OPEN ACCESS

Journal of Plant Breeding and Crop Science

September 2018
ISSN 2006-9758
DOI: 10.5897/JPBCS
www.academicjournals.org

ACADEMIC JOURNALS
expand your knowledge

ABOUT JPBCS

The **Journal of Plant Breeding and Crop Science (JPBCS)** is published monthly (one volume per year) by Academic Journals.

The Journal of Plant Breeding and Crop Science (JPBCS) (ISSN: 2006-9758) is an open access journal that provides rapid publication (monthly) of articles in all areas of the subject such as Sustainable use of plant protection products, Agronomic and molecular evaluation of recombinant inbred lines (RILs) of lentil, Pollen behaviour and fertilization impairment in plants, Development of a fast and reliable ozone screening method in rice etc.

The Journal welcomes the submission of manuscripts that meet the general criteria of significance and scientific excellence. Papers will be published shortly after acceptance. All articles published in JPBCS are peer-reviewed.

Contact Us

Editorial Office: jpbcs@academicjournals.org

Help Desk: helpdesk@academicjournals.org

Website: http://www.academicjournals.org/journal/JPBCS

Submit manuscript online http://ms.academicjournals.me/

Journal of Plant Breeding and Crop Science

Table of Contents: Volume 10 Number 9 September 2018

ARTICLES

Vol. 10(9), pp. 218-227, September 2018
DOI: 10.5897/JPBCS2018.0755
Article Number: 3DAAD9858157
ISSN: 2006-9758

http://www.academicjournals.org/JPBCS

ACADEMIC JOURNALS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Stability for descriptors of *Solanum aethiopicum* Shum group (family Solanaceae)

Nahamya Pamela Kabod[1,2], Godfrey Sseremba[1,3], Ruth Buteme[1], Michael Masanza[1] and Elizabeth Balyejusa Kizito[1*]

[1]Department of Agricultural and Biological Sciences, Faculty of Science and Technology, Uganda Christian University, P. O. Box 4, Mukono, Uganda.
[2]Department of Agricultural Production, College of Agricultural and Environmental Sciences, Makerere University, P.O. Box 7062, Kampala, Uganda.
[3]West Africa Centre for Crop Improvement, University of Ghana, P. M. B 30, Accra, Ghana.

Received 5 June, 2018; Accepted 27 July, 2018

***Solanum aethiopicum* Shum group is a nutrient-rich and income-generating crop enterprise in various sub-Saharan Africa countries. Despite its importance, the development of its improved varieties has not been prioritized. Until now, no field-based descriptor development reference for the crop is available for testing candidate varieties for distinctiveness, uniformity and stability. The purpose of this study is to identify morphological variables that provide identity of *S. aethiopicum* Shum group accessions across environments. With ten accessions across three test locations, it was observed that the highly polymorphic morphological variables were majorly vegetative and a few reproductive ones. They include plant height at flowering, plant canopy breadth, plant branching, petiole color, petiole length, leaf blade length, leaf blade width, leaf lobbing, leaf tip angle, flowering time, style length, fruit position, fruit flesh density, fruits per inflorescence and fruit flavor. A static stability analysis, a common selection technique for obtaining consistence in performance of genotypes, showed that accessions varied in their interaction with environments for different descriptors. The most statically stable accessions were 184P and 163P while the least stables were 168P, 148, 141, and 137. The findings indicate the potential for identifying unique and stable varieties of *S. aethiopicum* Shum group for the processing of official release to farmers.**

Key words: Polymorphic morphological markers; static stability coefficient; field characterization; *Solanum aethiopicum* Shum; genotype by environment interaction.

INTRODUCTION

Shum is one the four recognized morphological groups of the African eggplant (Abukutsa-Onyango et al., 2010; Adeniji et al., 2012; Horna and Gruere, 2006). It is desired for its nutrient-rich leaves (Bisamaza and Banadda, 2017; Ebert, 2014; Ojiewo et al. 2013; Pincus, 2015; Rubaihayo et al., 2003).

*Corresponding author. E-mail: lkizito08@gmail.com.

The rest of its groups are Gilo, Kumba and Aculeatum, and they are cultivated for other purposes (Adeniji et al., 2012; Prohens et al., 2013; Sakhanokho et al., 2014; Sękara et al., 2007). All the four groups are diploid (2n = 24) and they are indigenous to Africa (Prohens et al., 2013; Sakhanokho et al., 2014). The diversity for the Shum group of African eggplant (*Solanum aethiopicum*) is believed to be richest in Uganda, owing to favorable agroecologies and the contribution of the leafy vegetable to household diets and incomes (Cernansky, 2015; Ojiewo et al., 2013; Omulo, 2016; Rubaihayo et al., 2003; Ssekabembe, 2008; Ssekabembe et al., 2003; Stone et al., 2011). Elsewhere, the crop receives commercial attention in countries like Cameroon, Burkina Faso, Ghana, Nigeria, India and Brazil (Abbiw, 1997; Bationo-Kando et al., 2015; Gramazio et al., 2016; Kouassi et al., 2014; Ojiewo et al., 2013; Osei et al., 2010; Rémi et al., 2005).

There is an increasing interest among researchers and policy makers in promoting variety development, cultivation, value-addition and consumption of vegetables (Bisamaza and Banadda, 2017; Cernansky, 2015; Ebert, 2014; FAO, 2005; Pincus, 2015; Rubaihayo et al., 2003; Stone et al., 2011). The breeding and exploitation of new varieties is an avenue that can contribute significantly to improving rural income and overall economic development especially in the third world. For instance, development of new varieties with higher yields increases the value and marketability of crops. New varieties should however, meet the distinctiveness, uniformity and stability (DUS) tests as criteria used by national variety release systems (Mendes de Paula et al., 2014; UPOV, 2002). Distinctness describes the extent to which a descriptor can demonstrate differences between varieties; uniformity, on the other hand, describes the level of homogeneity within a variety. Stability of a genotype refers to its tendency to conserve performance across environments (Becker and Leon, 1988; Kamidi, 2001). Plant morphological characters are universally accepted descriptors for DUS testing and varietal characterization of crop species and are useful for distinguishing different varieties. Determining whether descriptors comply with the above mentioned prerequisites can best be done by evaluation of characteristics in field trials in which various genotypes are grown under identical conditions.

Coefficients of stability are used to identify the genotypes exhibiting same performance for specific variables (Balestre et al., 2009; Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Temesgen et al., 2015). Stability coefficients are commonly used with yield estimates but the same principle can be extended to morphological descriptors (Mendes de Paula et al., 2014; Sabaghnia et al., 2012; Temesgen et al., 2015). Performance stability refers to a genotype's ability to perform consistently, whether at high or low levels, across a wide range of environments. Most stability measures relate to either of two contrasting concepts of stability: "static" and "dynamic" (Eberhart and Russell, 1966; Finlay and Wilkinson, 1963; Lin and Binns, 1988). Static stability is analogous to the biological concept of homeostasis: a stable genotype tends to maintain a constant performance for a particular variable across environments (Lin and Binns, 1988; Palanog et al., 2015). This study aims at identifying: variables that provide identity of Shum accessions across environments, and accessions that are stable in morphological traits. The study generated results on reliable descriptors for field characterization of *S. aethiopicum* Shum group genotypes. The study accessions had earlier been characterized under screen house conditions (Sseremba et al., 2017) but needed field verification.

MATERIALS AND METHODS

Testing sites and germplasm

Three evaluation sites in Uganda were used; Ntawo village in Mukono Municipality in the Central region. Ntawo is an on-station field testing site for the Department of Agricultural and Biological Sciences, Uganda Christian University, Mukono. Butiki village in Jinja Municipality was used (near East), and Busamaga village in Mbale Municipality (Far East) in Eastern Uganda. Mukono, Jinja and Mbale are located at about 24, 70 and 230 km, respectively, East of Kampala.

The study accessions were obtained from farming households in Uganda through a field survey in 2014/2015, followed by on-station seed increase and purification by self-pollination. The accessions were assigned codes; some with stem color suffices such as G and P for green and purple, respectively, whenever more than one accession from same survey location possessed similar other attributes other than stem color. Ten accessions were used in this study: 108, 137, 141, 145, 148, 163P, 168P, 183P, 184G and 184P, and they have been described earlier under screen house conditions (Sseremba et al., 2017).

Experimental design

A randomized complete block design (RCBD) with three replications was used at each of the three test sites; Jinja, Mbale and Mukono. The evaluation was carried out during the first rainy season (February to June 2016). Four-row plots of length 4 m were used at an inter-row spacing of 30 cm. Direct sowing into the experimental field was used. The within-row sowing was done by drilling followed by thinning to 10 cm at 4-leaf stage (1 month after sowing). The testing fields were prepared by hand hoeing and use of Glyphosate to reduce on the weeds burden before the germination of planted seed. At planting, D.A.P fertilizer at a rate of 50 kg/acre was applied. Topdressing with N.P.K (25:5:5) was carried after thinning and at 2 months after sowing. Hand weeding within established fields was used.

Data collection

Data were collected during the opening of first flower until physiological ripening of fruit stages, depending on the variable. Forty one morphological variables were measured according to Adeniji et al. (2013) and Sseremba et al. (2017), with some modifications. A brief description of the various variables measured is included in Table 1.

Table 1. Description of variables measured to characterize *Solanum aethiopicum* Shum accessions.

S/N	Variable	Scale/units
1	Plant growth habit (PGH)	3-upright; 5-intermediate; 7-prostrate
2	Stem ridging (STR)	0-absent; 3=shallow; 5-intermediate; 7-prominent
3	Spines on stem (SOS)	0-absent; 3-short; 5-intermediate; 7-long
4	Stem pubescence (SPU)	0-absent; 1-few; 2-intermediate; 3-many; 4-very many
5	Plant height at flowering (PHF)	1-very short(<20); 3-short(~30); 5-intermediate(~60); 7-tall(~100); 9-very tall
6	Plant canopy breadth (PCB)	1-very narrow(<30); 2-narrow(~40); 5-intermediate; 7-broad(~90); 9-very strong(>130)
7	Plant branching (PB)	Number of primary branches per plant
8	Petiole color (PC)	1-green; 2-greenish-violet; 3-violet; 7-dark violet; 9-dark brown
9	Petiole length (PL)	Measured in centimeters (cm)
10	Leaf blade length (LBL)	Measured in centimeters (cm)
11	Leaf blade width (LBW)	Measured in centimeters (cm)
12	Leaf blade lobbing (LL)	1-very weak; 3-weak; 5-intermediate; 7-strong; 9-very strong
13	Leaf tip angle (LTA)	1-very acute(<15°); 3-acute(~45°); 5-intermediate(~75°); 7-obtuse(~110°); 9-very obtuse (~160°)
14	Leaf blade color (LBC)	1-light green; 3-green; 5-dark green; 7-greenish violet; 9-violet
15	Leaf prickles (LPR)	1-very few (1-2); 3-few (3-5); 5-intermediate (6-10); 7-many (11-20); 9-very many (>20)
16	Flowering time (FLW)	Number of days from sowing till first flower opening
17	Stamen length (STL)	Measured in centimeters (cm)
18	Petal length (PEL)	Measured in centimeters (cm)
19	Sepal length (SEL)	Measured in centimeters (cm)
20	Corolla color (COC)	1-greenish white; 3-white; 5-pale violet; 7-light violet
21	Relative style length (RSL)	Measured in centimeters (cm)
22	Pollen production (POP)	0-none; 3-low; 5-medium; 7-high
23	Style exsertion (STE)	3-inserted; 5-intermediate; 7-exerted
24	Fruit length (FRL)	Measured in centimeters (cm)
25	Fruit breadth (FRB)	Measured in centimeters (cm)
26	Fruit length / breadth ratio (FLBR)	Ratio of fruit length to fruit breadth
27	Fruit curvature (FRC)	1-none (fruit straight); 3- slightly curved; 5-curved; 7-snake shaped; 8-sickleshaped; 9-U shaped
28	Fruit shape (FRS)	3-about 1/4 way from the base to tip; 5-about 1/2 way from base to tip; 7-aboit 3/4 way from base to tip
29	Fruit apex shape (FAS)	3- protruded; 5-rounded; 7-depressed
30	Fruit color at commercial ripeness (FCCR)	1-green; 2-milk white; 3-deep yellow; 4-fire red; 5-scarlet red; 6-lilac gray; 7-purple; 8-purple black; 9-black
31	Fruit color distribution at commercial ripeness (FCDC)	1-uniform; 3-mottled; 5-netted; 7-striped
32	Fruit color at physiological ripeness (FCPR)	1-green; 2-deep yellow; 3-yellow-orange; 4-deep orange; 5-fire red; 6-poppy red; 7-scarlet red; 8-light brown; 9-brown
33	Fruit position (FPO)	1-erect; 3-semierect; 5-horizontal; 7-semipedant; 9-pedant
34	Fruit calyx length (FCL)	Measured in centimeters (cm)

Table 1. Description of variables measured to characterize *Solanum aethiopicum* Shum accessions.

35	Fruit cross section (FCS)	1-circular, no grooves; 3-elliptic, no grooves; 5-few grooves (~4); 7-many grooves (~8); 9-very irregular
36	Locules per fruit (LPF)	Number of locules per fruit (N=10)
37	Fruit flesh density (FFD)	1-very loose (Spongy); 3-loose (Crumbly); 5-average density; 7-dense; 9-very dense
38	Fruits per inflorescence (FRPI)	Number of fruits per inflorescence
39	Fruit flavor (FFL)	3-bitter; 5-intermediate; 7-sweet
40	Varietal mixture condition (VMC)	0-pure; 3-slight mixture; 5-medium mixture, 7-serious mixture
41	Flesh browning (FBR)	1 = Immediate browning 0 ~ 1 minute; 2- > 1 ~ 3 minute; 3- > 3 ~ 5 minute; 4-> 5 ~ 7 minute; 5-> 7 ~ 9 minute; 6-> 9 ~ 12 minute; 7-> 12 ~ 15 minute; 8-> 15 ~ 20 minute; 9-> 20 ~ 30 minute; 10 = > 30 minutes

Data analysis

A restricted (residual/reduced) maximum likelihood analysis considering accession and location as factors was implemented in *BreedingView* statistical software (VSN International Ltd, Hemel Office). A boxplot of each of the 41 variables measured was generated from mean values of each accession per location. Presence of spread (or absence of it) in the boxplot was used as criteria for distinguishing variables as either monomorphic or polymorphic. A variable was identified as monomorphic when all accessions had the same mean performance across test locations (Jinja, Mbale and Mukono). It was considered as slightly polymorphic when at least one of the test sites produced similar traits of a character (variable) for all accessions. Highly polymorphic variables (or descriptors) are ones clearly spread (large variation) among accessions at each of the three test locations. A static stability analysis (Finlay and Wilkinson, 1963; Lin and Binns, 1988; Palanog et al., 2015) was then carried out in *Breeding View* on variables which were qualified as highly polymorphic. Coefficients of static stability were used to select the most and least stable accessions per descriptor.

RESULTS

Variables that distinguished study accessions

Based on spread in means of study accessions for measured traits, some variables were monomorphic while the rest were polymorphic. Out of the 41 variables measured, nine were monomorphic although an analysis of variance (ANOVA) revealed detectable variation (Tables 2 to 4). The monomorphic variables namely plant growth habit (PGH), spines on stem (SOS), stem pubescence (SPU), leaf blade color (LBC), leaf prickles (LPR), fruit curvature (FRC), fruit shape (FRS), fruit color distribution at commercial ripeness (FCDC) and varietal mixture condition (VMC) are shown in Figure 1.

A graphical display of some of the monomorphic descriptors is shown in Figure 2. Some variables which were shown as monomorphic using boxplots were confirmed through the ANOVA as non-significant among accessions (Tables 2 to 4). The remaining 32 variables were generally polymorphic. They include stem ridging (STR), plant height at flowering (PHF), plant canopy breadth (PCB), plant branching (PB), petiole color (PC), petiole length (PL), leaf blade length (LBL), leaf blade width (LBW), leaf blade lobbing (LL), leaf tip angle (LTA), flowering time (FLW), stamen length (STL), petal length (PEL), sepal length (SEL), corolla color (COC) and relative style length (RSL). Others include pollen production (POP), style exsertion (STE), fruit length (FRL), fruit breadth (FRB), fruit length / breadth ratio (FLBR), fruit apex shape (FAS), fruit color at commercial ripeness (FCCR), Fruit color at physiological ripeness (FCPR), fruit position (FPO), fruit calyx length (FCL), fruit cross section (FCS), locules per fruit (LPF), fruit flesh density (FFD), fruits per inflorescence (FRPI), fruit flavor (FFL) and flesh browning (FBR).

Of the 32 generally polymorphic variables, 17 were only slightly polymorphic. Those that exhibited slight polymorphism include STR, PEL, SEL, COC, RSL, POP, STE, FRL, FRB, FLBR, FAS, FCCR, FCPR, FCL, FCS, LPF and FBR. A graphic display for some of the slightly polymorphic descriptors is shown in Figure 3. The variables that were highly polymorphic include PHF, PCB, PB, PC, PL, LBL, LBW, LL, LTA, FLW, STL, FPO, FFD, FRPI and FFL. Some of the highly polymorphic descriptors are shown in Figure 4. The 15 variables that exhibited high polymorphism are the only ones which were considered in the analysis of accession stability across environments.

Static stability of accessions across test locations

The static stability represents consistence in

Table 2. Mean squares of measured variables to characterize *Solanum aethiopicum* Shum accessions (part 1 of 3).

Source	d.f	COC	FAS	FBR	FCCR	FCDC	FCL	FCPR	FCS	FFD	FFL	FLBR	FLW	FPO	FRB
Location (LOC)	2	55.116***	2.009***	34.903***	9.339***	1.072***	0.054	16.350***	16.523***	24.523***	0.578	2.226	3502.550***	7.119*	1.314***
Accession (ACC)	15	1.664	1.807***	78.706***	6.418***	0.368***	9.844***	3.610***	28.945***	39.291***	5.515***	1.860***	298.850***	41.182***	15.772***
LOC x ACC	22	1.549	0.717***	5.361***	3.243***	0.309***	0.217***	2.570***	1.883***	6.768***	3.416***	1.672***	108.090***	8.643***	0.170***
Error	332	1.549	0.171	0.526	0.896	0.096	0.062	0.932	0.827	1.072	0.638	0.685	27.42	1.857	0.066

*, ** and *** significance at 5, 1 and 0.1% error allowed, respectively. COC, corolla color; FAS, fruit apex shape; FBR, flesh browning; FCCR, fruit color at commercial ripeness; FCDC, fruit color distribution at commercial ripeness; FCL, fruit calyx length; FCPR, fruit color at physiological ripeness; FCS, fruit cross section; FFD, fruit flesh density; FFL, fruit flavor; FLBR, fruit length / breadth ratio; FLW, flowering time; FPO, fruit position; FRB, fruit breadth.

Table 3. Mean squares of measured variables (part 2 of 3).

Source	d.f	FRC	FRL	FRPI	FRS	LBC	LBL	LBW	LL	LPF	LPR	LTA	PB	PC	PCB
Location (LOC)	2	0.025	0.637***	7.322	0.414**	5.500***	232.184***	87.137***	22.311***	0.038	0.000	68.185***	792.984***	0.484	6758.720***
Accession (ACC)	15	0.042*	8.900***	30.387***	1.277***	2.219***	15.540***	7.045**	22.903***	0.172***	0.000	15.509***	78.514***	23.324***	250.210***
LOC x ACC	22	0.028	0.048	5.758*	0.268***	3.452***	21.279***	12.725***	9.019***	0.093*	0.000	6.159***	32.956***	2.025***	424.190***
Error	332	0.021	0.039	3.624	0.084	0.069	4.193	2.986	2.176	0.056	0.000	1.22	5.464	0.453	57.760

*, ** and *** significance at 5, 1 and 0.1% error allowed, respectively. FRC, fruit curvature; FRL, fruit length; FRPI, fruits per inflorescence; FRS, fruit shape; LBC, leaf blade color; LBL, leaf blade length; LBW, leaf blade width; LL, leaf blade lobbing; LPF, locules per fruit; LPR, leaf prickles; LTA, leaf tip angle; PB, plant branching; PC, petiole color; PCB, plant canopy breadth.

Table 4. Mean squares of measured variables to characterize *Solanum aethiopicum* Shum accessions (part 3 of 3).

Source	d.f	PEL	PGH	PHF	PL	POP	RSL	SEL	SOS	SPU	STE	STL	STR	VMC
Location (LOC)	2	0.063*	0.313**	28867.4***	4.196*	138.157***	0.546	0.972***	0.451***	0.451*	53.497***	0.265***	131.315***	2.191***
Accession (ACC)	15	1.659***	0.362***	1419.3***	9.833***	6.855***	1.613***	1.570***	0.488***	0.297***	5.208***	0.102***	7.535***	3.757***
LOC x ACC	22	0.722***	0.372***	660*0***	3.287***	2.283***	1.180***	0.185***	0.446***	0.355***	3.018***	0.017***	8.672***	1.701***
Error	332	0.013	0.058	117.2	1.156	0.190	0.216	0.005	0.067	0.007	0.460	0.004	0.623	0.097

*, ** and *** significance at 5, 1 and 0.1% error allowed, respectively. PEL, petiole length; PGH, plant growth habit; PHF, plant height at flowering; PL, petiole length; POP, pollen production; RSL, relative style length; SEL, sepal length; SOS, spines on stem; SPU, stem pubescence; STE, style exsertion; STL, stamen length; STR, stem ridging; VMC, varietal mixture condition.

expression of particular morphological traits across the three locations: Jinja, Mbale and Mukono. Accessions 163, 141, 145, 141 (and 145 and 148), 163P, 184P, 184P, 108, 163P, 148, 184P, 184P, 184G, 108 and 168P had the best stability for PHF, PCB, PB, PC, PL, LBL, LBW, LL, LTA, FLW, STL, FPO, FFD, FRPI and FFL, respectively (Table 5). Accession 184P was most frequent for high static stability followed by 163P. The least stable accessions were 168P, 168P, 163P, 108, 148, 141, 141, 168P, 148, 141, 148, 137, 137, 183P and 137 for PHF, PCB, PB, PC, PL, LBL, LBW, LL, LTA, FLW, STL, FPO, FFD, FRPI and FFL, respectively. Accessions 168P, 148, 141, and 137 featured most frequently for

Figure 1. Varietal mixture of *Solanum aethiopicum* Shum.

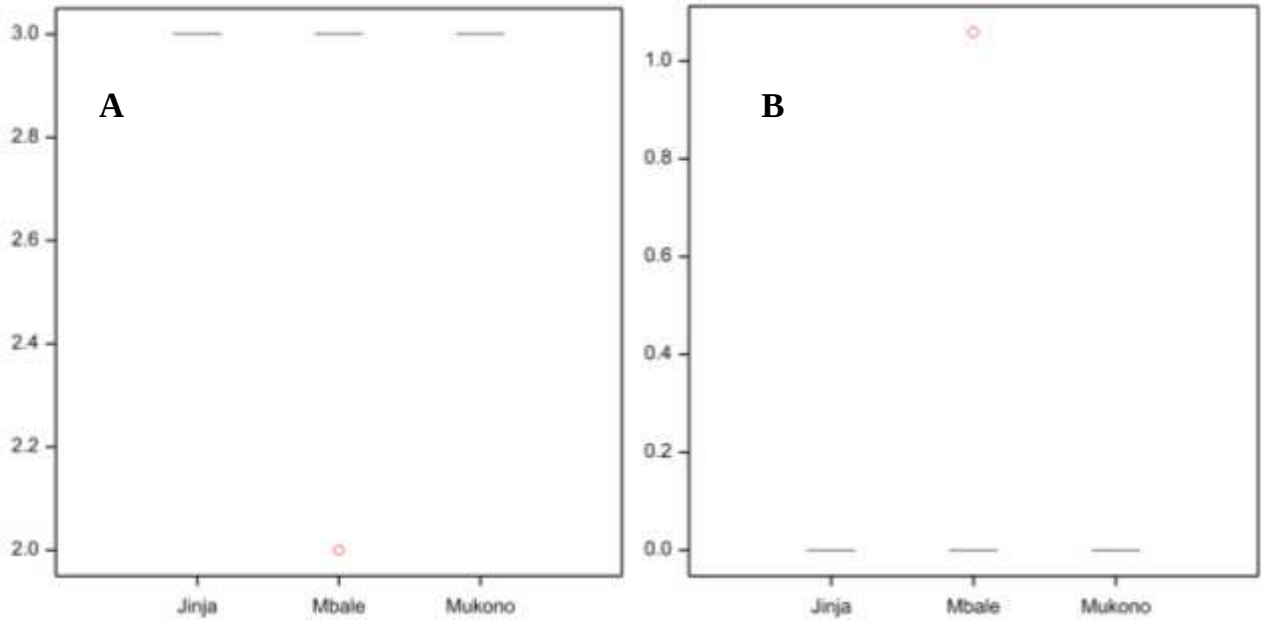

Figure 2. Performance of *S. aethiopicum* Shum accessions at different test locations showing monomorphism for plant growth habit (**A**) and spines on stem (**B**).

least static stability (thrice each).

DISCUSSION

It was observed that some of the variables had same form (or monomorphic) among accessions across test environments. The monomorphic variables are not useful markers for discriminating among genotypes (Odong et al., 2011; Prohens et al., 2013; Sseremba et al., 2017; Sseremba et al., 2018a). The variables namely plant growth habit, spines on stem, stem pubescence, leaf blade color, leaf prickles, fruit curvature, fruit shape, fruit color distribution at commercial ripeness, and varietal mixture condition, cannot be used as descriptors for purposes of identifying distinctiveness among the study accessions. If such monomorphic markers were the only available morphological descriptors, it would necessitate application of deoxyribonucleic acid (DNA) markers which are known for high discriminative power (Gramazio et al.,

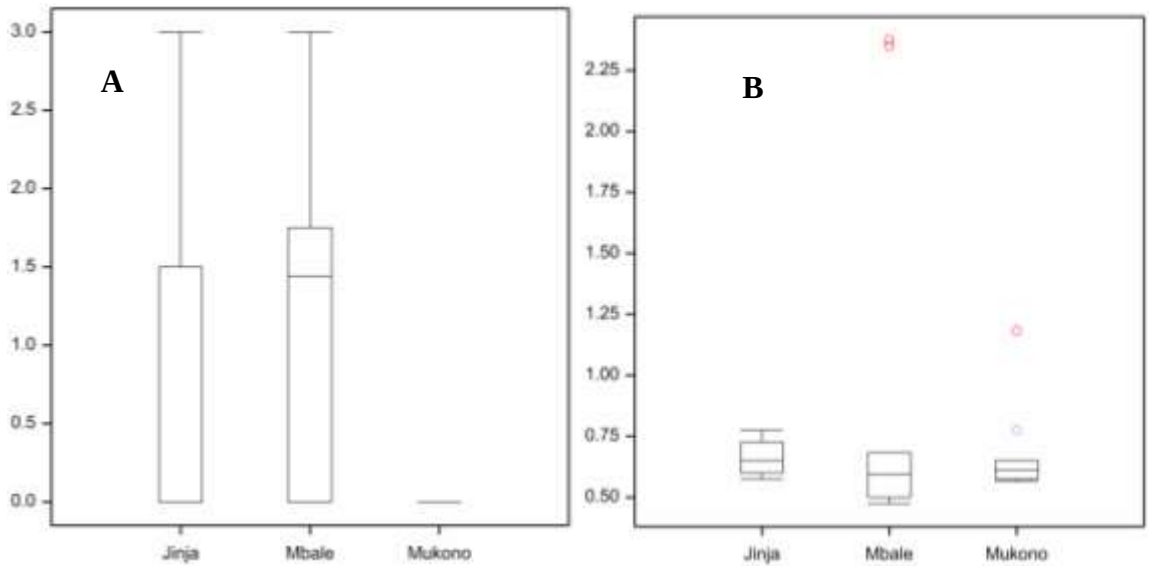

Figure 3. Performance of *S*. *aethiopicum* Shum accessions at different test locations showing slight polymorphism for stem ridging (**A**) and petal length (**B**).

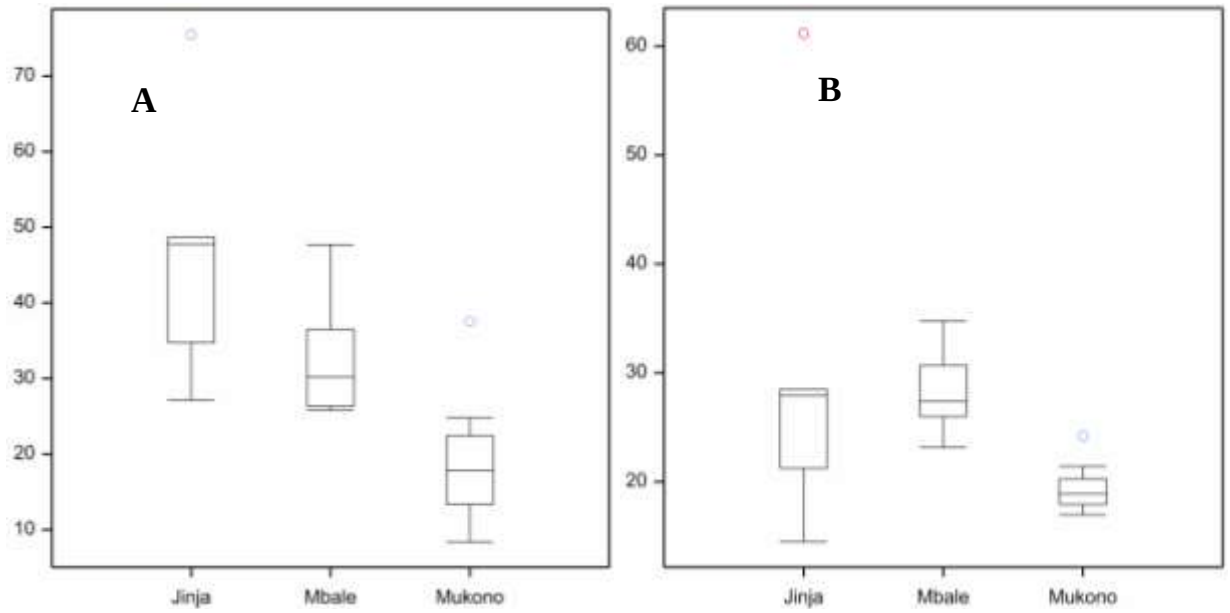

Figure 4. Performance of *S*. *aethiopicum* Shum accessions at different test locations showing high polymorphism for plant height at flowering (**A**) and plant canopy breadth (**B**).

2016). The DNA markers are however, very expensive particularly for crops such as the *S*. *aethiopicum* whose information on genomic resources is still scanty. Nonetheless, other morphological variables showed discriminative ability (of varying degrees) among the study accessions. Of the seventeen slightly polymorphic variables, only one (that is, stem ridging) was vegetative. The majority of slightly polymorphic variables were reproductive (flower or fruit related), suggesting a low discriminating power for reproductive structures. Similarly, nine (60%) out of fifteen highly polymorphic variables were vegetative, indicating a high discerning power for vegetative structures of *S*. *aethiopicum* Shum group (Adeniji et al., 2012).

The highly polymorphic vegetative variables were plant height at flowering, plant canopy breadth, plant

Table 5. Static stability coefficients for highly polymorphic descriptors measured to characterize *Solanum aethiopicum* Shum accessions.

ACC	PHF		PCB		PB		PC		PL		LBL		LBW		LL		LTA		FLW		STL		FPO		FFD		FRPI		FFL	
	Stability	Mean (cm)	Stability	Mean (cm)	Stability	Mean (#)	Stability	Mean (score)	Stability	Mean (cm)	Stability	Mean (cm)	Stability	Mean (cm)	Stability	Mean (score)	Stability	Mean (score)	Stability	Mean (days)	Stability	Mean (cm)	Stability	Mean (score)	Stability	Mean (score)	Stability	Mean (cm)	Stability	Mean (score)
108	200.3	32.5	23.5	24.6	16.5	8	0.5	3	0.2	2.9	1.0	9.1	0.5	7.0	0.1	5	0.4	5	79.1	55.6	0.00	0.37	3.0	6	5.3	6	0.1	4.2	0.0	3
137	276.1	29.6	32.9	24.6	7.2	9	0.0	2	0.1	2.7	2.1	8.2	0.6	6.4	1.7	6	0.2	4	7.0	54.0	0.00	0.42	3.4	7	5.4	4	0.9	4.5	3.7	3
141	192.3	24.1	2.2	21.6	4.8	6	0.0	1	0.0	1.1	12.0	10.2	4.6	7.2	1.2	6	1.2	5	120.6	60.8	0.00	0.62	1.3	8	5.3	6	0.1	4.3	1.3	4
145	78.2	21.7	33.9	19.7	0.2	4	0.0	1	0.5	1.8	4.6	9.2	2.8	6.7	0.6	4	3.7	5	33.6	67.1	0.02	0.55	0.5	8	4.8	6	0.6	4.8	0.5	5
148	198.8	35.2	15.0	28.0	12.8	5	0.0	1	0.8	2.6	8.1	8.6	3.9	6.9	2.3	4	4.4	6	0.4	54.7	0.02	0.51	2.6	6	3.0	6	1.7	2.3	0.3	3
163P	76.6	39.2	20.9	25.5	19.1	9	0.3	2	0.0	2.6	2.8	8.4	1.7	6.3	0.2	4	0.0	4	110.7	57.1	0.00	0.38	3.3	8	4.6	5	0.1	2.8	0.4	4
168P	656.2	48.0	508.9	35.6	2.9	9	0.3	2	0.4	2.9	1.8	9.8	1.6	6.9	2.8	5	1.3	4	41.4	57.1	0.00	0.38	1.0	7	1.8	5	0.3	4.2	0.1	4
183P	278.7	29.4	28.4	23.4	14.9	8	0.0	2	0.4	2.6	1.4	9.1	0.5	6.7	0.5	5	0.1	5	14.9	60.7	0.00	0.42	2.9	6	5.3	6	5.4	2.6	1.0	4
184G	172.1	35.2	22.7	26.7	4.4	9	0.3	1	0.5	3.4	0.5	9.1	0.3	7.1	1.4	6	0.7	5	38.2	55.1	0.00	0.43	3.1	6	0.3	4	0.2	3.4	0.0	4
184P	295.9	31.1	108.5	22.8	10.7	7	0.2	2	0.4	2.9	0.4	8.0	0.2	6.0	0.3	6	0.4	4	18.2	56.9	0.00	0.39	0.1	8	2.8	5	0.1	3.7	0.0	4

ACC, accession. Accessions with smaller static stability values are more stable. PHF, plant height at flowering (cm); PCB, plant canopy breadth (cm); PB, plant branching (#, number of primary branches); PC, petiole color; PL, petiole length (cm); LBL, leaf blade length (cm); LBW, leaf blade width (cm); LL, leaf lobbing (score 1-9); LTA, leaf tip angle; FLW, flowering date (days); STL, stamen length (cm); FPO, fruit position (score 1-9); FFD, fruit flesh density (score 1-9); FRPI, fruits per inflorescence (#); FFL, fruit flavor (score 3-7).

branching, petiole color, petiole length, leaf blade length, leaf blade width, leaf lobbing and leaf tip angle while reproductive ones were flowering time, style length, fruit position, fruit flesh density, fruits per inflorescence and fruit flavor. This observation generally agrees with a previous study in the screen house (Sseremba et al., 2017) but slightly deviates from the work of Adeniji *et al*. (2012) and Prohens et al. (2013). This study and that of Adeniji et al. (2012) were both field-based except the focus was on the leafy (Shum) and all the four recognized morphological groups of *S*. *aethiopicum*, respectively. Sseremba et al. (2017) compared the morphological attributes of *S*. *aethiopicum* and its progenitor, *S*. *anguivi* under screen house conditions; and it was observed that both vegetative and reproductive variates are useful in distinguishing between accessions of the two species. It is notable that *S*. *aethiopicum* Shum is leafy-type while its progenitor is fruit-type (Sękara et al., 2007; Sseremba et al., 2017). This study's observation that almost all the slightly polymorphic variables were reproductive characters suggests that leafy-type species should be described using vegetative structures (for morphological characterization).

From the static stability results, generally, different accessions showed higher stability for some than the rest of the variables. Accessions with the highest number of variables for best static stability were 184P followed by 163P. Conversely, accessions 168P, 148, 141, and 137 had the highest number of variables for least static stability. The observations suggest that either the parameters measured were at different fixation levels (level of homozygosity of same loci) in different accessions or there is a mere difference in form that a variable exhibits in relation to genotype and environment. The possibility of different fixation levels at same loci across accessions can be eliminated on grounds that *S*. *aethiopicum* is a predominantly self-pollinating species (Sakhanokho et al., 2014; Sękara et al., 2007); and pure line accessions were used in this study. Therefore, the effect of cross-pollination on genetic variability is ruled out. It is believed that some accessions were environmentally more robust than others on the account of their innate differences in genotype by environment interaction attributes (Donoso-Ñanculao et al., 2016; Kamidi, 2001; Sabaghnia et al., 2012; Temesgen et al., 2015). Thus, accessions 184P and 163P can be considered as the most stable across test environments while 168P, 148, 141, and 137 were the most sensitive. Sseremba et al. (2018b) had earlier obtained similar results when the environments were based on drought stress levels

in a screen house study.

Conclusion

The study aims at firstly, identifying variables that provide identity of Shum accessions across environments, and secondly, identifying accessions that are stable in morphological traits. From the first objective, it was observed that plant height at flowering, plant canopy breadth, plant branching, petiole color, petiole length, leaf blade length, leaf blade width, leaf lobbing, leaf tip angle, flowering time, style length, fruit position, fruit flesh density, fruits per inflorescence and fruit flavor are effective in distinguishing among Shum group accessions of *S. aethiopicum*. In the second objective, it was observed that accessions 184P and 163P were the most statically stable across test environments while 168P, 148, 141, and 137 were the least robust in conserving their morphological traits. A further study on static stability of Shum group genotypes that considers a more diverse source of accessions and additional testing environments is recommended so as to broaden the scope of inference for polymorphic descriptors of the subspecies. A combined use of molecular and morphological markers on same accessions is also recommended for further study; as it could play a cross-check role in attributing the observed morphological differences.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

This study was funded by European Union through the initiative – Promoting African and European Partnerships in Agricultural Research and Development (PAEPARD), under Forum for Agricultural Research in Africa (FARA) on a project titled '*Enhancing nutrition security and incomes through adding value to indigenous vegetables in East and Central Uganda* (FARA/PAEPARD-CRFII)'. Appreciation is also extended to the project partners: Dr. John Jagwe (Farmgain Africa), Dr. Apolo Kasharu (CHAIN UGANDA) and Dr. Debbie Rees (Natural Resources Institute, University of Greenwich, UK.

REFERENCES

Abbiw DK (1997). Traditional vegetables in Ghana. Promoting the Conservation and Use of Underutilized and Neglected Crops (IPGRI). Biodiversity International. Retrieved from http://www.bioversityinternational.org/fileadmin/bioversity/publications

Abukutsa-Onyango MO, Adipala E, Tusiime G, Majaliwa JGM (2010). Strategic repositioning of African indigenous vegetables in the Horticulture Sector. In Second RUFORUM Biennial Regional Conference on "Building capacity for food security in Africa", Entebbe, Uganda, 20-24 September 2010 (pp. 1413-1419). RUFORUM. Retrieved from http://www.cabi.org/gara/FullTextPDF/2013/20133184516.pdf

Adeniji OT, Kusolwa PM, Reuben SOWM (2012). Genetic diversity among accessions of *Solanum aethiopicum* L. groups based on morpho-agronomic traits. Plant Genetic Resources 10(03):177-185.

Adeniji OT, Kusolwa P, Reuben S (2013). Morphological descriptors and micro satellite diversity among scarlet eggplant groups. African Crop Science Journal 21(1):37-49.

Balestre M, de Souza JC, Von Pinho RG, de Oliveira RL, Paes JMV (2009). Yield stability and adaptability of maize hybrids based on GGE biplot analysis characteristics. Crop Breeding and Applied Biotechnology 9(3):219-228.

Bationo-Kando P, Sawadogo B, Nanema K, Kiebre Z, Sawadogo N, Traore RE, Sawadogo M, Zongo J (2015). Characterization of *Solanum aethiopicum* (Kumba group) in Bukina Faso. International Journal of Science and Nature 6(2):169-176.

Becker HC, Leon J (1988). Stability analysis in plant breeding. Plant Breeding 101(1):1-23.

Bisamaza M, Banadda N (2017). Solar drying and sun drying as processing techniques to enhance the availability of selected African indigenous vegetables, *Solanum aethiopicum* and Amaranthus lividus for nutrition and food security in Uganda. African Journal of Food Science and Technology 8(1):001-006.

Cernansky R (2015). Super vegetables. Nature 522(7555):146.

Donoso-Ñanculao G, Paredes M, Becerra V, Arrepol C, Balzarini M (2016). GGE biplot analysis of multi-environment yield trials of rice produced in a temperate climate. Chilean Journal of Agricultural Research 76(2):152-157.

Eberhart S, Russell W (1966). Stability parameters for comparing varieties. Iowa Agriculture and Home Economics, United States of America. Crop Science 6(1):36-40.

Ebert A (2014). Potential of Underutilized Traditional Vegetables and Legume Crops to Contribute to Food and Nutritional Security, Income and More Sustainable Production Systems. Sustainability 6(1):319-335.

Food and Agriculture Organization (FAO) (2005). Building on gender, agrobiodiversiy and local knowledge. Food and Agriculture Organization of the United Nations.

Finlay KW, Wilkinson GN (1963). The analysis of adaptation in a plant-breeding programme. Crop and Pasture Science 14(6):742-754.

Gramazio P, Blanca J, Ziarsolo P, Herraiz FJ, Plazas M, Prohens J, Vilanova S (2016). Transcriptome analysis and molecular marker discovery in *Solanum incanum* and S. aethiopicum, two close relatives of the common eggplant (*Solanum melongena*) with interest for breeding. BMC Genomics 17(1). https://doi.org/10.1186/s12864-016-2631-4

Horna D, Gruere G (2006). Marketing underutilized crops for biodiversity: the case of African garden egg (*Solanum aethiopicum*) in Ghana. In 8th Bioecon Conference. Kings College, Cambridge. pp. 29-30.

Kamidi RE (2001). Relative stability, performance, and superiority of crop genotypes across environments. Journal of Agricultural, Biological, and Environmental Statistics 6(4):449-460.

Kouassi A, Béli-Sika E, Tian-Bi T, Alla-N'Nan O, Kouassi A, N'Zi JC, Tio-Touré B (2014). Identification of Three Distinct Eggplant Subgroups within the *Solanum aethiopicum* Gilo Group from Côte d'Ivoire by Morpho-Agronomic Characterization. Agriculture 4(4):260-273.

Lin C, Binns M (1988). A superiority measure of cultivar performance for cultivar x location data. Canadian Journal of Plant Science 68:193-198.

Mendes de Paula TO, Marinho CD, Souza V, Barbosa MHP, Peternelli LA, Kimbeng CA, Zhou MM (2014). Relationships between methods of variety adaptability and stability in sugarcane. Genetics and Molecular Research 13(2):4216-4225.

Odong TL, van Heerwaarden J, Jansen J, van Hintum TJL, van Eeuwijk FA (2011). Determination of genetic structure of germplasm collections: are traditional hierarchical clustering methods appropriate for molecular marker data?. Theoretical and Applied Genetics

123(2):195-205.
Ojiewo C, Tenkouano A, Hughes JA, Keatinge JDH (2013). Diversifying diets: using indigenous vegetables to improve profitability, nutrition and health in Africa. Diversifying Food and Diets No. 291.
Omulo D (2016). Value addition on traditional vegetables: an impact assessment on women farmers in Lugari, Kenya. University of Nairobi, Nairobi, Kenya.
Osei MK, Banful B, Osei CK, Oluoch MO (2010). Characterization of African eggplant for morphological characteristics. Nong Ye Ke Xue Yu Ji Shu 4(3):33.
Palanog A, Endino-Tayson C, Ciocon IM, Ines LT, Tizon B, Bibar JE, Libetario E (2015). Grain yield performance and stability analysis of rice varieties under rainfed lowland conditions of Western Visayas, Philippines. The Asian International Journal of Life Sciences 24(1):399-408.
Pincus LM (2015). Increasing indigenous vegetable yield and nutritional quality through traditionally-and scientifically-informed soil fertility management. University of California, Davis. ProQuest LLC. 789 East Eisenhower Parkway P.O. Box 1346 Ann Arbor, MI 48106 – 1346.
Prohens J, Whitaker BD, Plazas M, Vilanova S, Hurtado M, Blasco M, Stommel JR (2013). Genetic diversity in morphological characters and phenolic acids content resulting from an interspecific cross between eggplant, *Solanum melongena*, and its wild ancestor (*S. incanum*): Morphology and phenolics in an interspecific family in eggplant. Annals of Applied Biology 162(2):242-257.
Rémi WS, Oluoch M, Silué D (2005). Improvement and distribution of seed of selected African indigenous vegetables for enhancing the livelihood of small-scale farmers in sub- Saharan Africa (Poster) (p. 1). Arusha, Tanzania: AVRDC-World Vegetable Center-Regional Center for Africa.
Rubaihayo E, Hart T, Kakonge E, Kaaya A, Kawongolo J, Kabeere F, Rubaihayo P (2003). Development of mechanisms for sustainable production and utilisation of indigenous vegetables and management of their genetic diversity in Uganda. Unpublished Report. Faculty of Agriculture, Makerere University Kampala.
Sabaghnia N, Karimizadeh R, Mohamadi M (2012). Genotype by environment interaction and stability analysis for grain yield of lentil genotypes. Žemdirbyst 99(3):305-312.
Sakhanokho HF, Islam-Faridi MN, Blythe EK, Smith BJ, Rajasekaran K, Majid MA (2014). Morphological and Cytomolecular Assessment of Intraspecific Variability in Scarlet Eggplant (*Solanum aethiopicum* L.). Journal of Crop Improvement 28(4):437-453.
Sękara A, Cebula S, Kunicki E (2007). Cultivated eggplants–origin, breeding objectives and genetic resources, a review. Folia Horticulturae 19(1):97-114.
Ssekabembe CK (2008). Effect of Proportion of Component Species on the Productivity of *Solanum aethiopicum* and *Amaranthus lividus* under Intercropping. African Journal of Agricultural Research 3(7):510-519.
Ssekabembe CK, Bukenya C, Nakyagaba W (2003). Traditional knowledge and practices in local vegetable production in central Uganda. African Crop Science Conference proceedings 6:4-19.
Sseremba G, Tongoona P, Eleblu JSY, Danquah EY, Kizito EB (2018a). Linear discriminant analysis of structure within African eggplant 'Shum'. African Crop Science Journal 26(1):37-48.
Sseremba G, Tongoona P, Eleblu JSY, Danquah EY, Kaweesi T, Baguma Y, Masanza M, Kizito EB (2018b). Stability of *Solanum aethiopicum* Shum accessions under varied water deficit stress levels and identification of pertinent breeding traits for resistance to water shortage. Euphytica 214(11):1-11.
Sseremba G, Tongoona P, Eleblu JSY, Danquah E, Kabod NP, Kizito EB (2017). Morphological distinctiveness between Solanum aethiopicum Shum group and its progenitor. Journal of Plant Breeding and Crop Science 9(8):118-129.
Stone A, Massey A, Theobald M, Styslinger M, Kane D, Kandy D, Davert E (2011). Africa's indigenous crops: State of the world 2011. Worldwatch Institute. Retrieved from www.NourishingthePlanet.org.
Temesgen T, Keneni G, Sefera T, Jarso M (2015). Yield stability and relationships among stability parameters in faba bean (*Vicia faba* L.) genotypes. The Crop Journal 3(3):258-268.
UPOV (2002). General introduction to the examination of distinctness, uniformity and stability and the development of harmonized descriptions of new varieties of plants. TG/1/3.ed. International Union for the Protection of New Varieties of Plants.

Vol. 10(9), pp. 228-238, September 2018
DOI: 10.5897/JPBCS2018.0747
Article Number: 555E91E58159
ISSN: 2006-9758

http://www.academicjournals.org/JPBCS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Inheritance and combining ability of cowpea resistance to bruchid (*Callosobruchus maculatus* F.)

Weldekidan Belay Miesho[1],*, Ulemu Mercy Msiska[1], Hailay Mehari Gebremedhn[1], Geoffrey Maxwell Malinga[2], Patrick Obia Ongom[1,3], Patrick Rubaihayo[1] and Samuel Kyamanywa[1]

[1]Department of Agricultural Production, College of Agricultural and Environmental Sciences, Makerere University, P. O. Box 7062, Kampala, Uganda.
[2]Department of Biology, Faculty of Science, Gulu University, P. O. Box 166, Gulu, Uganda.
[3]Makerere University Regional Center for Crop Improvement (MaRCCI), Kampala Uganda.

Received 17 May, 2018; Accepted 18 July, 2018

The bruchid, *Callosobruchus maculatus* (F.) is one of the most destructive pests and causes substantial losses to cowpea during storage in tropical and subtropical regions. The development of successful breeding strategy requires knowledge on gene action and trait inheritance in local and improved sources. In this study, the mode of inheritance, the types of gene action and maternal effects of cowpea resistance to bruchid was investigated. Nine parental lines and their 72 F_2 segregating populations, created in a full diallel Griffing's method 1 approach, were evaluated for resistance to bruchid attack in a randomized complete block design (RCBD) with three replications. Data were recorded on number of eggs laid by the bruchid (NE), adult bruchid emergence (NEI), median development period (MDP) and Dobie Susceptibility index (DSI) was computed. Genotype had highly significant effects on NE, NEI and MDP and DSI. General combining ability (GCA) effects of parents, specific combining ability (SCA) effects of crosses, and maternal and reciprocal effects were highly significant for all the traits. The ratios of GCA to SCA for all the traits were greater than 50% suggesting the preponderance of additive over non-additive gene action in the expression of the traits. Narrow sense heritability estimates were 64.12, 77.69 and 80.99% for NE, NEI and MDP, respectively. Parents 2419, TVu-2027 and IT84s-2246 were identified as promising general combiners for resistance to bruchid and the seven best selected crosses based on their SCA and DSI values were, IT84s-2246 × 2419, 2419 × MU9, TVu-2027 × SECOW2W and 2419 × IT90K-76, 2419 × WC69, 2419 × SECOW5T and 2419 × SECOW2W. The selected parents and/or crosses could be valuable genetic materials for breeding cowpea resistance to bruchid in Uganda or similar environments.

Key words: Additive gene action, heritability, median development period, reciprocal effects.

INTRODUCTION

Cowpea, *Vigna unguiculata* (L. Walp.) (Fabaceae) is one of the most important legume crops in arid and semiarid regions of Africa (NRC, 2006). It is a warm-weather crop, drought tolerant and well- adapted to the drier regions

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

of the tropics (Aliyu and Wachap, 2014). The crop represents one of the main sources of protein in human diet (Lima et al., 2014). Despite its relevance to agriculture in the developing world and its stress resilience, actual yields of cowpea are much lower than the known yield potential (Amatriaín et al., 2016). Production of this important crop has been constrained by insect pests among other factors (Boukar et al., 2012) and devastating effects in storage due to bruchid (Adebayo and Anjorin, 2018).

The cowpea bruchid, *Callosobruchus maculatus* F. (Coleoptera: Bruchidae), widely distributed in the tropical and subtropical regions (Adebayo and Anjorin, 2018), is the most destructive pest of cowpea during storage (Deshpande et al., 2011). *C. maculatus* attack cowpea in the field and continues after harvest, and if left unattended, cause up to 44.7% loss in weight, reduction in the germination ability, and the market and nutritional values of cowpea seeds (Oluwafemi, 2012; NARO, 2012; Adekunle and Ayodele, 2014; Miesho et al., 2018). Although several control measures for bruchids are available, such as, synthetic insecticides, plant extracts and other traditional methods such as mixing the cowpea seeds with ash (MBAZARDI, 2014), the use of host-plant resistant cultivar is currently viewed as the most economical and eco-friendly option (Orawu et al., 2013; Adebayo et al., 2016). To develop an appropriate breeding strategy, the search for sources of resistance to bruchids in cowpea must be followed with the study of the inheritance of resistant genes.

In an earlier study (Miesho et al., 2018), 18 bruchid resistant genotypes were identified from local and introduced cowpea genotypes; for example, 2419, IT84s-2046 and TVu-2027. However, knowledge regarding the genetic control and heritability of the resistance to *C. maculatus* was not studied and yet it is needed to optimize breeding pipeline for bruchid resistance (Barelli et al., 1999; Viana et al., 1999). Previous genetic studies using TVu-2027 as donor suggested that maternal genes are involved in the inheritance of resistance to bruchid (Dobie, 1981). The same study highlighted involvement of a major recessive gene and modifiers, and also noted that either dominant or interactive effects were more important than additive types of gene effects (Dobie, 1981). Redden (1983) reported paternal and embryonic genotypic effect in certain backcross combinations of F_3 generation and digenic control of resistance in one of their cross and monogenic control in another cross, in conjunction with one or more modifier or minor gene loci. In contrast, Kitch (1987) and Adjadi et al. (1985) reported that resistance to bruchid resulted from two recessive genes. In Uganda, studies on inheritance of resistance to bruchid are scarce. It is important to understand the heritability of resistance to bruchid character and the gene action controlling it to help breeders select suitable parents for the breeding program. Therefore, the aims of the present study were to identify the mode of inheritance, estimate the gene effects as well as identify parents and crosses with good combining abilities for cowpea resistance to bruchid under the Uganda growing condition.

MATERIALS AND METHODS

Experimental procedures and diallel mating scheme

Nine cowpea genotypes comprising of five bruchid resistant (IT90K-76, IT97K-499-35, TVU-2027, 2419 and IT84s-2246) and four susceptible (SECOW2W, WC69, MU9 and SECOW5T) lines used as parents were selected from out of 145 cowpea genotypes by a no-choice laboratory bruchid damage bioassay (Miesho et al., 2018). These genotypes were selected based on their adaptation to wider agro-ecology, preference by farmers and resistance to other biotic and abiotic stresses.

The nine cowpea parental lines were each planted separately in a five-litter bucket (two seeds per bucket) in September 2015 in a screen house at Makerere University Agricultural Research Institute Kabanyolo (MUARIK), Uganda, located at 0°28'N and 32°37'E, at approximately 1200 m a. s. l. Each line was hand emasculated before pollen shading and crossed at flowering in all possible combinations following Griffing's (1956) method 1 approach to produce 36 F_1 plants and 36 reciprocal crosses. The F_1 seeds and the reciprocal crosses were selfed to produce F_2 generation in a screen house. The F_1 seeds were planted along with their parents to identify true crosses. The F_2 seeds were harvested and bulked for each of the 36 crosses and 36 reciprocal crosses.

Bruchid laboratory culture

Adults of *C. maculatus* (F.) were obtained from the National Agricultural Research Laboratory, Kawanda. A permanent laboratory culture of the insect was established at MUARIK by allowing the insects to lay eggs on a susceptible inbred line IT71. Insects were reared on 12 kg seeds kept in four transparent plastic buckets of 5 L capacity whose tops were covered with muslin cloth to provide aeration and prevent the insects from escaping. The insects were allowed to oviposit, and their progeny maintained by regularly replacing the infested seeds with fresh seeds.

Screening of cowpea seeds for resistance to *C. maculatus*

To evaluate for resistance to bruchids, 10 F_2 generation seeds of each of the 36 F_1 and 36 reciprocal crosses and the nine parents were weighed and separately put in a Petri-dish of 90 × 15 mm. Thirty seeds were randomly selected from each of the bulked F_2s and parental seeds and oven dried at 40°C for 24 h to destroy any insects or eggs that could have been present and to standardize moisture levels of the seeds (Amusa et al., 2014). The experiment was laid in randomized complete block design with three replications. Time was used as blocking factor and infestation was done at an interval of eight days in order to ease data collection. To each Petri dish containing the ten seeds, two pairs of three-day old male and female adult bruchids from laboratory culture were introduced and the top covered to prevent the insects from escaping. The insects were left undisturbed in the Petri-dishes for three days to allow for mating and oviposition and then removed (Amusa et al., 2013). Data on number of eggs, daily insect emergence, number of exit holes, number of damaged and undamaged seeds, initial seed weight (g) and residual seed weight (g) were recorded for 44 days after insect introduction, and percentage weight loss and percentage pest tolerance computed.

Table 1. Analysis of variance for resistance of cowpea genotypes to *C. maculatus* infestation.

Source of variation	df	NE	NEI	ANH	MDP	PWL	PPT	DSI
Genotype	80	1831.45***	888.50**	9.14***	155.00***	543.23**	2766.76**	16.45**
Replication	2	16.807ns	5.94ns	0.75*	4.49*	0.45ns	153.10ns	0.95***
Residual	160	7.32	3.55	0.64	1.45	1.96	61.42	0.11

NE= Number of eggs; NEI= Number of emerged insects; ANH= Average number of holes; MDP= Median development period; PWL= percentage weight loss; PPT= percentage pest tolerance; DSI= Dobie susceptibility index. ***, **, * and ns; significant at P ≤ 0.001, P ≤ 0.01, P ≤ 0.05 and non-significant, respectively.

The number of emerged adult bruchids was recorded daily until no more adults emerged for five days. At the end of the experiment, Dobie Susceptibility Index (DSI) was calculated for each genotype using the data on total number of adult bruchid that emerged on each genotype and their median development period (that is the time from the middle of oviposition to the emergence of 50% of adult bruchids) using the formula of Dobie (1974):

$$DSI = \frac{\text{Loge F1} \times 100}{MDP}$$

Where, F1 is the total number of emerging adults and MDP is the median developmental period (days).

The susceptibility index ranging from 0 to 11 was used to categorize the cowpea genotypes; where; 0-3 = resistant, 4-7 = moderately resistant, 8-10 = susceptible and ≥10 = highly susceptible (Dobie, 1974).

Data analysis

General analysis of variance, using GenStat discovery 16.1th Edition statistical package, was performed for all quantitative data.

Diallel analysis was performed for all quantitative data of the populations developed by Griffing's (1956) Method 1 using Genetic Designs in R (AGD-R) Version 3.0 (Rodríguez et al., 2015). In this model, genotypes were considered as a fixed effect whereas replication effects were regarded as random.

Estimation of heritability, general and specific combining ability, reciprocal and maternal effects, and Bakers ratio

The general combining ability (GCA) effects were analyzed for each parent. Specific combining ability (SCA) and reciprocal effects were analyzed for the F2 crosses and their reciprocals, respectively. Similarly, maternal effects were analyzed for each parent. Confirmation of the adequacy of the additive and non-additive variances was estimated. Coefficient of genetic determination in the narrow (CGD-NS) and broad sense (CGD-BS), analogues of the narrow sense (h2) and broad sense heritability (H2), respectively were estimated. All the analysis was done using Genetic Designs in R (AGD-R) Version 3.0 (Rodríguez et al., 2015).

Phenotypic correlation analysis was used to investigate the relationship among number of eggs, adult bruchid emergence, median development period, percentage pest tolerance and Dobie susceptibility index. The analysis was done with GenStat Discovery, 16th Edition statistical package using data from the reciprocals, crosses and the nine parents.

RESULTS

There were significant differences in the responses of the parents and the F_2 segregating populations to bruchid infestation for all the traits measured (Table 1).

The observed significant differences among progenies were for number of eggs laid (NE), number of holes per seed (AHS), median development period (MDP), adult bruchid emergence (NEI), percentage seed weight loss (PWL), percentage pest tolerance (PPT) and Dobie susceptibility index (DSI) suggested the presence of genetic variability among the cowpea parental lines and the populations tested.

Total number of genotypes identified as susceptible, moderately resistant and resistant based on the DSI value were 15, 38 and 28, respectively (Table 5), indicating their continuous distribution to the different resistance classes (Table 2).

The Highest Dobie susceptibility index and adult emergence was recorded from the parental genotypes WC69, MU9, SECOW2W and SECOW5T than their crosses and reciprocals. The Dobie susceptibility ranged from zero for the resistant (TVu-2027 × IT97K-499-35) to 8.46 for the susceptible genotype (WC69). The number of emerged insects ranged from zero (2419 × IT84s-2246, IT84S-2246, IT84S-2246 × 2419, TVu-2027, TVu-2027 × 2419 and TVu-2027 × IT97K-499-35) to 69 (SECOW2W). Similarly, number of holes per seed was low for the resistant and high for the susceptible suggesting resistance. The correlation coefficients (r) of cowpea bruchid resistance parameters are presented in Table 3.

Percentage grain weight loss was significant (P<0.001) and positively correlated with the number of eggs (r = 0.70) and number of holes (0.80). Number of emerged insects showed significant (P<0.001) but negative correlations with MDP (-0.53) and PPT (-0.78). Dobie Susceptibility index showed significant (P<0.001) but negative correlations with insect development period (-0.81) and pest tolerance (-0.86); and positively correlated with number of eggs (0.80), growth index (0.7), number of emerged insects (0.88), number of holes (0.88), and weight loss (0. 57). These results imply that number of emerged insects and insect development period could be used as good indicators of cowpea resistance to bruchid.

Combining ability and maternal effects

The results of diallel analysis for the parents and F_2

Table 2. Evaluation of F_2 generation and parental seeds for bruchid resistance (some representative parental and F_2 populations).

Genotypes	Type of cross	NE	NEI	AHS	MDP	PWL	PPT	DSI
WC69	Parent	130	61.33	6.2	21.17	35	0	8.46
MU9	Parent	70	65	6.5	22	19	10	8.24
SECOW2W	Parent	95	69	6.9	23	30	3.33	7.99
SECOW5T	Parent	61	55	5.2	22	26	6.67	7.91
MU9 × SECOW5T	S×S	57	55	5.4	24	22	3.33	7.25
SECOW5T × WC69	S×S	45	36	3.5	22	38	3.33	7.07
MU9 × 2419	S×R	74	39	3.9	23	12	20	6.92
MU9 × SECOW2W	S×S	63	49	5	25.5	50	3.33	6.63
SECOW2W × 2419	S×R	40	27	2.9	24.5	15.63	30	5.84
SECOW2W × TVu-2027	S×R	32	15	1.6	23	5.42	43.33	5.11
SECOW5T × 2419	S×R	28	14	1.4	25	14.18	50	4.58
2419 × WC69	R×S	25	10.67	1.07	37.67	6.36	43.33	2.72
2419 × SECOW5T	R×S	12	9	0.8	38	2.37	56.67	2.63
2419 × SECOW2W	R×S	12	8	0.8	34.67	3.94	50	2.6
TVu-2027 × IT90K-76	R×R	12	5	0.5	28	1	76.67	2.5
TVu-2027 × SECOW2W	R×S	16	5	0.5	34	5	60	2.06
2419 × MU9	R×S	13	4	0.4	37	3.47	73.33	1.63
WC69 × 2419	S×R	5	2	0.2	21	5	70	1.43
2419	Parent	43.33	0.67	0.07	40.67	0.09	96.67	0.24
IT84S-2246	Parent	0	0	0	44	0	100	0
IT84S-2246 × 2419	R×R	0	0	0	44	0	100	0
TVu-2027	Parent	4	0	0	44	0	96.67	0
TVu-2027 × 2419	R×R	14	0	0	44	0	100	0
LSD		**4.36**	**3.04**	**1.29**	**1.94**	**2.26**	**12.64**	**0.54**

R= Resistance; S= susceptible.

Table 3. Correlation coefficients (r) for cowpea genotype bruchid resistance parameters under *C. maculatus* artificial infestation.

	NE	NEI	ANH	MDP	PWL	PPT	DSI
NE	1						
NEI	0.89***	1					
ANH	0.80***	0.90***	1				
MDP	-0.48***	-0.53***	-0.48***	1			
PWL	0.70***	0.78***	0.69***	-0.50***	1		
PPT	-0.71***	-0.78***	-0.71***	0.63***	-0.75***	1	
DSI	0.80***	0.88***	0.80***	-0.81***	0.76***	-0.86***	1

*** = significant at P ≤ 0.0001.

segregating populations and the different genetic variance components for number of eggs, adult emergence, and median development period are presented in Table 4.

The GCA and the SCA effects were both significant (P ≤ 0.001). Highly significant (P ≤ 0.001) difference was also observed among the reciprocal crosses for the traits measured, indicating significant diversity among the genotypes. Additionally, maternal effect was significant (P ≤ 0.001) for NE, NEI and MDP. The number of eggs laid by the bruchid, adult bruchid emergence, and median development period accounted for 52.42, 64.34, 64.11 and 51.51% of the sum of squares for the parents and 29.15, 18.24 and 11.69% of the sum of squares for the crosses, respectively (Table 4). The result also provided evidence for the existence of wide variation among both

Table 4. Combined ANOVA for GCA and SCA, heritability and degree of dominance of F_2 population and parents' diallel analysis for number of eggs, *C. maculatus* emergence and median development period.

Source	DF	NE	NEI	MDP
GCA	8	10056.36***	6031.5***	917.94***
SCA	36	1242.39***	379.94***	46.29***
Reciprocal	36	592.76***	234.49***	94.37***
Maternal	8	867.85***	577.82***	231.05***
Residual	160	7.32	4.6	1.52
$\delta^2 GCA$		186.09	111.61	16.97
$\delta^2 SCA$		205.84	62.56	7.46
BR		0.64	0.78	0.82
CGDNS (%)		64.12	77.69	80.99
CGDBS (%)		99.74	99.92	98.53
Degree of dominance		1.05	0.75	0.66

*** Data significant at P ≤ 0.001; GCA, the general combining ability; SCA, the specific combining ability; Reciprocal the reciprocal crosses; BR the Baker's ratio; $\delta^2 GCA$ = variance of general combining ability; $\delta^2 SCA$ = variance of specific combining ability of parents; CGDNS, the coefficient of genetic determination – narrow-sense heritability estimates; CGDBS, the coefficient of genetic determination – broad sense heritability estimates.

the parents and the resultant crosses, suggesting a high potential for selections for improvement in the resistance to bruchid. Values of Baker's ratio estimated for all the traits were greater than 50% suggesting the predominance of additive over non-additive gene action in the expression of these traits.

The observed high level of coefficient of genetic determination – broad sense (H^2) also corroborated the finding that both additive and non-additive gene effects conditioned the inheritance of bruchid resistance. The coefficient of genetic determination – narrow sense (h^2) estimates for number of eggs (64.12%), emerged insects (77.69%) and median development period (80.99%) were also high, supporting the Baker's ratio which revealed that additive gene effect was more important than non-additive gene effects for controlling the inheritance of the traits.

General combining ability (GCA) effects

Results of the general combining ability effects for the nine selected parents for bruchid resistance traits are shown in Table 5.

All the parents, except IT97k-499-35 for median development period, showed significant (P ≤ 0.001) GCA effects for number of eggs laid by the bruchid, adult bruchid emergence and median development period suggesting a greater contribution of additive gene effects in determining resistance to *C. maculatus* among the studied genotypes. Lines 2419, TVu-2027 and IT84s-2246 contributed significant (P < 0.001) GCA effects of -10.55, -10.03 and -8.57 for number of emerged insects and 6.19, 4.98 and 4.49 for median development period, respectively, suggesting that the genotype performed far better in the crosses for these specific traits. Conversely, genotypes SECOW2W, WC69, SECOW5T and MU9 contributed significant (P ≤ 0.001) and positive GCA effects of 10.97, 11.58, 13.34 and 8.10 for number of emerged insects and -3.35, -3.68, -3.17 and -4.02 GCA effects for median development period, respectively indicating their negative contribution to resistance.

Specific combining ability (SCA) and maternal effects

The majority of the F_2 generation seeds showed significant (P < 0.001) SCA effects for median development period, adult bruchid emergence and number of eggs laid by the bruchid (Table 6).

Significant SCA effects for median development period (MDP) were observed in 25 crosses, indicating the presence of non-additive gene effects. The lowest SCA values for MDP were observed from crosses 2419 × TVu-2027 (-5.04), IT84s-2246 × SECOW5T (-4.49), IT84s-2246 × IT90K-76 (-3.73) and 2419 × SECOW2W (-2.79), and the highest were recorded from TVu-2027 x IT97K-499-35 (6.64). Likewise, significant SCA effects for number of emerged insects were observed in 29 crosses ranging from -14.93 (2419 x WC69) to18.45 (SECOW2W). These results suggested that resistance of these genotypes was higher or lower than would be expected from the average resistance of their respective parents and therefore, these crosses could be selected for the improvement of resistance to bruchid.

All parents, except IT84s-2246, showed significant (P ≤

Table 5. Estimates of general combining ability effects for median development period, adult bruchid emergence and number of eggs laid by the bruchid in the F2 population diallel analysis.

Parent	NE	NEI	MDP
SECOW2W	11.66***	10.97***	-3.35***
WC69	19.99***	11.58***	-3.68***
MU9	16.95***	13.34***	-3.17***
SECOW5T	5.47***	8.10***	-4.02***
IT90K-76	-7.80***	-7.64***	-1.29***
IT97k-499-35	-7.71***	-7.20***	-0.15ns
TVu-2027	-15.06***	-10.03***	4.98***
2419	-9.16***	-10.55***	6.19***
IT84s-2246	-14.34***	-8.57***	4.49***

***, **,* and ns; significant at P ≤ 0.001, P ≤ 0.01, P ≤ 0.05 and non-significant, respectively.

Table 6. Estimates of specific combining ability effects for median development period, adult bruchid emergence and number of eggs laid by the bruchid in the F_2 population diallel analysis.

Female	Male	MDP	NEI	NE
SECOW2W	Secow2W	2.47*	18.45***	36.27***
WC69	Secow2W	0.42ns	5.55***	-4.07***
WC69	WC69	-0.01 ns	17.11***	52.27***
MU9	Secow2W	1.83***	-4.71***	-7.86***
MU9	WC69	-0.27 ns	-1.82*	25.97***
MU9	MU9	-0.19 ns	13.25***	-0.99ns
SECOW5T	Secow2W	1.81***	12.40***	11.62***
SECOW5T	WC69	-0.58***	-2.58***	-13.05***
SECOW5T	MU9	1.91***	2.16***	-4.68***
SECOW5T	SECOW5T	2.19***	15.39***	12.30***
IT90K-76	Secow2W	0.28***	-5.23***	-7.10***
IT90K-76	WC69	1.6***	-8.51***	-15.60***
IT90K-76	MU9	-0.41***	0.40***	-0.23ns
IT90K-76	SECOW5T	-0.80 ns	-12.53***	-5.58***
IT90K-76	IT90K-76	-0.95ns	0.22ns	-6.14***
IT97k-499-35	Secow2W	-0.86ns	-7.01***	-0.36ns
IT97k-499-35	WC69	1.21**	0.22ns	-2.53**
IT97k-499-35	MU9	-1.54***	-10.38***	-20.99***
IT97k-499-35	SECOW5T	-0.61ns	-10.47***	-13.01***
IT97k-499-35	IT90K-76	-1.76ns	11.77***	11.27***
Female	Male	MDP	NEI	NE
IT97k-499-35	IT97k-499-35	-1.56*	-4.34***	2.01ns
TVu-2027	Secow2W	-2.66***	-9.84***	-8.68***
TVu-2027	WC69	1.17***	1.38ns	-9.84***
TVu-2027	MU9	-2.34***	2.96***	5.36***
TVu-2027	SECOW5T	-0.15ns	0.36ns	7.84***
TVu-2027	IT90K-76	-0.72ns	4.27***	7.45***
TVu-2027	IT97k-499-35	6.64***	-1.34ns	-4.64***
TVu-2027	TVu-2027	5.51***	-0.67ns	0.05ns
2419	Secow2W	-2.79***	-2.99***	-14.08***
2419	WC69	-1.21*	-14.93***	-29.92***
2419	MU9	-0.72***	-3.52***	-0.71ns

Table 6. Contd.

2419	SECOW5T	0.72ns	-5.79***	-10.73***
2419	IT90K-76	6.48***	8.46***	17.38***
2419	IT97k-499-35	-1.99***	16.85***	22.12***
2419	TVu-2027	-5.04***	2.51***	0.30ns
2419	2419	-0.25ns	1.36ns	26.90***
IT84s-2246	Secow2W	-0.50ns	-6.64***	-5.73***
IT84s-2246	WC69	-2.34***	3.59***	-3.23***
IT84s-2246	MU9	1.73***	1.66*	4.14***
IT84s-2246	SECOW5T	-4.49***	1.06ns	15.29***
IT84s-2246	IT90K-76	-3.73***	1.142ns	-1.44ns
IT84s-2246	IT97k-499-35	0.46ns	4.70***	6.14***
IT84s-2246	TVu-2027	-2.42***	0.36ns	2.16*
IT84s-2246	2419	4.79***	-1.95*	-11.25***
IT84s-2246	IT84s-2246	6.49***	-3.93***	-6.07***

***, **,* and ns; significant at P ≤ 0.0001, P ≤ 0.001, P ≤ 0.05 and non-significant, respectively.

Table 7. Estimates of maternal effect of parents on median development period, adult bruchid emergence and number of eggs laid by the bruchid in the F_2 population diallel analysis.

Parent	MDP	NEI	NE
SECOW2W	-1.14***	3.61***	5.26***
WC69	-1.54***	0.13ns	-1.30***
MU9	-1.94***	6.70***	6.96***
SECOW5T	-2.01***	-0.68*	2.19***
IT90K-76	0.39*	-0.17ns	-0.5ns
IT97k-499-35	-0.68*	-0.65*	-3.07***
TVu-2027	3.45***	-2.89***	-3.83***
2419	3.19***	-3.19***	-4.48***
IT84s-2246	0.28 ns	-2.87***	-1.22***

0.01) maternal effects on median development period (Table 7).

Meanwhile, SECOW2W, MU9, TVu-2027, 2419 and IT84s-2246; and IT97k-499-35 and SECOW5T showed reciprocal effects on number of emerged insects at P ≤ 0.001 and P ≤ 0.01, respectively. Similarly, all genotypes, except IT90K-76, showed significant (P ≤ 0.001) maternal effect on number of eggs laid by bruchid.

Most crosses showed significant (P ≤ 0.001) reciprocal differences for number of eggs, number of emerged insects and median development period (Table 8).

Overall, 31 reciprocal crosses showed difference in median development period and number of eggs, and 35 reciprocal crosses for number of emerged insects. Low reciprocal combining ability (reciprocal effect) for median development period was also recorded from crosses IT84S-2246 × MU9 (-9.08), 2419 × IT97K-499-35 (-8.58) and from crosses 2419 × SECOW2W (-7.83). Crosses 2419 × IT97K-499-35 (9.33), IT84S-2246 × IT97K-499-35 (2.92) showed the highest reciprocal combining ability for median development period. Likewise, the lowest reciprocal combining ability for number of emerged insects was recorded from IT90K-76 × SECOW2W (-9.5), MU9 × SECOW2W (-8.67) and IT97K-499-35 × WC69 (-3.67), indicating the presence of maternal or cytoplasmic gene effects in the inheritance of resistance to the bruchid.

DISCUSSION

Phenotypic variability

The study demonstrated the existence of phenotypic differences among the parents and segregating F_2 generations for resistance to bruchid which could be

Table 8. Reciprocal effects for median development period, adult bruchid emergence and number of eggs laid by the bruchid in the F_2 population diallel analysis.

Female	Male	MDP	NEI	NE
WC69	SECOW2W	0.92***	4.17***	1.00ns
MU9	SECOW2W	0.33ns	-8.67***	-5.17ns
MU9	WC69	-0.58***	-2.83***	0.00***
SECOW5T	SECOW2W	0.54***	-1.54***	-0.50ns
SECOW5T	WC69	0.083ns	1.83***	-1.17***
SECOW5T	MU9	1.92***	8.33***	6.83***
IT90K-76	SECOW2W	-2.17***	8.17***	10.50***
IT90K-76	WC69	-0.83***	-9.50***	-20.67***
IT90K-76	MU9	0.33ns	8.17***	17.67***
IT90K-76	SECOW5T	-0.92***	1.67***	11.50***
Female	Male	MDP	NEI	NE
IT97k-499-35	SECOW2W	0.17***	8.83***	18.33***
IT97k-499-35	WC69	-1.08***	-3.67***	-2.83***
IT97k-499-35	MU9	-1.33***	7.50***	10.33***
IT97k-499-35	SECOW5T	-2.25***	-0.17***	6.17***
IT97k-499-35	IT90K-76	0.67***	4.33***	10.50***
TVu-2027	SECOW2W	-5.17***	6.17***	6.00***
TVu-2027	WC69	-3.33***	10.33***	14.50***
TVu-2027	MU9	-3.00***	2.33***	-3.67***
TVu-2027	SECOW5T	-5.33***	0.50***	7.00***
TVu-2027	IT90K-76	2.00***	2.33***	9.00***
TVu-2027	IT97k-499-35	-4.00***	2.50***	7.33***
2419	SECOW2W	-6.08***	10.50***	12.83***
2419	WC69	-7.83***	-3.50***	-9.00***
2419	MU9	-6.50***	16.00***	28.83***
2419	SECOW5T	-6.58***	2.83***	9.67***
2419	IT90K-76	-2.42***	-0.67*	-5.83***
2419	IT97k-499-35	-8.58***	6.50***	0.67ns
2419	TVu-2027	9.33***	-3.00***	3.17***
IT84s-2246	Secow2W	1.17***	4.83***	4.33***
IT84s-2246	WC69	0.67***	12.67***	8.50***
IT84s-2246	MU9	-9.08***	6.50***	-2.50***
IT84s-2246	SECOW5T	-0.50*	-2.33***	-9.50***
IT84s-2246	IT90K-76	-0.33ns	1.00***	0.83*
IT84s-2246	IT97k-499-35	2.67***	2.00***	6.83***
IT84s-2246	TVu-2027	2.92***	1.17**	2.50***
IT84s-2246	2419	0.00ns	0.00ns	0.00ns

useful to select the best parent or cross for production or further breeding. For instance, there was a wide variation among genotypes for susceptibility index, a measure of resistance to bruchid damage (Dobie, 1974), and other traits (Table 1). Zero DSI and 44 days of MDP were recorded from genotypes IT84S-2246, IT84S-2246 × 2419, 2419 × IT84S-2246, TVu-2027, TVu-2027 × 2419 and TVu-2027 × IT97K-499-35 (Table 2), suggesting that these genotypes were resistant. These results are in line with previous finding which suggested that resistant cowpea genotypes often show reduced insects emergence and delayed insect development (Amusa et al., 2017; Miesho et al., 2018). On the contrary, the highest number of insects was recorded from WC69 (8.46), suggesting susceptibility. Similar results were obtained by Amusa et al. (2017) and Miesho et al. (2018).

Genotypic variability

The genetics of insect development period (MDP), insect emergence (NIE) and number of eggs (NE) laid by bruchid were evaluated for the parents and the segregating F_2 population. Number of emerged insect and

bruchid development period which were strongly correlated to Dobie susceptibility index (DSI) were considered as the most important parameters to measure bruchid resistance in the tested cowpea genotypes (Redden and McGuire, 1983; Jackai and Asante, 2003; Miesho et al., 2018).

General and specific combining ability effects

The study demonstrated the existence of genetic variability among the tested genotypes in their resistance to bruchid. The GCA and SCA analysis revealed significant differences ($P < 0.001$) among genotypes for number of eggs, insect emergence and median development period (Table 4), suggesting the importance of additive and non-additive gene effects in determining the inheritance of resistance to cowpea bruchid. Dobie (1981) and Redden (1983) also reported significant GCA and SCA effects for insect emergence and median development period. A 6x 6 diallel analyses in common bean revealed significant GCA and SCA effects in the study of heritability of resistance genes to *Acanthoscelides obtectus* (Kananji, 2007). Similarly, Mwila (2013) using North Carolina Design II involving crosses among two resistant and six susceptible bean lines to *C. maculatus* also reported similar GCA and SCA effect results.

The results also showed that the inheritance of number of eggs, number of insect emergence, and median development period traits were predominantly controlled by additive gene actions (Table 4). GCA effects accounted for 52.42% (number of eggs), 64.34% (insect emergence) and 51.51% (median development period) of the sum of squares for the crosses and large (>50%) GCA/SCA ratios indicated the predominance of the additive gene action to the inheritance of resistance to bruchid (Baker, 1978). Negative combining ability values for NE and NEI, and positive values for MDP are an indicator of resistance to bruchid. Thus, genotypes that presented negative GCA values for number of eggs were TVu-2027 (-15.06), IT84s-2246 (-14.34), 2419 (-9.16), IT90K-76 (-7.80) and IT97k-499-35 (-7.71); while genotypes 2419 (-10.55), TVu-2027 (-10.03), IT84s-2246 (-8.57), IT90K-76 (-7.64) and IT97k-499-35 (-7.20) presented negative GCA values for insect emergence (Table 5). Likewise, genotypes that presented the highest positive general combining ability for MDP were 2419 (6.19), TVu-2027 (4.98) and IT84s-2246 (4.49). The negative GCA values of number of eggs and emerged insects and positive GCA values of median development period indicated that the parents contributed to reduced number of eggs, number of emerged insects and contributed to delayed insect emergence; thereby provide a positive contribution to resistance and therefore could be selected as a good parent for breeding resistance to bruchid. Kananji (2007) and Mwila (2013) reported similar results on the resistance of beans to *A.obtectus* and *C. maculatus*, respectively. Parents 2419, TVu-2027 and IT84s-2246 were identified as promising general combiners for resistance to bruchid. These genotypes revealed low seed damage, insect emergence, and weight loss; and high percentage pest tolerance and elongated insect emergence period (Table 2). Similarly, the specific combining ability effects were used to identify specific crosses with desirable traits (Acquaah, 2007). Accordingly, crosses IT84s-2246 × 2419, 2419 × MU9, TVu-2027 × SECOW2W, and 2419 × IT90K-76, 2419 × WC69, 2419 × SECOW5T and 2419 × SECOW2W which revealed lowest number of eggs and insect emergence and elongated insect development period were the best specific crosses for bruchid resistance (Table 6). The selection of parents based on data obtained from combining ability and understanding the genetic parameters controlling trait inheritance ensures the efficiency of breeding program (Sleper and Poehlman, 2006; Sharma et al., 2015).

Maternal effect

The majority of the crosses were affected by maternal genes in their resistance to bruchid (Table 7). Maternal effects are common in sexually reproducing crops, and these can be detected by investigating the existence of difference between individuals of the forward and reverse crosses (Eizadshenass, 2013). The maternal effects were significant among the reciprocals for number of eggs, insect emergence and median development period. Fewer numbers of eggs, insect emergence and extended insect development period were observed on the forward crosses involving the resistance parent as female than their counter reciprocals and the direction of crossing revealed an influence of maternal effects on the number of eggs, insect emergence and insect development period. The existence of maternal effect was also confirmed by the significant effects of reciprocal crosses and their varied SCA effects (Tables 4 and 8). Similar results were reported by Redden (1983) and Adjadi et al. (1985) in cowpea; and mungbean (Somta et al., 2007).

Heritability and gene action

Bruchid resistance traits had low magnitude of dominance variances, revealing higher estimates of broad and narrow-sense heritability. Narrow sense heritability of 64.12, 77.69 and 80.99% were recorded for number of eggs, emerged insects and median development period, respectively (Table 4). This implied that the heritability of the traits from the parents was highly predictable, thus explaining the very high values obtained for the narrow sense heritability. The results provide evidence for the presence of additive and non-additive gene effect on the

inheritance of cowpea resistance to bruchid. High heritability estimates indicated higher frequency of genes controlling the traits (Ma-Teresa et al., 1994) and expression of the reliability with which phenotypic value guides the breeding value. In the improvement of self-pollinated plants such as cowpea, additive variation is of great importance and makes it possible to successfully select better individuals in segregating populations (Warner, 1952). For this reason, backcross, pedigree, single-seed descent or gametic selection methods are recommended for advancing the segregating populations as proposed by Bernado (2003).

Conclusion and recommendation

Significant GCA, SCA and maternal effects; high levels of broad and narrow sense heritability were detected; and high GCA/SCA (>50%) ratios to all the traits revealed the predominance of additive gene action. Due to maternal effects; it is advisable to use the resistant line as female parent. The GCA results indicated parents 2419, TVu-2027 and IT84s-2246 as the best general combiners for better resistance to bruchid. The SCA results indicated IT84s-2246 × 2419, 2419 × MU9, TVu-2027 × SECOW2W, 2419 × IT90K-76, 2419 × WC69, 2419 × SECOW5T and 2419 × SECOW2W as the best crosses for direct production.

CONFLICT OF INTERESTS

The authors declare that they have no conflict of interest.

REFERENCES

Acquaah G (2007). Principles of plant genetics and breeding, 2nd edition. Oxford: Wiley-Blackwell.

Adebayo RA, Anjorin OO (2018). Assessment of entomocidal effects of solar radiation for the management of cowpea seed beetle, *Callosobruchus Maculatus* (F.) (Coleoptera: Chrysomelidae) in stored cowpea. Global Journal of Science Frontier Research 18:21-26.

Adebayo AM, Babarinde AS, Adesina OG, Oladoye OS (2016). Evaluation of selected cowpea lines and cultivars for inherent resistance against cowpea seed beetle, *Callosobruchus maculatus* Fabricius (Coleoptera: Chrysomelidae: Bruchinae). Journal of Natural Sciences Research 6:6-10.

Adekunle AO, Ayodele TF (2014). Insecticidal activity of the aqueous leaves extract of *Andrographis paniculata* as protectant of cowpea seeds from *Callosobruchus maculatus* infestation. Central European Journal of Experimental Biology 3:29-33.

Adjadi O, Singh BB, Singh SR (1985). Inheritance of bruchid resistance in cowpea. Crop Science 25:740-742.

Aliyu B, Wachap E (2014). Vegetable cowpea as a source of cheap protein and an environmentally friendly crop for urban cities. WIT Transactions on Ecology and the Environment 181:301-312.

Amusa DO, Ogunkanmi AL, Adetumbi JA, Akinyosoye TS, Ogundipe TO (2017). Genetics of bruchid (*Callosobruchus maculatus* Fab.) resistance in cowpea (*Vigna unguiculata* (L.) Walp.). Journal of Stored Products Research 74:13-21.

Amusa OD, Ogunkanmi LA, Bolarinwa K, Ojobo O (2013). Evaluation of four cowpea lines for bruchid (*Callosobruchus maculatus*) tolerance. Journal of National Science Research 13:46-52.

Amusa OD, Ogunkanmi LA, Adetunbi JA, Akinyosoye ST, Bolarinwa KA, Ogundipe OT (2014). Assessment of bruchid (*Callosobruchus maculatus*) tolerance of some elite cowpea (*Vigna unguiculata*) varieties. Journal of Agriculture and Sustainability 6:164-178.

Baker RJ (1978). Issues in diallel analysis. Crop Science 18:533-536.

Barelli MAA, Goncalves-Vidigal MC, Amaral Junior AT, Filho PV, Silverio L (1999). Genetic control on number of days to flowering and yield components in common bean (*Phaseolus vulgaris*). Acta Scientiarum, Agronomy 21:423-427.

Bernado R (2003). On the effectiveness of early selection in self-pollinated crops. Crop Science 43:1558-1560.

Dobie (1981). The use of resistant varieties of cowpeas (*Vigna ungviculata*) to reduce losses due to post-harvest attack by *Callosobruchus maculatus*. Series Entomologica 19:182-192.

Dobie P (1974). The laboratory assessment of the inherent susceptibility of maize varieties to post harvest infestations by *Sitophilus zeamais* Mots. (Coleoptera: Curculionidae). Journal of Stored Products Research 10:183-197.

Eizadshenass S (2013). Study of reciprocal cross differences in F1 females of *Drosophila mauritiana* and *D. simulans*. MSc thesis McMaster University.

Griffing B (1956). Concept of general and specific combining ability in relation to diallelcrossing system. Australian Journal of Biology and Science 9:463-493.

Jackai L, Asante SK (2003). A case for the standardization of protocols used in screening cowpea, *Vigna unguiculata* for resistance to *Callosobruchus maculatus* (Fabricius) (Coleoptera: Bruchidae). Journal of Stored Product Research 39:251-263.

Kananji G (2007). A study of bruchid resistance and its inheritance in Malawian dry bean germplasm. PhD. thesis, University of Kwazulu Natal, South Africa.

Lima MPL, Oliveira JV, Barros R, Torres JB (2014). Alternation of cowpea genotypes affects the biology of *Callosobruchus maculatus* (Fabr.) (Coleoptera: Bruchidae). Scientia Agricola Piracicaba 1:27-31.

Miesho BW, Hailay MG, Ulemu MM, Malinga GM, Sadik K, Odong TL, Rubaihayo P, Kyamanywa S (2018). New sources of cowpea genotype resistance to cowpea bruchid (*Callosobruchus maculatus* (F.) in Uganda. International Journal of Agronomy and Agricultural Research 12:39-52.

Mwila N (2013). Inheritance of bruchid (*Callosobruchus maculatus*) resistance in common beans (*Phaseolus vulgaris*). M.Sc. thesis, University of Zambia, Lusaka.

National Agricultural Research Organization (NARO) (2012). Agriculture in Uganda. Vol. II. Crops.

National Research Council (NRC) (2006). Lost Crops of Africa'. Vegetables, Volume II: The National Academies Press, Washington, D.C.

Oluwafemi AR (2012). Comparative effects of three plant powders and pirimiphos-methyl against the infestation of *Callosobruchus maculatus* (F.) (Coleoptera: Bruchidae) in cowpea seeds. Signpost Open Access Journal of Entomological Studies 1:87-99.

Orawu M, Melis R, Laing M, Derera J (2013). Genetic inheritance of resistance to cowpea aphid-borne mosaic virus in cowpea. Euphytica 189:191-201.

Redden RJ (1983). The inheritance of seed resistance to *Callosobruchus maculatus* F. in cowpea (*Vigna unguiculata* L.Walp.). II Analysis of percentage emergence and emergence periods of bruchid in F4 seed generation to two reciprocal crosses. Australian Journal of Agricultural Research 34:697-706.

Redden RJ, McGuire J (1983). The genetic evaluation of bruchid resistance in seed of cowpea. Australian Journal of Agricultural Research 34:707-715.

Rodríguez F, Alvarado G, Pacheco A, Burgueño J, Crossa J (2015). AGD-R (Analysis of Genetic Designs in R). CIMMYT-Knowledge-Center@cgiar.org or at Km. 45 Carretera Mexico-Veracruz, El Batán, Texcoco, Estado de México, México, C.P. 56237.

Sharma M, Adarsh MN, Kumari P, Thakur M, KUmar R, Sharma R, Gautam N (2015). Hybrid breeding in tomato. International Journal of Farm Sciences 1:233-250.

Sleper DA, Poehlman JM (2006). Breeding Field Crops, 5th edition. Iowa, IA: Blackwell Publishing.

Somta P, Ammaranan C, Ooi PAC, Srinives P (2007). Inheritance of seed resistance to bruchids in cultivated mungbean (*Vigna radiata*, L. Wilczek). Euphytica 155:47-55.
Viana JMS, Cruz CD, Cardoso AA (1999). Theory and analysis of partial diallel crosses. Genetics and Molecular Biology 22:591-599.
Warner JN (1952). A method for estimating heritability. Agronomy Journal 44:427-430.

Vol. 10(9), pp. 239-248, September 2018
DOI: 10.5897/JPBCS2018.0750
Article Number: B25C14D58161
ISSN: 2006-9758

http://www.academicjournals.org/JPBCS

ACADEMIC JOURNALS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Inheritance and combing ability in maize using a 7×7 diallel cross

S. Begum, S. S. Alam, S. H. Omy, M. Amiruzzaman and M. M. Rohman*

Plant Breeding Division, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh.

Received 28 May, 2018; Accepted 31 July, 2018

Twenty one F1s produced from 7×7 diallel mating along with the 7 parents were evaluated to notice the inheritance and combining ability of different traits to obtain high heterotic crosses. Genetic analysis and combing ability were analyzed following Hayman's and Griffing's diallel analyses, respectively. Hybrids projecting positive or negative potency ratio with >1.0 value for those traits is also the sign of incidence of over-dominance in desirable direction, and heterosis breeding is important to improve those traits in maize. Hayman's approach indicated dominance variance and the proportion of +/- genes was higher than additive variance in all characters. Griffing's analysis also demonstrated the presence of over-dominance governing the traits. The preponderance of dominant gene action coupled with low heritability observed for days to silking, ear length and grain yield suggests the importance of heterosis breeding. Substantial differences in general combing ability and specific combining ability were noticed in all the studied traits except 1000-grain weight. The parental line CML-509 was found to be the best general combiner for days to tasseling and silking, CML-498 for plant height, ear height and grain yield, CML-395 for ear length and grain yield. The crosses CML-498×CML-376, CML-498×CML-395 and CML-376×CML-247 showed significant positive specific combining ability effect for grain yield along with higher mean values over commercial check varieties.

Key words: Inheritance, combining ability, diallel mating, maize.

INTRODUCTION

Maize belongs to the grass family Poaceae. It is one of the most important cereal crops of the world. It is a major grain crop globally, which can be grown in comprehensive climatic conditions. Globally, maize is the third most important crop. It is a versatile crop grown over a wide range of agro-climatic zones. In fact, the suitability of maize to diverse environments is unmatched by any other crop. It is grown from below sea level to altitudes higher than 3000 m, and in areas with 250 mm to more than 5000 mm of rainfall per year; its growing cycle ranges from 3 to 10 months (Sheikh et al., 2017). According to FAO (2016), total area of maize cultivation was 188 million hectare (ha) with production of 1050.1 million ton and average yield of 5.64 ton ha^{-1}. Globally, maize is popular for its multipurpose uses with utmost grain yield. It is used as human food, poultry, livestock and fish feed. Due to increasing poultry and fish feed industry, its demand is increasing continuously.

*Corresponding author. E-mail: motiar_1@yahoo.com.

Keeping in mind the huge demand of maize as feed for poultry and livestock industry as well as food for human, new high yielding hybrid developing program has been going on. To achieve this target, yield improvement through genetic approaches that determine gene action is essential for formulating comprehensive breeding strategies. Yield improvement of any crop depends mostly on understanding the nature of gene action involved in a specific trait to be improved. In addition, the choice of competent breeding program depends on the large knowledge of the nature of gene action of yield related traits. Dominance gene action is desirable for developing hybrids while additive gene action effectively improves character (Edwards et al., 1976). One of the most helpful approaches in this concern is diallel analysis system extensively used in hereditary research to investigate the inheritance of important traits among a set of genotypes (Yan and Hunt, 2002). Components of genetic control and help breeders in the selection of desirable parents for crossing programs, and thus, facilitate in deciding a suitable breeding procedure for genetic improvement of various quantitative traits (Jinks and Hayman, 1963; Walters and Morton, 1978; Reza et al., 2004).

On the other hand, the ability of a line to transfer its performance to others is described as combining ability of inbred line. Combining ability of inbred lines provide information about genetic nature of quantitative traits as well as for selection of suitable parents to be used for heterosis breeding. General combining ability (GCA) is helpful for the improvement of selection efficiency in segregating populations (Bocanski et al., 2009). Specific combining ability (SCA) is specific performance of any two inbreeds in hybrid combination. Variance due to GCA is an indicator of the extent of additive gene action whereas variance due to SCA shows the extent of non-additive gene action (Hayman, 1954; Griffing, 1956).

The diallel cross technique was developed by Sprague and Tatum (1942). Hayman numerical approach (Haymen, 1954) provides information about inheritance pattern of particular character while Griffing (1956) provides a feature on gene action and combining ability of parental lines. The two main genetic parameters of diallel cross analysis are GCA and SCA. Since the GCA effects are endorsed by the preponderance of genes with additive effects and SCA indicates a predominance of genes with non-additive effects (Falconer, 1981), diallel crosses have been used for a long time in genetic research to determinate the inheritance of a trait among a set of genotypes and to identify superior parents for hybrid or cultivar development (Aliu et al., 2009). These methods have been extensively in different crops like maize (Njeri et al., 2017; Owusu et al., 2017; Brahmbhatt et al., 2018), rice (Huang et al., 2015; Kundan et al., 2013), Brassica (Tian et al., 2017) and cassava (Tumuhimbise et al., 2014). Therefore, it is necessary to understand the nature and magnitude of gene action as well as combining ability of yield and its attributes. The present investigation of 7×7 diallel cross I maize without reciprocal crosses was undertaken to supplement genetic parameters interpretations, pinpoint which parents contain the preponderance of dominance/recessive genes with increasing/decreasing character attributes, and isolate superior inbred lines and better combining parents for utilizing them judiciously in future breeding programs. Heterosis using commercial checks was also reported.

MATERIALS and METHODS

Plant materials

Seven maize inbred lines (CML 498, CML 376, CML 247, CML 509, CML 502, CML 144 and CML 395) collected from International Maize and Wheat Improvement Center (CIMMYT) were crossed in a diallel fashion excluding the reciprocals during the rabi season in 2014-15 at Bangladesh Agricultural Research Institute (BARI), Gazipur, Bangladesh. The resulting 21 F_1's and their 7 parents were evaluated along with two commercial checks (900M GOLD and NK40) in a randomized complete block design (RCBD) with three replications at the same location in the following rabi (winter) season of 2015- 2016.

Experiment settings, crop management and data recording

Seeds of each entry were sown in two rows of 4 m plot. The spacing between rows was 60 cm and plant to plant distance was 25 cm. Fertilizers were applied at 250, 55, 110, 40, 5 and 1.5 kg ha^{-1} of N, P, K, S, Zn, and B respectively. One plant per hill was maintained after proper thinning. Observations were recorded on five randomly selected competitive plants from each plot for days to 50% tasseling, days to 50% silking, plant height (cm), ear height (cm), ear length, number of grains/row, 1000-grain weight (g) and grain yield (t ha^{-1}). Data for 50% days to tasseling and 50% silking as well as grain yield were recorded on whole plot basis and finally, grain yield converted to t ha^{-1}. Data were analyzed for the variance for all the characters studied.

Statistical analysis

The mean performances of all characters were analyzed using Crop Stat software. Gene action was clarified by genetical analysis as proposed by Hayman's numerical approach (1954a, b). According to him, the size of mean degree of dominance $(H_1/D)^{.5}$ was categorized as $(H_1/D)^{.5} = 0$, mean no dominance, $(H_1/D)^{.5} = 1$, mean complete dominance, $(H_1/D)^{.5} > 1$, mean over dominance and $(H_1/D)^{.5} < 1$ mean partial dominance. The proportion of dominant and recessive alleles is ascertained by the ration $(4DH_1)^{.5} + F/(4DH_1)^{.5} - F$. Its value explain $(4DH_1)^{.5} + F/(4DH_1)^{.5} - F \cong 1.0$ means nearly equal proportion of dominance and recessive alleles in parents that is symmetrical distribution; p=q=0.5. If its value is >1.0 refers to an excess of dominant alleles and the minority of recessive alleles (p>q). If $(4DH_1)^{.5} + F/(4DH_1)^{.5} - F < 1.0$ means minority of dominant alleles and excess of recessive alleles (p<q). Mean covariance of additive and dominant variance was expressed by F. The value of F express if F=0 means balanced distribution (p=q=.5); F>0 (+) means dominant alleles are more frequent than recessive alleles (p>q); F>0 (-) means recessives are more prevalent than dominant alleles (p<q). The proportion of dominant

Table 1. Performance of hybrids obtained from 7 × 7 diallel crosses (without reciprocal cross) of maize.

Cross/ Hybrids		DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	GY (t ha^{-1})
1.	CML-498×CML-376	89	94	159	61	17	34	350	11.61
2.	CML-498×CML-247	88	94	159	65	14	25	320	10.24
3.	CML-498×CML-509	85	96	160	64	17	28	300	9.83
4.	CML-498×CML-502	92	96	167	65	15	28	320	6.25
5.	CML-498×CML-144	90	95	162	68	16	32	280	8.51
6.	CML-498×CML-395	93	97	187	78	17	24	370	11.55
7.	CML-376×CML-247	91	95	164	79	14	29	330	10.42
8.	CML-376×CML-509	85	91	162	72	16	30	370	8.62
9.	CML-376×CML-502	90	95	176	76	14	28	295	8.27
10.	CML-376×CML-144	90	94	168	70	15	30	310	8.88
11.	CML-376×CML-395	91	95	197	90	17	27	360	7.98
12.	CML-247×CML-509	88	92	164	77	16	30	355	10.28
13.	CML-247×CML-502	93	93	154	68	13	28	310	8.13
14.	CML-247×CML-144	92	96	168	68	13	29	320	8.46
15.	CML-247×CML-395	94	98	185	82	16	29	350	10.48
16.	CML-509×CML-502	84	90	177	78	14	26	400	8.07
17.	CML-509×CML- 144	86	90	171	73	16	29	385	8.90
18.	CML-509×CML-395	88	93	184	86	16	26	360	9.44
19.	CML-502×CML-144	92	96	185	80	14	28	310	8.65
20.	CML-502×CML-395	92	96	197	87	15	29	350	9.67
21.	CML-144×CML-395	92	96	191	81	16	27	355	9.16
22.	900 M Gold (Check 1)	88	92	177	79	15	34	310	9.87
23.	NK 40 (Check 2)	87	92	142	72	15	26	480	10.14
Mean		89	94	172	74	15	28	343	9.28
F-test		**	*	**	**	**	NS	NS	**
CV(%)		1.46	2.07	5.03	6.12	6.27	10.4	13.23	8.8
$LSD_{(5\%)}$		2.71	4.04	17.9	9.45	1.96	6.09	94.2	1.69

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

genes with positive or negative effects in parents is determined by the ratio: $H_2/4H_1$ with the maximum theoretical value of 0.25, which stands up when p=q=0.5 in all loci. A deviation from 0.25 would stem when $p \neq q$. Complete dominance was indicated when p = ±1; while partial dominance is indicated when "P" is between (-1 and +1), except the value zero, which indicates absence of dominance. Over-dominance was considered when potency ratio exceeds ±1. The positive and negative signs indicate the direction of dominance of either parent (Pujer and Badiger, 2017). Heritability values were categorized as follows: low, <30%; moderate, 30-60% and high, >60% (Johnson et al., 1955a).

General combining ability (GCA) and specific combining ability (SCA) were estimated following Model I, Method II of Griffing (1956). The standard heterosis (against the best standard check variety) was estimated and tested according to Singh and Singh (1994). Potency ratio was calculated according to Smith (1952) to determine the degree of dominance as follows:

$$P = \frac{F_1 - M.P.}{0.5\,(P_2 - P_1)}$$

Where, P: relative potency of gene set, F_1: first generation mean, P1: the mean of lower parent, P2: the mean of higher parent, M.P.: mid-parents value = (P1 + P2)/2.

RESULTS and DISCUSSION

Mean performance

Significant differences were found among the genotypes for days to tasseling (DT), days to silking (DS), plant height (PH), ear height (EH) and grain yield (GY) (Table 1). Though none of the hybrids showed significantly higher yield over the best check NK-40, six cross combinations, CML-498×CML-376 (11.61 t ha^{-1}), CML-498×CML-247 (10.24 t ha^{-1}), CML-498×CML-395 (11.55 t ha^{-1}), CML-376×CML-247 (10.42 t ha^{-1}), CML-247×CML-509 (10.28 t ha^{-1}) and CML-247×CML-395 (10.48 t ha^{-1}) showed better yield than commercial check NK40 (10.14

Table 2. Genetic variance components and related statistics for 8 traits in a 7×7 diallel cross (without reciprocal cross) of maize.

	DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW(g)	GY (t ha$^{-1)}$
D	9.74**	7.76**	194.41**	103.97**	2.19**	7.62**	742.78**	0.15**
H_1	138.17**	92.46**	2449.78**	1306.84**	26.96**	71.97**	11644.16**	2.40**
H_2	-451364**	-497967**	-1455289**	-255704**	-11508**	-38749**	-6065272**	-3717**
h^2	28182**	30403**	17559**	893.64**	245.58**	683.70**	226299**	0.37**
E	0.58**	0.69**	10.71**	7.99**	0.17**	1.67**	406.03**	0.23**
$(H_1/D)^{.5}$	0.94	0.86	0.89	0.89**	0.88	0.77	0.99	1.00
F	-8.76**	2.55**	-24.00**	-3.95**	0.20**	15.08**	-60.32**	0.44**
$H_2/4H_1$	-816.70	-1346.43	-148.51	-48.92	-106.70	-134.60	-130.22	-387.08
Prop. Dom/rec gene	0.35	1.47	0.87	0.96	1.11	-7.94	0.92	-5.22
h^2n (%)	18	25	22	22	23	44	14	12

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGR=number of grains per row, TGW=1000-grain weight, GY=grain yield, D= Additive variance, H_1= Dominance variance, H_2= Proportion of +/- genes, h^2= Over all dominance effect, E= Environmental variance, H_1/D= Mean degree of dominance, H2/4H1= Proportion of genes with ± effects, Prop. Dom/rec gene= Proportion of dominant and recessive genes, h^2_n= Heritability in narrow sense.

t ha^{-1}). The highest yielder cross CML-498×CML-376 had higher NGR (34) with shortest EH (61 cm) compared to the best check. Although none of the higher yielder crosses were earlier than the best check, the highest cross was almost similar.

Nature of genetic variance

The analysis of genetic variance components indicated that both additive variance (D) and dominance variance (H_1 and h^2) were significant for all the traits (Table 2). These results focused that the expression of all characters was conditioned by both additive and dominance gene action. However, dominant variance (H_1) was more predominant than additive variance (D) for all traits indicating the presence of over dominance controlling the traits (Radha, 2014). The dominance is also reflected by the high degree of dominance effect, that is sum total of all loci in the heterozygous state (h^2). The dominance was in partial dominance range because of $(H_1/D)^{.5} < 1.0$ for all traits except grain yield. The dominance is complete dominance in case of grain yield because of $(H_1/D)^{.5} = 1.0$. Though, the environmental variance (E) was significant but much lower than additive variance (D) and dominant variance ($H_{1)}$ for all traits. From proportion of dominant (p) and recessive (q) alleles days to tasseling, plant height, ear height and 1000-grain weight showed asymmetry of distribution ($p \neq q$) and the minority of dominant alleles and excess of recessive alleles ($p<q$) because of the proportion of dominance and recessive gene <1. On the other hand, days to silking, ear length, number of grain per row and grain yield also showed asymmetry of distribution, but excess of dominant alleles and minority of recessive alleles ($p>q$) as proportion of dominance and recessive gene >1. The symmetry of dominant and recessive allele distribution in parents is further established by relative sizes of dominance variance ($H_{1)}$ and proportion of (+/-) genes (H_2) as $H_1 \neq H_2$ means asymmetry of distribution ($p \neq q$. In the present study, $H_1<H_2$ for all traits indicated an uneven distribution of dominant and recessive alleles. The symmetry of distribution of dominant and recessive alleles in parents is also verified by the direction (sign) of F (mean covariance of D and H_1). In the present study, F<0 (-) for days to tasseling, plant height, ear height and 1000-grain weight which indicated recessives were more prevalent than dominant alleles ($p<q$). On the other hand, F>=0 (+) for days to silking, ear length, number of grain per row and grain yield which means dominant alleles were more frequent than recessive alleles ($p>q$). The proportion of dominant genes with positive or negative effects in parents is determined by the ratio: $H_2/4H_1$ with the maximum theoretical value 0.25. $H_2/4H_1 \neq 0.25$ means asymmetry of the distribution. In the present study, $H_2/4H_1 \neq 0.25$ and negative sign for all studied traits, hence dominant genes having decreasing and increasing effects on all characters were irregularly distributed

Table 3. Mean squares due to GCA and SCA for 8 traits in a 7×7 diallel cross (without reciprocal cross) of maize.

Sources of variation	df	Mean of squares							
		DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	GY (t ha^{-1})
Genotype	27	23.8**	15.9**	1240**	463**	7.03**	28.5**	2357	7.55**
GCA	6	64.6**	34.5*	1218**	547**	12.1**	22.3**	5025	3.34**
SCA	21	12.1**	10.6**	1247**	439**	5.58**	30.2*	1595	8.76**
Error	27	1.86	3.46	68.7	27.8	0.89	7.57	2139	0.59
GCA: SCA		5.34	3.25	0.98	1.25	2.17	0.74	3.15	0.38

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGPR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

in parents. Heritability estimate (h^2_n) was <30% for the studied traits except for number of grain per row (44%) that indicated these traits are less heritable and highly influenced by environment. On the other hand, heritability for number of grain per row was moderate. The predominance of dominant gene action coupled with low heritability observed for days to silking, ear length and grain yield suggesting the importance of heterosis breeding (Radha, 2014).

Analysis of variance

The mean square of genotypes (diallel hybrids) was highly significant for all the traits except 1000-grain weight (Table 3). Further, analysis of variance for combining ability showed that estimates of mean squares due to GCA and SCA were also highly significant for all the characters except 1000-grain weight. This indicated the importance of both additive and non-additive components of genetic variance in controlling these traits. Importance of both GCA and SCA variances for yield and yield contributing traits in maize was reported in various previous studies (Ahmed et al., 2008; Gurung et al., 2008; Mousa, 2014; Hoque et al., 2016). However, in the present study variances due to GCA were much higher in magnitude than SCA for the characters of days to 50% tasseling and silking, ear height, ear length, number of grains per row and 1000-grain weight, which revealed the prevalence of additive gene action for controlling these traits. The predominance of additive gene action for days to tasseling, days to silking and number of grain per row was reported by Hoque et al. (2016) which supports the present study. On the other hand, non additive gene action for ear height and 1000-grain weight was supported by Hoque et al. (2016) and Kadir (2010). On the other hand, the magnitude of SCA was higher than GCA for plant height, number of grain per row and grain yield, indicating non-additive gene action in controlling these traits. Non-additive gene action was also reported on plant height (Kadir, 2010), number of kernel per row (Abdel-Moneam et al., 2009) and grain yield (Abdel-Moneam et al., 2009; Kadir, 2010; Barakat and Osman, 2008; Gouda et al., 2013; Hoque et al., 2016) in their study. These investigations supported the present study.

General combining ability (GCA) effects

The GCA effects were shown in Table 4. None of the parents were found to be a good general combiner for all the characters studied. A wide range of variability in GCA effects was observed among the parents. In case of maize, the inbred lines with significant and negative GCA effects are considered as good general combiners for days to 50% tasseling, days to 50% silking, plant height as well as ear height to utilize these for developing early and short stature plants. On the other hand, for yield and other yield components, those with significant and positive GCA effects are considered as good general combiners.

In the present study, the parent CML-509 was a good general combiner for days to tasseling and silking due to its significant negative GCA value. In addition, it was also a good general combiner for 1000-grain weight for its significant positive GCA value. Parent CML-498 and CML-376 showed expected significant negative GCA value for plant height where CML-498 had significant negative value for both plant and ear height. So these parents could be a good source for the development of short stature plant. Significant and negative GCA for ear height was observed in different studies (Malik et al., 2004; Alam et al., 2008; Amiruzzaman, 2010). Inbred CML-498 and CML 395 exhibited significant positive GCA for grain yield. This result was supported by different studies (Malik et al., 2004; Uddin et al., 2006; Ahmed et al., 2008; Abdel-Moneam et al., 2009). They reported that parents with good general combiners for grain yield showed good performance for various yield components.

Higher significant positive GCA for ear length and yield were found in parent CML-395 while in case of number of grains per row and 1000-grain weight, parents CML-144

Table 4. General combining ability effects for different traits in a 7× 7 diallel cross (without reciprocal cross) of maize.

Parents	DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	GY (t ha^{-1})
1. CML-498	0.06	0.75	-7.13**	-7.63**	0.38	-0.27	-13.8	0.53*
2. CML-376	-0.16	-0.19	-5.02*	-0.96	0.34	1.51*	-6.59	-0.17
3. CML-247	1.51**	0.87	-5.57*	-2.29	-0.78**	-0.99	-4.37	0.08
4. CML-509	-3.88**	-2.75**	-3.79	0.37	0.34	-0.49	31.7*	-0.13
5. CML-502	0.12	-0.30	0.65	-0.79	-1.35**	-0.60	-6.59	-0.71**
6. CML-144	0.34	0.03	4.65*	0.48	-0.04	1.67*	-13.8	-0.12
7. CML-395	2.01**	1.59**	16.2**	10.8**	1.11**	-0.83	13.4	0.51*
SE(gi)	0.30	0.41	1.81	1.15	0.21	0.60	10.1	0.17
LSD $_{(5\%)}$	0.73	1.00	4.43	2.81	0.51	1.47	24.71	0.42
LSD $_{(1\%)}$	1.11	1.52	6.71	4.26	0.78	2.22	37.44	0.63

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGPR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

and CML-509 expressed positive significant GCA. Higher significant and positive GCA effect for 1000-grain weight was also observed in different studies (Alam et al., 2008; Abdel-Moneam et al., 2009; Uddin et al., 2006).

Specific combining ability (SCA) effects

The SCA effects of the crosses for eight characters are presented in Table 5. The hybrid CML-498×CML-247 exhibited significant negative SCA effects for days to tasseling and days to silking. In addition, the hybrid CML-509×CML-502 and CML-247×CML-502 exhibited significant negative SCA effects for days to tasseling and days to silking respectively, indicating earliness of the hybrids. These crosses mostly involved average × low, high × average, low × average general combining parents. These findings are consistent with the results of Ahmed et al. (2008).

Considering the results, out of 21 hybrids, nine crosses (viz.,CML-498×CML-376, CML-498×CML-247, CML-498×CML-509, CML-498×CML-395, CML-376×CML-247, CML-247×CML-509, CML-247×CML-395, CML-502×CML-144 and CML-502×CML-395) exhibited significant positive SCA effects for grain yield (Table 5), and most of them also possessed high *per se* performance for the same trait (Table 1). These crosses involved high × high, high × average, high × low, average × high and average × average general combining parents. These crosses involving parents with one or both parents were related to good combiners, indicating GCA of the parental lines plays a key role in producing high yield. Vasal (1998) recommended to include one good combiner (especially female parent) during the crossing to obtain higher heterosis. Xingming et al. (2002) also drew a similar conclusion. On the other hand, an appreciable amount of the SCA effects expressed by low × low crosses might be ascribed to dominance × dominance type of non-allelic gene action produced over-dominance and are non-fixable. It appears that superior performance of most hybrids may be largely due to epistatic interaction. If the inbreed does not show good GCA effect but have good SCA effect, these materials could be successively used for further breeding (Aliu et al., 2009). The SCA effects of the crosses exhibited no specific trends in cross combinations between parents having high, medium and low GCA effects. Any combination of the parents may produce hybrid vigor over the parents which might be due to dominance, over dominance or epistatic gene action. So, the crosses which showing desirable SCA effects can be used in the future breeding program.

None of the crosses exhibited significant and negative SCA effects for plant height and ear height. In case of ear length and number of grains per row, five crosses for each character expressed significant and positive SCA effect. For 1000-grain weight, none of the crosses showed significant and positive SCA effects.

Heterosis and potence ratio

Standard heterosis is important for selecting new variety (Amiruzzaman, 2010; Kadir, 2010). The standard/ economic heterosis expressed by the F_1 hybrids over the best commercial check variety NK 40 for yield and yield related traits are shown in Table 6. All the traits showed more or less significant heterosis in different crosses.

For grain yield (t ha^{-1}), only one cross CML-498×CML-395 (9.9%) showed significant positive heterosis over the standard check variety NK-40. Significant negative heterosis was exhibited by four and two crosses for days to tasseling as well as days to silking respectively, indicating earliness (Table 6). Heterosis ranged from -3.4

Table 5. Specific combining ability (SCA) effects for different traits in 7× 7 diallel cross (without reciprocal cross) in maize.

Cross	DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	Y (t ha^{-1})
1. CML-498×CML-376	-1.46	-1.65	10.3	1.82	1.43*	5.83**	39.9	2.92**
2. CML-498×CML-247	-4.13**	-3.21*	10.3	7.65*	0.26	-0.67	7.64	1.29*
3. CML-498×CML-509	-1.74	2.40	10.0	3.99	1.43*	1.83	-48.5	1.09*
4. CML-498×CML-502	1.26	0.46	12.1*	5.65	1.12	2.44	9.86	-1.91**
5. CML-498×CML-144	-0.96	-1.38	3.1	7.88*	0.81	4.17*	-22.9	-0.23
6. CML-498×CML-395	0.38	-0.43	16.5**	7.04*	1.17	-1.83	39.9	2.17**
7. CML-376×CML-247	-0.90	-0.76	13.2*	14.5**	0.10	1.56	10.4	2.17**
8. CML-376×CML-509	-1.51	-1.15	9.4	5.32	1.28*	2.06	14.3	0.58
9. CML-376×CML-502	-1.01	-0.10	19.5**	9.99**	0.67	0.17	-22.4	0.82
10. CML-376×CML-144	-1.24	-1.43	7.0	2.71	0.36	0.39	-0.14	0.84
11. CML-376×CML-395	-1.40	-1.49	24.4**	12.4**	1.21*	-0.11	22.6	-0.70
12. CML-247×CML-509	-0.68	-1.21	12.0*	11.2**	2.10**	5.06**	-2.92	2.00**
13. CML-247×CML-502	0.32	-2.65*	-2.5	3.82	0.39	2.67	-9.58	0.42
14. CML-247×CML-144	-0.90	-0.49	7.5	2.04	-1.02	1.39	7.64	0.17
15. CML-247×CML-395	-0.57	-0.04	13.0*	6.21	1.13	3.89*	10.4	1.55**
16. CML-509×CML-502	-3.29**	-2.04	18.8**	10.7**	0.67	0.17	44.3	0.57
17. CML-509×CML-144	-1.51	-2.38	8.8	4.38	0.86	1.39	36.5	0.82
18. CML-509×CML-395	-0.68	-1.43	10.7	7.54*	-0.29	0.39	-15.7	0.72
19. CML-502×CML-144	0.49	1.18	18.8**	13.0**	1.04	0.10	-0.14	1.15*
20. CML-502×CML-395	-1.18	-0.88	18.8**	9.21*	0.40	4.00*	12.6	1.52**
21. CML-144×CML-395	-1.40	-1.21	9.3	2.43	0.49	-0.78	24.9	0.44
SE(ij)	0.87	1.18	5.26	3.35	0.58	1.75	29.4	0.49
LSD $_{(5\%)}$	1.81	2.46	10.97	6.99	1.21	3.65	61.33	1.02
LSD $_{(1\%)}$	2.48	3.36	14.96	9.53	1.65	4.98	83.64	1.39

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGPR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

Table 6. Percent heterosis over the best check NK40 for different characters in 7×7 diallel crosses (without reciprocal cross) of maize.

Cross/ Hybrids	DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	GY (t ha^{-1})
1. CML-498×CML-376	2.33**	2.20**	10.56**	-15.1**	-6.25**	21.4**	-37.5**	2.9
2. CML-498×CML-247	1.16	1.10	12.68**	-9.59**	-12.5**	-18.0**	-37.5**	-10.6**
3. CML-498×CML-509	-3.49**	7.69**	13.38**	-5.48*	12.50**	7.14*	-50.0**	-1.7
4. CML-498×CML-502	5.81**	4.40**	18.31**	-6.85**	-6.25**	0.00	-45.8**	-32.5**
5. CML-498×CML-144	3.49**	2.20**	16.20**	-1.37	-6.25**	17.8**	-58.3**	-26.5**
6. CML-498×CML-395	5.81**	4.40**	30.28**	9.59**	12.50**	3.57	-20.8**	9.9**
7. CML-376×CML-247	5.81**	4.40**	15.49**	13.70**	-12.5**	3.57	-45.8**	-1.1
8. CML-376×CML-509	-3.49**	-2.2**	11.27**	6.85**	6.25**	25.0**	-25.0**	-15.3**
9. CML-376×CML-502	3.49**	2.20**	21.83**	6.85**	-6.25**	3.57	-37.5**	-15.0**
10. CML-376×CML-144	2.33**	1.10	24.65**	8.22**	-6.25**	10.7**	-33.3**	-16.8**
11. CML-376×CML-395	5.81**	4.40**	37.32**	24.66**	12.50**	-3.57	-25.0**	-24.4**
12. CML-247×CML-509	2.33**	1.10	18.31**	8.22**	0.00	7.14*	-27.1**	-13.5**
13. CML-247×CML-502	6.98**	5.49**	14.79**	4.11	-18.8**	-3.57	-33.3**	-26.8**
14. CML-247×CML-144	3.49**	2.20**	18.31**	-1.37	-12.5**	21.4**	-37.5**	-17.4**
15. CML-247×CML-395	6.98**	5.49**	35.21**	21.92**	0.00	7.14*	-29.2**	4.2
16. CML-509×CML-502	-3.49**	-1.10	23.94**	6.85**	-12.5**	-11.0**	-20.9**	-29.4**
17. CML-509×CML-144	-2.33**	-2.2**	16.90**	1.37	0.00	10.7**	-6.25*	-18.8**

Table 6. Contd.

18. CML-509×CML-395	-1.16	-1.10	23.24**	17.81**	0.00	-11.0**	-29.2**	-7.5**
19. CML-502×CML-144	5.81**	5.49**	16.20**	1.37	-12.5**	0.00	-37.5**	-26.9**
20. CML-502×CML-395	5.81**	4.40**	38.03**	19.18**	-6.25**	7.14*	-25.0**	-7.2
21. CML-144×CML-395	6.98**	5.49**	31.69**	12.33**	0.00	-14.3**	-27.1**	-11.6**
Mean	2.87	2.33	21.71	3.27	0.87	8.19	-29.56	-8.79
SE	0.81	0.61	1.87	2.28	1.96	2.57	2.52	2.60
$CD_{(0.05)}$	1.68	1.27	3.90	4.75	4.08	5.35	5.26	5.42
$CD_{(0.01)}$	2.29	1.74	5.32	6.48	5.57	7.30	7.17	7.39

* Significant at 5% level, ** Significant at 1% level.
DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGPR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

Table 7. Potence ratio of 21 F_1 hybrids of maize for various studied characters.

Name of crosses	DT	DS	PH (cm)	EH (cm)	EL (cm)	NGR	TGW (g)	GY (t ha^{-1})
CML-498×CML-376	0.0	-17.0	13.4	6.3	17.0	3.4	25.0	0.0
CML-498×CML-247	-5.0	-5.0	10.5	11.0	7.3	3.6	2.0	46.9
CML-498×CML-509	-1.8	0.0	28.7	4.0	0.0	0.0	-0.8	7.3
CML-498×CML-502	-1.7	-1.5	24.5	12.1	3.0	31.0	5.0	10.4
CML-498×CML-144	0.0	-15.0	2.3	2.9	6.0	2.7	-1.0	17.9
CML-498×CML-395	1.7	-2.2	3.5	1.7	3.0	2.5	7.0	8.7
CML-376×CML-247	3.0	-3.0	6.8	37.5	3.5	1.1	2.6	48.4
CML-376×CML-509	-1.8	-1.5	10.1	12.3	16.2	2.2	0.8	5.5
CML-376×CML-502	-5.0	-3.7	11.8	27.8	2.0	1.5	0.3	22.0
CML-376×CML-144	0.0	0.0	0.0	4.5	9.0	4.5	11.0	19.6
CML-376×CML-395	-3.0	-3.0	3.6	2.9	3.5	2.0	5.0	4.0
CML-247×CML-509	-1.0	-1.1	19.0	10.2	12.4	9.0	0.3	9.5
CML-247×CML-502	-1.0	-2.6	18.4	113.0	2.4	5.7	1.0	71.6
CML-247×CML-144	-2.7	-2.7	3.5	3.6	0.4	1.4	1.7	38.6
CML-247×CML-395	0.0	0.0	0.0	2.2	1.8	3.9	0.0	8.5
CML-509×CML-502	-2.6	-2.3	115.0	9.9	2.6	21.0	1.5	5.9
CML-509×CML- 144	-1.6	-1.9	3.2	8.5	6.0	1.8	1.1	8.3
CML-509×CML-395	-0.9	-1.0	3.6	3.0	1.8	4.5	0.4	50.2
CML-502×CML-144	-2.3	-1.7	4.6	5.5	1.6	1.3	2.0	80.0
CML-502×CML-395	-1.4	-1.4	4.6	2.5	1.0	10.3	9.0	7.8
CML-144×CML-395	-2.7	-2.7	23.0	3.0	2.9	0.0	4.0	7.5

DT=Days to 50% tasseling, DS=days to 50% silking, PH=plant height, EH=ear height, EL=ear length, NGPR=number of grains per row, TGW=1000-grain weight, GY=grain yield.

to 6.98% and -2.2 to 7.69% for days to tasseling and silking, respectively. Similarly, significant and negative heterosis was exhibited by four crosses for ear height ranging from -15.1 to -5.48%, indicating short stature. All crosses expressed significant and negative heterosis for 1000-grain weight.

The potency ratio of 21 F_1 crosses is presented in Table 7. Positive values ratio specified the degrees of dominance, that is partial to over-dominance and negative values ratio signposted the degrees of recessiveness, that is partial to under recessiveness (Solieman et al., 2013). For Days to 50% tasseling (DT), the potency ratio ranged from -5 (CML-498 × CML-247 and CML-376 × CML-502) to 3 (CML-376 × CML-247). Among them the value of potency ratio was zero (0) for four crosses indicating absence of dominance; two crosses showed complete dominance (-1.0), one cross namely CML-509 × CML-395 exposed partial dominance (-0.9) and the rest 14 crosses exhibited over-dominance (>±1). For days to 50% silking (DS), the range of potency

ratio was -17.0 (CML-498 × CML-376) to 0.0 with three crosses showing absence of dominance (0); one cross (CML-509 × CML-395) showed complete dominance (-1) and the rest 17 crosses showed over-dominance (>±1). For plant height (PH), the range of potency ratio was 0.0 (CML-376 × CML-144 and CML-247 × CML-395) to 115 (CML-509 × CML-502), with two crosses showing absence of dominance while the rest 19 crosses showed over-dominance (>±1). For ear height (EH) the range of potency ratio was 1.7 (CML-498 × CML-395) to 113.0 (CML-247 × CML-502) with all crosses exhibiting over-dominance (>+1). For ear length (EL) the range of potency ratio was 0.0 (CML-498 × CML-509) to 17.0 (CML-498 × CML-376) with one cross showing absence of dominance (0), one exhibiting complete dominance (+1) and one exhibiting partial dominance (0.4) and the rest 18 crosses showed over-dominance (>+1). For the number of grain per row (NGR), the range of potency ratio was 0.0 (CML-498 × CML-509 and CML-144 × CML-395) to 31.0 (CML-498 × CML-502) with two crosses showing absence of dominance and the rest 19 crosses showed over-dominance (>+1). For 1000-grain weight, the range of potency ratio was 0.0 (CML-247 × CML-395) to 25 (CML-498 × CML-376) with two crosses showing complete dominance (±1), one showed absence of dominance, five crosses showed partial dominance (-1 to +1) and the rest 13 crosses showed over-dominance. For grain yield (GY) the range of potency ratio was 0.0 (CML-498 × CML-376) to 80 (CML-502 × CML-144) with only one cross showing absence of dominance and the rest 20 cross exhibited over dominance.

Conclusion

The results of the study revealed that the value of dominance variance (H_1) and the proportion of +/- genes (H_2) were higher than additive variance (D) in all characters. Therefore, over-dominance controlled the studied traits. Hybrids projecting positive or negative potence ratio with >1.0 value for those traits is the sign of incidence of over dominance in desirable direction and heterosis breeding is important to improve those traits in maize. The parental lines CML-498 and CML-395 were found to be the best general combiner for yield. The good combiner parents for different trait could be used in hybridization to improve yield as well as with other desirable traits as donor parents for the accumulation of favorable genes. Three hybrids namely, CML-498×CML-376, CML-498×CML-395 and CML-376×CML-247 need to be further evaluated at different agro-ecological conditions in a multi-year to evaluate their performance.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Abdel-Moneam MA, Attia AN, El-Emery MI, Fayed EA (2009). Combining ability and heterosis for some agronomic traits in crosses of maize. Pakistan Journal of Biological Science 12(5):433-438.

Ahmed S, Khatun F, Uddin MS, Banik BR, Ivy NA (2008). Combining ability and heterosis in maize (*Zea mays* L.). Bangladesh Journal of Plant Breeding and Genetics 21(2):27-32.

Alam AKMM, Ahmed S, Begum M, Sultan MK (2008). Heterosis and combining ability for grain yield and its contributing characters in maize. Bangladesh Journal of Agricultural Research 33(3):375-379.

Aliu S, Fetahu S, Kaciu S, Salillari A (2009). Combining ability study for kernel yield per ear of maize (*Zea mays* L.) hybrid. 44th Croatian and 4th International Symposium on Agriculture pp. 476-480.

Amiruzzaman M (2010). Exploitation of hybrid vigor from normal and quality protein maize crosses. Ph.D Dissertation, Dept. Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh P 200.

Barakat AA, Osman MMA (2008). Evaluation of some newly developed yellow maize inbred lines for combining ability in two locations. Journal of Agricultural Science Mansoura University 33:4667-4679.

Bocanski J, Zorana S, Aleksandra N (2009). Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). Original science, paper. Genetika 41:145-154. http://dx.doi.org/10.2298/GENSR0902145B.

Brahmbhatt BN, Kuchhadiya GV, Gosai MA, Joshi NR, Kanjariya KG (2018). Study of combining ability through diallel crosses in maize (*Zea mays* L.) for grain yield and protein content. Journal of Pharmacognosy and Phytochemistry 7(2):1754-1755.

Edwards LH, Ketata H, Smith EL (1976). Gene action of heading date, plant height, and other characters in tow winter wheat crosses. Crop Science 16:275-277.

Falconer DC (1981). Introduction to quantitative Genetics, 2nd edition, Longman Group Ltd. New York, 67-68.

Food and Agriculture Organization (FAO) (2016). Agriculture Organization of the United Nations Statistics Division. www.fao.org/faostat/en

Gouda RK, Kage U, Lohithaswa HC, Shekara BG, Shobha D (2013). Combining ability studies in maize (*Zea mays* L.). Molecular Plant Breeding 3:116-127.

Griffing B (1956). Concept of general and specific combining ability in relation to diallel crossing systems. Australian Journal of Biological Science 9:463-493.

Gurung DB, George MLC, Delacruz QD (2008). Heterosis and combining ability of Nepalese Yellow maize Populations. Book of Abstracts. The 10th Asian Reg. Maize Workshop. October 20-23, Makassar, Indonesia P 88.

Hayman BI (1954). The analysis of variance of diallel tables. Biometrics 10:235-244. http://dx.doi.org/10.2307/3001877

Hoque M, Akhter F, Kadir M, Begum HA, Ahmed S (2016). Study on combining ability and heterosis for earliness and short statured plant in maize. Bangladesh Journal of Agricultural Research 41(2):365-376.

Huang M, Chen L, Chen Z (2015). Diallel analysis of combining ability and heterosis for yield and yield components in rice by using positive loci. Euphytica 205:37. https://doi.org/10.1007/s10681-015-1381-8

Jinks JL, Hayman BL (1963). The analysis of diallel crosses. Maize Genetic Cooperative Newsletter 27:48:54.

Johnson HW, Robinson HF, Comstock RE (1955). Estimates of genetic and environmental variability in soybean. Journal of Agronomy 47:314-318.

Kadir MM (2010). Development of quality protein maize hybrids and their adaptation in Bangladesh. PhD Dissertation, Dept. Genetics & Plant Breeding, Bangladesh Agricultural University, Mymensingh.

Kundan K, Shailesh M, Binod K (2013). Combining ability analysis in diallel crosses of wheat (*Triticum aestivum* L). The Bioscan 8:1557-1560.

Malik SI, Malik HN, Minhas NM, Munir M (2004). General and specific combining ability studies in maize diallel crosses. International Journal of Agriculture and Biology 6(5):856-859.

Mousa STM (2014). Diallel analysis for physiological traits and grain yield of seven white maize inbred lines. Alexandria Journal of Agricultural Research 59(1):9-17.

Njeri SG, Makumbi D, Warburton ML, Diallo A, Jumbo MB, Chemining'wa G (2017). Genetic analysis of tropical quality protein maize (*Zea mays* L.) germplasm. Euphytica 213:261 https://doi.org/10.1007/s10681-017-2048-4.

Owusu GA, Nyadanu D, Obeng-Antwi K, Amoah RA, Danso FC, Amissah S (2017). Estimating gene action, combining ability and heterosis for grain yield and agronomic traits in extra-early maturing yellow maize single-crosses under three agro-ecologies of Ghana. Euphytica 213: 287. https://doi.org/10.1007/s10681-017-2081-3.

Pujer P, Badiger M (2017). Heterosis and potence ratios for growth, earliness, yield and quality traits in cherry tomato (*Solanum lycopersicum* L. var. *Cerasiforme* Mill). International Journal of Chemical Studies 5(4):1000-1006.

Radha RK (2014). Diallel analysis for different horticultural traits in bitter gourd (*Momordica charantia* L.) using Hayman's numerical and graphical approach. Tropical Plant Research 1(2):60-64.

Reza A, Yazdisamadi B, Zali A, Tallei A, Zeinali H, Rezael A (2004). Estimate of heterosis and combining ability in maize (*Zea mays* L.) using diallel crossing method. pp. 395-397. In: Genetic Variation for plant breeding. 2004 *EUCARPIA, BOKU*, Vienna, Austria.

Sheikh FA, Dar ZA, Sofi PA, Lone AA (2017). Recent Advances in Breeding for Abiotic Stress (Drought) Tolerance in Maize. International Journal of Current Microbiology and Applied Sciences 6(4):2226-2243.

Singh RK, Singh PK (1994). A manual on Genetics and Plant Breeding. Experimental Techniques. Kalyani Publishers. Ludiana, New Delhi pp. 99-107.

Smith HH (1952). Fixing Transgressive Vigour in *Nicotiana rustica*. In: Gowen JW, editor. Heterosis. Ames (IA), Iowa State University Press. pp. 161-174.

Solieman THI, El-Gabry MAH, Abido AI (2013). Heterosis, potence ratio and correlation of some important characters in tomato (*Solanum lycopersicon* L.). Scientia Horticulturae 150:25-30.

Sprague GF, Tatum LA (1942). General vs. specific combining ability in single crosses of corn. Journal of American Society of Agronomy 34:923-932.

Tian HY, Channa SA, Hu SW (2017). Relationships between genetic distance, combining ability and heterosis in rapeseed (*Brassica napus* L.) Euphytica 213:1. https://doi.org/10.1007/s10681-016-1788-x

Tumuhimbise R, Melis R, Shanahan P (2014). Diallel analysis of early storage root yield and disease resistance traits in cassava (*Manihot esculenta* Crantz). Field Crops Research 167:86-93. doi.org/10.1016/j.fcr.2014.07.006.

Uddin SM, Khatun F, Ahmed S, Ali MR, Begum SA (2006). Heterosis and combining ability in corn (*Zea mays* L.). Bangladesh Journal of Botany 35:109-116.

Vasal SK (1998). Hybrid maize technology: Challenges and expanding possibilities for research in the next century. In: Vasal SK, Gonzalez CF, Xingming F (ed). Proc. 7th Asian Reg. Maize workshop.Los Banos, Philippines, February 23-27, pp.58-62.

Walters DS, Morton JR (1978). On the analysis of variance of a half diallel table. Biometrics 34:91-94.

Xingming F, Tan J, Chen Z, Yang J (2002). Combining ability and heterotic grouping of ten temperate, tropical and subtropical quality protein maize. *In:* Srinivasan, G, Zaidi PH, Prasanna BN, Gonzalez FC, Lesnick K (ed). Proc. 8th Asian Reg. Maize Workshop. Bangkok, Thailand, August 5-8, pp. 10-18.

Yan W, Hunt LA (2002). Biplot analysis of diallel data. Crop Science 42: 21-30.

Zare M, Choukan R, Bihamta MR, Heravan EM, Kamelmanesh MM (2011). Gene action for some agronomic traits in maize (*Zea mays* L.). Crop Breeding Journal 1(2):133-141.

Vol. 10(9), pp. 249-257, September 2018
DOI: 10.5897/JPBCS2018.0753
Article Number: 73AA0C758163
ISSN: 2006-9758

http://www.academicjournals.org/JPBCS

ACADEMIC JOURNALS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Genotype by environment interaction and stability analysis of cowpea [*Vigna unguiculata* (L.) Walp] genotypes for yield in Ethiopia

Tariku Simion[1*], Wassu Mohammed[2] and Berhanu Amsalu[3]

[1]Southern Agricultural Research Institute, Arbaminch Agricultural Research Center, Arba Minch, Ethiopia.
[2]School of Plant Sciences, Haramaya University, Ethiopia.
[3]Ethiopian Agricultural Research Institute, Melkassa Agricultural Research Center, Melkassa, Ethiopia.

Received 3 June, 2018; Accepted 25 July, 2018

Ethiopia is claimed to be a center of diversity for cowpea production. The crop is the most drought tolerant and could help the country overcome the recurrent drought problem; however, the yield is very low due to lack of effort to develop varieties. This research was conducted to evaluate the stability of cowpea genotypes and to estimate the magnitude of genotypes by environment interaction (GEI) effect on grain yield. Sixteen cowpea genotypes were tested at seven environments in an experiment laid out in a 4 × 4 triple lattice design during 2016/17 cropping season. The combined analysis of variance over environments showed significant differences among genotypes and environments, along with significant effect of GEI on grain yield, days to flowering, days to maturity, plant height and pods per plants. Analysis of variance for grain yield from AMMI model indicated the contribution of genotype and environment, with GEI accounting for about 63.3, 5.3 and 29.7% of the total sum of squares, respectively. The result indicated that environments contributed much to the observed variations suggesting the need to test cowpea genotypes in diverse environments. Considering all stability parmeters, viz; deviation from regression (S^2di), coefficient of regression (bi) from ER's model, IPCA1, IPCA2 and AMMI stability value (ASV) from AMMI model, GGE biplot and variety TVU was identified as the most stable with mean yield above the mean grain yield of genotypes. Two genotypes: IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to both environments but more to favorable environments suggesting the need to further test and develop as varieties. The other two genotypes: 95K-1095-4A and 93K-619-1, identified as unstable and highly responsive to environments suggested to consider the genotypes as candidate varieties where they performed best. Melkassa, Sekota and Jinka were identified as more descrimnating environments, whereas Arbaminch and Kobo were ideal for selecting superior genotypes; however, Babile and Meisso were non descrimnating environments.

Key words: Additive main effects and multiplicative interaction (AMMI) stability value, Eberhart and Russell, deviation from regression and triple lattice.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is an annual herbaceous legume that belongs to Fabaceae family. It is one of the widely cultivated and consumed grain legumes globally, especially in the arid and semi-arid tropics (Baidoo and Mochiah, 2014; Noubissietchiagam et al., 2010). Generally, cowpea production and utilization in

Ethiopia is very low as compared to other African countries though the country is claimed to be the center of diversity and/or origin. The country has high potential for the production of the crop as more than 66.5% of the arable land is very suitable for cowpea production (Collaborative Crop Research Program (CCRP), 2015). It plays a critical role in the lives of millions of people in the developing world, providing them a major source of dietary protein that nutritionally complements low protein staple cereal and tuber crops. Its grain is the most important part of the plant for human consumption (Agbogidi and Egho, 2012). Drought is the most important abiotic stress limiting production of all crops worldwide, even the most drought tolerant cowpea (Hall, 2004). More importantly, Ethiopia is known as a victim with recurrent droughts that causes partial or total crop failure, and subsequently, famine in the country. In such situations, cowpea can be a potential crop to reduce the consequences of drought because of its drought tolerant nature more than other staple crops. The relative magnitude of environment, genetic and their interaction effects are a challenge that makes production difficult (Hall et al., 2003). Therefore, in the process of developing cowpea varieties for desirable traits, it is necessary to evaluate genotypes in contrasting environments in the country. However, information on the effect of genotype, environment, and their interaction on cowpea grain yield under diversified agro-climatic conditions of Ethiopia is limited. The present study was initiated to estimate the magnitude of genotype, environment and genotype by environment interaction for grain yield of cowpea and characterize yield stability of cowpea genotypes across different environments.

MATERIALS AND METHODS

The experiment was conducted in seven environments during 2016/17 cropping season in Ethiopia (Table 1). Sixteen cowpea genotypes (14 advanced lines and two standard checks) were used for this study (Table 2). The experiment was laid out in 4 × 4 triple lattice experimental design with three replications. The seeds of the experimental genotypes were planted on 4 m × 3.6 m plots (14.4 m^2) having six rows, with inter-row spacing of 60 cm and 20 cm within rows. Fertilizer (DAP 100 kg/ha) was applied for the experiment along with other agronomic managements based on the recommendation. Data were collected on the basis of five sample plants randomly taken from the four central rows, viz. plant height at maturity, number of pods per plant, and number of seeds per pod, and on the basis of entire plot, such as days to 50% emergence, days to 50% flowering, days to 75% maturity, grain yield per net plot and 100-seeds weight. All data were subjected to analysis of variance (ANOVA) separately for individual environment and other environments. ANOVA is important in revealing the presence of GEI, but it does not indicate genotypes contribution to the interaction and which genotype was stable across environments. Stability was computed for grain yield by SPAR 2.0 software for Eberhart and Russell's stability parameters along with Genstat statistical software (16^{th} edition) for AMMI stability parameters and GGE biplot. Mean that differ significantly were separated by Duncan Multiple Range Test. The regression coefficient (b_i) (Eberhart and Russell's stability parameters) measures the response of genotypes to environments. When the regression coefficient of the genotype is nonsignficant from unity/one (b_i= 1), the genotype is said to be averagely responsive and suitable for both poor and good environments; when the b_i value of genotypes is signficantly different from one/unity (bi >1), the genotype is said to be highly responsive above the average and suitable only in good environment; whereas, when the genotype b_i value is signficantly different from one/unity (b < 1), it indicates the genotype is low reponsive and suitable for poor environment (Wachira et al., 2002). No significant S^2di (deviation from regression) value from zero indicates stable genotypes across environments and with significant S^2di value from zero considered as unstable genotypes across environments. AMMI stability value (ASV) is used to judge stable genotypes (the smaller the value, the more stable the genotype is).

RESULTS AND DISCUSSION

The combined analysis of variance over environments showed significant ($p<0.01$) mean squares of genotypes, environments and interaction of genotypes × environments (GEI) for grain yield (Table 3). The results indicated the presence of significant variations among genotypes and environments and the genotypes had inconsistent performance across the test environments for the mentioned traits. This in turn, suggested the need to conduct further GEI and thereby stability analyses to understand the nature of GEI and stability of the performance of genotypes across environments. Akande (2009) in cowpea, Kaya et al. (2002) in wheat, Solomon et al. (2008), Wende (2013) and Workie et al. (2013) in maize and Yayis et al. (2014) in field pea also reported the significant effect of genotype, environment and GEI on yield and some other yield related traits and suggested the importance of further stability analysis.

Mean performance of genotypes for grain yield

The first three genotypes (Table 4) with highest mean grain yield were IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) without significant differences between the two followed by 95K-1095-4A (1321.8 kg/ha). The three genotypes with lowest mean grain yield were IT-96D-610 (1112.5 kg/ha), Kenketi (1128.5 kg/ha) without significant difference among the two and IT-97K-568-18 (1007.0 kg/ha).

*Corresponding author. E-mail: trk2011smn@gmail.com.

Table 1. Description of test environments.

Environments	Soil type	Altitude (masl)	Average rainfall (mm)	Temperature(^{O}C)		Geographical location	
				Minimum	Maximum	Latitude (N)	Longitude (E)
Arbaminch	Vertisols	1216	1000.0	16.0	37.0	06° 06' 41"	37° 35'
Babile	*	1650	671.0	15.5	28.1	9° 13' 09"	42° 19'
Sekota	*	*	1043.0	12.9	32.9	38 ° 56'00"	12 ° 14'
Kobo	Vertisol	1450	673.4	13.0	34.0	12° 8' 21"	39 ° 18'
Melkassa	Andosol	1500	763.0	14.0	24.8	8° 30'00"	39° 21'
Jinka	Vertilsol	1383	1274.7	16.6	27.6	5° 52'00"	36° 38'
Meisso	Vertisol	1332	787.0	14.9	28.2	9° 28' 00"	38° 08'

Source: Arba Minch University and Melkassa Agricultural Research Center, *= Data not available.

Table 2. List of experimental materials.

Code	Genotype	Status
G1	KENKETI	Standard check
G2	86D-378	Advanced line
G3	IT-89KD	Advanced line
G4	MEL-NURL-96-3	Advanced line
G5	IT-96D-610	Advanced line
G6	IT-93K-556-4	Advanced line
G7	IT-97K-568-18	Advanced line
G8	IT-99K-1060a	Advanced line
G9	95K-1095-4A	Advanced line
G10	IT-87D-1137	Advanced line
G11	IT-96D-604	Advanced line
G12	93K-619-1	Advanced line
G13	IT-93K-293-2-2	Advanced line
G14	IT-99K-1060	Advanced line
G15	IT-960-604	Advanced line
G16	TVU	Standard check

Source: Melkassa Agricultural Research Center.

The AMMI for grain yield showed the significant ($p<0.01$) effect of environment, genotype, and genotype by environment interaction. Environment, genotype, and genotype by environment interaction accounted for about 63.3, 5.3, and 29.7% of the total sum of squares, respectively. Most of the total sum of squares of the model was attributed to the environment and the interaction effect. This result is in agreement with the results reported by Akande (2009), Sarvamangala et al. (2010) and Nunes et al. (2014) in cowpea along with Taye et al. (2000) in fieldpea which revealed that the contribution of environment to the observed variation of yield was large. The larger sum of squares of GEI compared to the genotype indicated larger differences in genotypic response across environments. In cowpea (Stanley Omar et al., 2005) and chickpea (Solomon et al., 2008), larger contribution of GEI than genotype effect for the observed yield variation was also reported. The greater contribution of the treatment (98.3%) than the error (1.53) indicated the reliability of the multi-environment experiment. The AMMI model further partitioned the genotype by environment interaction sum of square into interaction principal component axes (IPCA) and residual term. The mean squares of the first three IPCAs were signficant and all togther contributed 79.33% of the total sum of squares of GEI. The IPCA 1, IPCA 2 and IPCA 3 accounted for 37.93, 24.67 and 16.73%, respectively, for the observed variation due to GEI. For the validation of the variation explained by GEI, the first three multiplicative component axes are adequate (Gauch, 2006). This is because of notable reduction of dimensionality and graphical visualization for the stability patterns of genotypes (Annicchiarico, 2002) (Tables 5 and 6).

Table 3. Combined analysis of variance for yield and yield related traits.

Source of variation	Degree of freedom	DF	DM	PH (cm)	PPP	GY (kg)
Replication (R)	14	0.8	2.5	33.0	16.1	206.8
Genotype (G)	15	52.4**	122.8**	479.0**	107.4**	210611.0**
Environment (E)	6	2387.4**	1611.6**	14274.5**	1894.7**	6251125.2**
G × E	90	35.8**	65.8**	774.0**	69.2**	195706.1**
Error	335	8.5	6.1	81.8	23.7	4788.8
CV%		4.8	2.7	15.3	23.4	5.6
SEM		1.7	1.4	5.2	2.8	39.9
Mean		61.0	90.3	59.0	20.5	1237.4

**: Significant at p≤0.01, DF= days to flowering, DM=days to maturity, PH (cm) = plant height in centimeters, PPP= pods per plant, GY (kg) = grain yield in kilo gram, CV (%) =coefficient of variation in percent and SEM=mean standard error.

Table 4. Mean grain yield (kg/ha) of genotypes.

Genotype	Environment								
	Arbaminch	Babile	Sekota	Kobo	Melkassa	Jinka	Meisso	Gm	R
Kenketi	1206.7^{ef}	856.0^{c}	1766.3^{c}	1415.0^{gh}	645.3^{g}	1013.7^{e}	996.7^{ef}	1128.5^{hi}	14
86D-378	1947.7^{a}	524.0^{fg}	2078.7^{a}	1736.7^{e}	851.0^{de}	1478.3^{b}	1023.7^{ef}	1377.1^{a}	2
IT-89KD	1520.7^{d}	450.3^{g}	1795.7^{c}	2351.7^{a}	783.0^{def}	977.7^{ef}	1033.7^{de}	1273.2^{cde}	7
MEL-NURL-96-3	1222.3^{ef}	848.3^{cd}	1951.7^{b}	2069.7^{b}	799.7^{def}	766.7^{gh}	1254.7^{b}	1273.3^{cde}	6
IT-96D-610	1563.0^{cd}	1026.0^{b}	1523.3^{e}	1332.3^{h}	614.7^{g}	674.0^{h}	1054.3^{cde}	1112.5^{i}	15
IT-93K-556-4	1011.7^{g}	780.3^{cd}	2139.7^{a}	1541.3^{f}	693.3^{fg}	1620.7^{a}	1056.0^{cde}	1263.3^{cde}	8
IT-97K-568-18	900.7^{h}	879.7^{c}	1395.7^{f}	1134.0^{i}	840.3^{de}	706.0^{h}	1192.7^{bc}	1007.0^{j}	16
IT-99K-1060a	1629.0^{c}	802.7^{cb}	1754.3^{c}	1985.7^{bc}	1514.0^{a}	1020.3^{e}	1085.3^{cde}	1398.8^{a}	1
95K-1095-4A	1727.7^{b}	610.0^{ef}	1593.7^{de}	1734.3^{e}	1115.3^{c}	1009.7^{e}	1461.7^{a}	1321.8^{b}	3
IT-87D-1137	1208.0^{ef}	1149.3^{a}	1819.3^{c}	1512.7^{fg}	709.3^{efg}	749.7^{gh}	1013.3^{ef}	1166.0^{gh}	13
IT-96D-604	1544.0^{cd}	752.0^{d}	1648.0^{d}	1723.0^{e}	816.0^{def}	1336.3^{c}	883.3^{f}	1243.2^{def}	9
93K-619-1	2014.3^{a}	626.3^{e}	1845.3^{c}	1925.0^{cd}	819.0^{def}	876.0^{fg}	990.0^{ef}	1299.4^{bc}	4
IT-93K-293-2-2	1490.0^{d}	780.7^{cd}	1430.7^{f}	1183.7^{i}	1273.3^{b}	1043.0^{e}	1479.3^{a}	1240.1^{ef}	10
IT-99K-1060	1142.7^{f}	1066.0^{ab}	1566.7^{de}	1411.7^{gh}	790.3^{def}	1286.7^{cd}	1176.3^{bcd}	1205.8^{fg}	11
IT-960-604	1255.3^{e}	985.7^{b}	1540.7^{e}	1501.0^{fg}	863.3^{d}	1010.0^{e}	1241.3^{b}	1199.6^{fg}	12
TVU	1543.3^{cd}	994.3^{b}	1426.7^{f}	1850.3^{d}	831.7^{def}	1171.0^{d}	1199.3^{bc}	1288.1^{bcd}	5
Overall mean	1432.9	820.7	1704.8	1650.5	872.5	1046.2	1133.9	1237.4	
CV (%)	4.1	7.4	3.4	4.2	7.5	7.9	6.7		
SEM	32.17	31.27	30.78	37.55	42.5	42.9	45.5		

Means in the same column followed by the same letters are not significantly different at 5% level of significance, Gm=grand mean of genotypes, R=mean grain yield rank of genotype in descending order and CV (%) =coefficient of variation in percent, SEM=mean standard error.

Stability analysis for grain yield estimates of stability parameters from Eberhart and Russell's model

The six genotypes viz.; IT-960-604, Kenketi, IT-99K-10609, TVU, IT-96D-604 and IT-97K-568-18 with non-significant S^2di values from zero indicated the genotypes were stable. However, all genotypes had lower yield than overall mean of genotypes (1237.4 kg/ha) except TVU and IT-96D-604 which indicated the genotypes were not desirable for cultivation though they were stable. The desirable genotypes are expected not only to be stable in all environments but also have (high mean values). Ten genotypes viz.; 86D-378, IT-89KD, MEL-NURL-96-3, IT-96D-610, IT-93K-556-4, IT-99K-1060a, 95K-1095-4A, IT-87D-1137, 93K-619-1 and IT-93K-293-2-2 had significant S^2di values from zero indicating the genotypes were unstable. TVU was the desirable genotype for cultivation in all environments having static stability evident from non-significant value S^2di from zero, with non-significant bi value (bi=1) from unity/one and higher mean grain yield above average mean grain yield of genotypes. IT-99K-1060 was a low responsive genotype to varied

Table 5. AMMI analysis of variance for grain yield.

Source of variation	DF	SS	MS	Sum of square explained		
				%Total	% G × E	% G × E cumulative
Total	335	59287984	176979			
Treatments	111	58279428	525040**	98.3		
Genotypes	15	3159168	210611**	5.3		
Environments	6	37506751	6251125**	63.3		
Interactions (G × E)	90	17613509	195706**	29.7		
IPCA 1	20	6680777	334039**	11.3	37.93	
IPCA 2	18	4349683	241649**	7.3	24.67	62.6
IPCA 3	16	2946860	184179**	4.97	16.73	79.33
Residuals	36	3636189	101005**	6.1		
Error	335	908139	4324			

ns and **, nonsignificant and significant at p<0.01, respectively. DF = Degree of freedom, SS = Sum of square, MS = Mean square, G = Genotype, E = Environment, G x E = Genotype by environment interaction, IPCA 1, IPCA 2 and IPCA 3 = Interaction principal component axis one, two and three, respectively. In the joint regression analysis of variance, all effects were significant (p<0.01), which indicated contrasts between the environments and the occurrence of differential response of genotypes across environment (Table 6). These results are similar to those reported by Akande (2009), Sarvamangala et al. (2010) and Nunes et al. (2014) in cowpea.

Table 6. Joint regression analysis of variance for grain yield.

Source of variation	DF	SS	MS
Total	111	19426476.1132	175013.3
Genotype	15	1053056.1030	70203.74**
Environment+ (Genotype x Environment)	96	18373420.0102	191389.8**
Environment linear	1	12502250.2023	12502250**
GxE (linear)	15	1721084.0049	114738.9**
Pooled deviation	80	4150085.8030	51876.07**
Kenketi	5	99553.9451	19910.79**
86D-378	5	386414.6073	77282.92**
IT-89KD	5	257322.7465	51464.55**
MEL-NURL-96-3	5	252998.3918	50599.68**
IT-96D-610	5	281839.2433	56367.85**
IT-93K-556-4	5	739493.2260	147898.6**
IT-97K-568-18	5	176478.3714	35295.67**
IT-99K-1060a	5	385325.1075	77065.02**
95K-1095-4A	5	268299.5908	53659.92**
IT-87D-1137	5	280016.9027	56003.38**
IT-96D-604	5	173031.5005	34606.3**
93K-619-1	5	248038.7147	49607.748**
IT-93K-293-2-2	5	289537.9642	57907.59**
IT-99K-1060	5	129666.3231	25933.26**
IT-960-604	5	35612.2136	7122.443**
TVU	5	146456.9544	29291.39**
Pooled error	224	336185.3234	1500.827**

**: Significant at p<0.01, DF = Degree of freedom SS = Sum of square and MS = Mean square.

environments and suitable only for unfavorable environments with b_i value signficantly different from one/unity (bi <1).

Seven genotypes 86D-378, IT-89KD, MEL-NURL-96-3, IT-93K-556-4, 95K-1095-4A, IT-96D-604 and 93K-619-1 had mean yield greater than the mean yield of genotypes

over seven environments ranging from 2.1 to 11.3%. However, all genotypes had S^2di values significantly different from zero and significant bi values (bi>1) from unity/one. This suggested that the genotypes were not stable and highly responsive to favorable environments. These were desirable genotypes for cultivation in favorable environments for the crop having dynamic stability (mean value higher in favorable environments than the average yield of favorable environments).

Two genotypes (IT-99K-1060 and IT-97K-568-18) had non-significant S^2di value from zero ($S^2di>0$), significant bi value (bi<1) from unity/one and lower mean yield than average mean yield of genotypes. These genotypes were stable and more responsive to unfavorable environments for the crop, but the low yield of these genotypes did not promote its being recommended for cultivation in environments where they perform.

IT-96D-604 had non-significant S^2di value from zero ($S^2di>0$), significant bi value (bi>1) from unity/one and high mean yield above average mean yield of genotypes which suggested it was a desirable genotype for cultivation in all environments and more responsive in favorable environments. TVU had yield advantage of 4.01% over grand mean yield of genotypes and fifth ranking mean yield, zero (0) IPCA 1 score and relatively low IPCA 2 (negative); also, ASV suggested that this genotype could be considered for cultivation in unfavorable environments. This result indicated a proportionate genotype response (Silveira et al., 2013).

The genotypes with lower IPCA1 scores would produce a lower G×E interaction effect than those with higher IPCA1 scores and have less variable yields (more stable) across environments (Oliveira et al., 2014). The second group of genotypes consisted of IT-99K-1060a, 86D-378, 95K-1095-4A, 93K-619-1, MEL-NURL-96-3, IT-89KD and IT-96D-604 of which the first four ranked 1 - 4 high yields in the experiment while the last three ranked 6, 7 and 9 high yields. All had higher mean yields above the grand mean yield of genotypes, negative IPCA 1 scores, low ASV ranked 1 - 6 except 95K-1095-4A and MEL-NURL-96-3 with ASV ranked 11 and 14, respectively. The first four high yielding genotypes (IT-99K-1060a, 86D-378, 95K-1095-4A, 93K-619-1) except (86D-378) had same sign of IPCA 1 and IPCA 2 scores while the other genotype was suitable in unfavorable environments with opposite sign of IPCA 1 and IPCA 2. Therefore, the three genotypes could be considered for cultivation in all environments. Other genotype (86D-378) could be considered for cultivation in environments where it performed well. Dynamic stability implies for a stable genotype, a yield response that is always parallel to the mean response of the tested environments, that is, zero GEI (Annicchiarico, 2002). The third group of genotypes consisted of IT-99K-1060, IT-960-604, IT-87D-1137, Kenketi, IT-96D-610 and IT-97K-568-18 which had mean yields lower than grand mean yield of genotypes, with mean yield ranked 11 - 16 having relatively high and positive IPCA 1 scores, of which IT-96D-610, IT-99K-1060 and IT-87D-1137 had high ASV ranked 12, 13 and 15, respectively. The results suggested that these genotypes could not be considered for cultivation. Usually, in crop improvement programs, tests of performance across a wide range of environments is conducted to reduce the effect of GEI and to ensure that the selected genotypes have a high yield and stable performance across several environments (Stanley et al., 2005) (Table 7).

Which-Won-Where" Patterns

In Figure 1, a polygon view of GGE was formed by connecting the vertex genotypes with straight lines and the rest of the genotypes were placed within the polygon. The vertex genotypes were 86D-378 (G2), IT-89KD (G3), IT-93K-556-4 (G6), IT-97K-568-18 (G7), IT-99K-1060a (G8), 95K-1095-4A (G9) and IT-93K-293-2-2 (G13) and 93K-619-1 (G12) having the largest distance from the origin which were more responsive to environmental change and gave high yield except IT-97K-568-18 (G7) which was considered as specially adapted genotypes. The vertex genotypes in each sector are the best genotype at environments whose markers fall into the respective sector. Environments within the same sector share the same winning genotypes, and environments in different sectors have different winning genotypes. The genotypes within the polygon and nearer to origin were less responsive than vertex genotypes (Yan and Hunt, 2001; Yan and Tinker, 2006). Accordingly, the genotypes Kenketi (G1), MEL-NURL-96-3 (G4), IT-96D-610 (G5), IT-87D-1137 (G10), IT-96D-604 (G11), IT-99K-1060 (G14), IT-960-604 (15) and TVU (G16) were located within polygon which were less responsive. Genotype TVU (G16), located near to the origin indicated stablity. Winner and higher yielder genotype at Jinka (E6) and Sekota (E3) was IT-93K-556-4 (G6). IT-89KD (G3) and IT-99K-1060a (G8) were winners and highest yielders at Kobo (E4) and Melkassa (E5) respectively. Genotype 93K-619-1 (G12) and IT-93K-293-2-2 (G13) were winner and high yielder genotypes at Arbaminch and Meisso, respectively. Genotype IT-97K-568-18 (G7) was winner but lowest yielder at Babile (E2) which was relatively not conducive for cowpea genotypes to express their potentials. Yan et al. (2000) and Yan and Kang (2003) reported the polygon view of GGE biplot as the best way for identification of winning genotypes with visualizing the interaction patterns between genotypes and environments. The GGE biplot has therefore, been used in crop genotypes trials to effectively identify the best-performing genotype(s) across environments, identify the best genotypes for specific environments delineation, whereby specific genotypes can be recommended to specific environments and can be used to evaluate the yield and stability of genotypes (Yan and Kang, 2003;

Table 7. Stability parameters from AMMI analysis and Eberhart and Russel's models for grain yield.

Genotype	Pooled mean over seven environments	AMMI model stability parameter				ER's model stability parameter		
		IPCA 1	IPCA 2	IPCA 3	ASV	bi	S^2di	S^2di R
Kenketi	1128.5 (14)	4.2	6.8	1.18239	8.55 (5)	0.97	18409.9617^{ns}	2
86D-378	1377.1 (2)	-12.8	7.1	11.4536	8.72 (6)	1.48	75782.0941**	15
IT-89KD	1273.2 (7)	-18.5	1.3	-6.7099	8.105 (3)	1.7163	49963.722*	9
MEL-NURL-96-3	1273.3 (6)	-4.1	1.8	-0.6522	20.292 (14)	1.3881	49098.851*	8
IT-96D-610	1112.5 (15)	4.6	-6.3	-12.365	18.941 (12)	0.8685	54867.0213*	12
IT-93K-556-4	1263.3 (8)	3.9	23.3	-2.2022	15.423 (10)	1.0717	146397.8179**	16
IT-97K-568-18	1007 (16)	15.2	-4	1.67856	10.067 (7)	0.4678	33794.8469^{ns}	6
IT-99K-1060a	1398.8 (1)	-5.7	-9.6	0.83635	2.8393 (1)	0.9791	75564.1942**	14
95K-1095-4A	1321.8 (3)	-3.5	-11.4	-14.602	17.424 (11)	1.0162	52159.0908**	10
IT-87D-1137	1166 (13)	6.7	2.7	8.33403	23.019 (15)	0.9288	54502.5532**	11
IT-96D-604	1243.2 (9)	-5	5.2	17.1131	5.4225 (2)	1.0573	33105.4728^{ns}	5
93K-619-1	1299.4 (4)	-15.7	-5.9	3.0611	8.4902 (4)	1.5643	48106.9156*	7
IT-93K-293-2-2	1240.1 (10)	11.3	-12.8	-4.9588	23.775 (16)	0.3926	56406.7655**	13
IT-99K-1060	1205.8 (11)	11.4	6.2	3.28577	19.295 (13)	0.5615	24432.4373^{ns}	3
IT-960-604	1199.6 (12)	8	-1.5	0.15715	11.908 (8)	0.6894	5621.6154^{ns}	1
TVU	1288.1 (5)	0	-2.8	-5.6117	12.19 (9)	0.8542	27790.5636^{ns}	4

ns, * and **, non-significant, significant at $p<0.05$ and $p<0.01$, respectively. Numbers in parenthesis represent the pooled mean and ASV rank of genotypes in descending and ascending order, respectively. IPCA 1, IPCA 2 and IPCA 3 = interaction principal component axis one, two and three, respectively, ASV = AMMI stability value, ER's = Eberhart and Russel's model, bi and S^2di, regression coefficient and deviation from regression, respectively, S^2di R= rank of deviation from regression.

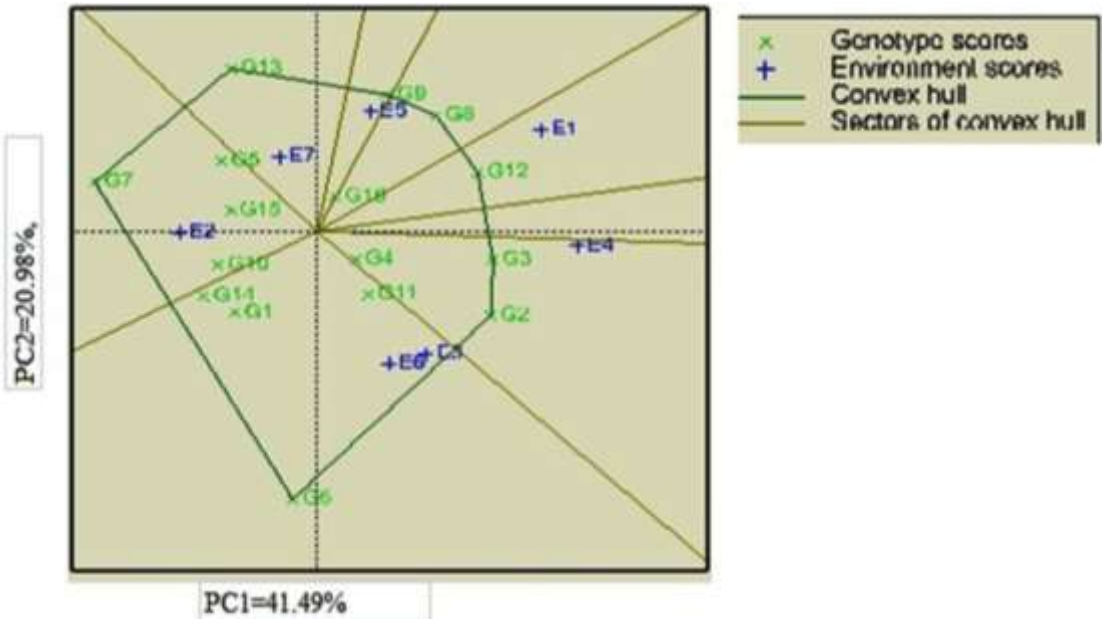

Figure 1. Polygon view of genotype by environment interaction for cowpea genotypes.

Yan and Tinker, 2006).

Figure 2 shows the discriminating ability and representativeness of test environments. Acordingly, Melkassa,Sekota and Jinka were more descrimnating environments with longer vector and larger angle which provides much more information about differences among genotypes. These environments cannot be used in selecting superior cowpea genotypes, but are useful in culling unstable genotypes. Babile and Meisso had relatively short vectors and close to origin that all

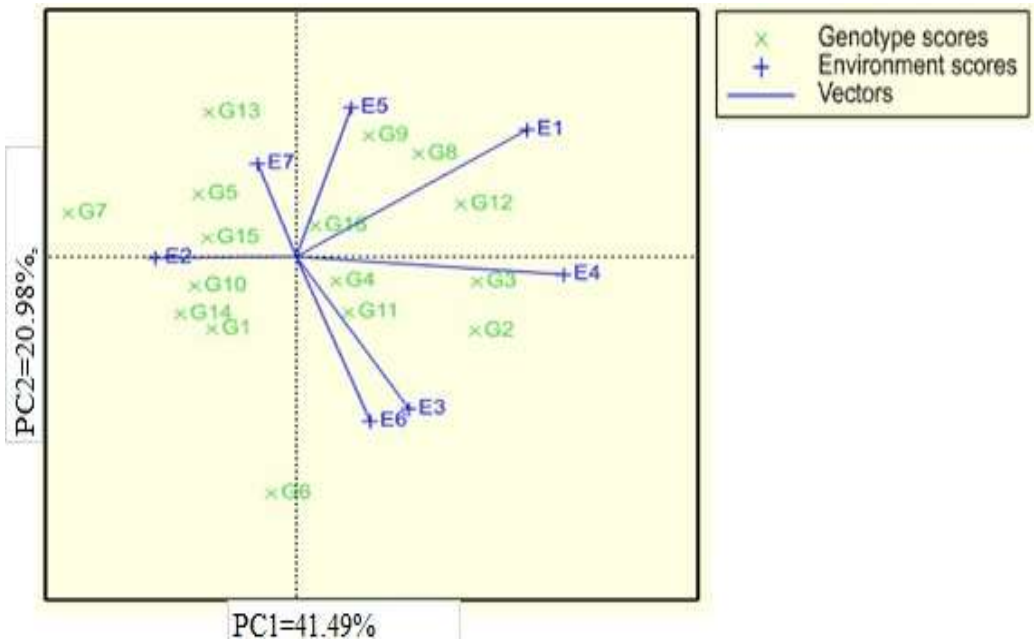

Figure 2. Discriminating power and representativeness of test environments.

genotypes performed similarly, and therefore provides little or no information about the genotypes difference. Thus, it should not be used as test environments for cowpea genotypes. However, identification and removal of non-informative test environments as well as identification of test environments for yield evaluation trial requires multiyear data (Yan et al., 2007). Arbaminch and Kobo had long vectors and small angles with the abscissa and were ideal for selecting superior genotypes. If budgetary constraints allow only a few test environments, these test environments would be the first choice.

According to Yan and Hunt (2001), discriminating ability and representativeness are the important properties of test environments. An ideal environment should be highly differentiating for the tested genotypes and at the same time representative of the target environment (Yan et al., 2007). Representativeness of the test environment is visualized by the angle formed between the environment vector and abscissa of average environment axis. The smaller the angle, the more representative the environment is (Yan et al., 2007). Environments with longer vectors are more discriminating of the genotypes, whereas environments with very short vectors are little or not informative on the genotype difference (Yan et al., 2007).

CONCLUSION

TVU (check variety) was identified as the most stable with mean yield above the mean grain yield of genotypes. Two genotypes, IT-99K-1060a (1398.8 kg/ha) and 86D-378 (1377.1 kg/ha) had first and second highest yield, identified as responsive to favorable environments suggested the need to further test to develop as varieties. Other two genotypes, 95K-1095-4A and 93K-619-1, identified as unstable and highly responsive to environments suggested considering the genotypes as candidate varieties where they performed best. Melkassa, Sekota and Jinka were identified as more descrimnating environments, Arbaminch and Kobo were ideal for selecting superior genotypes, but Babile and Meisso were not descrimnating environments.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

REFERENCES

Agbogidi OM, Egho EO (2012). Evaluation of eight varieties of cowpea [*Vigna unguiculata* (L.) Walp] in Asaba agro-ecological environment, Delta State, Nigeria. European Journal of Sustainable Development 12:303-314.

Akande SR (2009). Biplot analysis of genotype by environment interaction of cowpea grain yield in the forest and southern guinea savanna agro-ecologies of Nigeria. Journal of Food and Agricultural Environment 5:464-467.

Annicchiarico P (2002). Genotype x environment interactions - challenges and opportunities for plant breeding and cultivar recommendations. FAO plant production and protection Paper-174, Rome, Italy.

Aremu CO, Ariyo OJ, Adewale BD (2007). Assessments of selection techniques in genotype by environment interaction in cowpea [*Vigna*

unguiculata (L.) Walp]. Africa Journal of Agricultural Research 2:352-355.
Baidoo PK, Mochiah MB (2014). Varietal susceptibility of improved cowpea [Vigna unguiculata (L.) Walp] cultivars to field and storage pests. Sustainable Agricultural Research 3:69-76.
Collaborative Crop Research Program (CCRP) (2015). Collaborative Crop Research program. Cowpea stalkholder workshop,Accra,Ghana.
Gauch H (2006). Statistical analysis of yield trials by AMMI and GGE. Crop Science 46(4):1488-1500.
Hall AE, Cisse N, Thiaw S, Elawad HOA, Ehlers JD (2003). Development of cowpea cultivars and germplasm by the Bean/Cowpea CRSP. Field Crops Research 82:103-134.
Hall AE (2004). Breeding for adaptation to drought and heat in cowpea. Europe Journal of Agronomy 21:447-454.
Kaya YC, Palta S, Taner (2002). Additive main effects and multiplicative interactions Analysis of yield performance in bread Wheat genotypes a cross environments. Turkish Journal of Agriculture 26:275-279.
Nunes HF, Freire Filho FR, Ribeiro VQ, Gomes RL (2014). Grain yield adaptability and stability of blackeyed cowpea genotypes under rainfed agriculture in Brazil. African Journal of Agricultural Research 9(2):255-261.
Noubissietchiagam JB, Bell JM, Guissaibirwe S, Gonne S, Youmbi E (2010). Varietal response of cowpea [*Vigna unguiculata* (L.) Walp] to *Striga gesnerioides* (Wild.) Vatke race SG5 infestation. Horticulture, Agrobotanici, Cluj-Napoca 38:33-41.
Oliveira EJ, Freitas JP, de Jesus ON (2014). AMMI analysis of the adaptability and yield stability of yellow passion fruit varieties. Scientia Agricola. 71:139-145.
Sarvamangala C, Uma MS, Biradar S, Salimath PM (2010). Stability analysis for yield and yield components over seasons in cowpea [Vigna unguiculata (L.) Walp]. Electronic Journal of Plant Breeding 1:1392-1395.
Silveira LC, Kist V, Paula TOM, Barbosa MHP, Peternelli LA, Daros E (2013). AMMI analysis to evaluate the adaptability and phenotypic stability of sugarcane genotypes. Scientia Agricola 70:27-32.
Solomon A, Mandefro N, Habtamu Z (2008). Genotype-Environment Interaction and Stability Analysis for Grain Yield of Maize (*Zea mays* L.) in Ethiopia. Asian Journal of Plant Sciences 2:163-169.
Stanley OPB, Samonte LT, Wilson AM, McClung JC (2005). Targeting Cultivars onto Rice Growing Environments Using AMMI and SREG GGE Biplot Analyses. Crop Science 45(6):2414-2424.
Taye G, Getachew T, Bejiga G (2000). AMMI adjustment for yield estimate and classification of genotypes and environments in field pea (*Pisum sativum* L.). Journal of Genetics and Breeding 54:183-191.
Wachira F, Wilson NG, Omolo J, Mamati G (2002). Genotype x environment interactions for tea yields. Euphytica 127:289-296.
Wende A (2013). Genetic Diversity, Stability, and Combining Ability of Maize Genotypes for Grain Yield and Resistance to NCLB in the Mid-Altitude Sub-Humid Agro-Ecologies of Ethiopia. PhD. Dissertation. School of Agricultural, Earth and Environmental Sciences College of Agriculture, Engineering and Science University of KwaZulu-Natal, Republic of South Africa.
Workie A, Habtamu Z, Yigzaw D (2013). Genotype X environment interaction of maize (*Zea mays* L.) across North Western Ethiopia. Journal of Plant Breeding and Crop Science 5(9):171-181.
Yan W, Hunt LA, Sheng Q, Szlavnics Z (2000). Cultivar evaluation and mega-environment investigation based on GGE biplot. Crop Science 40:596-605.
Yan W, Hunt LA (2001). Interpretation of genotype by environment interaction for winter wheat yield in Ontario. Crop Science 41:19-25.
Yan W, Kang MS (2003). GGE Biplot Analysis: A graphical tool for breeders, geneticists, and agronomists. CRC Press, Boca Raton.
Yan W, Tinker NA (2006). Biplot analysis of multi-environment trial data. Principles and applications. Journal of Plant Science 86:623-645.
Yan W, Kang MS, MB, Woods S, Cornelius PL (2007). GGE Biplot vs. AMMI Analysis of Genotype-by-Environment data. Crop Science 47:643-655.
Yayis R, Agdew B, Yasin G (2014). GGE and AMMI biplot analysis for field pea yield stability in SNNPR State, Ethiopia. International Journal of Sustainable Agricultural Research 1(1):28-38.

Vol. 10(9), pp. 258-261, September 2018
DOI: 10.5897/JPBCS2017.0685
Article Number: 5C3263D58165
ISSN: 2006-9758

http://www.academicjournals.org/JPBCS

ACADEMIC JOURNALS

Journal of Plant Breeding and Crop Science

Full Length Research Paper

Evaluations of faba bean (*Vicia faba* L.) varieties for yield and yield related traits in central zone of Tigray, Northern Ethiopia

Kiros Wolday

Department of Crop, Axum Agricultural Research Center, Ethiopia.

Received 22 August, 2017; Accepted 18 September, 2017

A field experiment was carried out at Laelay maichew and Tahtay maichew districts in central zone of Tigray, Northern Ethiopia, for two consecutive seasons (2014/2015 to 2015/2016) under rain fed conditions. The objective of the study was to evaluate and select best performing faba bean varieties. Ten faba bean varieties including the local check were evaluated in randomized complete block design (RCBD) in three replications. The data on days to maturity, plant height, number of podsplant^{-1}and number of seed spod^{-1}, grain yield and hundred seed weight were collected. The collected data were subjected to analysis of variance using statistical analysis software (SAS). Combined analysis of variance revealed that there was no significant difference for all studied traits. However, there were significant differences among varieties for all traits in each location. The highest grain yield was recorded from Walki (1943.2 kgha^{-1}), followed by Hachalu (1836.70 kg ha^{-1}). Regarding the hundred seed weight, Hachalu possessed the 4th heaviest in seed weight (g) among the ten varieties, and 2nd in seed yield next to Walki. Highly significant and positive association of grain yield with plant height and number of pods per plant were found. Based on the result obtained, Walki was the best performing variety and selected to be promoted in farmer's field in the study areas and similar agro-ecologies.

Key words: Faba bean, *Vicia faba*, grain yield, yield characters, randomized complete block design (RCBD), Central Tigray.

INTRODUCTION

Faba bean (*Vicia faba* L.) is also referred to as broad bean, horse bean or field bean (Sainte, 2011). Ethiopia is one of the largest faba bean producing country in the world next to China (Hebblethwaite et al., 1993).

Faba bean (*V. faba* L.) is one of the major pulse crops occupying about 35% both in terms of area coverage and volume of annual production of all pulses produced in the country and grown in the highlands (1800 to 3000 meter above sea level) of Ethiopia (Gemechu et al., 2003). Ethiopia is now considered as one of the center of secondary diversity for faba bean (Yohannes, 2000). The crop occupies close to 459,183.51 hectares of land with an annual production close to 6977,983.87 tons (CSA, 2011).

E-mail: kiroswolday@gmail.com.

The grain of faba bean contains a high protein content of 24 to 33% (Winch, 2006). It serves as a source of food and feed with a valuable and cheap source of protein. It is a suitable rotational crop with nationally important cereal crops like teff, wheat and barley etc due to its nitrogen fixing capacity (MoA, 2014). It is a good source of cash to the farmers, and generates foreign currency to the country. However, its share in the countries pulse export is small (Newton et al., 2011; Amanuel et al., 1993)

Production has been constrained by several yield limiting factors. The inherent low yielding potential of the local varieties is one of the most important production constraints. Even the yields of improved varieties of faba bean varieties are severely affected by the variability among locations and years. Therefore, the present investigation aimed at finding out high yielding and most adaptable faba bean varieties in central zone of Tigray, northern Ethiopia. We hypothesized that at least one of the released faba bean variety group means would be significantly higher yielder than the local check.

MATERIALS AND METHODS

Study areas description

Field experiments were carried out in Laelay maichew and Tahtay maichew districts of the Central zone of Tigray, northern Ethiopia. They are located at 14°6'N to 38°46'E and 14°11'N to 38°43'E, and at an altitude of 1500 to 2250 and1500 to 2260 meters above sea level, respectively. They are situated in the northern semi-arid tropical belt of Ethiopia. The rainy season is mono modal concentrated in one season from July to September and receives from 700 to 800 mm rainfall per annum.

Experimental design, treatments and procedures

Nine released faba bean varieties (Walki, Hachalu, Tumsa, moti, Dagm, Obse, Gebelcho, Dosha, and Lalo) and one local check were evaluated for their yield and yield contributing characters at Laelay maichew and Tahtay maichew districts. Varieties were obtained from Holetta Agricultural Research Center (45 km from Addis Ababa) and Debrebirhan Agricultural Research Center in (130 km from Addis Ababa) in 2014. Treatments were laid out in randomized complete block design (RCBD) with three replications. Seed rate of 200 kg ha^{-1} was used. The plots were 4 m (length) x 2.4 m (width) with six total rows (4 middle or harvested rows). Spacing between replications was 1.5 m and spacing between plots, rows and plants were 1 m, 40 and 10 cm, respectively. Two seeds where planted per hill. After emergence, plants where thinned to one seed to maintain normal plant density. DAP (Di-ammonium phosphate) fertilizer at 100 kg ha^{-1} rate was whole applied at sowing. Weeds were controlled by hand weeding.

Data collected

Data were collected on plant and plot bases on yield and yield related traits. Data on days to 50% maturity was taken on plot bases. Whereas, data like plant height, numbers of pods per plant, and number of seeds per pod were determined on plant bases from the 4 middle rows of 10 randomly pre-tagged plants. Grain yield was recorded from 4 harvested middle rows. Grain yield was separated from the straw after sun drying for two weeks and yield per plot was converted into kg ha^{-1}. Finally, hundred seed weight was recorded by counting 100 seeds from each harvested plots.

Data analysis

Prior to analysis of the data, homogeneity of residual variances were assessed whether the normality assumptions of the data was violated. Thus, data were homogenous and showed normal distribution. All the collected data were subjected to analysis of variance (ANOVA) with statistical analysis software (SAS) computer software version 9.2 (SAS, 2002). Correlation analysis and treatments means were compared using least significance difference (LSD) at 5% probability level (Fisher, 1935).

RESULTS AND DISCUSSION

Statistical analysis shows that there was significant difference among varieties for all yield and yield related traits (days to maturity, plant height, Number of pods per plant, number of seeds per pod, grain yield and hundred seed weight). However, the combined results showed no significant difference for genotype environment interaction for all studied traits (Table 1).

Analysis of variance revealed that days to 50% maturity had significant ($P< 0.05$) effect at each location. Local check (104.5) and Moti (104.5) matured early compared to Tumsa (188) and Gebelcho (107.42). However, no significant difference was observed with Walki (106.41), Hachalu (106.58), Dagm (105.83), Obse (104.83), Dosha (105.50) and Lalo (106.83) (Table 1).

The result is in line with the finding of Ashenafi and Mekuria (2015) and Tafere et al. (2012) who reported that Moti was the early maturing genotype; whereas Gebelcho (107.42) and Tumsa (108) were late maturing varieties. Early maturing varieties are the most adaptable varieties and have advantage over the late maturing varieties in areas where rain starts late and withdraws early.

Combined analysis for the two years showed that the highest grain yield was obtained from Walki (1943.2 kg ha^{-1}) followed by Hachalu (1836.70kgha^{-1}) and Dosha (1828.10), and in each locations. Similar results were reported by Ashenafi and Mekuria (2015) at Sinana and Agarfa areas. The highest plant height was recorded in local genotype (94.97cm) followed by Dosha (94.83cm).

Similar result was found by Tafere et al. (2012) who reported Dosha was the tallest in plant height. It may be due to the fact that plant height is highly affected by the genetic make of the varieties. Moreover, Talal and Munqez (2013) reported that plant height was significantly affected by faba bean accessions.

The highest values for number of pods per plant were recorded from Dagm (17.6) followed by local check (17.1) and Lalo (17.02). Whereas, Obse and Gebelcho possessed the lowest values for the number of pods per plant. Regarding the number of seeds per pod,

Table 1. Combined mean performance of different faba bean varieties for different yield and yield related traits across years and locations.

Variable	50% DM	PH (cm)	NPP	NSP	GY (kg ha^{-1})	HSW(g)
Hachalu	106.58^{abcd}	92.82^{abc}	14.37^{bcd}	2.42^{b}	1836.70^{ab}	64.10^{a}
Tumsa	108^{a}	93.40^{abc}	11.83^{cde}	2.48^{ab}	1494.70^{ed}	64.33^{a}
Moti	104.75^{d}	88.88^{bc}	11.58^{e}	2.62^{ab}	1443.00^{ed}	60.76^{a}
Dagm	105.83^{bcd}	91.97^{abc}	17.6^{a}	2.82^{a}	1606.80^{bcd}	37.31^{c}
Obse	104.83^{dc}	88.68^{c}	10.23^{e}	2.72^{ab}	1270.70^{e}	66.60^{a}
Gebelcho	107.42^{ab}	94.80^{a}	10.28^{e}	2.37^{b}	1510.90^{cde}	64.64^{a}
Dosha	105.50^{bcd}	94.83^{a}	14.93^{abc}	2.50^{ab}	1828.10^{abc}	64.08^{a}
Lalo	106.83^{abc}	90.35^{abc}	17.017^{ab}	2.38^{b}	1270.40^{e}	42.22^{c}
Local	104.75^{d}	94.97 ^{a}	17.10^{ab}	2.48^{ab}	1605.10^{bcd}	36.63^{c}
GMS	15.86*	71.28*	106.31**	0.27*	643966**	19.35**
EMS	9205**	5540.64**	1244**	1.12*	468025^{ns}	24.30**
GxE	4.19^{ns}	40.35^{ns}	16^{ns}	0.31^{ns}	163526^{ns}	145^{ns}
CV	2.38	7.22	27	17	25	17.17
LSD	2.06	5.41	3.1	0.35	321.43	7.71

*, **Significant at 0.05 and 0.01 probability level respectively; and NS: Non significant; DM: Days to maturity; PH: Plant height; NPP: Number of pods per plant; NSP: Number of seeds per pod; GY: Grain yield; HSW: Hundred seed weight, GMS: Genotype mean square; EMS: Environment mean square; GxE: genotype by Environment interaction.

Table 2. Pearson's correlation coefficient among faba bean yield and yield related traits.

Trait	PH	NPP	NSP	GY	HSW
Maturity	0.35879**	0.19212*	-0.3489**	-0.3502**	-0.1958*
PH	-	0.51381**	0.11926^{ns}	0.30346**	-0.1813*
NPP	-	-	0.03865^{ns}	0.42136**	-0.4708**
NSP	-	-	-	0.16961^{ns}	0.03143^{ns}
GY	-	-	-	-	-0.074^{ns}

*, ** Significantly correlated at 5 and 1% probability levels, respectively. NS: Non significant; PH: plant height (cm); NPP: number of pods per plant; NSP: Number of seeds per pod; GY: Grain yield (kg ha^{-1}); HSW: Hundred seed weight (g).

maximum number of seeds per pod were obtained from Dagm (2.82), and followed by Obse (2.72). Obse possessed the heaviest seed weight (66.60g) among the ten varieties followed by Gebelcho (64.64g), Tumsa (64.33 g) and Hachalu (64.10 g). Similar result was reported at Sinana on Gebelcho and Hachalu by Ashenafi and Mekuria (2015). However, local check and Dagm possessed the lowest value for hundred seed weight (HSW).

Grain yield showed highly significant and positive association with plant height and number of pods plant^{-1} (Table 2). These findings are in line with the findings of Abdelmula and Abuanja (2007) who reported significant and positive correlation of seed yield with plant height and number of pods per plant. HSW is significantly and negatively associated with plant height, number of pods/plant and number of seeds per pod. Similar results were also reported by Ashenafi and Mekuria (2015). Hence, faba bean production and productivity could be improved by selecting faba bean yield traits like number of pods per plant and plant height.

CONCLUSION AND RECOMMENDATION

The lack of best performing and high yielding variety is the main challenge for faba bean production and productivity in central zone of Tigray. Ten varieties including the local check were evaluated for their adaptability, yield and yield related traits. Walki variety was found to be the most adaptable and high yielding genotype followed by Hachalu. Hence, faba bean production and productivity could be improved by using better yielding varieties such as Walki and Hachalu. In addition, a strong and positive correlation between the different traits and seed yield of faba bean could be used as a selection criterion in order to improve faba bean production and productivity.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

The authors would like to thank Tigray Agricultural Research Institute for their financial support. In addition to this, they are sincerely grateful to the research members of crop core process of Axum Agricultural Research Center for their support during the entire period of the study.

REFERENCES

Abdelmula AA, Abuanja IK (2007). Genotypic Responses, yield Stability, and association between characters among some of Sudanese faba bean (*Vicia faba L.)*genotypes under heat stress. Conference on International Agricultural Research for Development (pp. 1-6). Khartoum: University of Kassel-Witzenhausen and University of Göttingen October 9-11, 2007.

Amanuel G, Tanner DG, Assefa T, Duga D (1993). Observation on wheat and barley-based cropping sequences trials conducted for eight years in South-eastern Ethiopia. Paper presented at the 8th Regional Workshop for Eastern, Central and Southern Africa, 7-20 June 1993, Kampala, Uganda.

Ashenafi M, Mekuria W (2015). Effect of faba bean (*Vicia faba L*.) Genotypes on Yield Attributes at Sinana and Agarfa Districts of Bale Zone, Southeastern Ethiopia. Jordan Journal of Biological Science 8(4):281-286.

Central Statistical Authority (CSA) (2011). Agricultural sample survey. Report on area and production for major crops (private peasant holdings, *meher* season). Addis Ababa, Ethiopia.

Fisher RA (1935). The design of experiments. Oliver and Boyd (Edinburgh).

Gemechu K, Mussa J, Tezera W (2003). Faba bean (*Vicia faba* L.) genetics and Breeding Research in Ethiopia: A Review. In: Ali k, kenneni G, Ahmed S (eds). Food and Forage legumes of Ethiopia: Progress and prospects. Proceedings of the workshop on Food and Forage Legume, 22-26 September, 2003. Addis Ababa, Ethiopia.

Hebblethwaite PD, Ingram J, Scott RK, Elliot J (1993). Some factors influencing yield variation of field beans (*Vicia faba L.).* In: Thompson, R (ed.). Proceedings of the Symposium on the Production, Processing and Utilization of the Field Beans (*Vicia faba L.*). Bulletin No. 15, Scottish Horticultural Research Institute, Invergrowie, U.K. pp. 20-27.

Ministry of Agriculture (MoA) (2014). Plant variety release, protection and seed quality control directorate. Crop variety register. Addis Ababa, Ethiopia. Issue No. 17. P 81.

Newton Z, Ann C, Rowland M (2011). Grain legume impacts on soil biological processes in sub-Saharan Africa. African Journal of Plant Science 5:1-7.

Sainte M (2011). The magazine of the European Association for Grain Legume Research. Issue No. 56 Model Legume Congress, France, 15-19 May, 2011.

Statistical Analysis System (SAS) (2002). Statistical analysis software Version 9.1.3 SAS Institute Inc., U.S.A.

Tafere M, Tadesse D, Yigzaw D (2012). Participatory varietal selection of faba bean (*Vicia faba* L.) for yield and yield components in Dabat district, Ethiopia. Wudpecker Journal of Agricultura Research 1:270-274.

Talal AB, Munqez JY (2013). Phenotypic Characterization of Faba Bean (Vicia faba L.) Landraces Grown in Palestine. Journal of Agricultural Science 5:110-117.

Winch T (2006). Growing Food. A Guide to Food Production. Springer. 333 p.

Yohannes D (2000). Faba bean (Vicia faba *L.*) In Ethiopia. Institute of Biodiversity Conservation and Research (IBCR) Addis Ababa Ethiopia.

Related Journals: