

Full Length Research Paper

Genetic variability of some chickpea (*Cicer arietinum* L.) genotypes and correlation among yield and related traits in humid tropics of southern Ethiopia

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Received 15 January, 2018; Accepted 10 August, 2018

The current investigation evaluated the genetic variability of some chickpea (*Cicer arietinum* L.) genotypes and correlation among yield and related traits in Abaya Woreda. Five improved chickpea genotypes along with one local variety were laid out in randomized complete block design with three replications. Data were recorded from phenological, growth parameters; and yield and related traits depicted the ranges of mean values for most of the traits were large depicting the existence of genetic variations among the tested genotypes. Phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV) for all the traits. Higher heritability values were obtained from seed yield per hectare, days to maturity, seed yield, yield per plot, hundred seed weight, number of pod length, plant height, number of primary branch per plant, days to emergence and days to flowering whereas low heritability was obtained from number of secondary branch per plant, number seed per pod and of pod per plant. Positive and highly significant correlation were reported between grain yield and yield per plot, hundred seed weights and yield per plot while negative and significant correlation was obtained between pod length and yield per plot. Thus, genetic evaluation in these genotypes indicated that there were genotypic and phenotypic variation, positive and significant correlation and moderate to high heritability in the most studied traits that will be utilized in the future breeding program. Finally, this investigation should be repeated over years and locations to confirm future breeding program.

Key words: *Cicer arietinum*, correlation, genetic variation, heritability.

INTRODUCTION

Chickpea is the third most important pulse crop after faba bean and haricot beans in production and area coverage with annual production of 225,607.53 hectares and

average productivity of 19.69 Qt./ha in the country (CSA, 2016/2013). On the contrary, in areas where improved chickpea technologies were adopted and used, yield

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levels of up to five tons per hectare have been achieved (Tabikew et al., 2009). This huge productivity gap warrants wider dissemination of the improved chickpea technologies in order to substantially boost up the overall productivity and production in the country.

The principal uses of chickpea in Ethiopia include: as good source of protein (20 to 30%) as compared with cereals (8 to 10%), about 40% carbohydrates and 3 to 6% oil (Gil et al., 1996). It is also a good source of calcium, magnesium, potassium, phosphorous, iron, zinc and manganese (Ibrikci et al., 2003). Two main types of chickpea cultivars are grown globally: the desi and kabuli types. The total yield production is quite low in most chickpea growing countries and a wide gap exists between the potential (5 ton ha⁻¹) and actual (0.96 ton ha⁻¹) yields (FAOSTAT, 2013). The low yields have been attributed to low genetic diversity of cultivated chickpea for yield and yield components (Malik et al., 2014) and various biotic (Aschochyta blight, Fusarium wilt, Pod borer dry root rot etc.).

Plant breeders are continuously engaged to improve the genetic yield potential of this crop to meet the demands of ever-increasing population. Heritability explains whether the differences observed among individuals arose because of differences in genetic makeup or due to environmental factors. Genetic advance gives an idea of possible improvement of new population through selection, when compared to the original population. The information on nature and magnitude of genetic variation in quantitative characters and their inter-relationship in population comprising diverse genotypes is an important prerequisite for systematic breeding program. Therefore, several research workers (Malik et al., 1983; 1988; Saleem et al., 2002a, b; Parshuram et al., 2003; Ali et al., 2008) have emphasized the utility of the estimates of genetic components in the response prediction of quantitative characters to selection as well as the correlated response of various traits to grain yield.

To formulate proficient breeding program and for developing high-yielding varieties, it is essential to understand the genetics of the yield and related traits. It is recognized that, correlation coefficient indicates relation between any two traits. In order to tracing any possible causes of correlation between seed weight per plant and other yield related traits, correlation coefficient is calculated.

Selection criteria based on yield components would be helpful than direct selection in selecting suitable plant types as yield is quantitative trait that is affected by environmental variation. Thus, construction of selection indices will be highly helpful to discriminate desirable genotypes. The discriminant function provides an efficient method for simultaneous selection (Smith, 1936).

For this reason, to estimate expected genetic gain of the character through discriminant function methods is necessary. This method has been successfully followed

by various researchers in various crops such as Deb and Khaleque (2007) in chickpea, Ferdous et al. (2010) in bread wheat, Kumar et al. (2012) in Rabi sorghum and Sarker et al. (2013) in chickpea. Hence, available information will be very helpful for an efficient selection criterion in selecting the most desirable and high yielding genotypes of chickpea.

Genotypic and phenotypic variances make available the information of variability only but the heritable portion of this variation is determined by the estimates of heritability. Genetic structure of the breeding materials determines the extent of heritability of various characters (Kahirizi et al., 2010). For that reason, awareness of these values of the resources in which breeders are paying attention is of enormous importance. High heritability estimates signify the effectiveness of these characters through selection for crop improvement, as less environmental influences are involved in it (Maniee et al., 2009). Malik et al. (2011) reported highest heritability together with high genetic advance expressed as percent average in 100 seed weight, seed volume and swelling index suggested effective selection for these characteristics.

The most common chickpea genotypes; Minjar, Natoli, Ejere, Mestawel, Fetenech and Cheffe (local variety) were selected to study their genetic variability. In spite of all the multi benefits of chickpea, its productivity has remained low in Ethiopian agriculture. Reasonable grain yield in chickpea could be achieved by using improved genotypes with appropriate agronomic practices. There was no research work that has been done so far on genetic variation of chickpea genotypes and correlation among yield and related traits in West Guji zone Gedeo zone.

The present investigation was to determine the genetic variation of some selected chickpea (*Cicer arietinum L.*) genotypes and correlation among yield in related Abaya areas; to estimate genetic advance and heritability of chickpea genotypes and to evaluate the correlation among yield and related traits for some selected chickpea (*C. arietinum L.*) genotypes.

MATERIALS AND METHODS

Description of experimental site

The experimental site was located in southern Ethiopia in the Oromia Regional State and the study was conducted at local farmers land, in Abaya sub site. Abaya is found in southern Ethiopian Rift valley 365 km away south from Addis Ababa. It is situated in Kolla (70%) and Woina Dega (30%). Abaya is bordered on the south by Gelana district, on the north by Gedeo Zone, on the east by Lake Abaya and on the west by Yirga Chafe District. The altitude of the district ranges from 1200-2060 m.a.s.l. Abaya receives annual rainfall ranging from 700 to 11000 mm and the average annual temperature ranges from 16 to 28°C. The rainy season occurs from April to October and the maximum rain is received in the months of May (Abaya Agricultural Office Profile and GPS readings taken from the site, 2017).

Treatments and experimental design

Some released chickpea genotypes were obtained from Debre Zeit Agricultural Research Center. A field experiment was conducted to study growth and yield of six chickpea genotypes (Ejere, Fetenech, Mestawel, Minjar, Natoli and local variety/Cheffe) evaluated in Chromic Luvisols, Eutric Fluvisols and Dystric Nitosols (Tadesse, 2002) of Abaya wereda at Guangoa Badiya site. The experiment was laid out in a randomized complete block design with three replications and the net plot size was 2.0 x 1.5 m = 3 m²; 30 cm x 15 cm of inter and intra-row spacing; comprising of 5 rows with 13 seeds per rows were used and seedbed was prepared by ploughing 3 times followed by plantings.

Traits evaluated

The data for the following traits were recorded from ten randomly selected plants from each experimental plot, and the average value was considered: plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, pod length, days to 50% flowering, days to 95% maturity, 100 Seed weight, and seed yield per plot.

Statistical analysis

Analysis of variances

All collected data were subjected to analysis of variance using appropriate computer software (SAS, 2004) and Duncan's Multiple Range Test (DMRT) at probability of 0.05 was used to separate the means and ranges for significant parameters.

Phenotype and genotype

The variability was estimated using range, mean, standard error, phenotypic and genotypic variance and coefficient of variation and the resulting components of variances were used to compute the phenotypic and genotypic variation and genetic advances as:

$$\sigma^2_g = (\sigma^2_t - \sigma^2_e) / r$$

Where, σ^2_g = genotypic variance, σ^2_t = mean square of treatment and σ^2_e = error mean square, r = number of replication.

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

Where, σ^2_p = phenotypic variance.

According to Singh and Chaudhary (1999), the phenotypic and genotypic coefficients of variances (GCV) are expressed by the following formula:

$$GCV (\%) = (\sqrt{\sigma^2_g} / X) \times 100$$

$$X = \text{Mean value of the trait and } PCV (\%) = (\sqrt{\sigma^2_p} / X) \times 100,$$

Where, PCV = phenotypic coefficient of variation

Heritability in broad sense was calculated for each trait by using the following formula (Allard, 1960):

$$H (\%) = (\sigma^2_g / \sigma^2_p) \times 100$$

The expected genetic advance (GA) under selection, assuming the selection intensity of 5% was calculated as proposed (Johanson et al., 1955):

$$GA = K \cdot (\sqrt{\sigma^2_p}) \cdot \sigma^2_g / \sigma^2_p = K \cdot H \cdot \sqrt{\sigma^2_p} = K \cdot H \cdot \sigma$$
 (Standard deviation), K = standardized selection differential ($K = 2.06$ at 5% selection intensity).

$$GAM = (GA / X) \times 100$$

Where, GAM = Genetic expected mean.

Correlation coefficient

Both genotypic and environmental effects, which are the inherent correlation between two variables, were estimated by the formula of (Al- Jibouri et al., 1958):

$$r_g = Gcovx.y / \sqrt{(\sigma^2_{gx} \cdot \sigma^2_{gy})}$$

Where, r_g = genotypic correlation coefficient, $Gcovx.y$ = genotypic covariance between variables x and y , σ^2_{gx} = genotypic variance for variable x and σ^2_{gy} = genotypic variance for variable y .

RESULTS AND DISCUSION

Phenotypic and genotypic coefficient

Success of plant breeders in selecting genotypes that produces higher yield and quality traits depends on existence and exploitation of genetic variability to the fullest extent. Estimation of phenotypic coefficient of variation showed that environment does have significant effect on the studied traits. The lower phenotypic and genotypic coefficient of variations were recorded from plant height, number of pod per plant, pod length, hundred seed weight and yield per pod (Table 1). The difference between phenotypic and genotypic coefficient of variations revealed that there was a little environmental influences on the traits except for seed yield per hectare, number of secondary and primary branches per plant. These results are in confirmation with those of Malik et al. (2011) and Lokare et al. (2007) who reported little influence of environment on seed physiochemical traits in chickpea.

Heritability in broad sense

Phenotypic and genotypic variances make information available for the variability only but the heritable portion of this variability was determined by the estimates heritability. Broad sense heritability (H), an estimate of the total contribution of the genotypic variance to the total phenotypic variance ranged from 34.06% for number of secondary branch per plant to 97.36% for yield per plot (Table 1).

All traits had high heritability estimates as followed for yield per plot (97.36%), days to maturity (95.51%), pod length (93.83%), 100 seed weight (87.63%), seed yield per hectare (86.92%), plant height (84.52%), days to emergence (77.46%), days to flowering (77.12%), and number of primary branch per plant (75.21%). Highest

Table 1. Estimates of genetic variability in chickpea genotypes.

Traits	Range	± SE	Mean	(σ^2_p)	(σ^2_g)	(σ^2_e)	PCV	GCV	H%	GA	GA as (%)
DE	1.1-2.01	1.15	1.56	23.47	18.18	5.29	6.21	5.47	77.46	7.72	9.89
DF	50.33-54.83	1.17	52.58	23.82	18.37	3.45	6.18	5.43	77.12	7.74	9.80
DM	50.5-85.67	0.70	68.09	43.62	41.66	1.96	3.92	3.83	95.51	12.97	7.69
PBPP	41.17-46.50	1.83	43.84	54.25	40.80	13.45	4.17	3.62	75.21	11.39	6.45
SBPP	41-44.17	2.69	42.59	43.86	14.94	28.92	7.47	4.36	34.06	4.64	5.23
PH	42.50-55.50	0.12	49.00	0.39	0.33	0.06	45.44	41.77	84.52	1.08	78.95
PPP	22.75-70.67	0.97	46.71	7.32	3.55	3.77	15.06	10.49	48.48	2.70	15.01
PL	7.5-12.50	0.13	10.00	1.14	1.07	0.07	24.60	23.83	93.83	2.06	47.47
SPP	3.07-3.30	1.35	3.19	14.03	6.69	3.74	10.98	7.59	47.68	3.67	10.77
HSW	14.00-16.17	0.34	13.49	3.72	3.26	0.46	14.29	13.38	87.63	3.47	25.75
YLD	180.24-437.42	1.91	308.83	112.04	97.39	14.65	2.62	2.44	86.92	18.92	4.68
YPP	11.08-17.96	0.12	14.52	2.27	2.21	0.06	16.93	16.70	97.36	3.02	33.89

DE days to emergence; DF, days to flower; DM days to maturity; PBPP, number of primary branch per plant; SBPP, number of secondary branch per plant; PH, plant height; PPP, number of pod per plant; PL, pod length; SPP, number of seed per plant; HSW, hundred seed weight; YLD, grain yield; YPP, yield per plot.

heritability of 97.36 for yield per plot along with high genetic advance indicated that maximum improvement by selection could be possible considering this trait whereas relatively moderate estimates of heritability were recorded from number of pod per plant (48.48%), number of seed per pod (47.68%), and number of secondary branch per plant (34.06%) indicating that all the studied traits may positively respond to phenotypic selection (Table 1).

High heritability estimates signify the effectiveness of these traits through selection for crop improvement, as less environmental effects were involved in the traits (Maniee et al., 2009). In addition, the current observations were in agreement with the findings of Malik et al. (2011) genetic analysis of physiochemical traits in chickpea; the highest heritability was obtained from 100 seed weight (99%) followed by seed volume (95%), swelling index (91%) indicating additive genetic variation was the major component of genetic variation in the inheritance of these traits and the effectiveness of selection in the early generation.

Estimates of expected genetic advance

The genetic advances as percent of the mean (GAM) at 5% selection intensity is presented in Table 1. It ranged from 4.68% for seed yield to 78.95% for plant height (Table 1). This showed presence of high genetic variability in the case of plant height; but most traits showed low to moderate genetic advance for these parameter, which were also reflected by their respective low genotypic and phenotypic variations. This in turn showed the importance of genetic variability for the improvement of the traits through selection. The current observations are in confirmation with the findings of Malik

et al. (2011) who reported similar results in their study on genetic analysis of physiochemical traits in chickpea genotypes.

Estimates of expected genetic advance

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Correlation coefficient of six chickpea genotypes

Days to emergence showed positive and significant to highly correlations with number of pod per plant, number of seed per pod, hundred seed weight, and grain yield. Positive and significant correlations were observed between number of secondary branch per plant and yield per pod and hundred seed weights. Positive and highly significant correlation were reported between grain yield and yield per plot, hundred seed weights and yield per plot, while negative and significant correlation was obtained between pod length and yield per plot (Table 2). Similarly, Qurban et al. (2011) showed positive and significant correlation of anthesis-silking interval with ear

Table 2. Genotypic coefficient of variation in chickpea genotypes.

Traits	DE	DF	DM	PBPP	SBPP	PH	PPP	PL	SPP	HSW	YLD	YPP
DE	1.00	0.11	-0.01	-0.14	0.19	0.15	0.24*	-0.01	0.21*	0.30**	0.39**	0.16
DF		1.00	-0.07	-0.56	0.21	-0.11	0.10	-0.06	-0.06	0.05	0.10	-0.02
DM			1.00	0.07	0.07	-0.01	0.01	0.00	-0.12	0.07	-0.06	0.03
PBPP				1.00	-0.07	0.15	-0.05	-0.05	-0.13	0.05	0.01	-0.02
SBPP					1.00	0.04	0.06	0.04	0.10	0.13	0.15	0.25*
PH						1.00	0.05	-0.16	0.20*	0.26*	0.03	0.15
PPP							1.00	-0.10	-0.08	0.35**	0.47**	0.40**
PL								1.00	-0.01	0.02	-0.09	-0.25*
SPP									1.00	0.03	0.01	0.05
HSW										1.00	0.48**	0.32**
YLD											1.00	0.33**
YPP												1.00

height. Sharanappa et al. (2014) and Saurabh et al. (2017) also reported similar results.

Conclusion

The ranges of mean values for most of the traits were large showing the existence of variation among the tested genotypes. Phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (PCV) for all the traits. The two values differed slightly indicating less influence of the environmental factors.

Moderate heritability values were obtained for days to maturity, days to flowering, number of primary branch per plant, yield per plant, number of secondary branch per plant, plant height, pod length, number of pod per plant, days to emergence, grain yield per hectare, whereas number of seed per pod had low heritability and hundred seed weights showed very low heritability. Positive and highly significant correlation were reported between grain yield and yield per plot, hundred seed weights and yield per plot, while negative and significant correlation was obtained between pod length and yield per plot.

Genetic evaluation in these genotypes indicated that there were genotypic and phenotypic variation, positive and significant correlation as well as high heritability in the most studied traits that will be utilized in the future breeding program. The study has to be repeated over years and location by increasing number of genotypes to confirm the future breeding programs.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENT

The authors extend their deepest gratitude to Dilla

University Research and Dissemination Office for funding the research project.

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