized soil with manure and organic residues for cultivating the white lupin has higher availability of Ca composition (Khetarpaul et al., 2004). The high concentration of Fe in white lupin may be due to the fact that these ions are readily transferred from the soil to plants, and accumulate in plants (Soetan et al., 2010; Saadia and Nabila, 2013). This indicated that white lupin genotype cultivation was possible on unfertile soil which prevents environmental pollution by fertilizer. Lupin generally contains about twice the protein found in those legumes normally consumed by humans; not only protein but also Ca level content of white lupin genotype was higher than many other crop foodstuffs including wheat, maize, and soybean as reported by Tizazu and Emire (2010). White lupin is mainly consumed and grown in different parts of Ethiopia with different agronomic and climate conditions. The wide variation in white lupin grain protein and mineral composition was important during selection for improvement in breeding of these crops within good grain composition to alleviate food insecurity due to climate change effects such as drought. The mineral composition of the white lupin genotype was aimed at mitigating the micronutrient malnutrition of the developing regions of the world as it compares with that of other dry beans (Tizazu and Emire, 2010).

Estimates of variability components

Phenotypic and genotypic variances

Estimates of phenotypic (σ^2p) and genotypic (σ^2g) variances, and phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) are presented in Table 10. The genotypic and phenotypic coefficients of variation ranged between 4.39 to 29.54%,

Table 10. Mean, range, genetic and phenotypic variances, heritability and genetic advance of white lupin landraces.

Trait	Range	Mean	δ^2g	δ^2p	GCV (%)	PCV (%)	H^2%	GAM	GAM (5%)
DFE	8-13.5	10.55	1.92	3.60	13.14	17.98	53.42	2.09	19.79
DFF	70-84	78.45	9.20	20.42	11.72	12.76	45.04	4.19	5.34
D50%F	74-85.75	81.66	7.76	12.85	3.41	4.39	60.36	4.46	5.46
DM	163-196	184.1	48.12	95.12	3.77	5.30	50.59	10.16	5.52
HLPB	21.05-32.05	25.99	13.88	17.95	14.33	16.30	77.31	6.75	25.96
PH	64.75-93.2	80.67	61.93	94.11	9.75	12.03	65.80	13.15	16.30
PTL	5.1-7.2	6.16	0.25	0.38	8.05	9.98	65.02	0.82	13.37
IFL	13.30-23.29	17.63	3.57	5.72	10.73	13.57	62.50	3.08	17.47
NBPP	5.35-8.5	6.23	0.46	0.57	10.93	12.11	81.47	1.27	20.32
STY	0.83-2.43	1.14	0.07	0.11	22.92	29.21	61.58	0.42	37.05
LL	9.75-14.9	12.27	1.62	2.36	10.36	12.51	68.61	2.17	17.68
VN	15.1-23.85	18.76	3.14	5.74	9.44	12.76	54.76	2.70	14.40
NPPP	24.85-48.1	38.11	31.80	41.61	14.80	16.92	76.42	10.16	26.64
PL	5.91-7.61	6.81	0.12	0.29	5.11	7.88	42.07	0.46	6.83
PT	1.14-2.25	1.28	0.04	0.06	16.54	18.69	78.31	0.39	30.14
NSPP	26.31-32.8	5.26	0.52	0.69	13.68	15.83	74.69	1.28	24.36
SWPP	24.57-59.42	44.56	56.86	78.64	16.92	19.90	72.31	13.21	29.65
GY	530.0-4374.6	3170	775807.2	872306.2	27.78	29.46	88.94	1711.1	53.98
Pr	28.55-35.81	31.88	2.92	5.78	28.00	29.54	50.44	2.50	7.84
P	268.1-3423.2	2763	38595.00	53375.00	7.11	8.36	72.31	344.14	12.45
Ca	635.67-1043.7	772.3	15854.32	17995.46	16.30	17.37	88.10	243.46	31.52
Fe	68.67-104.69	81.59	136.75	203.16	14.33	17.47	67.31	19.76	24.22

δ^2g= Genotypic variance, δ^2p= Phenotypic variance, GCV (%) =Genotypic coefficient of variation, PCV (%) =Phenotypic coefficient of variation, H2 (%) = Heritability in broad sense, and GAM (5%) = Genetic advance as percent of mean at 5% selection intensity. DFE= Day to 50% emergence, DFF= Days to first flowering, D50%F= Day to 50% flowering, DM= Day to maturity, HLPB=Height lowest primary branch, PH=Plant height (cm), PTL=Petiole length, IFL=Inflorescence length, NBPP=Number of branch/plant, STY=Stem thickness, LL=Leaf length, VN=Verticil number, NPPP=Number of Pod/plant, PL=Pod length, PT=Pod thickness, NSPP= Number of seeds per pod, SWPP=Seed weight/plant, GY=Grain yield, Pr=Protein, P=Phosphorus, Ca=Calcium, Fe=Iron.

and 3.41 to 28% respectively, for 22 traits of 25 white lupin genotypes.

According to Sivasubramaniah and Madhavamenon (1973), the estimate of PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (> 20%). The GCV and PCV were estimated <10% for days to 50% flowering, days to maturity, petiole length, pod length and phosphorous content of the grains. This indicated the lesser phenotypic variability among white lupin genotype for these traits that might be due to the environmental influence of environmental factors, but improvement of these traits by selection is not possible as the heritable variation among genotypes is not enough. In support of this study results, Georgieva and Kosev (2016) observed low GCV and PCV was estimated for pod length in two white lupin genotypes Garant and Chernilovec. Also, low GCV was estimated for pod length for white lupin genotype as reported by Hibstu (2016), and Georgieva and Kosev (2018). The GCV and PCV were estimated as moderate (10-20%) inflorescence length.

The estimates of genotypic and phenotypic coefficients of variations were high (> 20%) for stem thickness and grain yield. This suggested that the traits were less influenced by environmental factors and selection based on phenotypic expression of the genotypes could be applied as a breeding method to identify genotypes for higher mean values. High phenotypic and genotypic coefficients of variation is an indication of the less influence of environmental factors in the expression of traits and the higher chance to improve the traits through selection inbreeding (Swati et al., 2014; Bharathiveeraman et al., 2012; Nwangburuka et al., 2012; Saleh et al., 2010). A similar finding by Annicchiarico et al. (2010) and Mera et al. (2006) reported high GCV and PCV for stem thickness and grain yield in white lupin genotypes. Also, Georgieva and Kosev (2016) observed high GCV for grain yield Chernilovec white lupin genotype.

Moderate GCV and PCV was estimated for days to 50% emergence, days to first flowering, days to maturity, height of lower branch, inflorescence length, number of branch per plant, leaf length, numbers of pod per plant, pod thickness, seed number per pod, seed weight per plant, calcium and iron content traits. Similarly, Dutta et al. (2013) and Jain et al. (2013) reported moderate GCV

and PCV for inflorescence length. Similar result by Temesgen (2019) showed low genetic advance as percent of means for number of primary branches and pod length. Generally, the phenotypic variance exceeded the genotypic variance though little difference indicated small environmental influence contribution on the performance of the traits in addition to genotypic variance. This further indicates that the contribution of environmental variance was less than that of genotypic variance to selection for improvement of white lupin crops.

Estimates of heritability and genetic advance

Estimates of heritability in a broad sense (H^2) and genetic advance as percent of the mean (GAM) for 22 quantitative traits of 25 white lupin genotypes are presented in Table 10. The heritability values ranged from 42.07% (pod length) to 88.94% (grain yield) while GAM was in the range between 5.34 (days to first flowering) and 53.98% (grain yield). As suggested by Johnson et al. (1955), heritability values are categorized as low (<30%), moderate (30-60%) and high (>60%) and GAM was classified as low (<10%), moderate (10-20%) and high (>20%).

High H^2 and GAM estimates for height of lower branch, number of branch per plant, stem thickness, number of pod per plant, pod thickness, number of seed per plant, seed weight per plant, grain yield, and calcium and iron contents of grain. High heritability coupled with high genetic advance as percent of mean indicates function of additive gene action which is important for direct selection based on these traits to that diverse material which could be effective for desired improvement. In the light of this, Tesfaye et al. (2014) reviewed that high H^2 couple with high GAM would give better information about genotypes than the individual parameter for selection. The recent study is in agreement with Temesgen (2019) who reported higher values of the coefficient of heritability and genetic advance as percent of means for number of primary branches per plant, pod thickness, number of pod per plant, seed number per pod, seed yield per plant in gram, and seed yield per hectare. Also, Georgieva and Kosev (2016) observed in both varieties Garant and Chernilovec an established high coefficient of heritability (H^2) in the traits number of seeds per plant and higher values of the coefficient of heritability for number of pod per plant in Chernilovec, while the inheritance had a very low coefficient in Garant. Similarly, Hibstu (2016) reported higher genetic advance as percent of means for number of pods per plant and grain yield. Also, Mera et al. (2006) reported high broad sense heritability for pod wall proportion. Mohammadi and Pourdad (2009) and Hefny (2013) have reported high values of heritability, which are similar to those in the present study for grain yield per plant.

The moderate H^2 with low GAM were estimated for day to first flowering, day to maturity and protein content while the moderate H^2 and GAM were estimated for day to 50% emergency and vertical numbers. These show the influence of environmental effect on the expressions of the trait than that of genetic effect; so, selection based on this trait was not rewarded for improvement. Also, high heritability estimates was accompanied with moderate genetic advance as percent of the mean (10-20%) for plant height, petiole length, inflorescence length, leaf length and phosphorus contents. Selection of genotypes based on mean performances may be effective to improve traits that had high heritability estimates coupled with moderate or high genetic advance as percent of mean (Sivasubramanian and Madhavamenon, 1973).

Conclusion

The research results showed the presence of significant differences among white lupin landraces for agronomic traits, protein and mineral contents of grains. The landraces were collected mainly from northwestern Ethiopia and few from southern Ethiopia indicated the existence of variations for different agronomic traits and nutrient contents of grain in germplasm of white lupin. The variation of genotypes for yield ranged from 122 to 3206 kg with a mean grain yield of 1938.13 kg ha^{-1}. The genotypes grain protein content was in the range between 28.55 and 35.81% with an average of 31.88%, and the grain of genotypes had phosphorus, calcium and iron contents of 268.1 to 3423.2, 635.67 to 1043.72 and 68.67 to 104.69 mg/kg, respectively. The phenotypic (PCV) and genotypic (GCV) coefficient of variations varied from 4.39 to 29.54% and 3.41 to 28%, respectively. Heritability in a broad sense (H^2) and genetic advance as percent of the mean (GAM) ranged from 42.07 to 88.94% and 5.34 to 53.98%, respectively. The estimates of GCV, PCV, H^2 and GAM were moderate to high for numbers of pod per plant, seed weight per plant, pod length, pod thickness, inflorescence length and verticil number, days to first flowering and number of branches per plant, plant height and stem thickness, numbers of seed per plant pod length and pod thickness. The observed variations among landraces suggested the higher chance of identifying genotypes for desirable traits either to be used as a variety after consecutive evaluation or used in crossing program for genetic recombination and selection of potential progenies in the subsequent generation. The improvement of white lupin for agronomic and nutrient contents of grain can contribute to adapting to climate variability and change in Ethiopia.

CONFLICT OF INTERESTS

The author has not declared any conflict of interests.

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Full Length Research Paper

Evaluation of improved pigeon pea (*Cajanus cajan*) varieties for organoleptic dal quality in India

Fromm I.[1*], Bollinedi H.[2], Dheer M.[2], Goel P.[2], Nehra P. [2], Raje R. S. [2], Singh G.[3], Singh N. K.[2], Jha S. K. [4] and Singh A.[5]

[1]School of Agricultural, Forest and Food Sciences, Bern University of Applied Sciences, Zollikofen, Switzerland.
[2]Division of Genetics, ICAR-IARI, New Delhi, India.
[3]ICAR- NRCPB, New Delhi, India.
[4]Division of Food Science and Postharvest Technology, IARI, New Delhi, India.
[5]Division of Agricultural Economics, IARI, New Delhi, India.

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Pigeon pea (*Cajanus cajan* L.) is an important pulse crop in the Indian diet and one of the most important sources of dietary protein for the population. Organoleptic qualities of pigeon pea dal were tested to draw conclusions on the preferred varieties. Organoleptic qualities such as taste, texture, aroma, tenderness, sweetness and overall acceptance were tested by a trained sensory panel. Available and commercially viable improved varieties were selected for the analysis. All samples were milled and cooked under the same conditions. Results indicated that PUSA ARHAR 16, one of the improved varieties, presents a good potential in terms of agronomic characteristics for farmers and is also well accepted by the sensory panel during the organoleptic evaluation. Generating sound scientific evidence on organoleptic characteristics of pigeon pea is important for the breeders, as they will evaluate which varieties have a commercial potential and are accepted by the consumers.

Key words: Consumer preferences, organoleptic qualities, pigeon pea, India

INTRODUCTION

Pigeon pea (*Cajanus cajan*) is an important pulse crop in the Indian diet and one of the most important sources of dietary protein for the population. In the context of the fifth phase of the Indo-Swiss Collaboration in Biotechnology (ISCB), an assessment of the physical and organoleptic qualities of dal made from pigeon pea seed was carried out. In India, pigeon pea is mainly consumed as dal which is the preparation in the form of soup made from split seeds of pigeon pea. Its preparation involved cooking (boiling) of split seeds in water followed by frying in vegetable oil with various spices. Dal of pigeon pea is consumed all over the India and constitutes the main constituent of vegetarian diet. Studies of the natural genetic variability of pigeon pea and the presence of its wild relatives in the region indicate that India is the primary center of origin of pigeon pea (Joshi et al., 2001; Saxena, 2008; Saxena et al., 2010; Parray et al., 2019). Several physical, biochemical and organoleptic factors affect dal quality (Singh Raghuvanshi et al., 2011; Chandegara and Joshi, 2002). Thus, an assessment of

*Corresponding author. E-mail: ingrid.fromm@bfh.ch.

Table 1. Varieties evaluated for organoleptic traits.

Varieties	Pedigree	Agronomic characteristics	Seed color	Seed weight (g/100 seeds)	Place of origin	Year of release
PUSA 992 (Control)	Selection of 90306	Indeterminate growth, semi-spreading, early maturing (135-140 days), yields about 1200-1500 kg/ha, suitable for pigeon pea and wheat cropping system	Yellow brown	8.2	IARI, New Delhi	2002 (CVRC)
AL 882	PUSA 982 X ICPL 85024	Determinate growth habit, early maturing (132 days)	Yellow brown	7.6	IARI, New Delhi	2018
PAU 881	H-89-5 X ICPL 85024	Indeterminate growth, early maturing, semi-spreading, suitable for pigeon pea and wheat cropping system	Yellow brown	7.5	PAU, Ludhiana	2007 (SVRC)
PUSA ARHAR 16	Selection of single plant progeny of superior recombinants selected from the population improvement approach involving diverse genotypes viz., ICP 85059, ICPL 390, ICPL 267, Manak, H-92-39 and ICP 85024	Determinate, erect and compact, extra early, matures in about 120 days, yields about > 1000 kg/ha	Brown	7.4	IARI, New Delhi	2018 (SVRC)
BSMR 853	(ICPL 736 X BDN 1) X BDN 2	Indeterminate growth, spreading, resistant to wilt and sterility mosaic disease	White	11-12	ARS, Badnapur	2001 (SVRC)
BSMR 736	CTP 7217 X No. 148	Red seeds, resistant to wilt and SMD	Red	10-11	ARS, Badnapur	1994 (SVRC)
BDN 711	Sel. From BPG 111	Indeterminate growth, spreading, resistant to wilt and sterility mosaic disease, escape terminal drought	White	10-12	ARS, Badnapur	2012 (SVRC)

these factors and acceptance to consumers is an important aspect of quality in pigeon pea. The overall goal of the ISCB program was to contribute towards food security and sustainable agriculture in India through innovative biotechnology approaches. One component of the program was to breed pigeon pea varieties to overcome production constraints such as low yields, resistance to pod borer (*Helicoverpa armigera*) and maruca pod borer (*Maruca vitrata)*, and early maturity. The study also aimed at identifying market preferred seed types and traits; and understanding of seed supply systems along with utilization of quality seed of improved varieties. Additionally, the study determined which types of pigeon pea varieties farmers grow, the farmers', processors' and consumers' preferences in choice of the grain type, and constraints to production. With these results, research strategies for improvement of pigeon pea production could be formulated (Fromm and Egger, 2018; Fromm and Singh, 2019). An organoleptic evaluation of selected improved pigeon pea varieties was conducted using methods and recommendations found in the literature on best practices for sensory evaluations (Beckley and Kroll, 1996; Lawless and Heymann, 1998; Moskowitz et al., 2003; Lyon, 2001). The aim of this organoleptic evaluation was to identify which newly released variety had acceptable sensory characteristics and is preferred by the panelists.

MATERIALS AND METHODS

Plant material and sample collection

The seeds of the varieties were procured from the Breeding Institutes which developed that variety (Table 1). In the present investigation, the leading pigeon pea varieties of India were utilized to assess the organoleptic evaluation. The major pigeon pea growing area in India is Central zone which comprises about 82% area of India. The leading varieties of these zones are BSMR 853, BDN

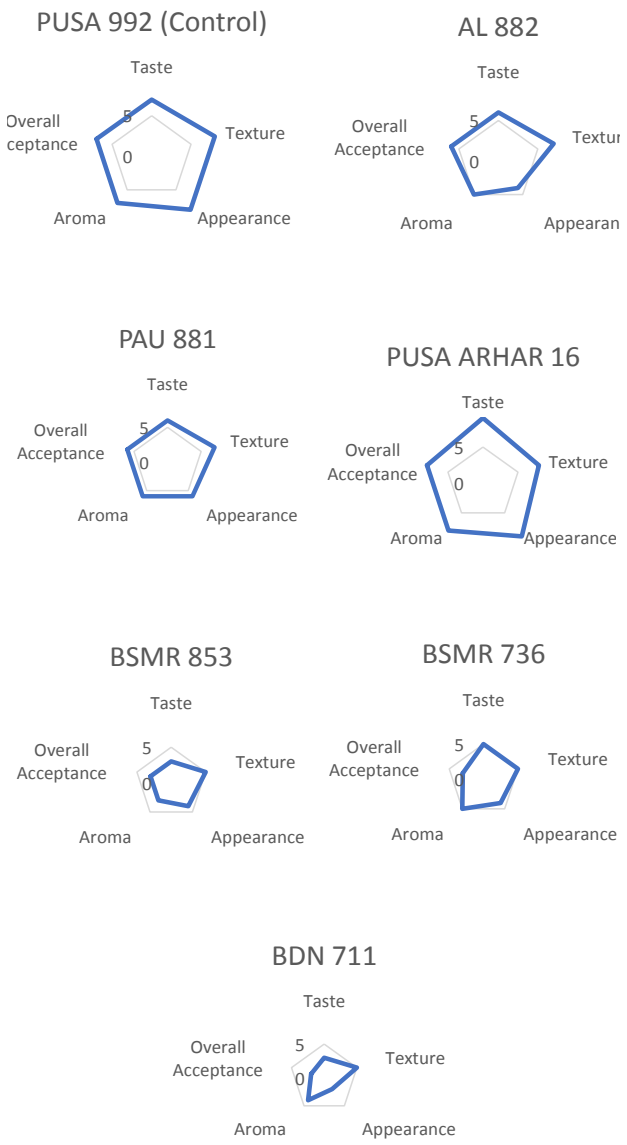

Figure 1. Comparison of organoleptic evaluations.

711, BSMR 753, Maruti and Asha. Out of these, three latest varieties BSMR 853, BDN 711 and BSMR 753 were included in the study. Moreover, from the NWPZ (North West Plain Zone), 5 varieties PUSA 992, PUSA ARHAR 16, AL 882 and PAU 881 were evaluated. In this zone, varieties with short vegetation period are preferred as in the Rabi season wheat crop is taken up after the harvest of pigeon pea. The demand for such varieties with short vegetation is increasing day by day. However, there is always a concern about the organoleptic quality of the pigeon pea dal made from the seeds of such varieties. There is a common understanding that the early maturing varieties do not have good organoleptic quality of dal as compared to traditional varieties. Therefore, it was imperative to test the varieties to come up with conclusive and scientific evidence for the breeders.

Milling of pigeon pea varieties into split dal

A standard protocol was used for milling of seeds into split dal as described (Wani et al., 2011; Navnath et al., 2018). The grains were cleaned and graded initially. Before milling clean-graded grains were subjected to thermal treatment in a temperature controlled rotary roasting equipment in which heating element was centrally placed. Rotational speed of the equipment was adjusted in such a way to have residence time of the grains 3 min. Temperature of roasting was set at 250°C using temperature controller. An amount of 0.5 kg of thermally treated pigeon pea seeds sample was milled in a small manually operated disc mill made up of two iron discs with corrugations. The distance between lower stationary and upper moving disc was kept constant for all samples. After milling, fractions of the samples (gota, unmilled grain, hull, split cotyledons that is, dal and fines) were separated and dhal was obtained (Table 1).

Sensory evaluation

Pigeon pea dal/ soup from the mentioned varieties was prepared by mixing in 1:3 ratio of split dal and water, and pressure cooked until three whistles. The pressure was allowed to be released on its own and then prepared for serving to a trained group of panelists in three sessions. A sensory evaluation of pressure-cooked pigeon pea dal was conducted with an expert panel, using on a 9-point hedonic scale for the traits like appearance, texture, taste, aroma, and overall acceptance. The hedonic scale defined was:

9= Like extremely
8= Like very much
7= Like moderately
6= Like slightly
5= Neither like nor dislike
4= Dislike slightly
3= Dislike moderately
2= Dislike very much
1= Dislike extremely

Sweetness and tenderness were evaluated using a 5-point scale. The defined criteria for sweetness was:

5= Sweet
4= Moderately sweet
3= Neither sweet nor tasteless
2= Tasteless
1= Undesirable

The 5-point scale used to evaluate tenderness was:

5= Desirably soft
4= Moderately soft
3= Neither soft nor hard
2= Moderately hard
1= Very hard

No further statistical analysis was made due to the small sample of pigeon pea.

RESULTS AND DISCUSSION

The results of the sensory evaluation indicated that pigeon pea variety PUSA ARHAR 16 was favored in terms of taste, texture, appearance, aroma and overall acceptance (Figure 1). Pigeon pea variety PUSA 992 was used as the control variable and was favored by the panel in terms of the organoleptic characteristic tested. Pigeon pea varieties BSMR 853 and BDN 711 were the

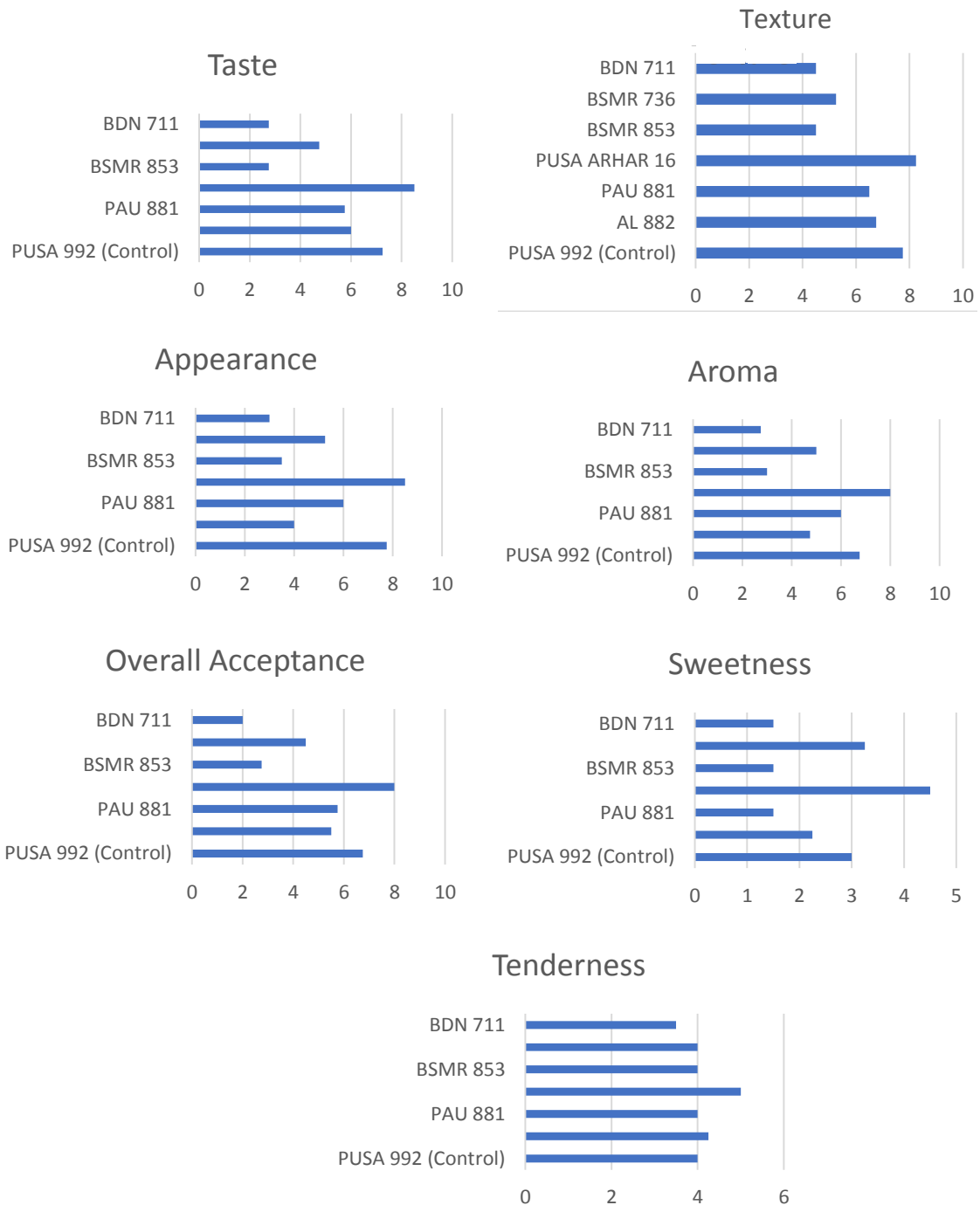

Figure 2. Ratings of organoleptic evaluations per characteristic.

least favored varieties.

Pigeon pea variety PUSA 992 was used as a control because of its wide availability in the market and wide consumption across India. Both the control and improved variety PUSA ARHAR 16 was rated highest scores, 8 and 9, for overall acceptance (Figure 2). Sweetness and tenderness where rated using a different scale. Sweetness of pigeon pea dal in India is understood as a positive characteristic and although dal is consumed as a savory dish, notes of sweetness are favored by the local consumers. PUSA ARHAR 16 and BSMR 736 were evaluated as having this sweetness quality. The results indicated that most varieties are moderately soft, PUSA ARHAR 16 having the most tender quality. Tenderness is also considered a desirable trait by the local consumers and is also perceived as an indication of faster cooking

time.

Conclusion

The organoleptic evaluation of the selected improved pigeon pea varieties gives an indication of which of the varieties can be released to the market with a higher possibility of commercial success. It is of paramount importance to breeders that the genetic material and varieties they have worked on for many years are not only accepted by the farmers because of their improved characteristics (that is early maturity, drought and pest resistance, higher yields) but also accepted by the consumers because of their good organoleptic characteristics. Based on the results of the organoleptic evaluation, PUSA ARHAR 16 presents the most favorable scores, which are likely to be accepted by consumers. The agronomic traits of this improved variety are also favorable for the farmers and present a good potential for wider cultivation in India.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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Full Length Research Paper

Inheritance pattern of resistance to Fusarium wilt (*Fusarium oxysporum f*. sp *sesame*) in sesame

Z. S. Ngamba[1], G. Tusiime[1], P. Gibson[1], R. Edema[1], M. Biruma[2], P. A. L. Masawe[3], E. Kafiriti[3] and F. Kapinga[3]

[1]Department of Agricultural Production, College of Agricultural and Environmental Sciences, Makerere University, P. O. Box 7062, Kampala, Uganda.
[2]National Semi-Arid Resources Research Institute (NaSARRI), P. O. Box 56, Soroti, Uganda.
[3]Tanzania Agricultural Research Institute Naliendele, P. O. Box 509, Mtwara, Tanzania.

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Fusarium wilts (*Fusarium oxysporum* f.sp. *sesame)* is among of the most destructive soil-borne disease of sesame in Uganda. The disease may cause yield loss of up to 100% if not controlled. Breeding and use of resistant varieties is the most economic and eco-friendly solution to the disease since majority of sesame growers are resource constrained. Some genotypes were reported to be moderately resistant to the disease in Uganda. However its nature of inheritance was not studied. Successful breeding requires selection of suitable parents and whose pattern of inheritance of disease resistance is known. In this study, eight parental genotypes of sesame with different levels of resistance to Fusarium wilt pathogen were used in a full diallel to produce F1 progenies. The eight parents and F1 progenies were evaluated in the screen house under high pathogen pressure through artificial infection in an Alpha Lattice Design of three replicates. The results revealed that additive and non-additive gene actions contributed to controlling resistance to Fusarium wilt. However non-additive were more predominant which were signposted by moderate Baker's ratio (53.9%) and low Coefficient of Genetic Determination narrow sense (h^2 = 45.1%). Moreover, the study indicated that maternal effects have influence toward resistance to Fusarium wilt in sesame. Among eight parents used parent Sesim 2 (with EM% GCA effect 7.32, and DI% GCA effect -4.02) and EM15-1-5 (with EM% GCA effect 3.07%, and DI% GCA effect -11.58%) were good combiner parents for transmitting resistance and are recommended for use in breeding for Fusarium wilt resistance.

Key words: Fusarium wilt, inheritance, incidence, resistance, sesame,

INTRODUCTION

Fusarium wilt (*Fusarium oxysporum* f.sp. *sesami*) is a soilborne disease in which its pathogen interacts with the host plant and when inside the plant interfere with the water supply system hence the plant wilt (Bayoumi and EL-Bramawy, 2007; Elewa et al., 2011; Joshi, 2018). Fusarium wilt is among factors responsible for low yield of sesame in Uganda. Elsewhere, the disease has been reported to cause yield loss ranging from 50 to 100%

*Corresponding author. E-mail: zngamba@yahoo.com.

Table 1. Sesame parental genotypes used in the *Fusarium oxysporum f.sp. sesame i*resistance inheritance study.

S/N	Genotype	Code number	Origin	Categoriesof resistance
1	4036-1-10-2//Renner1-3-16-2	P1	Ugandan pure line	Susceptible
2	Lindi 02	P2	Tanzanian variety	Moderate susceptible
3	Sesim 3	P3	Ugandan variety	Susceptible
4	Sesim 1	P4	Ugandan variety	Susceptible
5	Renner1-3-1-17	P5	Ugandan pure line	Moderate susceptible
6	Mtwara 09	P6	Tanzanian variety	Susceptible
7	Sesim 2	P7	Ugandan variety	Moderate resistance
8	EM15-1-5	P8	Ugandan pure line	Moderate resistance

Source: Ngamba et al. (2020).

(El-Bramawy et al., 2009). Some agronomic recommendations (such as early planting, intercropping, burning of leftovers and crop rotation) have been made by researchers to manage the disease in Uganda. However these agronomic practices faces some challenges like early planting aimed at helping the plant to escape from the disease which becomes severe toward the end of the rainy season; Contrariwise, this practice expose the crop to other disease like leaf spot and waterlogging effect (Egonyu et al., 2005). Crop rotation, intercropping and burning of leftovers intended to reduce the population of the pathogen in the soil but they are not efficient due to effective survival strategies of the pathogen (Okungbowa and Shittu, 2012). The best approach for managing this disease is to grow resistant varieties. Resistant varieties are efficient, long term solution, environment friendly and affordable to smallholder resource constrained farmers (Bayoumi and EL-Bramawy, 2007; Jyothi et al., 2011; Shabana et al., 2014). Unfortunately in Uganda, there are no sesame varieties with good levels of resistance to wilt. There is great need therefore to develop resistant varieties. However, successful breeding requires selection of suitable parents whose pattern of inheritance of disease resistance is known (Chataika et al., 2011). Inheritance pattern is fundamental in breeding activities since it provides information on superior parents which can easily combine to produce an offspring with desired traits. Furthermore, it provides information on the choice of breeding methods to use in relation to the trait in question (Chandra, 2011). In a study done by Ngamba et al. (2020) some of the varieties with moderate levels of resistance to Fusarium wilt were identified. These could be useful in breeding for enhanced resistance to the disease. This study was therefore carried out todetermine the mode of inheritance of resistance to *F. oxysporum* f. sp. sesami in sesame genotypes.

MATERIALS AND METHODS

F1 progenies generation

Eight parents (Table 1) were selected and crossed in the field at NaSARRI-Serere in all possible combinations to produce F1 progenies. Full Diallel mating design method 1 was used (Griffing, 1956). The eight (8) parents and fifty six (56) F1 progenies (crosses and reciprocal crosses) were evaluated in the screen house against the isolate SEFU2 of *F. oxysporum* f.sp*. sesame* following artificial inoculation. Isolate SEFU2 was among of the isolates of *F. oxysporum f*. sp*. sesame* tested by Ngamba et al. (2020) and reported to be more aggressive compared to other tested isolates. During this study, the isolate was obtained from laboratory of Makerere University Agriculture Research Institute Kabanyolo (MUARIK). The pathogen was firstly cultured on sterilized sorghum in the laboratory for 21 days at room temperature. The fully colonized sorghum seeds were then used to inoculate the sterilized soil in plastic pots.

Experimental design

The design of the study was an Alpha Lattice Design (8 blocks x 8 genotypes) with three replicates. A block was made of 8 plastic pots (2 kg capacity). Pots were filed with sterilized soil and thereafter inoculated with Fusarium wilt pathogen (SEFU2) two days prior to planting at a ratio of 75 g of isolate per pot of 2 kg of soil. Un-inoculated controls were included in the study. Fifteen seeds from the same cross were planted in each pot. Plants were watered as the conditions necessitated, and observed daily for disease symptoms.

Data collection

Data were collected for plant stand per pot and number of diseased plants per genotype. Plant stand was collected at fourteen days after planting and was used to deduce emergence percentage (EM %) while number of diseased plants per genotype was used to compute disease incidence (DI %). The following equations were used to estimate EM% and DI%.

$$\text{EM } \% = \frac{\text{Number of emerged plants}}{\text{Total number of plant sown}} * 100$$

$$\text{DI } \% = \frac{\text{Number of diseased plants}}{\text{Total number of plant emerged}} * 100$$

The linear model used during analysis of variance was,

$$Y_{ijk} = \bar{\bar{Y}} + G_i + R_j + (R/B)_k + E_{ijk}$$

Y_{ijk} is the observation value for genotype ith and jth $\bar{\bar{Y}}$ is mean, G_i is

Table 1. Scale for classification of the genotypes.

Scale number	Infection percentage	Category of resistance
1	0.00	Immune (I)
2	0.1 -20	Resistant (R)
3	20.1 - 40	Moderately resistant (MR)
4	40.1 - 60	Moderately susceptible (MS)
5	60.1 - 80	Susceptible (S)
6	80.1 - 100	Highly susceptible (HS)

Table 3. Analysis of variance for the emergence percentage (EM %) and disease incidence (DI %) of 56 progenies of sesame with their eight parents.

SOV	df	EM%	DI%
Replication	1	50	725.96**
Parental/crosses	63	636.56***	507.66***
Residual	63	29.43	57.51
Total	127	330.77	286.08
CV%		9.26	10.96

SOV= Source of Variance, Values with **and *** represent significance at P≤0.01 and P≤0.001 respectively.

the genotype effect for ith , R_j is the replication effect for jth ,$(R/B)_k$is the replication block nested effect for the kthand E_{ijk} is the experimental error effect.

Data analysis

Data were subjected to Analysis of Variance (ANOVA) in Genstat 18th edition Software to determine significant treatment effects. Fisher Protected Least Significant Difference (LSD) test at 5% probability level was used to compare means. Progenies were then grouped according to their resistance levels using the scale developed by Kavak and Boydak (2006) with slight modification (Table 2). Combining ability analysis was carried out following Griffing (1956) method 1 model. The estimates of general combining ability (GCA) for the parents, specific combining ability (SCA) for the crosses and reciprocal effect were calculated according to the linear model,

$$Y_{ijkl} = \bar{\bar{Y}} + gca_i + gca_J + sca_{ij} + r_{ij} + P_k + (P/B)_l + e_{ijkl}$$

Where, $Y_{ijkl}$is the observed value for genotype ith and jth, $\bar{\bar{Y}}$ the grand mean, $gca_i\ and\ gca_J sca_{ij}$ and r_{ij} are the general combining and specific combining ability and reciprocal effect for ith, jth and ijth respectively, P_k replication effect for kth, *(P/B)ₗ* is the replication nested block effect for the lth and e_{ijkl} is the experimental error effect.

For gene action determination,parents were considered to be fixed. The estimated variance components (σ^2) of GCA and SCA were used to calculate the coefficient of genetic determination (CGD) both broad sense (BS (H)) and narrow sense (NS (h^2)) heritability (Equation 1 and 2). Baker's ratio (1978) which determines the fraction of genetic variation that is due to additive effects was calculated according to equation 3.

$$\text{CGDBS (H)} = \frac{2\delta^2\text{gca} + \delta^2\text{sca}}{2\delta^2\text{gca} + \delta^2\text{sca} + \delta^2\text{e}} \quad (1)$$

$$\text{CGDNS } (h^2) = \frac{2\delta^2\text{gca}}{2\delta^2\text{gca} + \delta^2\text{sca} + \delta^2\text{e}} \quad (2)$$

$$\text{BR} = \frac{2\delta^2\text{gca}}{2\delta^2\text{gca} + \delta^2\text{sca}} \quad (3)$$

RESULTS

Responses of parents and crosses on emergence and disease incidence

On analysis of data, it was realized that the block effect was not effective in an alpha lattice design, so analysis was done following the randomized complete block design model. The results showed significant differences among parent/crosses for all the traits tested (P≤0.001) (Table 3). The means of emergence ranged from 26.0 to 98.0% with a grand mean of 58.6% and disease incidence that ranged from 33.3 to 96.0% with grand mean of 69.2% (Table 4). Parents Sesim 2 (36.7%) and EM15-1-5 (39.1) continued to be moderately resistant with the rest of the parents being susceptible or highly susceptible. Only one, a reciprocal cross (EM15-1-5 x Sesim 1) (33.3%) was recorded as moderately resistant. The other crosses were ranged from susceptible to highly susceptible (Table 4).

Combining ability and gene action

Table 5 represents analysis of variance for combining ability of emergence (EM %), disease incidence (DI %),

Table 4. Means of emergence, disease incidence and categories for resistance performance of eight parents and 56 F1 progenies in response to *Fusarium oxysporum* f.sp. *sesami* in screen house.

Genotype	EM%	DI%	Category
P8 X P4	60.0	33.3	MR
P7	98.0	36.7	MR
P8	82.0	39.0	MR
P7 X P8	84.0	43.0	MS
P4 X P2	50.0	44.6	MS
P8 X P3	52.0	45.8	MS
P2 X P6	46.0	47.7	MS
P3 X P1	36.0	50.0	MS
P8 X P6	62.0	51.5	MS
P1 X P2	46.0	51.9	MS
P7 X P5	68.0	53.1	MS
P5 X P1	44.0	54.5	MS
P8 X P1	50.0	56.1	MS
P5 X P2	50.0	56.8	MS
P4 X P6	46.0	56.9	MS
P4 X P7	80.0	57.8	MS
P3 X P6	60.0	60.0	MS
P3 X P5	60.0	60.2	S
P7 X P3	60.0	60.3	S
P8 X P5	50.0	60.4	S
P3 X P2	82.0	60.8	S
P4 X P3	48.0	62.1	S
P8 X P7	64.0	62.7	S
P1 X P4	76.0	62.8	S
P4 X P8	70.0	63.1	S
P2 X P8	66.0	63.9	S
P5 X P8	56.0	64.3	S
P1 X P8	40.0	64.6	S
P3 X P8	40.0	65.0	S
P7 X P4	52.0	65.5	S
P5 X P4	64.0	65.7	S
P2 X P1	68.0	67.7	S
P7 X P6	62.0	67.7	S
P2 X P7	38.0	68.9	S
P5 X P3	54.0	70.6	S
P4 X P5	26.0	73.8	S
P5 X P7	62.0	74.2	S
P1 X P5	56.0	75.1	S
P8 X P2	66.0	75.9	S
P7 X P2	44.0	77.5	S
P3 X P7	72.0	77.8	S
P2 X P4	56.0	77.9	S
P2 X P5	46.0	78.0	S
P3	94.0	78.5	S
P6 X P5	40.0	79.2	S
P5	86.0	79.2	S
P1 X P7	60.0	79.5	S
P2 X P3	50.0	79.8	S
P6 X P4	30.0	80.6	HS

Table 4. Contd.

P5 X P6	32.0	81.7	HS
P3 X P4	60.0	83.5	HS
P4	86.0	83.5	HS
P6 X P3	26.0	84.5	HS
P1 X P3	76.0	86.9	HS
P7 X P1	80.0	87.5	HS
P4 X P1	36.0	88.7	HS
P6 X P2	36.0	88.9	HS
P2	90.0	91.0	HS
P6	78.0	92.5	HS
P6 X P7	32.0	93.8	HS
P6 X P8	62.0	93.8	HS
P1 X P6	44.0	95.8	HS
P1	92.0	95.8	HS
P6 X P1	66.0	96.9	HS
Minimum	26.0	33.3	
Maximum	98.0	96.9	
Grand Mean	58.6	69.2	

EM%-emergence percentage, DI%-disease incidence, MR-moderate resistant, S-susceptible, MS-moderate susceptible HS-highly susceptible and P-parent.

Table 5.ANOVA for combining ability for the emergence percentage and disease incidence of 56 crosses with their parents.

SOV	df	EM%	DI%
Crosses	63	318.28***	253.83***
GCA	7	354.93***	665.93***
SCA	28	419.05***	165.03***
Reciprocal	28	208.35***	239.61***
Error	63	14.72	28.76
VCgca		21.26	39.82
VCsca		202.16	68.13
H		0.94	83.71
h^2		0.16	45.12
Baker's ratio		0.17	53.90

SOV- Source of Variance, Values with *** represent significance at P≤0.001; EM%-emergence percentage; DI%-disease incidence; H- coefficient of genetic determination both broad sense; h^2- coefficient of genetic determination both narrow sense; VCgca and VCsca- variance components of general combining ability and specific combining ability respectively.

coefficient of genetic determination for broad and narrow sense ((CGD BS (H) and CGD NS (h^2)) and Baker's ratio (BR). Results showed that crosses, general combining ability (GCA), specific combine ability (SCA) and reciprocal effects were highly significant (P≤0.001) in all traits tested. Coefficient of genetic determination (broad sense) was high (>0.80) in all traits tested. The coefficient of genetic determination (narrow sense) was low (0.16 for EM% while 0.45 for DI %). Bakers' ratio was only medium (0.54) in disease incidence.

General combining ability effect of resistance to *Fusarium oxysporum* f. sp. *sesami* for parental genotypes

With exception of Lindi 02 and Sesim 1, all parents significantly influenced emergence (P≤0.001 to P≤0.05). For disease incidence, four parents (Lindi 02, Sesim 3, Sesim 1 and Renner 1-3-1-17) were not significant from each other while the remaining four parents (4036-1-10-2//Renner1-3-16-2, Mtwara, Sesim 2 and EM15-1-5) were

Table 6. General combining ability relative estimates for the emergence percentage and disease incidence of eight parents.

Parent name	EM%	DI%
4036-1-10-2//Renner1-3-16-2	1.57*	6.44***
Lindi 02	-0.82^{ns}	0.99^{ns}
Sesim3	1.69**	-0.14^{ns}
Sesim1	-0.69^{ns}	-1.465^{ns}
Renner1-3-1-17	-3.57***	-0.04^{ns}
Mtwara 09	-8.57***	9.82***
Sesim2	7.32***	-4.02***
EM15-1-5	3.07***	-11.58***

Values with *, **and *** represent significance at P≤0.05, P≤0.01 and P≤0.001 respectively while ns is non-significant; EM%-emergence percentage and DI%-disease incidence.

highly and significantly different (P≤0.001) (Table 6).

Specific combining ability effect of resistance to *F. oxysporum* f. sp*. sesami* for F1 progenies

Results for emergence indicated that the effect of seven crosses was highly significant (P≤ 0.001) and that of eleven other crosses significant (P≤ 0.01 to P≤0.05). The effect of the remaining ten crosses was not significant (Table 7). For disease incidence, 17 crosses were not significant while eleven had significant (P≤ 0.001 to P≤0.05) effects.

Reciprocal effects of resistance to *F. oxysporum* f.sp*. sesami* for F1 progenies

The reciprocal effects for emergence and disease incidence are shown in Table 8. Results showed that 18 crosses were highly significant for emergence (P≤ 0.001). For the same trait, eight crosses were significant (P≤ 0.01 and P≤ 0.05) while two crosses (EM15-1-5 x Lindi 02 and Sesim 2 x Sesim 3) were not significant. For disease incidence, 21 crosses were highly significant (P≤ 0.001) while the four crosses were not. The crosses Mtwara 09 x Sesim 1 and EM15-1-5 x Renner1-3-1-17 were significantly different at P≤ 0.05 while the cross Renner1-3-1-17 x Lindi 02 was the only highly significant one at P≤ 0.01.

DISCUSSION

Inheritance study is important on determining how gene of interest transferred from one generation to another generation, the best combiner parents for breeding program and also guide breeder to choose the best breeding methods regarding the trait of interest (Goffar et al., 2016). The study used eight promising parents of different reaction to Fusarium wilt with their 56 F1 progenies. From the results above, the parental/crosses response to EM% and DI% was highly significant suggesting that all materials responded differently to *F. oxysporum* f. sp*sesami.* This showed that there is genetic diversity within the tested materials providing a high possibility of obtaining materials with good wilt resistance. Only a cross EM15-1-5 x Sesim1 was moderate resistant (33.3%) while others ranged from moderately susceptible to highly susceptible. Combining ability analysis showed highly significant differences for crosses, GCA, SCA and reciprocal effects for all the traits tested (P≤ 0.001). This suggests that both additive and non-additive genetic variances are involved in controlling resistance to *F. oxysporum* f. sp*. sesami*. Highly significant GCA exhibited by parents is evidence that those parents had transferred their traits to the progenies. This implied that additive gene effects were involved in the transmission of the traits tested. SCA was also highly significant for all traits tested meaning that the observed and expected performance of the progenies due to allelic combination could be due to non-additive effects. Moreover, all traits observed had shown to be influenced by extra-chromosomal inheritance or maternal effects since the reciprocals effects were also significant. Different studies have shown that germination percentage is controlled by both additive and non-additive gene action and maternal effects (Donohue, 2009; Luzuriaga et al., 2006; Rix et al., 2012; Singh et al., 2017; Wanjala et al., 2017). Non-significance of SCA mean squares is a good indication that the performance of single cross progeny can be adequately predicted on the basis of GCA (Baker, 1978). From this study, it is very difficult to predict the performance of the progeny based on GCA since the SCA mean squares were significant. It was good to see that coefficient of genetic determination broad sense (H) was high (greater than 80%). This means that more than 80% of variance in phenotypic performance is genetically controlled. Coefficient of genetic determination narrow

Table 7. Specific combining ability for the emergence percentage and disease incidence of 28 crosses.

Genotype	EM%	DI%
4036-1-10-2//Renner1-3-16-2 x Lind 02	-2.31^{ns}	-16.78**
4036-1-10-2//Renner1-3-16-2 x Sesim 3	-5.81*	-7.00*
4036-1-10-2//Renner1-3-16-2 x Sesim 1	-3.44^{ns}	1.61^{ns}
4036-1-10-2//Renner1-3-16-2 x Renner1-3-1-17	-6.56**	-10.73***
4036-1-10-2//Renner1-3-16-2 x Mtwara 09	3.44^{ns}	10.92***
4036-1-10-2//Renner1-3-16-2 x Sesim 2	2.56^{ns}	11.89***
4036-1-10-2//Renner1-3-16-2 x EM15-1-5	-18.19**	-3.69^{ns}
Lindi 02 x Sesim 3	6.56**	0.31^{ns}
Lindi 02 x Sesim 1	-4.06^{ns}	-7.44*
Lindi 02 x Renner1-3-1-17	-6.19*	-2.69^{ns}
Lindi 02 x Mtwara 09	-8.19**	-11.66***
Lindi 02 x Sesim 2	-24.06***	7.06*
Lindi 02 x EM15-1-5	5.19*	11.33***
Sesim 3 x Sesim 1	-5.56*	5.25^{ns}
Sesim 3 x Renner1-3-1-17	0.31^{ns}	-3.60^{ns}
Sesim 3 x Mtwara 09	-8.69***	-6.59^{ns}
Sesim 3 x Sesim 2	-1.56^{ns}	4.01^{ns}
Sesim 3 x EM15-1-5	-17.31***	-2.03^{ns}
Sesim 1 x Renner1-3-1-17	-9.31***	2.05^{ns}
Sesim 1 x Mtwara 09	-11.31**	-8.79*
Sesim 1 x Sesim 2	0.81^{ns}	-2.07^{ns}
Sesim 1 x EM15-1-5	4.06^{ns}	-7.92*
Renner1-3-1-17 x Mtwara 09	-10.44***	1.51^{ns}
Renner1-3-1-17 x Sesim 2	2.69^{ns}	-1.47^{ns}
Renner1-3-1-17 x EM15-1-5	-5.06*	4.79 ^{ns}
Mtwara 09 x Sesim 2	-10.31***	5.76^{ns}
Mtwara 09 x EM15-1-5	8.94***	5.20^{ns}
Sesim 2 x EM15-1-5	5.06*	-0.72^{ns}

Values with *, **and *** represent significance at P≤0.05, P≤0.01 and P≤0.001 respectively while ns is non-significant; EM%-emergence percentage and DI%-disease incidence.

sense (h^2) for EM% was 0.16 while that of DI% was 45.12. This indicates that only 16% (for EM %) and 45.12% (for DI %) of the variance in the phenotypic performance is predictably transmitted, thus low predictability of progeny from parental performance. Baker's ratio was very low for EM% (0.17) while for DI% was fairly medium. This still suggests the predominance of non-additive gene action in controlling resistance to *F. oxysporum* f. sp*. sesami*in sesame. These results clearly suggest that selection during late generations would be the best breeding strategy for improving resistance in sesame to *F. oxysporum* f. sp*. sesami*. These findings correspond to other studies done under both natural and artificial inoculation using F1 progenies along with their parents. Those studies reported that gene action governing resistance to Fusarium wilt in sesame is predominantly controlled by non-additive gene action (Bayoumi and EL-Bramawy, 2007; El-Bramawy and Shaban, 2007). Furthermore, it was reported that in the late generations, resistance to Fusarium wilt is controlled by additive gene action (El-bramawy, 2006). The finding of this study could be influenced by type of genetic material used, mode of pollination, parent cross combination and method used to derive gene action (Goffar et al., 2016; Ulloa et al., 2013).

The parents 4036-1-10-2//Renner1-3-16-2, Sesim 3, Sesam 2 and EM15-1-5 showed positive desirable significant GCA effects for high germination. These could be associated with resistance to seed rot caused by *F. oxysporum* f. sp*. sesami* and are good combiners for improvement of this trait. On the other hand, Sesim 1, Mtwara 09, Renner1-3-1-17 had negative significant GCA effects for low germination. These genotypes were thus not associated with resistance to seed rot and are therefore poor combiners for improvement of sesame for this trait. Similarly, Lindi 02 had negative and non-significant GCA for germination suggesting that this parent was not associated with resistance to seed rot

Table 8. Reciprocal effect for the emergence percentage and disease incidence of 28 reciprocal crosses.

Genotype	EM%	DI%
Lindi 02 x 4036-1-10-2//Renner1-3-16-2	11.00***	7.89***
Sesim 3 x 4036-1-10-2//Renner1-3-16-2	-20.00***	-18.47***
Sesim 3 x Lindi 02	16.00***	-9.49***
Sesim 1 x 4036-1-10-2//Renner1-3-16-2	-20.00***	12.99***
Sesim 1 x Lindi 02	-3.00**	-16.70***
Sesim 1 x Lindi 02	-6.00***	-10.67***
Renner1-3-1-17 x 4036-1-10-2//Renner1-3-16-2	-6.00*	-10.29***
Renner1-3-1-17 x Lindi 02	2.00***	-10.61**
Renner1-3-1-17 x Ssesim 3	-3.00***	5.21^{ns}
Renner1-3-1-17 x Sesim 1	19.00***	-4.03^{ns}
Mtwara 09 x 4036-1-10-2//Renner1-3-16-2	11.00**	0.52***
Mtwara 09 x Lindi 02	-5.00***	20.58***
Mtwara 09 x Sesim 3	-17.00***	12.26***
Mtwara 09 x Sesim 1	-8.00***	11.82*
Mtwara 09 x Renner1-3-1-17	4.00**	-1.29^{ns}
Sesim 2 x 4036-1-10-2//Renner1-3-16-2	10.00***	4.02***
Sesim 2 x Lindi 02	3.00*	4.31***
Sesim 2 x Sesim 3	-6.00^{ns}	-8.75***
Sesim 2 x Sesim 1	-14.00***	3.85^{ns}
Sesim 2 x Renner1-3-1-17	3.00***	-10.52***
Sesim 2 x Mtwara 09	15.00***	-13.02***
EM15-1-5 x 4036-1-10-2//Renner1-3-16-2	5.00**	-4.25***
EM15-1-5 x Lindi 02	0.00^{ns}	6.02***
EM15-1-5 x Sesim 3	6.00***	-9.58***
EM15-1-5 x Sesim 1	-5.00***	-14.87***
EM15-1-5 x Renner1-3-1-17	-3.00*	-1.95*
EM15-1-5 x Mtwara 09	0.00*	-21.15***
EM15-1-5 x Sesim 2	-10.00***	9.90***

Values with *, **and *** represent significance at P≤0.05, P≤0.01 and P≤0.001 respectively while ns is non-significant; EM%-emergence percentage and DI%-disease incidence.

hence it is a poor combiner for improving this trait. Genotypes Sesim 2 and EM15-1-5 had significant negative GCA for disease incidence making them be good combiner parents for improving this trait. The susceptible parents (Mtwara 09 and 4036-1-10-2//Renner1-3-16-2) showed positive significant GCA effect indicating a possibility of these parents passing susceptibility to *F. oxysporum f.* sp*. sesami* to their progenies. Contrastingly, the susceptible parents Sesim1, Sesim 3 and Renner1-3-1-17 had non-significant negative GCA effects for disease incidence which implied that they could be good combiners and would pass resistance to *F. oxysporum* f. sp*. sesami* to their progenies. A high GCA estimate is the determinant of higher heritability with less environment effects, less gene interactions and high achievement in selection (Chigeza et al., 2013).

Although the crosses 4036-1-10-2//Renner1-3-16-2 x Lindi 02, and Lind 02 x Mtwara 09 were made from a combination of poor parents, they showed desirable highly negative significant SCA effects for disease incidence. This could be due to dominance x dominance type of non-allelic gene interaction produced over dominance (Wassimi et al., 1986). Furthermore, crosses 4036-1-10-2//Renner1-3-16-2 x Renner1-3-1-17, Sesim 3 x Renner1-3-1-17 and Sesim 1 x EM15-1-5 made from a combination of a poor and a good parent showed good SCA effects for disease incidence. This implied that favourable additive effects of the good general combiner parent contributed to the performance of these progenies (Verma and Srivastava, 2004). Therefore, the above crosses can be included in a breeding programme for developing wilt resistant sesame varieties.

Reciprocal effects showed that most of the crosses were highly and significantly influenced disease incidence. This suggests that maternal effects could be controlling resistance to *F. oxysporum* f. sp*. sesami* in sesame. This type of gene interaction is significant in a

breeding program which permits the determination of parent to be used as donor or recipients of pollen (Bahari et al., 2012). Reciprocal crosses of Renner1-3-1-17 x Lindi 02, Sesim 2 x Renner1-3-1-17, Sesim 2 x Mtwara 09 and EM15-1-5 x Mtwara 09 had positive and negative significant reciprocal effects for EM% and DI% respectively. This means that parents used as females were able to contribute much to the performance of the offspring due to maternal effects. These crosses can be used for breeding for wilt resistance in the future.

CONCLUSIONS AND RECOMMENDATIONS

Based on the results obtained from this study, inheritance of resistance to Fusarium wilt (*F. oxysporum* f. sp. *sesami*) in sesame among the studied genotypes is controlled by both additive and non-additive gene action as revealed by low coefficient of genetic determination narrow sense and moderate Baker's ratio. The study further showed that maternal effects influenced resistance to Fusarium wilt which was shown by highly significant performance among reciprocal crosses. Accordingly, selection for resistance to Fusarium wilt can be effective in late generations. The study also showed that genotypes Sesam 2 and EM15-1-5 were the best general combiner parents compared to the rest and can be used in routine breeding for resistance to Fusarium wilt. Overall, findings of this study have created the foundation for further studies upon which the sesame breeding program in Uganda can be based.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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