

# Genetic Variability and Heritability in Ethiopian Grasspea (*Lathyrus sativus* L.) Accessions

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## Abstract

Comprehensive information on genetic variability and selection parameters is very crucial to design breeding strategies. However, very limited information is available in Ethiopian grasspea germplasm. Therefore, the present study was conducted to estimate genetic variability, broad sense heritability and genetic advance; and determine scope of selection for 18 quantitative traits using 426 Ethiopian grasspea accessions. The analysis of variance showed highly significant ( $P < 0.0001$ ) differences for most of the traits demonstrating the presence of high genetic diversity among the studied grasspea accessions. Higher differences between PCV and GCV estimates were observed for number of pods, effective pods and seed yield signifying the importance of environmental factors influence. High heritability coupled with high genetic advance was observed for many of agronomically important traits indicating that the high heritability is due to additive gene effects and therefore, selection can be effective for the improvement of grasspea for those traits. On the contrary, low heritability coupled with low genetic advance was recorded for number of seeds per pod indicating greater contribution of non-additive gene effects on the expression of this trait.

**Keywords:** Additive effect, Coefficient of variation, Genetic advance

## Introduction

Grasspea (*Lathyrus sativus* L.,  $2n = 2x = 14$ ) is a grain legume cultivated for food, feed and fodder in many countries. It has very important economic and ecological significance in developing countries like Ethiopia, India, Bangladesh, Pakistan and Nepal

(Campbell, 1997; Dixit *et al.*, 2016). In Ethiopia, grasspea is one of the principal legumes cultivated by smallholder farmers for its drought tolerance, resistance to diseases and pests; and for its ability to restore soil fertility (Dejene and Lijalem, 2012). The annual total area of cultivation and production of the country was reported to be 159,105.70 ha and

287,674.40 tons, respectively (CSA, 2016). The crop is becoming more important than previous times in agricultural systems; and thus, its area of cultivation is expected to increase in the future (Dejene and Lijalem, 2012). It is also highly adapted to adverse edaphic conditions (Polignano *et al.*, 2005; Vaz-Patto *et al.*, 2006). For these reasons, grasspea is considered as a promising crop for climate change adaptation, diversification of cropping systems and sustainable agriculture (Vaz-Patto *et al.*, 2006; Hillocks and Maruthi, 2012). Despite these advantages, grasspea is one of the most inadequately studied and exploited crops (Polignano *et al.*, 2005; Kumar *et al.*, 2011).

Genetic variability plays the fundamental role in any plant breeding program. Quantifying genetic diversity present in crop species is of greatest importance as it provides the basis of selection for traits of interest (Singh, 2002). Additionally, reliable estimates of genetic and environmental variations are helpful in estimating the heritability and predicted genetic gain from selection (Singh and Narayanan, 1997; Holland *et al.*, 2003; Visscher *et al.*, 2008). Overall, comprehensive knowledge on genetic variability, heritability and genetic advance allows geneticists and breeders to design breeding strategies for the improvement of crop productivity and quality (Johnson *et al.*, 1955).

Heritability and genetic advance are important selection parameters (Singh and Narayanan, 1997). Heritability

estimates can be grouped as broad sense heritability or narrow sense heritability (Holland *et al.*, 2003). Broad sense heritability provides information on the relative magnitude of genetic and environmental variation in specific population (Singh, 2002; Holland *et al.*, 2003; Visscher *et al.*, 2008). Genetic advance is the measure of genetic gain under selection and depends on genetic variability, heritability and selection intensity. Genetic advance also indicates the mode of gene action in the expression of traits and helps in choosing breeding methods (Singh and Narayanan, 1997). Thus, heritability estimates coupled with genetic advance are more reliable and helpful in predicting the gain under selection than individual consideration of the parameters (Johnson *et al.*, 1955).

In grasspea, genetic variability studies had been conducted by many researchers (Wuletaw and Endashaw, 2003; Turk *et al.*, 2007; Sedehi *et al.*, 2008; Talukdar and Biswas, 2008; Rahman *et al.*, 2010; Hobdari *et al.*, 2012; Parihar *et al.*, 2015) using quantitative traits and proved the presence of high genetic variation among studied genotypes. Heritability and genetic advance had also been estimated for yield and related traits by several authors (Wuletaw and Endashaw, 2003; Turk *et al.*, 2007; Parihar *et al.*, 2015). However, very limited research has been done on variability, heritability and genetic advance in Ethiopian grasspea accessions. In addition, previous study considered only small number (50) of

accessions compared to the total accessions conserved in Ethiopian Biodiversity institute. Moreover, the accessions were evaluated for small number (9) of quantitative traits. As a result, very limited information is available on these parameters in Ethiopian grasspea accessions. Therefore, the present study was conducted to estimate genetic variability, heritability and genetic advance of yield and related traits and to determine scope of selection in Ethiopian grasspea accessions.

## **Materials and Methods**

### **Experimental Site, Materials and Design**

The experiment was conducted at Debre Zeit Agricultural Research Center (DZARC) in Central Ethiopia during 2013/14 main cropping season. The mean annual rainfall of the center during the cropping season was 850 mm. The minimum and maximum temperatures were 8°C and 26.1°C, respectively, with a mean annual temperature of 19.32°C. The soil of the testing site is characterized by dark

clay vertisols with pH of 7.45 (Niguse, 2014). The study was carried out using 426 grasspea accessions obtained from Ethiopian Biodiversity Institute, originated from different regions of Ethiopia (392), Eritrea (24) and Australia (10) (Figure 1). All the available accessions were included in the study purposively to generate comprehensive information. The experiment was laid down using randomized complete block design with two replications. The blocks were folded into six sub blocks to reduce variations within the block and each sub block was planted with 71 accessions. Accessions were assigned randomly to the rows within the blocks. Each accession was grown on a 3 m long single row with spacing of 30 cm between rows and 10 cm between plants within a row. Therefore, the area of each block was 21.3 m (71 accessions x 30 cm of space between rows) length by 20.5 m (6 blocks x 3 m long row + 2.5 m of total space between sub blocks) width. The distance between the two blocks was 1m.

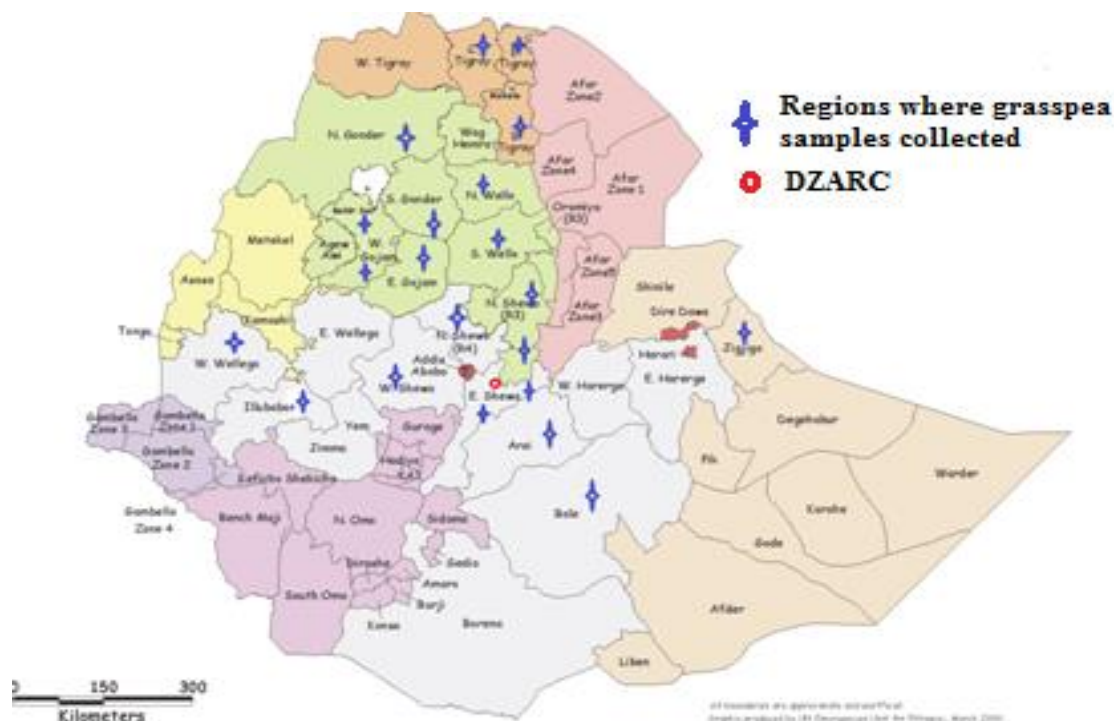


Fig. 1. Map of Ethiopia indicating different regions where 392 grasspea accessions collected for *ex situ* conservation and DZARC-the test site

## Data Collection

Data collection was started from seed emergence and date of planting was used as a basis for all data recording purposes. Data were collected both on plant and plot bases from a total of 23 quantitative traits using descriptors for *Lathyrus* species (IPGRI, 2000). On plant basis, data were collected for plant height (cm), number of primary branches, length of primary branch (cm), leaflet length (cm), leaflet width (cm), leaf petiole length (cm), number of pods per plant, number of effective pods, pod length (cm), pod width (cm), number of seeds per pod and seed yield per plant (g) from six randomly selected and tagged plants of each accession. On plot basis, data were recorded on date of emergence,

days to 50% flowering, days to maturity, 100-seed weight (g), biomass (g), grain yield per plot (g) and harvest index (%).

## Data Analyses

### Genotypic and phenotypic variability

Mean, range, standard error of the mean and coefficient of variation were computed for all recorded traits. All quantitative data were subjected to the analysis of variance (ANOVA) as suggested by Gomez and Gomez (1984) using SAS Software (SAS Institute, 2004) to evaluate the extent of genetic variability among accessions. The means were compared using Duncan's Multiple Range (DMRT) at  $\alpha = 0.05$  probability.

Genotypic and phenotypic variances and the respective coefficients of variation were estimated following the procedure given by Burton and De

Vane (1953) for traits showing significant variation among accessions. Thus,

Genotypic variance ( $\sigma_g^2$ ) = (MSg-MSe)/r, and

Phenotypic variance ( $\sigma_p^2$ ) =  $\sigma_g^2 + \sigma_e^2$

Where, MSg = mean square for genotypes

MSe ( $\sigma_e^2$ ) = mean square for error (environmental variance); and

r = number of replications.

Genotypic Coefficient of Variation (GCV) =  $[\sqrt{(\sigma_g^2) / (\bar{X})}] \times 100$

Phenotypic Coefficient of Variation (PCV) =  $[\sqrt{(\sigma_p^2) / (\bar{X})}] \times 100$

Where,  $\bar{X}$  is grand mean

### Heritability

Heritability ( $H^2$ ) in broad sense of traits was estimated as the ratio of the genotypic variance ( $\sigma_g^2$ ) to the phenotypic variance ( $\sigma_p^2$ ) (Burton and DeVane, 1953):  $H^2 = [\sigma_g^2 / \sigma_p^2] \times 100$  where;  $\sigma_g^2 = (MSg - MSe) / r$ ;  $\sigma_p^2 = \sigma_g^2 + MSe$ ; MSg, MSe and r = mean squares for genotypes, mean square for error and the number of replications, respectively.

### Genetic advance

Genetic advance (GA) of traits was computed using the formula suggested by Johnson et al. (1955) as follows:

GA = (k) ( $\sigma_p$ ) \* ( $H^2$ ); and GA (as % of the mean) =  $[GA / (\bar{X})] \times 100$

Where, k = selection differential (k = 2.06 at 5% selection intensity)

$\sigma_p$  = phenotypic standard deviation

$H^2$  = heritability (broad sense); and

$\bar{X}$  = Grand mean.

## Results and Discussion

### Analysis of Variance

The mean squares from the analysis of variance revealed highly significant ( $P \leq 0.0001$ ) differences among grasspea accessions for the traits like plant height, number of primary -branches, number of pod per plant, number of seeds per pod, days to flowering, days

to maturity, 100 seeds weight, seed yield per plant, biomass, and harvest index (Table 1). These results indicated the presence of genetic diversity among grasspea accessions and the possibility of improving these traits through strong selection. The existence of high variability for different traits among grasspea accessions had been reported by

previous authors (Wuletaw and Endashaw, 2002; 2003; Turk *et al.*, 2007; Talukdar and Biswas, 2008; Grela *et al.*, 2010; Parihar *et al.*, 2015). Most of these authors reported the presence of highly significant differences for plant height, number of primary branches, number of pod per plant, number of seeds per pod, days to flowering, days to maturity, 100 seeds weight, seed yield per plant, biomass, and harvest index. Furthermore, in other studies of similar nature, it was found that there was highly significant differences for plant height, number of primary branches, number of pod per plant, number of seeds per pod, days to flowering, days to maturity, 100 seeds weight, and seed yield per plant in filed pea, cowpea, soybean, faba bean and

chickpea genotypes, respectively (Singh *et al.*, 2011; Kumar *et al.*, 2013; Diriba *et al.*, 2014; Ammar *et al.*, 2015; Getachew *et al.*, 2015). Therefore, these findings showed the importance of these agronomic traits for diversity studies and crop improvement in legumes. However, on contrary to the present result, non-significant difference for plant height among 50 Ethiopian grasspea accessions were also reported (Wuletaw and Endashaw, 2003). This difference may be due to differences in accessions and environmental conditions of the research sites used by the researchers. In the present study, many more accessions were included than accessions used by the previous investigators.

**Table 1.** Mean squares and *simple statistics* for 18 quantitative traits of 426 grasspea accessions

Traits	MSg (425)	MSe (425)	Mean	Range	S.E	CV (%)
PH	184.39***	39.17	68.72	42.32 - 100.23	0.36	9.11
NPB	1.19***	0.38	4.26	2.00 - 7.17	0.03	14.50
LPB	171.01***	42.15	66.99	41.00 - 95.33	0.35	9.69
LL	0.27 <sup>ns</sup>	0.26	4.24	2.92 - 12.23	0.02	11.91
LW	0.015***	0.004	0.58	0.23 - 1.13	0.00	11.05
PtL	0.122 <sup>ns</sup>	0.11	2.08	1.02 - 5.40	0.01	15.84
ONPP	1406.57***	293.8	102.94	43.00 - 262.00	1.00	16.65
EPP	1084.82***	230.11	94.45	39.00 - 232.00	0.88	16.06
PL	0.055 <sup>ns</sup>	0.06	2.78	2.20 - 6.38	0.01	8.40
PW	0.0045 <sup>ns</sup>	0.004	0.87	0.60 - 1.33	0.00	7.53
NSP	0.13***	0.074	3.59	2.50 - 4.50	0.01	7.57
DF	55.02***	2.8	46.02	36.00 - 64.00	0.18	3.64
DM	127.53***	9.74	106.65	86.00 - 129.00	0.28	2.93
SW	0.82***	0.32	8.40	5.50 - 12.00	0.03	6.72
SYP	23.59***	6.72	14.30	3.45 - 30.79	0.13	18.12
GYP	0.8***	0.28	2.76	1.16 - 4.6	0.37	18.34
BY	4.91***	0.78	5.96	2.07 - 11.67	0.62	14.80
HI	0.0007***	0.002	0.47	0.32 - 0.81	0.03	9.72

Note: PH = plant height (cm), NPB = Number of primary branches per plant, LPB = Length of primary branch (cm), LL = Leaflet length (cm), LW = Leaflet width (cm), PtL = Petiole length (cm), NPP = Number of pod per plant, EPP = Effective pods per plant, PL = Pod length (cm), PW = Pod width (cm), NSP = Number of seeds per pod, DF = Days to flowering, DM = Days to maturity, SW = 100 seed weight (g), SYP = Seed yield per plant (g), GYP = Grain yield per hectare (t/ha), BY = Biomass (t/ha), and HI = Harvest index; ns, and \*\*\* indicate insignificance and very highly significance at 5% and 1%, respectively).

### Simple Measure of Variability

The mean values, ranges and coefficients of variation for 18 quantitative traits showed considerable variation among grasspea accessions (Table 1). The wide ranges especially for plant height, days to 50 % flowering, number of pods per plant, days to maturity, seed yield per plant, biomass and grain yield per hectare indicated the diversity among the grasspea accessions and suggest the possibility of improving these traits through selection, and hybridization. The existence of variability among grasspea accessions for these parameters had been reported previously by several authors (Wuletaw and Endashaw, 2002; 2003; Rahman *et al.*, 2010; Dikshit *et al.*, 2014; Ahmadi *et al.*, 2015; Parihar *et*

*al.*, 2015) . However, the results reported elsewhere revealed low mean performance with comparable ranges and coefficient of variation compared to the present results for most of traits considered (Rahman *et al.*, 2010; Ahmadi *et al.*, 2015). Similarly, lower mean values with comparable ranges but very high coefficient of variation were reported for many of the traits evaluated (Parihar *et al.*, 2015). These differences in mean performance might come from differences in genetic factors or environment conditions under which genotypes were evaluated.

**Table 2.** Estimates of coefficients of variation, heritability and genetic advance for 14 agronomic traits in 426 grasspea accessions

Traits	$\sigma^2_e$	$\sigma^2_g$	$\sigma^2_P$	GCV (%)	PCV (%)	H <sup>2</sup> (%)	GA (5%)	GAM (5%)
PH	39.17	72.61	111.78	12.40	15.39	64.96	14.15	20.59
NPB	0.38	0.41	0.79	14.94	20.80	51.59	0.94	22.10
LPB	42.15	64.43	106.58	11.98	15.41	60.45	12.86	19.19
LW	0.004	0.01	0.014	12.79	16.80	57.89	0.12	20.04
NPP	293.80	556.39	850.19	22.91	28.33	65.44	39.31	38.19
EPP	230.11	427.36	657.47	21.89	27.15	65.00	34.33	36.35
NSP	0.07	0.03	0.10	4.66	8.90	27.45	0.18	5.03
DF	2.80	26.11	28.91	11.10	11.68	90.31	10.00	21.74
DM	9.74	58.90	68.64	7.20	7.77	85.81	14.64	13.73
SW	0.32	0.25	0.57	5.95	8.99	43.86	0.68	8.12
SYP	6.72	8.44	15.16	20.31	27.22	55.66	4.46	31.21
GYP	0.28	0.26	0.54	18.47	26.62	48.15	0.73	26.41
BY	0.78	2.07	2.85	24.11	28.30	72.58	2.52	42.32
HI	0.002	0.003	0.005	10.64	14.27	55.56	0.08	16.33

Key: PH = plant height, NPB = Number of primary branches per plant, LPB = Length of primary branch, LW = Leaflet width, NPP = Number of pod per plant, EPP = Effective pods per plant, NSP = Number of seeds per pod, DF = days to flowering, DM = days to maturity, SW = 100 seed weight, SYP = seed yield per plant, GYP = Grain yield per plot, BY = Biomass, HI = Harvest index).

In the present study, the mean performance of grain yield per hectare varied from 1.16 to 4.6 t with the mean value of 2.76 t ha<sup>-1</sup> and coefficient of variation of 18.34%. The highest grain yield per hectare (4.6 t) was recorded from A60 followed by A385 (4.38 t) and A105 (4.33 t); while the lowest yield per hectare was obtained from A96 (1.16 t). Biomass per hectare also varied from 2.07 t to 11.67 t with the mean value of 5.96 t and coefficient of variation of 14.8%. The highest biomass per hectare (11.67 t) was recorded from A385 followed by 126 (10.72 t) and A60 (10.39 t); while the lowest biomass per hectare was obtained from A71 (2.07 t). Days to maturity ranged from 86.00 to 129.00 days with the mean value of 106.65 days and coefficient of variation of 2.93%, showing a wide range of variation among accessions. The earliest accession was A90, which took 87.00 days to mature, followed by A76 and A71 with 89.00 and 89.50 days to mature, respectively. The late maturing accession was A323, which took 126.00 days to mature. However, unlike to the present results, higher mean values and high coefficient of variation were reported by previous studies (Wuletaw and Endashaw, 2002; Wuletaw and Endashaw, 2003) for many of the traits considered in Ethiopian grasspea accessions. These differences in mean performance and coefficient of variation might be due to differences in environmental conditions of the two research sites. Grela *et al.* (2010) also reported that grain yield, plant height, biomass and number of pods per plant are highly

affected by rainfall amount and other environmental factors.

## **Estimates of variances and genetic parameters**

### **Estimates of variances**

Estimates of genotypic ( $\sigma^2_g$ ), phenotypic ( $\sigma^2_p$ ) and environmental ( $\sigma^2_e$ ) variances were estimated for the studied traits (Table 2). Phenotypic variance was relatively high for the traits like number of primary branches, number of seeds per pod, 100-seed weight, seed yield per plant and harvest index. This indicated that the phenotypic expression of these traits was greatly influenced by environmental factors; and selection on phenotypic bases of these traits may not be effective for genetic improvement unless the environmental conditions are optimized. Similarly, in another studies, relatively higher phenotypic variance for number of plant height, primary branches, number of pods per plant and seed yield per plant were reported (Wuletaw and Endashaw, 2003). On the contrary, degree of difference between phenotypic variance and genotypic variance was relatively low for leaflet width, days to 50% flowering, days to maturity and biomass. This shows that the phenotypic expression of these traits was relatively less affected by environmental factors; and selection on phenotypic bases of these traits will be effective. Wuletaw and Endashaw (2003) also indicated lower degree of difference between phenotypic and genotypic variances



for days to 50% flowering and biomass. However, the same authors reported relatively high and low degree of differences between phenotypic and genotypic variances for days to maturity and harvest index, respectively. This variation of phenotypic expression of the two traits between studies might be mainly due to differences in environmental conditions of the two research sites.

### **Coefficients of variation**

Genetic (GCV) and phenotypic (PCV) coefficients of variability values for 14 traits varied from 4.66% for number of seeds per pod to 25.2% for biomass per hectare and 7.77% for days to maturity to 29.11% for biomass per hectare, respectively (Table 2). Estimates of GCV and PCV had been reported for the same traits of grass pea by previous investigators (Kumar and Dubey, 2001; Wuletaw and Endashaw, 2002; Wuletaw and Endashaw, 2003; Ahmadi *et al.*, 2015; Parihar *et al.*, 2015). It has been reported that GCV and PCV values, > 20%, 10-20% and < 10% are regarded as high, moderate and low, respectively (Deshmukh *et al.*, 1986).

High GCV value was obtained for traits like number of pods per plant, effective pods per plant, seed yield per plant, grain yield per hectare and biomass (Table 2). This indicated the existence of considerable genotypic variability among grasspea accessions for these traits and greater influence of genetic factors for the expression of

these traits. High GCV estimates for number of pods and seed yield per plant were reported by several authors (Kumar and Dubey, 2001; Talukdar and Biswas, 2008; Parihar *et al.*, 2015). Similarly, Wuletaw and Endashaw (2003) reported high GCV for number of pods per plant and biomass. In the present study, moderate GCV estimate was revealed for traits like plant height, length of primary branches, number of primary branches, leaflet width, days to 50% flowering and harvest index; and low GCV estimate was observed for days to maturity, number of seeds per pod and 100-seed weight. These results indicated greater influence of environmental factors for the expression of these traits compared to traits revealed high GCV estimates.

In line with the present results, moderate GCV was reported by Kumar and Dubey (2001) for number of branches per plant; by Wuletaw and Endashaw (2003) for days to 50% flowering; and by Ahmadi *et al.* (2015) and Parihar *et al.* (2015) for harvest index. Similarly, low GCV estimates were reported by Wuletaw and Endashaw (2003) and Ahmadi *et al.* (2015) for days to maturity and 100-seed weight; and Parihar *et al.* (2015) for days to maturity and number of seeds per pod. However, on the contrary, low GCV estimate was reported by Wuletaw and Endashaw (2003) for number of primary branches; and by Ahmadi *et al.* (2015) for biomass. These differences might be due to differences between sets of accessions used for the studies or

environmental conditions of research sites where accessions were grown for characterization.

High PCV was revealed for traits like number of primary branches, number of pods per plant, effective pods per plant, seed yield per plant, grain yield per hectare and biomass (Table 2). These results reflected the presence of considerable phenotypic variation among grasspea accessions for these traits. The high PCV estimates for number of pods and seed yield per plant and biomass per hectare were in harmony with the previous reports by several authors (Kumar and Dubey, 2001; Wuletaw and Endashaw, 2003; Talukdar and Biswas, 2008). Similarly, Parihar *et al.* (2015) reported high PCV estimates for number of pods per plant, seed yield per plant, biomass and grain yield per hectare.

In the present study, moderate PCV values were exhibited for traits like plant height, length of primary branches, leaflet width, days to 50 % flowering and harvest index. On the contrary, low PCV was observed for days to maturity, number of seeds per pod and 100-seed weight, indicating existence of lesser phenotypic variability among grasspea accessions that might be due to greater influence of environmental factors for the expression of the traits. Similar results were reported by Wuletaw and Endashaw (2003) for days to 50% flowering and harvest index. Ahmadi *et al.* (2015) also reported moderate PCV estimate for harvest index. In

agreement with the present result, low PCV estimate was reported by Wuletaw and Endashaw (2003), Ahmadi *et al.* (2015) and Parihar *et al.* (2015) for days to maturity. However, in contrast to the present study, low PCV estimate was reported by Wuletaw and Endashaw (2003) for traits like number of primary branches and plant height; and by Ahmadi *et al.* (2015) for plant height. These differences might be due to differences in genetic bases of the studied materials for these traits or higher influence of environmental factors for their expression.

Higher differences between PCV and GCV estimates were observed for number of pods, effective pods and seed yield per plant, and grain yield per hectare (Table 2) indicating the complexity of these traits and the importance of environmental factors in influencing the expression of these traits. High differences between PCV and GCV were also reported in grasspea by previous authors (Wuletaw and Endashaw, 2003; Parihar *et al.*, 2015) for number of pods and seed yield per plant and biomass per hectare. Similar results were reported by Talukdar and Biswas (2008) for number of pods per plant and seed yield per plant. However, difference between PCV and GCV estimates was relatively very slight in the case of days to maturity and days to 50% flowering, signifying minimal influence of environment and a reasonable effect of genotypic factors on the expression of these traits. Similar results were reported

previously in grasspea by several authors (Wuletaw and Endashaw, 2003; Ahmadi *et al.*, 2015; Parihar *et al.*, 2015) for days to maturity and days to 50% flowering. In general, coefficients of genotypic and phenotypic variation suggest that there is good scope for improvement through selection for number of pods per plant, effective pods per plant, seed yield per plant, grain yield per hectare and biomass per hectare. Similar results were reported for traits like number of pods per plant, seed yield per plant and biomass per hectare in grasspea accessions (Wuletaw and Endashaw, 2003; Parihar *et al.*, 2015).

### **Broad sense heritability**

Heritability estimates for traits under study varied from 27.45% for number of seeds per pod to 90.3% for days to 50% flowering (Table 2). According to Johnson *et al.* (1955), these heritability estimates can be classified as low (< 30%), moderate (30-60%) and high (> 60%) levels. Hence, high heritability estimate was recorded for days to 50% flowering, days to maturity, followed by biomass per hectare, number of pods per plant, effective pods per plant, plant height and length of primary branches. These results indicated that expression of these traits was least influenced by the environmental factors, signifying a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotypic expression. However, selection may not be useful for these traits, because broad sense heritability is based on total genetic variance which includes both fixable

(additive) and non-fixable (dominance and epistatic) variances (Singh and Narayanan, 1997). Similarly, Wuletaw and Endashaw (2003) reported high heritability estimates for days to 50% flowering, number of pods per plant and biomass per hectare. High heritability had been also reported in grasspea for days to 50% flowering, days to maturity and plant height (Ahmadi *et al.* (2015; Parihar *et al.*, 2015).

Likewise, Kumar and Dubey (2001) revealed high heritability estimates for plant height in grasspea. Furthermore, similar to the present findings, high heritability estimates were reported (Kumar *et al.*, 2013; Diriba *et al.*, 2014; Getachew *et al.*, 2015) for days to 50% flowering and days to maturity in field pea, cowpea, mung bean and chickpea, respectively. However, on the contrary to the present result, low heritability was reported for plant height and biomass per hectare by Wuletaw and Endashaw (2003) and Parihar *et al.* (2015), respectively.

Traits like seed yield per plant, number of primary branches, harvest index, grain yield per hectare, leaflet width and 100 seeds weight revealed moderate level of heritability. For such traits, phenotypic expression is influenced by environmental factors and the non-additive gene effects; and hence, genetic improvement through selection is difficult due to masking effects of the environment on the genotypic effects (Johnson *et al.*, 1955). Further, the lowest heritability estimate was recorded for number of seeds per pod (27.45%); this indicated that a small proportion of the

phenotypic variation is caused by variation in genotypes, signifying that the phenotypic expression of this trait was highly influenced by environmental factors with less contribution of genetic factors. In agreement with the present results, Wuletaw and Endashaw (2003) and Parihar *et al.* (2015) reported moderate level of heritability for number of primary branches, 100 seeds weight, seed yield per plant and grain yield per hectare.

### **Genetic advance**

In present study, genetic advance as a percent mean (GAM) ranged from 5.03% for number of seeds per pod to 45.24% for biological yield per hectare (Table 2). These results indicated that selecting the top 5% of the accessions could result in an advance of 5.03% to 45.24% over the respective population mean. As suggested by Johnson *et al.* (1955), estimates of genetic advance can be classified as low (< 10%), moderate (10-20%) and high (> 20%).

High GAM was recorded for traits like biomass per hectare, number of pods per plant, effective pods per plant, seed yield per plant, grain yield per hectare, number of primary branches, days to 50% flowering, plant height and leaflet width. These results indicated that the expression of these traits is mainly governed by additive gene effects; and therefore, improvement of such traits can be achieved through selection. In harmony to the present findings, Wuletaw and Endashaw (2003) reported high GAM for days to 50%

flowering, number of pods per plant and biomass per hectare. Similarly, Parihar *et al.* (2015) reported high GAM for plant height, number of primary branches and pods per plant and seed yield per plant.

On the contrary, length of primary branches, harvest index and days to maturity revealed moderate level of GAM. In addition, low genetic advance was recorded for traits like number of seeds per pod and 100 seeds weight. This indicated that expression of these traits is governed by non-additive gene effects; and hence, heterosis breeding may be useful for the improvement of these traits than selection. Similarly, Parihar *et al.* (2015) reported low GAM for number of seeds per pod in grasspea accessions. However, in contrast to the present results, Wuletaw and Endashaw (2003) reported moderate level of GAM for 100 seeds weight and seed yield per plant; and low level of GAM for days to maturity, number of primary branches and plant height. Additionally, Parihar *et al.* (2015) reported moderate level of GAM for days to maturity and biomass per hectare. These differences might be due to difference in magnitude of the different gene effects or the influence of environmental factors.

### **Scope of selection**

In the present study, high heritability coupled with high GAM was observed for plant height, number of pods per plant, effective pods per plant, days to 50% flowering and biomass per hectare (Table 3), indicating greater

contribution of additive gene action for the expression of these traits; and therefore, improvement can be achieved through selection in these traits. Similarly, Wuletaw and Endashaw (2003) reported high heritability coupled with high GAM for days to 50% flowering, number of pods per plant and biomass per hectare. In addition, high heritability coupled with high GAM had been reported in grasspea accessions by Ahmadi *et al.* (2015) for biomass per hectare. However, it is not necessary for a trait showing high heritability to exhibit high GAM or the vice-versa (Johnson *et al.*, 1955). In the present study, moderate heritability and high GAM estimates were revealed for length of primary branches, number of primary branches, leaflet width, seed yield per plant and grain yield per hectare, indicating that these traits are governed by additive gene effects, however the exhibited low heritability might be due to high environmental influences. Therefore, selection for these traits may be effective in early generations of grasspea accessions with larger possibility of delay for further generations.

On the contrary, high heritability coupled with moderate level GAM was recorded for days to maturity. In addition, moderate heritability coupled with moderate genetic advance was recorded for harvest index. These results indicated the existence of intermediate expression in these traits for both additive and dominance gene effect. Similar results were reported for days to maturity (Ahmadi *et al.*,

2015; Parihar *et al.*, 2015). Furthermore, moderate heritability coupled with low GAM was recorded for 100 seeds weight, suggesting that the expression of seed weight is governed by non-additive gene action. However, the exhibited moderate heritability might be mostly due to favorable influence of the environment rather than the genetic factors. Additionally, low heritability and low GAM were recorded for number of seeds per pod indicating that the expression of this trait is governed by non-additive gene effects; and influenced negatively by environmental effects. In general, these results indicate the predominance of non-additive gene action in the inheritance of seeds per pod and seed weight, suggesting that selection may not be effective for the improvement of these traits, and rather heterosis breeding may be useful. Similar suggestion was given for the traits exhibiting non-additive gene action (Singh and Narayanan, 1997).

## Conclusions

In conclusion, the analysis of variance showed the presence of high genetic diversity among the studied grasspea accessions. Traits like pods per plant, seed yield per plant and grain yields per hectare were highly influenced by the environment factors compared to other traits. The role of additive gene action was high for the expression of plant height, pods per plant, days to 50% flowering and biomass yield; and therefore, selection can do

improvement on these traits. High heritability coupled with high GAM was observed for plant height, number of pods per plant, effective pods per plant, days to 50% flowering and biomass per hectare showing that the high heritability is most likely due to additive gene effects; and the importance of selection for the improvement of grasspea for these traits. On the contrary, the role of additive gene effects was low for seeds per pod indicating limited scope of selection for improvement for this trait; rather heterosis breeding may be useful.

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