

Genetic variability, heritability and genetic gain of common bean (*Phaseolus vulgaris* L.) genotypes in response to Mexican bean weevil (*Zabrotes subfasciatus* Boheman) infestation

Shiferaw G. Tigist^{1*}, Gemechu Keneni², Amelework Assefa³, Julia Sibiya⁴

¹Ethiopian Institute of Agricultural Research, Melkassa Agricultural Research Centre, P.O. Box 430, Adama, Ethiopia

²Ethiopian Institute of Agricultural Research, Holeta Agricultural Research Centre, P. O. Box 2003, Addis Ababa, Ethiopia

³Agricultural Research Council, Vegetable and Ornamental Plant, Private Bag X293, Pretoria, 0001, South Africa

⁴African Centre for Crop Improvement, University of KwaZulu-Natal, Private Bag X01, Scottsville 3209, Pietermaritzburg, South Africa

*Corresponding author: tshiferaw2006@gmail.com

Abstract

The aims of the study were to determine expected genetic gains from selection and the extent and pattern of genetic diversity of common bean genotypes to Mexican bean weevil. Three hundred bean genotypes were artificially infested with the Mexican bean weevil. The experiment was laid out in a randomized complete block design with three replications. Data on thirteen insect and seed related traits were recorded and subjected to statistical analysis. The broad-sense heritability values ranged from 68.5%–93.9% for the traits studied. The expected genetic gains from selection ranged from 5.9%–67.1% for insect related traits and from 0.2%–82.2% for seed related traits. Seed weight loss showed significant positive phenotypic and genotypic correlation with number of eggs, number of adults emerged, percent adult emergence, index of susceptibility, number of holes and first and second progeny damage. Cluster analysis classified the 300 genotypes into two major clusters and seven sub-clusters. Mahalanobis's D^2 value calculated among the sub clusters ranged from 5.6 to 191.6. There was no defined relationship between geographic origins and the pattern of genetic diversity in response to Mexican bean weevil infestation. Therefore, parental selection should be made based on genetic diversity and other special merits of the genotype for the resistance attributes. The introgression of the resistance gene into the adapted improved varieties and landraces, and increasing the frequency of resistance genes through selection could be used as a strategy to improve bruchid resistance in the future.

Keywords: Common bean, broad-sense heritability, genetic gains, correlation coefficient, Mexican bean weevil.

Introduction

Common bean (*Phaseolus vulgaris* L.) is the second most widely grown legume crop cultivated in Ethiopia after faba bean (*Vicia faba* L.) (Asfaw et al., 2009). It is one of the major pulse crops which played an important role to the Ethiopian national economy (Teshome et al., 2020). The crop is also an important source of protein, particularly to the rural poor who cannot afford to buy animal protein. Common bean is used for rotation to break the life cycles of crop-specific pathogens and to restores soil fertility through symbiotic nitrogen fixation and mineral solubilization (Kirkegaard et al., 2008). Despite the importance of the crop, the potential of common bean production has not been realized in tropical and sub-tropical regions of Africa due to several biotic and abiotic constraints.

Storage insect pests are among the most serious problems affecting common bean production. Two bean bruchid species, *Zabrotes subfasciatus* (Boheman) and

Acanthoscelides obtectus (Say), are the most important storage pests for common bean worldwide (Parsons and Credland, 2003). In Ethiopia, *Zabrotes subfasciatus* is the most common and causes severe qualitative and quantitative losses to stored common bean grains (Tadesse et al., 2008). Effective control of bruchids could commonly be achieved through storage environment management and through breeding for resistance. Breeding for resistance to bean bruchid is economically feasible and environmentally sound (Assefa, 2010).

Common bean is believed to be introduced into Africa within the 16th century alongside maize (Gentry, 1969). After its initial introduction, farmers in Africa have preserved and discovered important alleles that are adapted to their local environments, which led to the development of morphologically and genetic variants (Sperling, 2001). In the past three decades, the national bean research programs in

Africa have been introducing large number of common bean germplasm from different parts of the world. Ethiopia possesses a wide range of genetic diversity for common bean in Africa (Asfaw et al., 2009; Dagneu et al., 2014; Tigist et al., 2019).

Although there is a large collection of common bean germplasm maintained by the Ethiopian common bean breeding program (Asfaw et al., 2009; Dagneu et al., 2014; Tigist et al., 2019), the genetic value and the extent of the genetic diversity have not been studied well. The information on the genetics of resistance, the magnitude and pattern of the genetic diversity in response to the Mexican bean weevil has not yet been systematically studied. The aims of this study were to determine expected genetic gains from selection and the extent and pattern of genetic diversity of common bean genotypes to Mexican bean weevil.

Results

Performance of the genotypes for bruchid resistance

The analysis of variance showed a highly significant differences ($P \leq 0.01$) among the genotypes for all the traits (Tables 1), confirming the presence of adequate variability among the 300 genotypes for the response to bruchid. Highest coefficient of variations (CV%) were observed for adult dry weight, first progeny damage, infested seeds and seed weight loss. A wide range of variation was observed for number of adult emergence, percent adult emergence, number of holes and second progeny damage.

Broad-sense heritability and expected genetic gain from selection

Estimates of broad-sense heritability, expected genetic gain from selection and genetic advance as percentage of the means for different insect and seed related traits are presented in Figure 1. Broad-sense heritability values ranged from 77% - 91% for insect related traits and 82% - 100% for seed related traits. For the insect related traits, the genetic variances for percentage of adult's emergence and index of susceptibility were large relative to their respective environmental variances. Consequently, high heritability estimates of above 91% were observed. The same was true for seed related traits, except for total number of holes and seed density, where all traits showed broad-sense heritability estimates of above 87%.

The heritability estimates *per se* cannot give us information about the effectiveness of selection and estimation of the genetic advance is important (Shukla et al., 2006). The expected genetic gains from selection ranged from 5.9% to 67.1% for insect related traits and from 0.2% to 82.2% for seed related traits. The lowest expected genetic gains from selection were recorded for seed density (0.2), proportion of seed coat weight (3.2) and index of susceptibility (5.9). High genetic advance as a percentage of the mean were observed for number of percentage damage from the first progeny (156), seed weight loss (155), adults emerged (146.4), total number of holes (146), seed size (121) and number of eggs (115.0). Characters that showed low genetic advance as percentage of the means were proportion of seed coat weight (37.0) and seed density (11.7).

Interrelationship between traits

Phenotypic and genotypic correlation coefficients between the traits are presented in Table 2. Seed related traits such

as proportion of seed coat weight, seed density and seed size and insect trait of adult dry weight showed non-significant phenotypic or genotypic correlation with all other traits. However, adult dry weight revealed a strong positive relationship with number of adults emerged and total number of holes. Number of holes per seed showed a significant positive phenotypic correlation with index of susceptibility and percentage damages (1st and 2nd progeny) but significant positive genotypic correlation with infested seeds, number of adults emerged, percentage adult's emergence and total number of holes at level.

The number of eggs showed significant positive phenotypic and genotypic correlation with infested seeds, number of adults emerged, index of susceptibility, number of holes, first progeny damage and seed weight loss. Positive and significant phenotypic and genotypic correlations were observed between the number of adults emerged and the number of eggs, infested seeds, percentage of adults emerged, index of susceptibility, number of holes, progeny damage (1st and 2nd) and seed weight loss. Percent adult emergence had no significant association with infested seeds. Index of susceptibility and seed weight loss revealed a significant positive correlation with all the traits. However, infested seeds had no significant relationship with index of susceptibility and seed weight loss.

Cluster and distance analysis

The relationship among the 300 common bean genotypes was assessed based on the Ward's agglomerative hierarchical classification using Euclidean distance. The cluster analysis conducted using the mean values of 13 insect and seed related traits clearly classified the 300 genotypes into two distinct major clusters (I and II) and seven sub-clusters (SC1-3 and SC5-7) (Figure 2). The first cluster consisted of 58% of susceptible small and large seeded beans genotypes. Cluster I was further divided into four sub-clusters (SC1, 2, 3 and 4). The SC1 and 2 constituted of 134 small seeded genotypes whereas the remaining 40 genotypes grouped under SC3 and 4 were medium and large seeded genotypes. Cluster I consisted of 63.7% (130) landraces, of which 17 were breeding lines, 25 released varieties and one resistant line (MAZ 215). The second cluster was composed of 126 genotypes and organized under three sub (SC5-7) clusters with 23, 46 and 57 genotypes, respectively. Majority (97%) of the resistant lines, were grouped in Cluster II together with large seeded released varieties.

The pairwise generalized squared distance values (D^2) among the seven sub clusters are presented in Table 3. The distances between the eight pairs of the sub clusters were highly significant ($p < 0.001$). The maximum distance ($D^2 = 191.6$) was found between SC-3 and SC-5 followed by SC-1 and SC-5 ($D^2 = 176.2$) and SC-1 and SC-3 were being constituted very susceptible small and large-seeded genotypes, respectively. Genotypes grouped under SC-5 were small seeded (RAZ) and large seeded (MAZ) bruchid resistant lines.

Mean performance of clusters

The mean performances of the clusters in response to bruchid are presented in Table 4. SC-1 consisted of highly susceptible genotypes with the largest number of eggs, adults emerged, total number of holes, the highest index of susceptibility, seed weight loss, with the highest proportion of seed coat weight and seed density. SC-2 and SC-3 also

comprised of susceptible genotypes with the highest percentage of adults emergence, progeny damage (1st and 2nd), and number of holes per seed, high number of eggs, adults emerged, total number of holes, high index of susceptibility and seed weight loss. Genotypes under SC-2 had small seed size, whereas SC-3 constituted medium to large-seeded genotypes. SC-5, on the other hand, constituted of resistant genotypes with the lowest index of susceptibility, percentage of adult emergence, the least total number of holes and number of holes per seed as well as the lowest percentage damage and seed weight loss. Thus, SC-5 and SC-7 constituted of genotypes with good level of resistance to bean bruchid than the other sub-clusters specifically, SC-1 and SC-2 that constituted of genotypes that were more susceptible to bean bruchid. Genotypes, such as RAZ-11, RAZ-36, RAZ-2, RAZ-44, RAZ120, RAZ-40 and MAZ-203, which showed consistent complete resistance based on the univariate analysis previously reported by Tigist et al. (2018) grouped under SC-5. The other two promising resistance entries SCR-11 and NC-16 grouped under SC-7.

Pattern of phenotypic diversity

There was no clear association between geographic origin of the genotypes and their clustering pattern as genotypes from the same places of origin fell into different clusters and vice versa (Table 5). Most of the landraces (78.4%) grouped into SC-1, SC-2 and SC-3, which had a statistically non-significantly distance. Similarly, landraces from the same region were observed to be distributed over five of the seven sub-clusters except genotypes from Amhara region, which grouped under six clusters. Released varieties were found to be the most divergent as they were distributed over five clusters.

Discussion

The high levels of broad sense heritability values for insect related traits (77.2% - 91.2%) and seed related traits (> 82%) indicated that a greater proportion of the phenotypic expression of the genotypes was contributed by the genotypic variance with minimal environmental effects. Large heritability values were observed in most of the traits, suggesting selection schemes based on these traits would be effective towards improving bean bruchid resistance. The high heritability values are consistent with Kasozi (2013) who reported up to 89% heritability of maize weevil (*Sitophilus zeamais*) resistance traits (F₁ weevil progeny emergence, percentage grain damage and Dobie's index of susceptibility). Keneni (2012) also reported moderate to high broad-sense heritability (43-76%) for seed related traits such as seed weight loss, proportion of seed coat weight (%) and seed size for genotypes infested by the adzuki bean beetle (*Callosobruchus chinensis* L.) in chickpea (*Cicer arietinum*). However, the author also reported low broad-sense heritability estimates ranging from 0.20-11% for insect related traits (number of eggs, number of adults emerged, days to adult emerged, number of uninfected seed and percentage adult emergence). Except number of eggs, which showed 77.3% broad-sense heritability estimate, other insect and seed related traits revealed broad-sense heritability estimates over 82%, indicating that selection based on these traits will be effective for reducing the loss caused by the insect (Singh, 2002).

Many researchers agreed that heritability value *per se* cannot be used to predict the effectiveness of selection. Heritability estimates can be used to predict the genetic

advance that can tell us the effectiveness of selection (Shukla et al., 2006). Index of susceptibility, percentage of adult emerged, seed weight loss, percentage damage, and proportion of seed coat weight revealed the highest heritability values with high genetic advance as percentage of the mean. However, seed density and proportion of seed coat weight showed high genetic advance as percentage of the mean. This indicated that the resistance of bean bruchid could be improved through direct selection from lower percentage of adults emerged, index of susceptibility, seed weight loss and percentage damage. Hence, progress should be expected from selection between individual genotypes for these characters to reduce infestation and consequent seed damage by bean bruchid.

In the present study, with some exceptions, the genotypic correlation coefficients were generally greater than the corresponding phenotypic correlation coefficients, which indicated that the observed relationship between characters might be due to genetic reason. As expected, the correlation between number of eggs, number of adults emerged, percentage of adults emerged, index of susceptibility and seed weight loss were positive and significant. The phenotypic and genotypic correlation between seed coat weight (%), seed density and seed size were found to be non-significant with all other traits. Therefore, progress in breeding for resistance to bruchids could be achieved by selection of genotypes with low numbers of eggs, low adults emerged, low percentage of adults emerged, low total number of holes and genotypes with low susceptibility indices. Most of these traits have a high broad-sense heritability and expected genetic gain from selection and negatively significant correlation with seed weight loss. Similar results were reported on common bean and cowpea (*Vigna unguiculata*) infested by *C. maculatus* (Mwila, 2013), on chickpea infested by *C. Chinensis* (Keneni, 2012) and on maize infested by *Sitotroga cerealella* and *Sitophilus zeamais* (Demisse et al., 2015).

Guzzo et al. (2015) reported lack of correlation between seed size and genotype resistance for the two common bean storage insect pests (*Z. subfasciatus* and *A. obtectus*), suggesting the resistance level of the genotypes to these insects is not related to seed size. Kananji (2007) also reported that seed size did not affect the susceptibility of bean genotypes for *Z. subfasciatus*. On the other hand, other researchers found that seed size is important in the choice of the host by the Bruchidae (Janzen, 1969; Simmonds et al., 1989) and the small-seeded bean varieties were found to be relatively resistant than the large seeded varieties (Schoonhoven and Voysest, 1991). Beneke (2010) also reported seed size to exhibit a significant positive correlation with number of adults emerged for *A. obtectus*. Proportion of seed coat weight showed non-significant correlation with most of the important traits. According to Guzman Maldonado et al. (1996), seed hardness and seed coat thickness revealed no significant correlation in no-choice and free-choice conditions with oviposition and adult emergence for both *Z. subfasciatus* and *A. obtectus*. In addition, seed coat thickness is not important for resistance to *C. maculatus* on common bean and cowpea (Silva et. al., 2004). Other reports indicated that the proportion of seed coat weight had a strong negative correlation with seed weight loss in chickpea infested by *C. chinensis* (Keneni et al., 2012). Telxaira (2009) reported that female *Z. subfasciatus* lay large but fewer eggs on beans with a low seed density as compared to beans with a high bean density. In the present

Table 1. Mean and standard error, range, mean squares and coefficient of variation (CV) of 13 insect and seed related traits after infestation by bean bruchid.

Traits	Mean±SE	Range	CV (%)	Mean square
Number of eggs	53.1 ± 17.6	8.0 - 138.0	11.8	1716.5**
Days to adult emergence	22.6 ± 6.5	21.0 - 40.0	5.4	20.2**
Number of adults emerged	39.6 ± 13.6	0.0 - 110.0	13.0	1408.5**
Adult dry weight	0.04 ± 0.03	0.0 - 0.95	24.6	0.006**
Index of susceptibility	6.63 ± 0.9	0.0 - 11.0	16.7	12.9**
Percent adult emergence	74.65 ± 10.6	0.0 - 100.0	17.5	1662.7**
Infested seeds (%)	35.3 ± 9.8	3.7 - 85.5	21.3	786.3**
Number of holes	41.1 ± 14.2	0.0 - 114.0	13.0	1516.5**
Number of holes per seed	1.6 ± 0.3	1.0 - 4.0	19.8	0.79**
First progeny damage (%)	28.8 ± 8.4	0.0 - 75.4	22.1	780.9**
Second progeny damage (%)	86.7 ± 5.3	0.0 - 100	7.5	2236.2**
Seed weight loss (%)	24.0 ± 6.5	0.0 - 50.3	20.9	523.1**
Seed coat weight (%)	8.9 ± 0.4	6.2 - 15.7	5.5	3.66**
Seed density	1.4 ± 0.04	1.2 - 1.6	3.6	0.011**
Hundred seed weight	26 ± 0.01	10.7 - 50.8	4.6	321.0**

SE, standard error; CV, coefficient of variation.

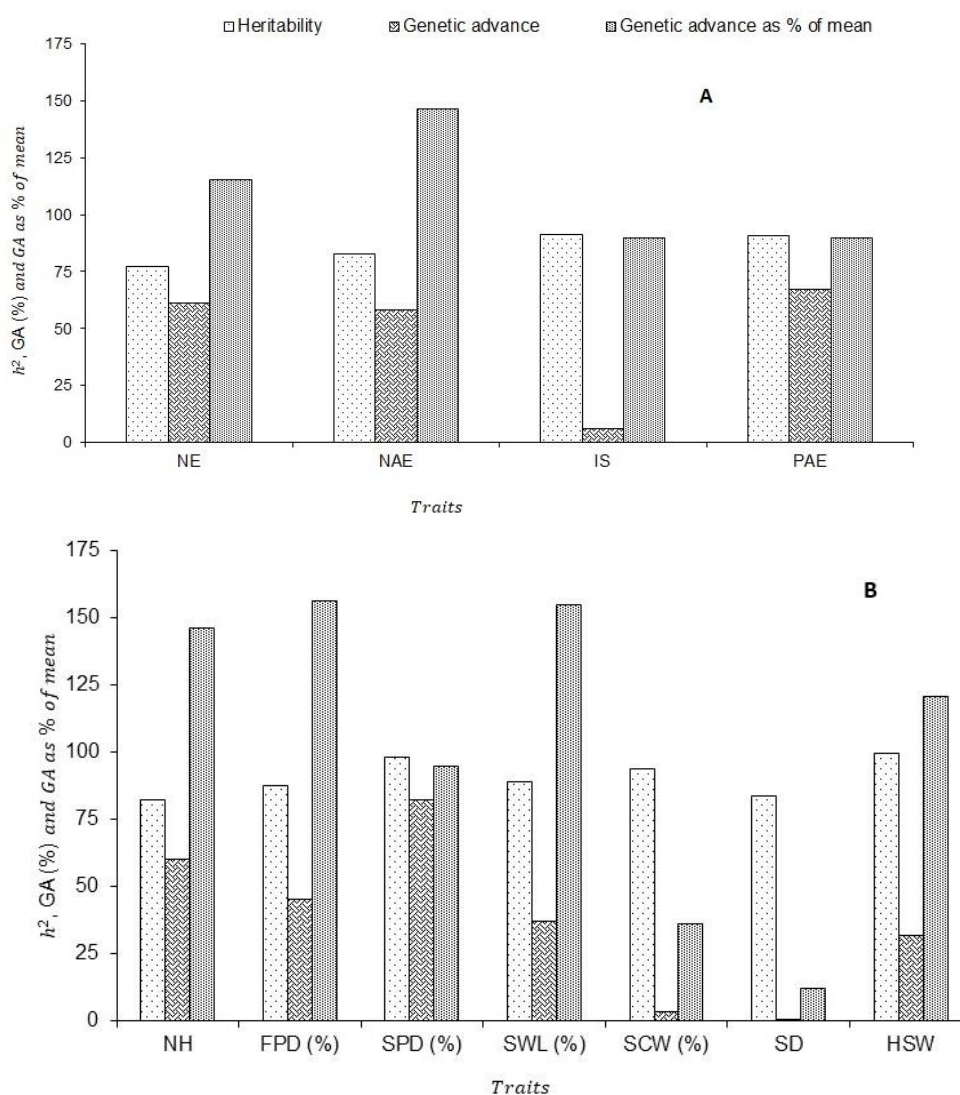


Figure 1. Estimates of broad-sense heritability (H^2), expected genetic advance (GA) and genetic advance as percentage of the mean for insect based (A) and seed-based (B) traits to bean bruchid infestation. NE = number of eggs; INS = infested seeds; NAE = number of adults emerged; PAE = percentage adults emergence; ADW = adult dry weight; IS = index of susceptibility; NH = number of holes; NH/S = number of holes per seed; FPD = first progeny damage; SPD = second progeny damage; SWL = seed weight loss; SCW = proportion of seed coat weight; SD = seed density; HSW = hundred seed weight.

Table 2. Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients among different response traits to bean bruchids infestation measured in 300 common genotypes.

Characters	NE	INS	NAE	PAE	ADW	IS	NH	NH/S	FPD	SPD	SWL	SCW	SD	HSW
NE		0.67**	0.83**	0.09	0.41	0.56*	0.84**	0.29	0.65**	0.3	0.57*	0.12	0.14	0.001
INS	0.70**		0.46*	-0.12	0.12	0.22	0.47*	0.45*	0.73**	0.09	0.37	-0.06	0.10	0.29
NAE	0.84**	0.51*		0.60**	0.54*	0.88**	0.99**	0.48*	0.77**	0.68**	0.78**	0.18	0.14	-0.10
PAE	0.05	-0.11	0.54*		0.35	0.84**	0.59*	0.52*	0.48*	0.89**	0.60*	0.18	0.04	-0.18
ADW	0.38	0.12	0.49*	0.29		0.42	0.54*	0.16	0.35	0.35	0.31	0.09	0.11	-0.13
IS	0.56*	0.27	0.86**	0.79**	0.38		0.88**	0.57*	0.70**	0.90**	0.79**	0.23	0.13	-0.11
NH	0.84**	0.51*	0.99**	0.53*	0.48*	0.86**		0.48*	0.78**	0.68**	0.79**	0.17	0.14	-0.08
NH/S	0.29	0.36	0.43	0.44	0.14	0.49*	0.43		0.61*	0.50*	0.47*	-0.04	0.13	0.18
FPD	0.66**	0.73**	0.78**	0.43	0.33	0.70**	0.79**	0.47*		0.63**	0.71**	0.05	0.09	0.17
SPD	0.26	0.09	0.61*	0.84**	0.3	0.85**	0.61**	0.49*	0.59*		0.74**	0.18	0.07	-0.12
SWL	0.52*	0.37	0.72**	0.54*	0.27	0.74**	0.72**	0.39	0.68**	0.71**		0.16	0.10	-0.04
SCW	0.10	-0.06	0.15	0.17	0.06	0.21	0.15	-0.02	0.05	0.18	0.15		0.08	-0.16
SD	0.10	-0.09	0.12	0.04	0.09	0.11	0.11	-0.11	-0.07	0.06	0.08	0.07		-0.08
HSW	0.002	0.26	-0.13	-0.17	-0.11	-0.07	-0.13	0.15	0.15	-0.12	-0.03	-0.16	0.08	

NE = number of eggs; INS = infested seeds; NAE = number of adults emerged; PAE = percentage adults emergence; ADW = adult dry weight; IS = index of susceptibility; NH = number of holes; NH/S = number of holes per seed; FPD = first progeny damage; SPD = second progeny damage; SWL = seed weight loss; SCW = proportion of seed coat weight; SD = seed density; HSW = hundred seed weight ** = Significant at $P \leq 0.01$; * = Significant at $P = 0.05$

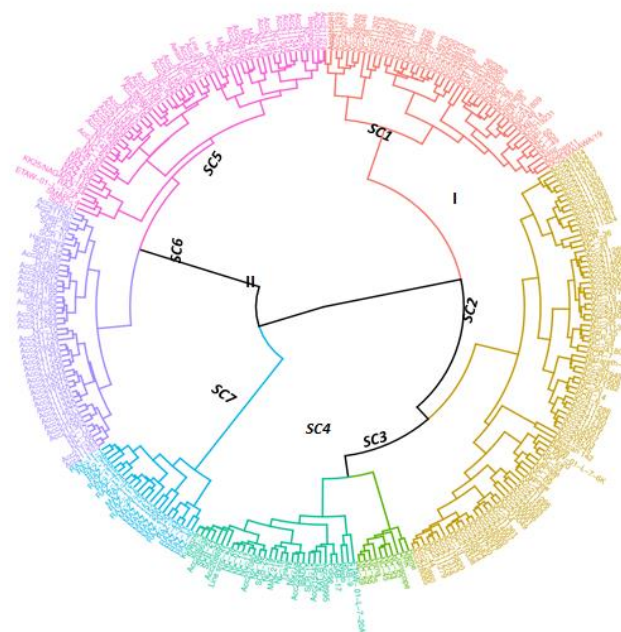


Figure 2. Cluster analysis of common bean genotypes using Ward's agglomerative hierarchical classification based on 13 insect and seed related traits after infestation by bean bruchid.

Table 3. Pair-wise generalized squared distances (D^2) among 300 common bean genotypes in seven sub-clusters.

Sub-cluster	1	2	3	4	5	6	7
1		8.6	17.2	27.0 *	176.2***	25.7*	46.0***
2			20.3	9.2	147.0***	5.6	18.9
3				17.6	191.6***	33.8**	50.8***
4					138.0***	6.2	13.8
5						126.7***	83.4***
6							7.2
7							

χ^2 =22.36, 27.69 and 34.53 at 5 %, 1% and 0.1% probability level, respectively. *** Significant at $P < 0.001$; ** Significant at $P = 0.01$; * Significant at $P = 0.05$.

Table 4. Performance difference among the two clusters of common bean genotypes for the mean of 13 response traits bean bruchids infestation.

Trait	Cluster means							Grand mean
	C-I (n=174)				C-II (n=126)			
	SC-1 (n=48)	SC-2 (n=86)	SC-3 (n=10)	SC-4 (n=30)	SC-5 (n=23)	SC-6 (n=46)	SC-7 (n=57)	
NE	89.92**	59.53	76.73	39.76	42.09	38.95	30.93*	35.33
INS (%)	89.92**	59.53	76.73	39.76	42.09	38.95	30.93*	35.33
NAE	89.92**	59.53	76.73	39.76	42.09	38.95	30.93*	35.33
PAE	78.64	84.72**	77.71	82.20	6.45*	83.89	71.65	74.64
IS	8.53**	7.72	8.13	6.67	0.97*	6.68	5.32	6.63
NH	73.01**	51.43	61.33	33.99	2.65*	32.84	20.95	41.09
NH/S	1.78	1.68	2.25**	1.82	0.80*	1.48	1.56	1.63
FPD	46.72	32.00	62.44**	34.22	3.23*	22.63	15.33	28.78
SPD	98.70	98.95	99.38**	97.50	5.02*	95.29	76.23	86.67
SWL	36.16**	31.22	32.76	25.04	1.48*	21.56	11.81	23.99
SCW	9.27**	9.23	8.43	8.30	8.22*	8.73	9.16	8.95
SD	1.39**	1.35	1.26*	1.33	1.34	1.37	1.33	1.35
HSW	23.56	22.12	49.25**	38.13	30.89	21.65*	24.44	25.90

NE = number of eggs; INS = infested seeds; NAE = number of adults emerged; PAE = percentage adults emergence; ADW = adult dry weight; IS = index of susceptibility; NH = number of holes; NH/S = number of holes per seed; FPD = first progeny damage; SPD = second progeny damage; SWL = seed weight loss; SCW = proportion of seed coat weight; SD = seed density; HSW = hundred seed weight. * Lowest value; ** Highest value.

Table 5. Clustering of 300 common bean genotypes based on the collection regions.

Collection regions	Total	Distribution over clusters						
		Cluster I				Cluster II		
		SC-1	SC-2	SC-3	SC-4	SC-5	SC-6	SC-7
Amhara	69	14	21	6	8	14	0	6
Somali	2	0	0	1	0	1	0	0
Oromia	54	11	19	9	4	11	0	0
Benishangul-Gumuz	13	4	3	6	0	0	0	0
SNNPR	50	5	23	12	0	10	0	0
Unknown	16	3	6	3	2	2	0	0
Improved varieties	36	6	8	4	7	7	0	4
CIAT breeding lines	25	4	6	5	8	2	0	0
CIAT resistance lines	33	9	0	0	1	0	23	0
Malawi	0	1	0	0	0	1	0	0
Total	300	57	86	46	30	48	23	10

SNNPR = South Nations, Nationalities and Peoples Region; CIAT = International Center for Tropical Agriculture.

maculatus was also found to be unaffected by seed coat thickness and seed density (Baker et al., 1989). Common bean seed morphological characters did not appear to affect female bruchid ovipositional preference and subsequent adult emergence and damage (Negasi, 1994).

Cluster analysis classified the 300 common bean genotypes into two main clusters and seven sub-clusters with varying number of genotypes, assuming maximum homogeneity within cluster and maximum heterogeneity between clusters in terms of the traits under consideration (Hair et al., 1995). The fact that most of the Ethiopian collections and released genotypes were grouped into the same cluster may indicate their similarity for a susceptible reaction to bean bruchid. An earlier study also depicted that most of the cultivated common bean varieties and landraces lack resistance to *Z. subfasciatus* (Schoonhoven and Cardona, 1982). Out of the 21 pairs of sub-clusters, divergence between 48% of the pairs was found to be non-significant. The genotypes in these pairs of clusters were more closely related than those genotypes in significantly diverged clusters (Singh and Chaudhary, 1985).

There was no defined relationship between geographic origin and the pattern of genetic diversity as a number of genotypes from the same source fell into different clusters, and vice versa. These results are consistent with those reported by Madakbas and Ergin (2011) and Boros (2014) who tested common bean landrace collections from Turkey and Poland for morphological, phenological and agronomical characters. Similar results were also reported from Ethiopian chickpea collections for response to adzuki bean beetle infestation (Keneni et al., 2011). These results suggested that genotypes from different regions might have the same genetic background, which may be partly due the informal seed exchange among farmers from different regions of the country or the germplasm exchange among international and national bean breeding programs.

Materials and Methods

Plant material

In this study, 300 genotypes, of which 204 landraces, 34 released varieties, 27 breeding lines and 35 exotic resistance lines for Mexican Bean Weevil, were evaluated. Of the 204 landraces, 148 were obtained from the Ethiopian Biodiversity Institute (EBI) and the remaining 56 were collected from the major bean growing areas of Ethiopia. The released varieties and breeding lines were obtained from Melkassa, Sirnka and Areka Agricultural Research Centers and Haramaya University, Ethiopia, whereas the Mexican Bean Weevil resistant genotypes were obtained from the International Center for Tropical Agriculture (CIAT), Uganda, Pannar Seed Company, South Africa, and Malawi National Bean Improvement Program, Malawi. The detail description of the genotypes used in this study is presented in supplementary Table 1.

Laboratory evaluation

The experiment was conducted at the Entomological Research Laboratory at Melkassa Agricultural Research Center, Ethiopia. The detailed evaluation protocol and data recording methods were described in Tigist et al. (2018). Data on number of eggs, number of adults emerged, percent adult emergence, index of susceptibility, total number of holes, number of holes per seed, 1st progeny percent damage, 2nd progeny percent damage, percent seed weight

loss, proportion of seed coat weight, seed density and hundred seed weight were recorded. Analysis of variance was done with the SAS software version 9.2 (SAS Institute, 2003).

Hierarchical cluster analysis was used to group the genotypes based on their similarities. The phenotypic distance among genotypes was measured using Euclidean distance and the distance matrix was used to construct the dendrogram using ward D² linkage method. The optimum number of clusters in the data set was determined using gap statistics (Tibshirani et al., 2001). Genetic distances between clusters were standardized with Mahalanobis's D² statistics using the formula:

$$D_{ij}^2 = (x_i - x_j)' \text{cov}^{-1} (x_i - x_j)$$

Where D²_{ij} = the distance between cluster i and j; x_i and x_j = vectors of the values of the variables for cluster i and j; and cov⁻¹ = the pooled within groups variance-covariance matrix. The D² values obtained for pairs of clusters were considered as the calculated values of Chi-square (x²) and were tested for significance both at 1% and 5% probability levels against the tabulated value of x² for 'P' degree of freedom, where P is the number of traits considered in this study (Singh and Chaudhary, 1985). Cluster analysis was done using different packages and functions of R in R environment (R Development Core Team, 2019).

Variance components due to genotype (σ²_g), environment (σ²_e) and broad-sense heritability (h²) and the expected genetic gain from selection (GA) were calculated from the analyses of variance as suggested by Singh and Chaudhary (1985).

$$\sigma_g^2 = [(\sigma_e^2 + r\sigma_g^2) - \sigma_e^2] / r = \frac{MS1 - MS2}{r}$$

$$\sigma_e^2 = MS2$$

Broad-sense heritability (h²) was calculated as:

$$H^2 = \sigma_g^2 / [\sigma_g^2 + \sigma_e^2]$$

The expected genetic advances (GA) were estimated using the below formula by assuming 10% of the genotypes were selected (selection intensity = 10%)

$$GA = K \cdot \sqrt{\sigma_p^2} \cdot \frac{\sigma_g^2}{\sigma_p^2} = K \cdot \sigma_p \cdot h^2$$

$$GA \text{ as \% of mean} = \frac{GA}{\bar{x}}$$

Where, GA = expected genetic advance from selection and K = the selection differential (K= 1.76 at 10% selection intensity), σ_p = square root of the phenotypic variance, h² = broad sense heritability and $\bar{x}$ = population mean.

Phenotypic and genotypic correlations were estimated using the standard procedure described by Miller et al. (1958) and Kashiani and Saleh (2010) using the following formula:

$$r_p = \frac{\text{cov}_{pxy}}{\sqrt{\sigma_{px}^2 * \sigma_{py}^2}}$$

$$r_g = \frac{\text{cov}_{gxy}}{\sqrt{\sigma_{gx}^2 * \sigma_{gy}^2}}$$

Where r_p = phenotypic correlation, r_g = genotypic correlation, cov_{pxy} = phenotypic covariance of traits x and y, cov_{gxy} = genotypic covariance of traits x and y, σ_{px}² = phenotypic variance of x, σ_{py}² = phenotypic variance of y, σ_{gx}² = genotypic variance of x and σ_{gy}² = genotypic variance of y.

Conclusions

This study clearly revealed the presence of useful genetic variability and the existence of a substantial level of diversity among common bean genotypes, which can be useful for

further breeding for bruchid resistance. By using direct selection for seed weight loss or indirect selection using other traits such as number of eggs, number of adults emerged, percentage of adults emerged, index of susceptibility, it could be possible to reduce the seed weight loss caused by bean bruchid. The high heritability and expected genetic gains from selection in most of the traits studied in the present study indicated that selection based on these traits would be effective towards improving of bean bruchid resistance and reducing seed weight loss. Complementing the conventional approach with the use of molecular markers could improve the efficiency of selection in developing bruchid resistant cultivars. There was no defined relationship between geographic origin and genetic diversity, suggesting that parental selection should be made based on genetic diversity and other special merits of the genotype for the resistance attributes. The introgression of the resistance gene into the adapted improved varieties and landraces, and increasing the frequency of resistance genes through selection could be used as a strategy to improve bruchid resistance in the future.

Acknowledgments

The authors wish to acknowledge the Alliance for Green Revolution in Africa (AGRA) for financial support and Melkassa Agricultural Research Centre (MARC) for providing the necessary material and technical support during the study period.

References

- Assefa TM (2010) Selection for drought and bruchid resistance of common bean populations. Dissertation, University of Padova, Italy.
- Asfaw A, Blair M.W, Almekinders C (2009) Genetic diversity and population structure of common bean (*Phaseolus vulgaris* L.) landraces from the East African highlands. *Theor Appl Genet*. 120: 1–12.
- Baker AT, Nielsen SS, Shades RE, Singh BB (1989) Physical and chemical attributes of cowpea lines resistant and susceptible to *callosobruchus maculatus* (f.) (Coleoptera: Bruchidae). *J. Stored Prod Res*. 25: 1-8.
- Beneke CJ (2010) The Expression and inheritance of resistance to *Acanthoscelides Obtectus* (Bruchidae) in South African dry bean cultivars. Msc thesis, University of the Free State, South Africa.
- Boros L., Wawer A, and Borucka K (2014) Morphological, phonological and agronomical characterization of variability among common bean (*Phaseolus vulgaris* L.) local population from the national center for plant genetic resources: Polish genebank. *Hortic Res*. 22: 123-130.
- Dagnew K, Haileselassie T, Feyissa T (2014) Genetic diversity study of common bean (*Phaseolus vulgaris* L.) germplasm from Ethiopia using inter simple sequence repeat (ISSR) markers. *Afr J Biotechnol*. 13: 3638-3649.
- Gentry HS. (1969) Origin of the common bean *Phaseolus vulgaris*. *Econ Bot*. 23: 55-69
- Guzman Maldonado, SH, Marin-Jarillo A, Castellanos JZ, Gonzalez de Mejia E, Acosta JAG (1996) Relationship between physical and chemical characteristics and susceptibility to *Zabrotes subfasciatus* (Boh.) (Coleoptera:Bruchidae) and *Acanthoscelides obtectus* (Say) in common Bean (*Phaseolus vulgaris* L.) varieties. *J Stored Prod Res*. 32: 53-58.
- Guzzo EC, Vendramim JD, Chiorato AF, Lourencao AL, Carbonell SAM, Correa OMB (2015) No correlation of morpho-agronomic traits of *Phaseolus vulgaris* (Fabaceae) genotypes and resistance to *Acanthoscelides obtectus* (Say) and *Zabrotes subfasciatus* (Boheman) (Coleoptera: Chrysomelidae). *Neotrop Entomol*. 44: 619-625.
- Hair JF, Anderson RE, Tatham RL, Black WC (1995) *Multivariate data analysis* Macmillan publishing company, New York, USA.
- Janzen DH (1969) Seed eaters versus seed size, number, toxicity and dispersal. *Evolution*. 23: 1-27.
- Kananji GAD (2007). A study of bruchid resistance and its inheritance in Malawian dry bean germplasm. Dissertation, University of KwaZulu-Natal, Pietermaritzburg, South Africa.
- Kashiani P, Saleh G (2010) Estimation of genetic correlations on sweet corn inbred lines using sas mixed model. *Am J Agric Biol Sci*. 5: 309-314.
- Kasozi LC Genetic analysis and selection for weevil resistance in maize (2013) Dissertation, University of KwaZulu-Natal, Pietermaritzburg, South Africa.
- Keneni G (2012) Genetic potential and limitation of Ethiopian chickpea (*Cicer arietinum* L.) germplasm for improving attributes of symbiotic nitrogen fixation, phosphorus uptake and use efficiency, and adzuki bean beetle (*Callosobruchus chinensis*) resistance. Dissertation, Addis Ababa University, Ethiopia.
- Keneni G, Endashaw B, Getu E, Muhammad I, Dagne K, Asefa F (2011) Characterization of Ethiopian chickpea (*Cicer arietinum* L.) germplasm accessions for response to infestation by adzuki bean beetle (*Callosobruchus chinensis* L.) II. Phenotypic diversity. *Ethiop J Agric Sci*. 21:66-83.
- Kirkegaard J, Christen O, Krupinsky J, Layzell D (2008) Break crop benefits in temperate wheat production. *Field Crops Res*. 107:185–195.
- Miller PA, Williams JC, Robinson HF, Comstock RE (1958) Estimates of genotypic and environmental variances and covariances in Upland cotton and their implications in selection. *J Agron*. 50: 126-131.
- Mwila N (2013) Inheritance of bruchid (*Callosobruchus maculatus*) resistance in common beans (*Phaseolus vulgaris*). Thesis, University of Zambia, Zambia.
- Negasi F (1994) Studies on the economic importance and control of bean bruchids in haricot bean, *Phaseolus Vulgaris* L., in Eastern and Southern Shewa. Thesis, Alemaya University of Agriculture, Alemaya, Ethiopia.
- Parsons DMJ, Credland PF (2003) Determinants of oviposition in *Acanthoscelides obtectus*: a nonconformist bruchid. *Physiol Entomol*. 28: 221-231.
- SAS Institute Inc. (2011) *SAS/STAT Users guide 9.3* SAS Institute, Cary, NC.
- Schoonhoven AV, Cardona C (1982) Low level of resistance to the Mexican bean weevil in dry beans. *J Econ. Entomol*. 75: 567-569.
- Schoonhoven AV, Voysest O (Eds.) (1991) *Common Beans: Research for crop improvement*. CAB International, Wallingford, UK.
- Shukla S, Bhargava A, Chatterjee A, Srivastava A, Singh SP (2006) Genotypic variability in vegetable amaranth (*Amaranthus tricolor* L.) for foliage yield and its contributing traits over successive cuttings and years. *Euphytica*. 151: 103-110.
- Silva LB, Sales PM, Olivera EAA, Machado LTO, Fernandes VSK, Xavier-Filho J (2004) The seed coat of *Phaseolus*

- vulgaris* interferes with the development of cowpea weevil *Callosobruchus maculatus* (F.) (Coleoptera., Bruchidae). Annals of the Brazilian Academy of Sciences. 76: 57-65.
- Simmonds MSJ, Blaney WM, Birch ANE (1989) Legume seeds: the defenses of wild and cultivated species of *Phaseolus* against attack by bruchid beetles. Ann Bot. 63: 177-184.
- Singh RK, Chaudhary BD (1985). Biometrical methods in quantitative genetic analysis, Kalyani publishers, New Delhi, India
- Singh BD (2002) Plant breeding: principles and methods. Kalyani Publishers, New Delhi-Ludhiana.
- Sperling, L (2001) The effect of the civil war on Rwanda's bean seed systems and unusual bean diversity. Biodivers. Conserv. 10:989-1009.
- Tadesse A, Amare A, Emana G, Tadele T (2008). Review of research on post-harvest pests. In: T. Abraham, editor Proceedings of the 14th Annual Conference of the plant Protection Society of Ethiopia (PPSE). PPSE and EIAR, Addis Abeba, Ethiopia. p. 475-562.
- Telxeira IRV, Barchuk AR, Medeiros L, Zucoloto FS (2009) Females of the weevil *Zabrotes subfasciatus* manipulate the size and number of eggs according to the host seed availability. Physiol Entomol. 34: 246–250.
- Teshome A, Hailu S, Habte E, Deribe Y, Amsalu B (2020). Factors Affecting the profitability of smallholder common bean producers in central Rift Valley of Ethiopia. Ethiop J Agric Sci. 30(3): 99-118.
- Tibshirani, GW, Robert, Trevor H (2001) Estimating the number of clusters in a data set via the gap statistic. J R Stat Soc Series B. 63: 411–23.
- Tigist, SG, Melis R, Sibiya J, Amelework AB, Keneni G, Tegene A (2019). Population Structure and Genome-Wide Association Analysis of Bruchid Resistance in Ethiopian Common Bean Genotypes. Crop Sci. 12: 1–12.
- Tigist, SG, Melis R, Sibiya J, Keneni G (2018). Evaluation of different Ethiopian common bean, *Phaseolus vulgaris* (Fabaceae) genotypes for host resistance to the Mexican bean weevil, *Zabrotes subfasciatus* (Coleoptera: Bruchidae). Int J Trop Insect Sci. 38: 1–15.