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Evaluation of large seeded faba bean genotypes for agronomic performance in vertisol areas of Southern Tigray, Ethiopia

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Thirty-two faba bean genotypes were evaluated for their yield and yield components in verstisol areas of Hashenge and Aiba in 2015. Alpha lattice design with two replications was used for the experiment. The Analysis of Variance showed highly significant differences (P<0.01) for thousand seed weight over locations. Based on this, genotype EH 06007-2 scored highest 1000 seed weight (1111 g) followed by EH 06088-6 (971.5) and EH 06007-4 (938.5 g) over locations. Least thousand seed weight was obtained from the local genotype (505.5 gm) followed by the standard check Walki (587.3) and ET 07017-bulk (648.0 g). Grain yield showed significant differences (p<0.05) at Aiba location but no significant differences in Hashenge. At Aiba, genotype ET 07013-1 gave the highest grain yield (59.31 qt/ha) followed by genotype ET 07005-1 (57.85) and EH 06088-1 (54.77 qt/ha). Significant positive correlations were recorded between TSW with DM (0.624), number of seeds per pod (0.567) and NTPP (0.427) but it was negatively correlated with NPPP (-0.487). Grain yield was significantly and positively correlated with plant height (0.49) and NPPP (0.369). The highest distance (0.692) was between cluster V and IV, which suggested that the members of these clusters diverge on most of the studied traits and could be used in breeding programs. Principal component (PC) analysis revealed that the first four PCs explained 83.7% of the total variation. The variance explained by PC1 was mostly due to traits related to DM, TSW, NSPP and NTPP, whereas PC II was mostly related to grain yield, plant height, NPPP and thousand seed weight traits. The PC analysis ultimately showed the amount of variability for the traits that could be used for the improvement of large seed sized faba bean genotypes.

Key words: Large seed size, genotypes, grain yield, faba bean *Vicia faba*, vertisols

INTRODUCTION

Faba bean (*Vicia faba*) has been grown in various parts of the world including Ethiopia, which is the 2nd largest producer after China (Biruk, 2009). According to the CSA (2013), faba bean grows in the highland areas of northern and central Ethiopia and the total cultivated area and average yield of the crop in 2008/2009 was 538, 820.5 ha and 12.92 qt/ha, respectively. Regional shares of faba bean production area are 4.11%, 48.05%, 37.46%, and 10% for Tigray, Amhara Oromia, and SNNPR regions, respectively.

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Faba bean (*V. faba* L.) is one of the major pulse crops grown in the highlands (1800 – 3000 m asl) of Ethiopia (Temesgen and Aemiro, 2012). Faba bean is a valuable protein-rich leguminous crop cultivated and consumed as human food in the specified areas. In addition, its straw is used as animal feed. With a cheap protein source, it partly compensates for the large deficiency in animal protein sources. Faba bean plays a significant role in improving the productivity of soil by fixing atmospheric nitrogen and is a suitable rotation crop for cereals as well as in interrupting disease and insect pest cycles (Barri and Shtaya, 2013).

Vertisols cover 10.3% (about 12.7 million ha) of the Ethiopian land mass and are the fourth most abundant soils after Histosols, Cambisols and Nitosols. It is estimated that Vertisols comprise about 24% of the country's cropped highland soils (Tekalign et al., 2002). Vertisols are potentially among the most productive soils of sub-Saharan Africa, but they are agriculturally underutilised within the traditional farming practices due to water logging during heavy rains. High moisture level limits faba bean production on vertisol as the crop is highly sensitive to water logged conditions (Getachew et al., 2003). Moreover, the problem of black root rot (*Fusarium solani*) is widely present in the vertisols (Beniwal and Dereje, 1987).

The highland area of Southern Tigray is suitable for the production of not only faba bean but also other pulse crops. In spite of this, however, faba bean production and productivity is by far below the genetic potential of the crop (MoARD, 2008). Low access of improved varieties and susceptibility of the available varieties of faba bean to water logging becomes the most important constraint in this region. The problem of water logging has resulted in the outbreak of not only root rot but also to chocolate spot and ascochyta blight (Couchman and Hollaway, 2016). The objective of this study was to evaluate faba bean genotypes for agronomic performance in vertisol areas of southern Tigray.

METHODOLOGY

Description of study area

The experiment was conducted at Hashenge and Aiba, located in the southern zone of Tigray Region and 148 and 102 km south of Mekelle (capital city of Tigray), respectively. These locations have an altitude of 2420 and 2700 m above sea level, respectively, and the soils are vertisols. The study areas were selected based on their suitability for faba bean production and presence of water logging condition.

Experimental materials

The materials used in this experiment comprised of 32 large seed size Faba bean genotypes (New, EK 05024-2, EK 05023-1, EK 05014-3, EK 05027-5, EK 05002-3, EK 05005-4, ET 07002-1, ET 07002-2, ET 07002-bulk, ET 07005-1, ET 07005-2, ET 07005-3, ET 07005-bulk, ET 07013-1, ET 07017-bulk, ET 07019-bulk, EH 06007-2, EH 06007-4, EH 06088-1, EH 06031-3, EH 06023-4, EH 06022-4, EH 06022-1, EH 06028-1, EH 06070-3, EH 06007-6, EH 06022-3, EH 06088-6 as well as Hachalu. Walki and local). These materials were sourced from Holleta Agricultural Research Center in 2014. The experiment was conducted using Alpha Lattice Design with two replications and plots of 2 m long and 2.4 m wide and inter- and intra-row spacings of 40 and 10 cm, respectively. Four rows were harvested for yield and yield component evaluation. DAP fertilizer at the rate of 100 kg/ha was applied at planting. During growth, data were recorded on various agronomical traits including days to maturity, stand count at harvest, plant height, number of pods per plant, number of seeds per pod, grain yield, thousand seed weight, and diseases reaction.

Statistical analysis

Data collected from the experiment were analyzed using SAS (1999) for the analysis of variance and Minitab Version 14 (Minitab 1998) for Multivariate analysis (cluster analysis) statistical packages. Analysis of variance (ANOVA) and Pearson correlation analyses were performed according to the methods described by Gomez and Gomez (1984). All the quantitative and qualitative data were used for principal component analysis (PCA) and cluster analyses. The mean data were standardized prior to multivariate analysis to eliminate the effects resulting from using different scales. To separate the 32 genotypes into groups and to evaluate the patterns of similarity and dissimilarity, the data were subjected to cluster analysis according to Gower distance (Gower 1971), using PAST software version 2.15 (Hammer et al., 2001). Principal component analysis (PCA) of the correlation matrix was performed with the same software to determine the sources of variation among genotypes.

RESULTS AND DISCUSSION

Seed size and disease reaction of faba bean genotypes

Since seed size, grain yield and disease reaction are the most important traits for pulse crops in general and faba bean crop in particular, analysis was focused to these characters, Based on this, there was highly significant difference ($P<0.01$) for thousand seed weight at Hashenge and Aiba locations. Genotype EH 06007-2 scored highest 1000 seed weight (1111 g) followed by EH 06088-6 (971.5) and EH 06007-4 (938.5 g) over locations. On the other hand, least seed size was recorded from the local (505.5 gm) genotype followed by the standard check Walki (587.3) and ET 07017-bulk (648.0 g) genotypes. From the tested genotypes, about 25 genotypes scored more 1000 seed weight than the standard check (Hachalu) but the other standard checks (Walki and local) showed least seed weight (Table 1).

The most important diseases affecting faba bean at Aiba and Hashenge locations are Chocolate spot, Ascochyta blight and Faba bean gall (Teklay et al., 2014). In 2015, these diseases did not occur at Hashenge. For this, disease severity scoring was taken only at Aiba location for Chocolate Spot and Ascochyta Blight (Table 1).

As indicated in Table 1, the analysis of variance for

Table 1. Thousand Seed weight, Grain yield and disease severity score of Faba Bean Genotypes grown at Hashenge and Aiba in 2015.

Genotype	Thousand seed weight (g)			Grain yield (kg/ha)			Disease score at Aiba (0 – 9)	
	Hashenge	Aiba	Mean	Hashenge	Aiba	Mean	Chocolate spot	Ascochyta blight
EH 06007-2	1102	1120.	1111.3	3716	4774	4245	2.5	2
EH 06088-6	1012	931	971.5	3399	4236	3818	4	3
ET 07005-2	947	802.5	874.8	3301	4604	3953	2.5	2.5
EH 06070-3	946	857.5	901.8	3073	3587	3330	4	2
ET 07005-1	937.5	815	876.3	3808	5785	4797	4.5	2
EH 06007-6	923	862	892.5	3225	4680	3953	3	2.5
EH 06022-1	906.5	706	806.3	3251	2519	2885	3	2
EH 06088-1	900.5	843	871.8	3514	5477	4496	2.5	2
ET 07002-bulk	899.5	824	861.8	3487	3643	3565	4.5	2
EH 06028-1	872.5	918	895.3	2868	2778	2823	4	2.5
EH 06022-3	863.5	762	812.8	3733	4161	3947	2	1.5
EH 06007-4	837.5	1039.	938.5	3273	4994	4134	3	1.5
ET 07005-3	836	883.5	859.8	3770	4501	4136	2.5	1
EH 06022-4	835	792	813.5	3484	3555	3520	4	2
EK 05027-5	834	759	796.5	3364	2557	2961	4	2.5
ET 07002-2	834	776.5	805.3	3677	3685	3681	5	3
EH 06023-4	831.5	757.5	794.5	3513	5315	4414	2.5	2
EH 06031-3	815.5	720	767.8	3414	3852	3633	4	2.5
New	813	818.5	815.8	3318	4719	4019	3.5	2.5
EK 05024-2	810	833.5	821.8	3849	5279	4564	3	2.5
ET 07019-bulk	804.5	808	806.3	3535	4605	4070	3.5	3
ET 07002-1	769.5	735.5	752.5	3773	3610	3692	3.5	3
EK 05023-1	766	668.5	717.3	3898	4381	4140	2	1.5
Hachalu	736.5	655.5	696.0	3583	4041	3812	2.5	2
ET 07013-1	724.5	669	696.8	3627	5931	4779	2.5	1.5
EK 05014-3	721	687	704.0	3566	5069	4318	2	1.5
ET 07005-bulk	715.5	751	733.3	3484	4404	3944	3.5	3
EK 05005-4	696.5	651	673.8	3684	2720	3202	5	2.5
EK 05002-3	685	591	638.0	3575	2915	3245	3.5	2
Walki	647.5	527	587.3	4218	4367	4293	4.5	2.5
ET 07017-bulk	642	654	648.0	2918	3726	3322	4	3
Local	517	494	505.5	3838	3497	3668	4	2.5
S. E (m)	50.2	47.94	48.01	5.93	8.53		0.97	0.62
LSD (5%)	115.4***	110.2***	44.2 ***	NS	17.43 *		NS	NS
CV (%)	6.14	6.21	6.04	16.89	20.1		29	27.6

* implies significant difference at 0.05, Disease score of 0 = most resistant; Disease score of 9 = most susceptible.

disease reaction has shown non-significant difference. Accordingly, although the severity scores of chocolate spot for all the genotypes were slightly higher than those for ascochyta blight, the scores were in the range of 1 to 5 for both diseases thus indicating resistant to moderately resistant disease reaction.

Variations of faba bean genotypes for grain yield

The analysis of variance for grain yield has showed significant difference ($p<0.05$) among genotypes at Aiba location but no significant difference in Hashenge. At Aiba location, 15 genotypes gave statistically more grain yield than the first standard check of walki (43.66 qt/ha). Accordingly, genotype ET 07013-1 gave the highest grain yield (59.31 qt/ha) followed by genotype ET 07005-1 (57.85) and EH 06088-1 (54.77 qt/ha).

Even though no statistical significant difference has showed for grain yield at Hashenge, the above genotypes (ET 07013-1, ET 07005-1 and EH06088-1) scored higher grain yield as 36.27, 38.08 and 35.14 qt/ha in that order. In this location, the highest grain yielder gave 42 18 qt/ha, which indicated a very similar in yielding potential

Table 2. Pearson correlation coefficients for 8 quantitative traits of 32 faba bean genotypes grown in 2015 at Hashenge and Aiba.

Traits	DM	SCH	NTPP	PHT	NPPP	NSPP	GY	TSW
DM	**1**							
SCH	0.085	**1**						
NTPP	0.679***	-0.238	**1**					
PHT	0.079	0.100	0.091	**1**				
NPPP	-0.377*	-0.063	0.068	0.116	**1**			
NSPP	0.606***	0.107	0.434*	0.223	-0.220	**1**		
GY	0.072	0.087	0.272	0..493**	0.369*	0.249	**1**	
TSW	0.624***	-0.214	0.427*	-0.016	-0.487**	0.567***	0.100	**1**

DM: Days to mature; SCH: Stand Count at Harvest; NTPP: Number of Tillers per Plant: PHT: Plant height; NPPP: Number of pods per plant; NSPP: Number of seeds per pod; TSW: Thousand seed weight and GY for Grain yield. ***, ** and * significant at p ≤ 0.001, p ≤ 0.01 and p ≤ 0.05, respectively.

with the highest yielder genotype. In general, the genotypes that showed significant yield difference at Aiba had also higher and reasonable grain yield at Hashenge location (Table 1).

Correlation analysis

Pearson correlation coefficients between different pairs of characters were computed and are shown in table 2. The correlation coefficients of the 1000 seed weight trait showed that it was positively and significantly correlated (P<0.01) with days to maturity (0.624), number of seeds per pod (0.567) and number of tillers per plant (0.427). On the other hand, thousand seed weight was highly and negatively correlated with number of pods per plant (-0.487). As pods of faba bean per plant increases, seed size decreased to accommodate more pod clusters in a node. Similarly, highest and positive significant correlations were found between number of tillers per plant and days to maturity (0.679), number of seeds per pod and days to maturity (0.606).and grain yield with plant height (0.49). These results reflected the importance of days to maturity, number of seeds per pod and number of pods per plant in the determination of thousand seed weight in faba bean. Al Barri and Shtaya (2013) reported the importance of number of seeds per pod and number of pods per plant on 100 seed weight determination.

Cluster analysis

Cluster analysis was used to further investigate the inter-relationships of the genotypes using eight agronomic traits (days to maturity; stand count at harvest; number of tillers per plant: plant height; number of pods per plant; number of seeds per pod; thousand seed weight and grain yield). The genotypes were grouped into two main clusters (A and B). Main cluster A was also divided into four sub clusters and cluster B was divided in to three sub clusters (Figure 1).

Among the seven clusters, cluster I comprised of 7 genotypes (ET 07005-1, EH 06023-4, ET 07005-3, ET 07019 - -bulk, New, ET 07005-bulk and ET 07005-2) that have similar maturity time and number of tillers per plant. From this cluster, genotypes ET 07005-3 and New had the lowest dendrogram distance (1.21). Cluster II comprised six genotypes, including two standard checks and they were characterized by relatively early maturation, high number of pods per plant and more grain yield but lower thousand seed weight. The third cluster that consisted of six genotypes had highest thousand seed weight, more number of seeds per pod and late matured varieties. The genotypes in the fourth cluster were characterized by lowest thousand seed weight and lowest number of seeds per pod. The local check with its lowest seed size was included in this cluster. Cluster V that consisted of only one genotype (ET 06007- 6) has showed late maturation, poor in stand establishment but highest in tillering capacity. This cluster has more dendrogram distance (24.18) than others. On the other hand, cluster VI, comprising of five genotypes has less number of pods per plant. Finally, the lowest grain yield was recorded from the genotype in the seventh cluster. This cluster which includes only two genotypes also had low stand count at harvest and short plant height. Even though these genotypes were moderately resistant to Ascochyta blight and Chocolate spot diseases, more scores were recorded from them.

To evaluate the genetic variability or similarity of the genotypes among the clusters, the inter-cluster Gower distance and relationships were calculated using PAST software (Table 3). The highest distance (0.692) was between cluster V and IV, which suggested that the members of these clusters diverge on most of the studied traits and could be used in breeding programs. The lowest distance (0.148) was between cluster III and cluster I, suggesting that their maternal origin may be

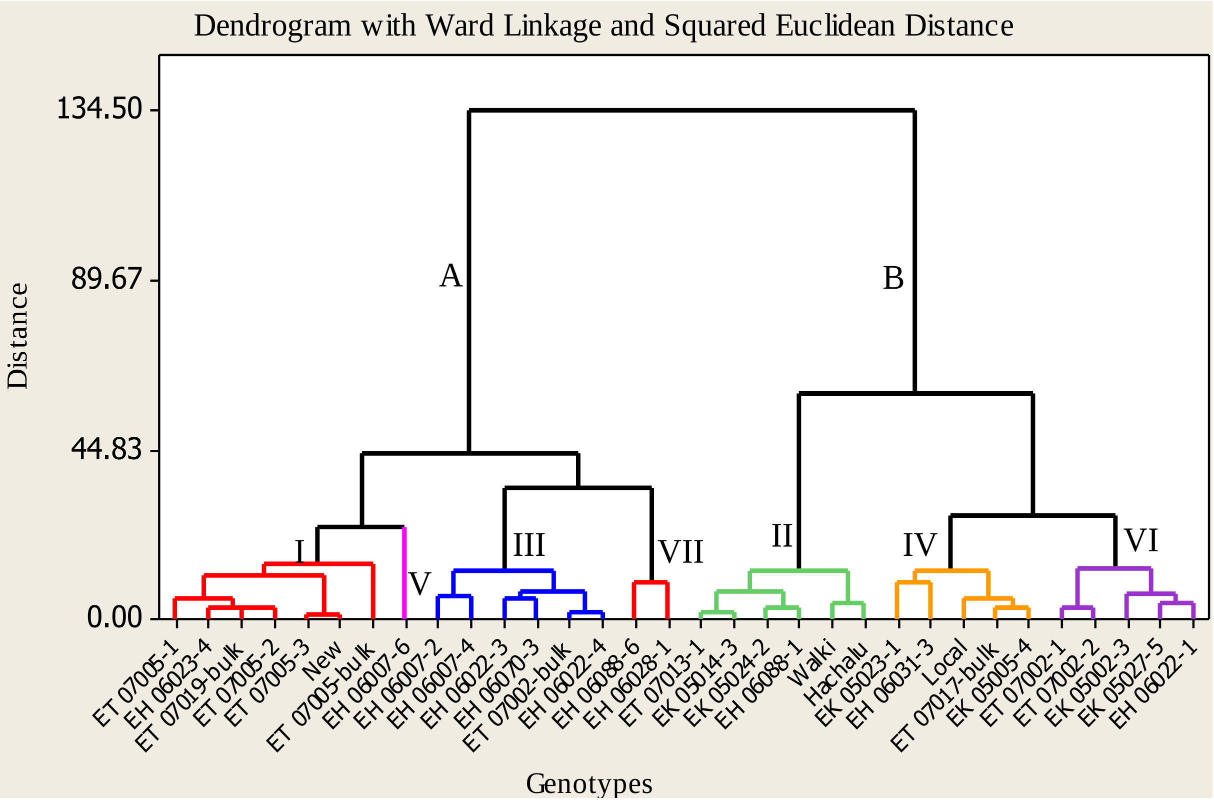

Figure 1. Cluster analysis showing relationships among faba bean genotypes determined on the basis of 8 yield traits.

Table 3. Gower distance and similarities among seven clusters of 32 genotypes of faba bean.

Cluster	I	II	III	IV	V	VI	VII
I	0						
II	0.387	0					
III	**0.148**	0.497	0				
IV	0.535	0.335	0.505	0			
V	0.285	0.601	0.321	**0.692**	0		
VI	0.393	0.327	0.365	0.272	0.544	0	
VII	0.370	0.580	0.346	0.465	0.444	0.378	0

very closely related (Kumar et al., 2013).

Principal component analysis

Principal component analysis (PCA) was used to identify hidden patterns in the data and was performed to obtain more reliable information on how to identify groups of genotypes that have desirable yield traits for breeding. Eight components were extracted from the 8 studied traits by PCA analysis. But based on Diana (1999 as cited from Kaiser, 1960), factors to be retained should have more than 1 eigenvalues, at least 5% variance explained for each component, and/or more than 75% cumulative proportion of variance explained.

The results (Table 4) indicated that the first four components accounted for 83.7% of the total variation, whereas, the remaining 4 components accounted for only 16.3% of the morpho-agronomic diversity. PC I explained the most variability (36.1%), followed by PC II (22.3%), PC III (15.4%) and PC IV (10.0%). In the first principal component, DM, TSW, NSPP and NTPP were more important traits contributing more to the variation and this component was more associated with the high values of the above traits negatively.

The sign indicates the direction of the relationship

Table 4. Eigenvalues, proportion of variance and cumulative variance for 8 quantitative characters in Faba bean genotypes.

Character	PC1	PC2	PC3	PC4
DM	-0.520	0.086	-0.074	-0.280
SCH	0.038	-0.104	-0.791	-0.471
NTPP	-0.429	-0.152	0.389	-0.385
PHT	-0.118	-0.515	-0.240	0.552
NPPP	0.229	-0.512	0.341	-0.402
NSPP	-0.470	-0.087	-0.191	-0.024
GY	-0.154	-0.620	-0.002	0.099
TSW	-0.482	0.200	0.080	0.274
Eigenvalue	2.8847	1.7873	1.2303	0.7966
% of total variance	36.1	22.3	15.4	10.0
Cumulative variance	36.1	58.4	73.8	83.7

* DM: Days to mature; SCH: Stand count at harvest; NTPP: Number of tillers per plant: PHT: Plant height; NPPP: Number of pods per plant; NSPP: Number of seeds per pod; TSW: Thousand seed weight and GY for grain yield.

between the components and the characters (Yemane and Fasil, 2002). Due to more variation explained by the PC 1 (Table 4), its scores could effectively represent the genotype effect (Ali et al., 2011). In the second principal component, the observed variation (22.3%) was caused mainly by GY, PHT, NPPP and TSW and of which, TSW had positive relationship with this PC. PC III was positively dominated by the effect of number of tillers per plant and number of pods per plant and negatively by stand count at harvest. On the other hand, Plant height, stand count at harvest and number of pods per plant in the fourth principal component constituted large part of the total variation. In this experiment, the PC analysis ultimately showed the amount of variability for the traits that could be used for the improvement of large seed sized faba bean genotypes.

Conclusion

The combined analysis of variance for thousand seed weight indicated that there were highly significant ($p < 0.01$) differences among genotypes over locations. Genotype EH 06007-2 ranked highest in thousand seed weight followed by EH 06088-6 and EH 06007-4 as 1111, 971.5 and 938.5 g, respectively. The standard check (Hachalu) recorded low thousand seed weight (696 g) as compared with most faba bean genotypes under study. In addition, genotypes that out yielded the standard checks (Walki and Hachalu) in grain yield also had better seed size and lower disease reaction. In 2015, the faba bean crop was not attacked by diseases in Hashenge location and severity scores at Aiba location for Chocolate Spot and Ascochyta Blight were generally low to moderate.

Based on the inter-cluster Gower distance and relationships, the highest distance (0.692) was between cluster V and IV, which suggested that the members of these clusters diverge on most of the studied traits and could be used in breeding programs. The lowest distance (0.148) was between cluster III and cluster I, suggesting that their maternal origin may be very closely related. PCA showed that the first 4 PC accounted for 83.7% of the variability.

Conflict of Interests

The authors have not declared any conflict of interest.

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