ASSESSMENT OF GENETIC VARIABILITY AND HERITABILITY OF AGRONOMIC TRAITS IN ETHIOPIAN CHICKPEA (*CICER ARIETINUM* L) LANDRACES

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Abstract

Ethiopia has a large number of Desi type chickpea landraces. In the country, limited information is available on the performance of the landraces regarding of important agronomic traits. Thus, 202 chickpea landraces and two released varieties, Fetenech (early maturing) and Minjar (high yielding), were tested to evaluate the genetic variation and heritability for the selected agronomic traits. The experiment was conducted at Sirinka under rain fed condition in 2016 growing season using alpha lattice design with three replications. The data were collected, on days to 50 % flowering, days to 75 % maturity, plant height, number of pods per plant, number of seeds per pod, grain yield hectare and 100 seed weight, and analyzed by using SAS software. Analysis of variance showed highly significant difference (P<0.001) among the tested genotypes for all traits considered in the study, indicating the presence of genetic variability. Grain yield varied between 563 and 2794 kg/ ha. Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged between 4.2 – 28.64% and 3.91 – 27%, respectively. The lowest PCV and GCV (4.2 and 3.91%) were obtained for days to maturity, while the highest PCV and GCV values (28.64 and 27%) were obtained for grain yield, respectively. High heritability and genetic advance as the percent of the mean were observed for grain yield, number of pods per plant and biomass yield. This indicates that these traits are governed by additive gene action, implying the possibility for genetic gain through selection. The findings of this study show that traits such as grain yield, number of pods per plant, biomass yield and hundred seed weight, which had high heritability coupled with relatively high values of GCV, and genetic advance as percentage of mean, are the most important traits, which could be improved by selection.

Keywords: Desi type, Chickpea, Landraces, Variability, Heritability

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1. Introduction

Chickpea (*Cicer arietinum* L.) is self-pollinated diploid (2n=2×=16) annual leguminous plant in the family Fabacea, with a genome size of 738.09 Mbp (Varshney et al., 2013). Chickpea is the third most important pulse crop in the world, after faba bean and field pea (Tesfamichael et al., 2015). India is the largest chickpea producing country accounting for 72% of the global production. The other major chickpea producing countries are Pakistan 5%, Iran 2%, Australia 6%, Turkey 4%, Myanmar 4%, Ethiopia 3.5%, Tanzania 1%, Mexico 2% and Malawi 0.5% (Ojiewo, 2016).

Chickpea has an importance due to its good nutritional value as it contain an average of 22% protein, 63% carbohydrate, 8% crude fiber 4.5% fat and 2.7% ash (Shafique et al., 2016). Besides being an important source of human food and animal feed, it is also an important contributor to soil fertility as it provides nitrogen to soil through fixation of atmospheric nitrogen (Gul et al., 2011).

Ethiopia is the largest producer, consumer and exporter of chickpea in Africa and shares 4.5% of global chickpea market and more than 60% of Africa's global chickpea market (Tebkew and Ojiewo, 2016). However, seed yield is quite low and a wide gap exist between the potential (5 ton ha-1) and actual (1.93 ton ha-1) yields (FAOSTAT, 2008). The low yields have been attributed to several factors among which include low genetic diversity of cultivated chickpea and several biotic and abiotic stresses (Gaur et al., 2012). Evaluation and assessment of genetic resources is a pre-requisite for which the future breeding work is based. The value of germplasm relies not only on the number of accessions it possesses, but also upon the genetic variability present in those accessions for agronomic and yield components (Reddy et al., 2012). Heritability act as predictive tool in expressing the reliability of phenotypic traits and thus high heritability could assist in effective selection of particular characters and devise future breeding programme of chickpea. In Ethiopia, limited information is available on the performance desi type chickpea landraces for the important agronomic traits and breeders lack baseline information needed to effectively improve chickpea productivity in the country. The objective of this study was to evaluate and assess the genetic variability and heritability of selected agronomic traits of the Ethiopian chickpea landraces.

2. Material and Method

2.1. Description of experimental site

After The experiment was executed under rain fed condition at Sirinka Agricultural Research Center, Habru district of North Wollo Zone, which is located at 110 08'N latitude and 390 28' E longitude and at an altitude of 1850masl. The annual rainfall of the site is 1006.3 mm with 13.6 °C minimum and 26.7 °C maximum temperature. According to Sirinka Agricultural Research Center soil classification, the soils of the site are classified as Vertisols.

2.2. Experimental materials and design

Two hundred two new Desi type chickpea landrace collections from Amhara, Oromiya and SNNP Regional States were used for this study. The landraces were collected from elevations ranging from 1174 to 2660masl. The desi chickpea landraces were collected in the years of 2013 (42) and in 2016 (160). Two standard checks Fetenech, early type, and Minjar high yielded varieties were included in the study. The experiment was planted on 02 September 2016 by using alpha lattice design with three replications at Sirinka and Jari under rain fed conditions. Each landrace was sown in two rows at 60 cm, 30 cm, and 10 cm spacing between plots, rows, and plants, respectively; with 1 m row length. All agronomic practices were done uniformly for all accessions as required. There was no fertilizer application. For controlling pod borer, we applied recommended insecticide Karate at the rate of 200ml/300 liter/ha during seedling stage and the mature larvae are picked up by hand at flowering stage of the crop.

2.3. Data collection

Data were recorded based on the descriptors for chickpea (IBPGR, ICRISAT and ICARDA, 1993). The data were taken on plot and plant basis. The data on plant basis were recorded from five pre tagged plants, which were randomly taken. Numbers of pods per plant, number of seeds per pod, plant height, number of primary branches and number of secondary branches were recorded from each plot on plant basis whereas data of days to 50% flowering, days to 75% maturity, biomass in gram per plot , hundred seed weight and seed yield in gram per plot were determined on plot basis.

2.4. Data analysis

Analysis of variance (ANOVA) was performed by using SAS computer software (SAS, 2004) as per the following

linear model for alpha lattice design.

$Y_{ijk}=\mu+R_i+B_{ij}+T_k+e_{ijk}$ Where, μ=the grand mean of trait Y; R_i= the effect of Replicate i; B_{ij}= effect of Block j within Replicate I; T_k=Effect of treatment k.

The variance components (phenotypic, genotypic, and error variances) and the phenotypic and genotypic coefficients of variation were estimated as per the expected mean squares of the alpha lattice ANOVA model as follows:

Genotypic variance (σ^2_g) = $(MSg - MSe)/r$;

Error variance (σ^2_e) = MSe

Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

where r = number of replications; MSg = mean square of genotype, and MSe = mean square of error.

Phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV) were estimated using the respective variance components according to Burton (1951) as follows:

$$PCV = \frac{\sqrt{\sigma^2 p}}{\overline{X}} x100 \quad GCV = \frac{\sqrt{\sigma^2 g}}{\overline{X}} x100$$, where $\overline{X}$ = mean value of the trait.

Broad sense heritability (H²) values were estimated based on the formula of Falconer and Mackay (1996) as follows:

$$H^2 = \frac{\sigma^2_g}{\sigma^2_p}x100;$$ σ^2_g = genotypic variance; σ^2_p = phenotypic variance.

Expected Genetic Advance (GA) was estimated using the formula suggested by Johnson et al., (1955).

$GA = k\sigma_p h^2$; Where, σ_p = the phenotypic standard deviation of the character; k = the standardized selection differential at 5% selection intensity (2.063), and h^2= broad sense heritability. In addition, the expected genetic advance as percent of the mean (GAM) was computed as suggested by Johnson et al. (1955) using the following formula.

$$GAM = \frac{GA}{\overline{X}}x100,$$ where $\overline{X}$ = grand mean for the character.

3. Results and Discussion

3.1. Phenotypic variability assessment

Analysis of variance revealed highly significant differences (P<0.001) among genotypes for all of the studied traits (Table 2), indicating genetic variability in the characters studied. Similarly, previous studies on chickpea landraces indicated significant variations for traits like plant height, days to flowering, days to maturity, number of pods per plant, hundred seed weight and grain yield (Tesfamickael et al., 2014; Uday et al., 2012).

Table 1. Mean squares for different sources of variation and the corresponding coefficient of variation (CV) for the 10 traits studied at Sirinka under rain fed condition

| Traits | Source of variation | | | | |
	Genotypes (df = 203)	Replication (df = 2)	Bloc (REP) (df = 33)	Error (df = 373)	CV %
DF	24.25**	25.83**	4.24**	1.95	6.56
DM	42.32**	22.08**	5.39**	2.3	4.28
PH	31.12**	86.37**	8.61**	4.06	9.85
PB	0.72**	0.05ns	0.11ns	0.08	19.65
SB	11.11**	0.92ns	1.88*	1.21	17.16
NPP	520.46**	167.32*	50.90*	34.04	21.02
NSP	0.08**	0.02ns	0.029*	0.02	12.06
HSW	8.34**	5.27**	0.43ns	0.39	13.23
GY	441140.22**	93086.47*	23558.56ns	18940	28.66
BM	1936174.5**	734469.2*	123242.6ns	106305.2	25.97

DF = Days to flowering, DM = Days to maturity, PH = Plant height (cm), PB = Primary branches, SB = Secondary branches, NPP = Number of pods per plant, NSP = Number of seeds per pod, HSW = Hundred seed weight, GY = Grain yield kg/ha, BM = Biomass kg/ha, ns = non – significant and *, ** significant at 5% and 1% probability level, respectively.

The magnitude of mean squares due to genotypes was high for grain yield, biomass yield, and number of pods per plant; while low genotype mean square values exhibited for number of seed per pod, primary branches per plant and hundred seed weight (Table 2). This low magnitude of mean squares indicated that these traits were relatively sensitive to environmental effects and

reflected non-significant variability. The results reported by Zerihun (2011) and Melese (2005) also agree with the present finding.

3.2. Range and means

The range for biomass spans 1624.93 – 5852.05 kg/ha, for grain yield 563.46 – 2794.6 kg/ha and for number of pods per plant 42.17 – 170.47. This shows the existence

of considerable variation for these traits. However, number of seeds per pod (0.99 – 2.05), and primary branches (2.11 – 5.53) had low range. As to phenological traits, the number of days needed for flowering and maturity ranged from 36 to 64 and 89 to 107 days, respectively (Table 3). Tesfamichael et al. (2014) had also reported variation for these traits in different chickpea genotypes. The variation among the chickpea landraces in this study would provide ample opportunities for the genetic improvement of the crop through direct selection from the landraces and/ or through hybridization using parents possessing the desirable traits.

3.3. Phenotypic and genotypic coefficients of variation

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) across the 10 traits ranged between 4.20 – 28.64% and 3.91 – 27%, respectively (Table 4). The lowest PCV and GCV (4.2% and 3.91%) were obtained for days to maturity, while the highest PCV and GCV values of 28.64% and 27%; respectively, were obtained for grain yield. For most of the traits studied, phenotypic coefficient of variation was slightly higher than the corresponding genotypic coefficient of variation.

Table 2. Variation in agro-morphological traits of 204 chickpea genotypes at Sirinka Sirinka under rain fed condition

Traits	Range (max to min)	Range difference	SD
Days to flowering (days)	36 – 64	28	3.15
Days to maturity (days)	89 – 107	18	4.18
Plant height (cm)	27 – 48	21	3.85
Primary branches	2 – 6	4	0.57
Secondary branches	8 – 18	10	2.19
Number of pods per plant	42 – 171	129	14.41
Number of seeds per pod	1 – 2	1	0.21
Hundred seed weight (gm)	11 – 24	13	1.80
Grain yield kg/ha	564 – 2795	2231.14	412.18
Biomass kg/ha	1625 – 5852	4227.12	877.22

This relative narrow gap between the corresponding PCV and GCV values for the traits indicates small environmental effects on these parameters. PCV and GCV values of more than 20% are considered to be high, values less than 10% as low, and values between 10 – 20% as medium (Deshmukh et al., 1986). In this study, grain yield and biomass had very high PCV. On the other hand, days to flowering, days to maturity and plant height had very low PCV values. The number of primary branches, secondary branches, number of seeds per pod and hundred seed weight had moderate values of PCV. In case of GCV, grain yield and biomass had high values, while days to flowering, days to maturity, plant height and number of seeds per pod had very low magnitude. Moderate GCV values were obtained for primary branches, secondary branches, pods per plant, and hundred seed weight.

This result agrees with Uday et al., (2012) who reported low PCV for days to maturity (3.81%) and days to 50% flowering (6.52%); high PCV for grain yield per plant (29.69%), and moderate PCV for primary branches per plant (17.96%), seeds per pod (17.34%) and plant height (11.18%). Narendra (2004) also reported greater genotypic and phenotypic coefficient of variation for the most of the characters in chickpea. Melese (2005) also reported a wide range of variation for most of characters studied in chickpea. He reported PCV and GCV values of more than 54.0% and 37.48%, respectively for the biomass and grain yield.

3.4. Estimates of heritability and expected genetic advance

Phenotypic

In addition to genetic variation, heritability of economically important traits is essential for effective breeding programme and selection of specific traits. In this study estimate of broad sense heritability ranged from 59.05% for number of seeds per pod to 88.86% for grain yield (Table 4). According to Singh (2001), if heritability of a character is very high, i.e., 80% or more, selection for that character could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. Whereas, for characters with low heritability, i.e., 40% or less, selection may be considerably difficult or impractical due to the masking effect of the environment. Considering this bench-mark, in this study, heritability estimate was high for grain yield (88.86%), hundred seed weight (87.82%), biomass yield (86.15%) , and number of pods per plant (83.53%) while it was moderate for days to flowering (79.85%), plant height (70.89%), primary branches (74.44%), secondary branches (74.44%) and number of seeds per pod (59.05%). Tesfamichael et al. (2014) also reported high heritability for grain yield and hundred seed weight. Muhammad et al. (2005) also reported high heritability for number of pods per plant (88%), hundred seed weight (97.7%) and grain yield (90.9%). These authors reported moderate heritability for days to flowering, days to maturity, primary branches, and for secondary

branches. Highest heritability for hundred seed weight was also reported by Uday et al, (2012). Qurban et al., (2010) also reported high heritability for biomass, grain yield, hundred seed weight and number of pods per plant. The higher value of heritability for grain yield, hundred seed weight and number of pods per plant indicate that these traits can be used for selection of high yielding genotypes (Qurban et al., 2010). High broad sense heritability has been reported in chickpea for 100 seed weight and number of seeds per plant (Ali and Ahsan, 2012), number of secondary branches per plant and seed yield (Malik et al., 2009), days to flowering and plant height (Khan et al., 2011). Okonkwo and Idahosa (2013) reported high broad sense heritability for yield and some agronomic traits in soybean.

Genetic advance under selection (GA) refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Estimates of GA for grain yield at 5% selection intensity was 755.61 kg ha-1, indicating that whenever we select the top 5% high yielding genotypes, mean grain yield of genotypes in the next generation could be improved by 755.61 kg ha-1 per one cycle of selection.

Genetic advance as percentage of the mean (GAM) was high for grain yield (52.5%), biomass yield (46.1%), number of pods per plant (36%) hundred seed weight (24.6%) while low GAM was obtained for days to maturity (7.5%), days to flowering (10.6%), plant height (13.9%) and number of seeds per pod (14.5%). High heritability estimates along with high genetic advance is more helpful in predicting gain under selection than heritability estimates alone (Johnson et al., 1955; Singh, 1993). According to Panse (1957) higher heritability coupled with high genetic advance as percent of mean suggest that the traits are controlled by additive gene action. Therefore, in this study, the traits such as grain yield, number of pods per plant, biomass yield, and hundred seed weight, which had relatively high values of GCV, heritability and genetic advance as percentage of mean, are the most important traits which could be easily be improved through selection.

Table 3. Estimates of means, standard error, variance components, PCV, GCV, H2, GA, and GAM for 10 traits of chickpea genotypes

Traits	Means	SE(±)	σ^2g	σ^2p	PCV (%)	GCV (%)	h2 %	GA	GAM (%)
DF	48.04	0.13	7.76	9.72	6.49	5.80	79.85	5.13	10.69
DM	97.55	0.17	14.54	16.82	4.20	3.91	86.41	7.31	7.50
PH	39.04	0.17	9.81	13.84	9.53	8.02	70.89	5.44	13.93
PB	2.91	0.02	0.24	0.32	19.45	16.77	74.33	0.87	29.82
SB	12.76	0.09	3.52	4.73	17.04	14.71	74.44	3.34	26.17
NPP	68.57	0.58	172.05	205.97	20.89	19.13	83.53	24.69	36.00
NSP	1.72	0.01	0.02	0.04	11.92	9.19	59.05	0.25	14.53
HSW	13.23	0.07	2.83	3.23	13.58	12.72	87.82	3.25	24.60
GY	1439.18	16.67	150969.0	169894.5	28.64	27.00	88.86	755.61	52.50
BY	3377.57	35.46	662192.0	768619.7	25.96	24.09	86.15	1558.22	46.13

DF = Days to flowering, DM = Days to maturity, PH = Plant height, PB = Primary branches, SB = Secondary branches, NPP = Number of pods per plant, NSP = Number of seeds per pod, HSW = Hundred seed weight, GY = Grain yield, BY = Biomass yield, SE = Standard error of mean, σ^2_g=genotypic variance, σ^2_p= phenotypic variance, PCV (%)=phenotypic coefficient of variation, GCV (%) =genotypic coefficient of variation, h2 =heritability, GA= genetic advance, GAM (%)=genetic advance as percentage of mean.

4. Conclusions

Analysis of variance showed highly significant differences among the tested genotypes for all 16 quantitative traits, indicating the presence of genetic variability in the traits studied. Biological yield exhibited the widest range (1624.9 – 5852.1 kg/ha) followed by grain yield (563.5 – 2794.6 kg/ ha), number of pods per plant (42.2 – 170.5 pods per plant), days to maturity (89.27 – 106.5 days), and hundred seed weight (11.2 – 24.2gm).

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) ranged between 4.2% – 28.64% and 3.91% – 27%, respectively. The lowest PCV and GCV (4.2% and 3.91%) were obtained for days to maturity, while the highest PCV and GCV values (28.64% and 27%) were obtained for grain yield, respectively. Estimates of GA for grain yield at 5% selection intensity was 755.61 kg ha-1, indicating that whenever we select the top 5% high yielding genotypes, mean grain yield of genotypes in the next generation could be improved by 755.61 kg ha-1 per one cycle of selection. Twelve genotypes out yielded the best released variety (Minjar), indicating the possibility of identifying superior genotypes for release.

High heritability and genetic advance as the percent of the mean were observed for grain yield, number of pods per plant and biomass yield. This indicates that these traits are governed by additive gene action, implying the possibility for genetic gain through selection. The

findings of this study show that traits such as grain yield, number of pods per plant, biomass yield and hundred seed weight, which had high heritability coupled with relatively high values of GCV, and genetic advance as percentage of mean, are the most important traits which could be improved by selection.

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