

Phenotypic Variability and Association (among yield components and) Yield Related Trait in desi Type Chickpea (*cicer arietinum* L.) in Raya Kobo District, Northern Ethiopia

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ABSTRACT

Chickpea is the most important pulse grown in Ethiopia however; its production is limited due to lack of improved varieties that is adaptable to both biotic and abiotic factor as well as to give high grain yield. Twelve varieties of chickpea collected from Sirinka Agriculture Research Center (SARC) were evaluated at SARC Kobo branch using irrigation with the objectives evaluating the variability of chickpea varieties for grain yield and yield related traits, determination of association among yield components and identify traits that can be used mainly to explain variation among desi chickpea varieties. The study was laid out in randomized complete block design with three replications. Analyses of variance, the mean square due to accession were highly significant for all of the characters studied such as plant height, biological yield and grain yield. The range for PCV was 3.96% days to maturity to 30.1% for biological yield. As to the GCV, it ranged from 1.24% for days of maturity to 28.153% for biological yield. Heritability estimates vary as small value recorded for days to maturity (9.74%) and high value recorded for hundred seed weight per plant (96.52%). Hundred seed weight, biological yield, plant height, grain yield and harvest index have high heritability and high expected genetic advance. Most of the characters studied show high heritability estimate indicating the possibility of improving these traits through selection. Grain yield showed positive and highly significant association with biological yield, number of pod, number of primary branch, hundred seed weight, and days to maturity. The dendrogram obtained from the hierarchical cluster analysis grouped the original 12 accessions into four clusters and two solitary accessions. The principal component analysis revealed that four principal components PC1 to PC4 with eigen values greater than one accounted for 98.2% of the total variation. The present study indicates the presence of high heritability with high values of genetic advance which showed the possibility of selection to improve yield and yield related traits in desi type chickpea genotypes.

Keywords: Chickpea; Correlation; Genetic advance; Genetic variability; Grain yield; Heritability

INTRODUCTION

Chickpea (*Cicer arietinum*) is the third most important pulse grown in the world next to dry bean and pea, and constitutes about one fifth of the world's pulse production [1]. Chickpea originated in southeastern Turkey and spread west and south via the Silk Route [2]. As Zeeshan *et al.*, [3] reported that four centers of diversity have been identified in the Mediterranean, Central Asia, the Near East and India, as well as a secondary center of origin in Ethiopia. As Choudhary *et al.*, [4] confirmed chickpea is the inexpensive and readily available source of carbohydrates, fats and protein. It is also marketed as dry chickpeas and ground flour for baking purposes. Research is currently underway to develop chickpea milk [5].

Global chickpea production was 8.24 million tons from an area of

9.4 million hectares and mean production of 0.77 t ha⁻¹ while, contribution of Asia was 7.36 million tons (89.4%) [6]. In Ethiopia mean production of chickpea 19.69 Qt. ha⁻¹ and area coverage with annual production of 225,607.53 hectares [7]. On the opposite, as Tabikew *et al.*, [8] reported in developed countries where improved chickpea technologies were embraced and utilized, yield levels of up to 50 Qt.ha⁻¹ have been attained. This big productivity difference warrants having a great extent circulation of the improved chickpea technologies in order to significantly boost up the overall productivity and production in the country. Different crop management problems limited the supply of production in Ethiopia. The main problem of chickpea includes lack of improved varieties that is adaptable to both biotic and abiotic factor as well as to give high grain yield [9].

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Selection for productivity needs an integral approach because the nature of the yield contributing is variable and mainly modified by external factor that reduce the increment of yielding ability. The effectiveness of selection relies on the amount of variability present in the genetic material for yield and yield related traits [10]. Hence, estimation of variability is prime importance.

Plant breeders focus on manipulating plant heredity to release new and improved varieties to enhance the genetic yield potential of the crop. The genetic properties of a population are determined by the relative magnitudes of the components of variance. The amount of genetic and phenotypic variability that exist in a species is most important in efforts to initiating a breeding program and developing better varieties in any crop. Heritability indicates how it is effective in selection based on phenotypic performance and explains whether the differences observed among individuals arose in genetic makeup or due to environmental factors [11]. Genetic advance express the expected genetic improvement that result from selecting the best performing accession. The information on nature and magnitude of genetic variation in quantitative characters in population is an important prerequisite for every plant breeding program. Accordingly, several researchers Johanson *et al.*, [12]; Rao and Hodgkin [13]; Noor *et al.*, [14]; Zeeshan *et al.*, [3] have emphasized on estimation of genetic components of quantitative characters to selection as well as the associated response of various traits to grain yield.

Some of the characters are highly associated among themselves and with grain yield. The most important method to improve yield of chickpea would be improved by an understanding of how agromorphological traits associate with one another in affecting yield [15]. The most important logical step to know the type of plant traits are correlation coefficient, path coefficient and factor analysis [16]. Low genetic diversity for yield, yield components and resistant against major diseases in plant genetic diversity are major limitation in achieving high yield capability and enhancing food production. Daba *et al.*, [17] suggested that the available information about the performance of the chickpea in Ethiopia is very limited and the knowledge of genetic diversity helps in the tagging of germplasm, identification of gene stock and establishment of core collections. Therefore, the general objective of the present study was to determine the morphological variability and association among chickpea yield and yield related traits of chickpea in Ethiopia and specific objectives were:

- To study the variability of chickpea cultivars for yield and yield related traits.
- To determine the association among chickpea grain yield and yield components.
- To determine which traits can be used mainly to explain variation among desi chickpea varieties.
- To estimate genetic advance and heritability of chickpea genotypes.

MATERIALS AND METHODS

Description of the study area

The experiment was conducted at SARC Kobo branch from February to April 2015 using irrigation. Kobo is located in North wollo Zone, which is one of the districts of ANRS (Amhara National Regional State) of Ethiopia. It is 565 km north of Addis

Ababa. It is also far from 400 km away east of Bahir-Dar. This site is lying between 12° 08' 21" north latitude and 39° 38' 21" east longitudes. Kobo district comprise an altitude 1470 m above sea level. The mean annual minimum and maximum temperature is 15 and 31°C, respectively, and has an average annual rainfall of 668 mm.

Plant material

Twelve genotypes of chickpea germplasm that consists of eight accessions of the landraces and four released varieties obtained from SARC were used for the study (Table 1).

Treatment and experimental design

The experiment was laid out in randomized complete block design (RCBD) with three replications. Each experimental plot size was 2 m long and 2 m wide and consists of five rows with 15 plants per row. The spacing between plots and blocks was 1.5 m and 1.5 m respectively. Five rows of 2 m length for each genotype in each replicate were planted with 10 cm intra-row where as inter-row distance was kept 30 cm. Sowing was done by hand drilling on February 1, 2015 at SARC Kobo branch. For data collection, the middle three rows were used. All experimental factors were applied uniformly to the entire plot.

Data Collection: Data were collected on plant basis and plot basis.

- 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 branch, number of secondary branch, number of pods per plant, number of seeds per pod, grain yield per plant, biological yield and harvest index.
- The other traits such as number of days to maturity, number of days to flowering and hundred Seed weight were collected on plot basis.

Statistical procedures: The collected grain yield was subjected to moisture content analysis using Grain Analysis Computer (GAC) at Sirinka Agriculture Research Center in order to know the moisture content of the harvested grain and readjusted the grain yield weight and hundred seed weight value using the standard moisture content that is 10%. Then the data were subjected to analysis of variance (ANOVA), cluster analysis, correlation analysis, and principal component analysis which were done with SAS version 9.1 SAS software [18]. Mean separation was also carried out

Table 1: Lists of desi type chickpea germplasm used in the study.

Serial No.	Genotype	Type	Source
1	41039	Landraces	SARC
2	41041	Landraces	SARC
3	41056	Landraces	SARC
4	41098	Landraces	SARC
5	41263	Landraces	SARC
6	207700	Landraces	SARC
7	209115	Landraces	SARC
8	742124	Landraces	SARC
9	Kutaye	Released	SARC
10	Fetenech	Released	SARC
11	Mastewal	Released	SARC/DZARC
12	Minjar	Released	SARC/DBARC

using Duncan's Multiple Range Test (DMRT) to test the significant difference among genotype means.

Phenotypic and genotypic variation: The variability present in population was estimated by simple measure, such as range, mean, standard error, phenotypic and genotypic variation, and coefficient of variation. The phenotypic genotypic variance and coefficient of variation was estimated according to the method suggested by Singh and Chaundhary as follow [19]:

$\delta^2_p = \delta^2_g + \delta^2_e$ Where, δ^2_p -phenotypic variance; δ^2_g -genotypic variance

$\delta^2_g = \frac{mg - me}{r} \delta^2_e$ e- environment (error variance); mg- mean square of genotype

me- mean square of error and r -number of replication

Phenotypic coefficient of variance, $PCV = \frac{\sqrt{\delta^2_p}}{\bar{x}} \times 100$ where \bar{x} is

population mean Genotypic coefficient of variation $GCV = \frac{\sqrt{\delta^2_g}}{\bar{x}} \times 100$ where \bar{x} is population mean.

Estimates of heritability in the broad sense: Heritability was computed for each character based on the formula developed by Allard (1960) [11] as $H^2 = \frac{\delta^2_g}{\delta^2_p} \times 100$ where, δ^2_p - phenotypic variance, δ^2_g -genotypic variance.

Estimation of expected genetic advance: The genetic advance for selection intensity (K) at 5% was calculated by $GA = (K) (\delta P)(H^2)$ where GA -expected genetic advance δp =phenotypic standard deviation, H^2 =heritability, K =selections differentiation ($K=2.06$ at 5% selection intensity). The genetic advance as a percent of mean was calculated as $\frac{GA}{\bar{x}} \times 100$ Where \bar{x} =population mean [11].

RESULTS AND DISCUSSIONS

Variance analysis: The analysis of variance revealed significant differences among the genotypes for hundred seed weight, biological yield, grain yield, harvest index plant height, number of primary branch, number of secondary branch, number of pod per plant and days to flowering but there is no significant difference among genotypes for days to maturity and seed per pod (Table 2). The presence of significant differences among the genotypes indicates considerable magnitude of genetic variability of the material used

for the study. Similar results were reported in the previous study of chickpea [20].

Variability studies: The result of variance analysis for eleven measured traits showed significant differences among the examined characters indicating the presence of variability, which can be exploited through selection. High differences between the minimum and maximum mean values were found for majority of traits (Table 3). The studied genotypes showed hundred seed weight variation ranging from 12.1 g to 22.7 g in 41098 and 41263 genotypes respectively. Biological yield showed variation from 14.5 g to 34.0 g in 41098 and kutaye genotype respectively. Grain yield ranged from 6.9 g to 41056 to 17.4 g with a mean value of 11.8 for kutaye. Plant height show wide range of variation in which the shortest accession was kutaye that is 32.9 cm but the longest one was 41039, which was 42.2cm. The result of this study is similar to Talebi and Rokhza. They have reported that chickpea displayed wide range of variation observed for plant biomass, number of seeds per plant, hundred seed weight, and plant height.

The number of days required for flowering and maturity were with a range of 49 days to 54 days and 99 days to 106 days, respectively. Genotype 41039, 41041, mastewal, 41098, 41263, 41056 required the lowest number of days for flowering and 209115 and fetenech required the highest number of days for flowering. In addition, for maturity 41041, 41098, and 41056 needed the lowest number of days and mingar, fetenech, 212474 needed more days to maturity than others Appendix Table 1. The present study is in agreement with the finding of Dadi [21] and Noor *et al.*, [14] in which they considered eleven quantitative traits of chickpea and revealed considerable diversity for those traits that they consider and had wide range and high variance value for hundred seed weight, seed yield, days to flowering, days to maturity, plant height, pods per plant, biological yield and harvest index. However, little variability was observed for primary branches, secondary branches and seed per pod. High range of variation indicates availability of high genetic variation among chickpea genotypes and selection could be effective for such traits.

The mean for secondary branch, grain yield, and number of pod per plant in this experimental study was low due to adaptation of chickpea and sowing period to cause water deficiency because irrigation might not be adequate due to lack of power supply at this environment. This cause abort formation of pods and flower,

Table 2: Estimates mean square of 11 characters of chickpea genotypes.

Trait	Df	PH	PB	SB	DF	PPP	SPP	DM	HSW	BY	GY	HI
Rep	2	0.18	0.03	0.56	0.69	2.6	0.02	1.3	0.11	2.81	3.15	16.9
S.V	11	20.1*	0.03*	1.87**	11.3**	20.0**	0.18	13	48.8***	152.4***	31.4***	95.7***
Error	22	7.4	0.01	0.53	2.97	11.4	0.06	9.3	0.58	6.97	1.47	5.8
C.V		7.5	5.4	22	3.41	20	14.9	3	4.65	10.95	10.9	5.14
Mean		36.3	2.22	3.32	50.5	16	1.58	102	16.43	24.72	11.8	46.8
LSD		4.6	0.2	1.2	2.9	5.7	0.4	5.1	1.2	4.4	2	4

Rep= Replication, S.V= source of variation C.V= coefficient of variation Significant at $P < 0.001$, ***; $P < 0.01$, **; $P < 0.05$, PH= plant height, PB= primary branch, SB= secondary branch, DF= days to flowering, PPP= pod per plant, SPP= seed per plant, DM= days to maturity, HSW= hundred seed weight, BY= biological yield, GY= grain yield, HI= harvest index.

Table 3: Accessions' extreme values minimum and maximum, LSD and grand mean for 11 quantitative characters of desi type chickpea genotype.

Character	Minimum		Maximum		Grand mean	LSD	DMRT
	Accession number/variety	Value	Accession number/variety	Value			
Plant height (cm)	Kutaye	32.9	41039	42.3	36.28	4.608	*
Primary branch	41041	2	41263	2.4	2.22	0.203	*
Secondary branch	41098	2.26	41041	5.33	3.32	1.2385	**
Day to flowering	41056	49	209115	54	50.53	2.91	**
Pod per plant	41056	13.4	41039	21.18	15.8	5.71	**
Seed per pod	212474	1.4	Mastewal	2	1.58	0.44	
Day to maturity	41263	99	Fetenech	105.6	101.8	5.19	
100 seed weight	41098	12.1g	Kutaye	22.7g	16.43g	1.29	***
Biological yield	41098	14.5g	Kutaye	34g	24.72g	4.472	***
Grain yield	41056	6.9g	Kutaye	17.4g	11.8g	2.05	***
Harvest index	Kutaye	31.10%	212474	54.40%	46.80%	4.08	***

NB: *, ** and *** Significance difference at 0.05, 0.01 and 0.001 respectively.

biological yield, and number of branch reduced [22]. Similarly, Talebi and Rokhza reported that number of pod per plant, plant height per plant, seed yield per plant and secondary branch were affected too much by environmental factors [20].

Estimation of phenotypic and genotypic variation: Genetic parameters of yield and their components are given in (Table 4). In the present study, the highest genotypic variances were found for biological yield (48.443), hundred seed weight (16.07), and harvest index (29.98) while the lowest genotypic variance was found for plant height (4.22), primary branch (0.07), day to flowering (2.78) and secondary branch (0.4433). The highest phenotypic variances were found for biological yield (55.413), harvest index (35.76), day to maturity (16.64) plant height (11.6), number of pod per plant (14.27) and grain yield (11.5) while the lowest phenotypic variance was found for primary branch (0.017), secondary branch (0.973), time taken to flowering (5.74) and seed per pod (0.07).

The higher value of genotypic variance indicates that characters can be used as the genetic parameters for the improvement and selection of high yielding genotypes. These results were in accordance with the findings of Dasgupta *et al.*, [23] and as they indicated that biological yield per plant and grain yield per plant showed high genotypic variation by using Mather and Jinks [24] model of heritability. Crop improvement could be possible by simple selection because high genotypic variation revealed the presence of an additive gene effect [14]. On the other hand, low genotypic variation was observed for hundred seed weight, number of secondary branch, and number of primary branch. The result indicated that the environment influenced such traits [25].

Estimation of phenotypic (PCV) and genotypic (GCV) coefficients of variation: Although phenotypic coefficients of variation were found to be higher than genotypic coefficients of variation for all characters, the majority of the character considered in studies of two values i.e. PCV and GCV differ only slightly, indicating less influence of the environmental factors (Table 4). The range for PCV was 3.96% days to maturity to 30.1% for biological yield. As to the GCV, it ranged from 1.24% for days to maturity to 28.153% for biological yield.

According to Deshmukh *et al.*, [26], PCV and GCV values less than 10% were considered as low, between 10 and 20% to be medium and greater than 20% were considered as high. With this benchmark,

Table 4: Estimation of genetic variability parameters for quantitative traits of chickpea.

Character	(σ^2_g)	(σ^2_p)	(GCV %)	(PCV %)	(H ² %)	(GA)	(GA %)
PH	4.223	11.62	5.65	9.37	36.34	2.54	7.014
PB	0.007	0.017	3.6	5.86	41.18	0.12	4.967
SB	0.443	0.973	2.41	29.52	45.548	0.92	27.7
DF	2.78	5.75	3.29	4.73	48.32	2.38	4.71
PPP	2.887	14.28	10.7	23.86	20.219	1.57	9.94
SPP	0.01	0.07	6.329	16.46	14.286	0.0765	4.84
DM	1.62	16.64	1.236	3.96	9.714	0.8	0.792
HSW	16.07	16.65	24.4	24.83	96.517	8.11	49.37
BY	48.44	55.41	28.15	30.09	87.42	13.4	54.21
GY	10.03	11.5	26.7797	28.7288	87.21	6.1	51.62
HI	29.98	35.78	11.67	12.7587	83.79	10.32	22.0228

high GCV value was recorded for hundred seed weight (24.40%), grain yield (26.7798%) and biological yield (28.1523%), whereas medium GCV value was recorded for pods (10.696) and harvest index (11.67). High PCV value was observed in characters like number of secondary branch (29.53), grain yield (26.77), number of pod per plant (23.86 %), hundred seed weight (24.832), biological yield (30.0971) and grain yield (28.7288) whereas medium value was harvest index (12.75) (Table 4). This result is in line with the finding of Dadi in which the findings have displayed high genotypic and phenotypic coefficient of variation of chickpea genotypes for traits that includes biological yield, grain yield, number of pods per plant, number of seeds per plant, and number of secondary branches. This offers a wide scope of opportunity to select for these traits. Similar result was also reported by Padmavathi *et al.*, [27] in which higher amount of phenotypic and genotypic coefficients of variation was noticed for number of primary branches per plant, biological yield per plant, and seed yield per plant. These variations in characters may attribute to the geographical origin of these accessions and it offers relatively wide scope for selection among these characters.

The moderate and higher PCV and GCV value traits having considerable genetic variability, offer good opportunity for crop improvement through selection whereas lower value of PCV and GCV indicate limited scope for improvement of these traits through selection.

Estimates of heritability (H^2) in broad sense: Broad sense heritability was worked out for the 12 accessions ranged from 9.71% for time taken maturity to 96.51% for hundred seed weight per plot (Table 4). According to Singh (2001), heritability of a character is described very high (80% or more) selection for such characters was found easy. Most studied traits estimated high heritability such as biological yield (87.42%), grain yield (87.21%), hundred seed weight (96.51%) and harvest index (83.79). These results agreed with the findings of previous researchers Saleem *et al.*, [28]; Saeed *et al.*, [29], has been shown that hundred seed weight, biological yield, number of primary branches, hundred seed weight, harvest index, biological yield, and seed yield per plant.

Noor *et al.*, [14] also observed high heritability estimates for biological yield per plant (92%), grain yield per plant (85), day to maturity (71%), number of secondary branch (56%), and day to flowering (67%) and harvest index (56%). Moderate heritability estimate was observed for plant height (36.33%) and pod per plant (20.21) and lower in seed per pod (14.28) and days to maturity (9.7%). Tulu also confirmed the fluctuation of heritability in years and location for some traits [30]. Therefore, traits with high heritability could be utilized in the breeding program as high heritability signifies the proportion of total variability due to genetic makeup of plants.

Estimation of expected genetic advance (GA): The expected genetic advance expressed as a percentage of the mean by selecting the top 5% (high yielder) of the accessions, varied from 0.792% for days to maturity to 54.21 for biological yield (Table 4). Comparatively, high-expected genetic advance as percent of means were observed for number of secondary branch, grain yield, biological yield per plant, hundred seed weight and harvest index.

Selections for such characters were likely to be effective, as high heritability values were associated with high genetic advance. In agreement with this study, Habtamu *et al.*, [31] reported that high heritability associated with high genetic advance as percentage of mean were observed in case of secondary branches, pods per plant, hundred seed weight and grain yield per plant in chickpea.

Low values of genetic advance were recorded for days to flowering and maturity, primary branch per plant and seed per pod. Similar

observation was reported by Habtamu *et al.*, [31] that there was low genetic advance for days to flowering and maturity, primary branch per plant and seed per pod. The low expected genetic advance as percent of mean for days to flowering, pod filling duration and days to maturity is due to low variability for these traits indicated by their respective low GCV and PCV values [32].

Cluster analysis: In the present study, quantitative morphological characters were used for the cluster analysis. As shown in Figure 1, the dendrogram obtained from the hierarchical cluster analysis grouped the original 12 accessions that were obtained from SARC into four clusters and two solitary accessions.

Cluster A and C were the largest cluster containing three genotype each and cluster B and D were containing two genotype each. Kutaye and 41039 were solitary being ungrouped with the others. This experimental result agree with Keneni *et al.*, [32] report, variability among 40 genotypes of chickpea were grouped into four clusters each contain greater than seven accessions. In the current investigation the genotypes, having different traits were grouped into various clusters.

Cluster A is comprised of three accessions that were characterized by intermediate number of primary branch, plant height and they had early flowering time among the group. Similarly, they had lower number of pod per plant. In general, genotype 41056 and 41098 had close distance each other.

The number of accessions in cluster B was two and characterized by having lower hundred seed weight (12.95 and 13.5). Similarly, they had intermediate biological yield per plant, high number of secondary branch compared to others and lower grain yield per plant. There were three accessions in cluster C, characterized by greater numbers of Pod per plant, high hundred seed weight, an intermediate number of primary branches and longer plant height.

Cluster D contained two accessions, they were characterized by relatively higher biological yield, and they required long day for maturity had greater number of pod per plant and seed per pod. Kutaye is one of the released varieties, which remain ungrouped and was characterized by the shortest among the group (32.9 cm),

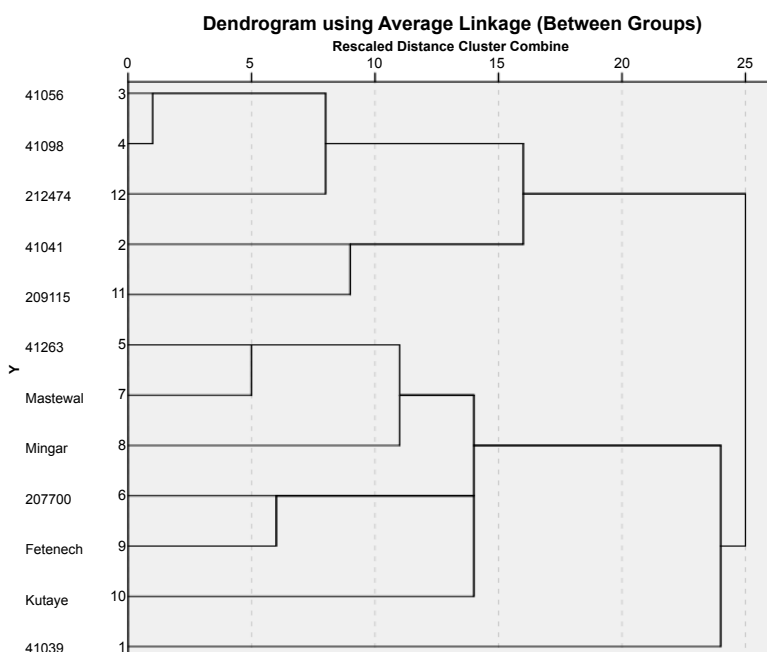


Figure 1: Dendrogram of 12 chickpea varieties based on evaluation for 11 morphological traits.

but with highest biological yield (34 g) and grain yield (17.4 g) compared to the other clusters. Finally, accession number 41039 remained solitary from the very beginning and it was characterized by longest among the group (42.2 cm) with highest number of pod per plant (21.18).

Correlation analysis: Correlation coefficients between all pairs of variables used in this experiment have been shown in Table 5. Grain yield per plant showed positively and significantly associated with biological yield per plant (0.92080**), number of pod per plant (0.49912**), number of primary branch (0.37202**), hundred seed weight (0.599723**) days to maturity (0.3799***) and days to flowering (0.268*) (Table 5). This experimental result was similar with the one reported by Bejiga *et al.*, [17] who described that yield per plant being positively and significantly correlated with days to maturity, biological yield, number of pod per plant and hundred seed weight.

Days to maturity was positively and significantly correlated with seed per pod, secondary branches per plant and hundred seed weight while negative and significant correlated with plant height, primary branch and number of pod per plant. Hundred seed weight was positively and significantly correlated with grain yield, primary branch, number of pod per plant, days to maturity and biological yield. Significant and positive correlations indicated that selection based on hundred seed weight and grain yield may be

helpful to improve grain yield production of chickpea [29,33-35].

Principal component analysis: The principal component analysis (Table 5) revealed four principal components PC1 to PC4 with Eigen values greater than one have accounted for 98.2% of the total variation. The first two principal components PC1 and PC2 with values of 61.1% and 26.1% respectively contributed more to the total variation. Talebi and Karami (2011) found that the first four PCs contributed 88.5% of the variability among 35 genotypes of chickpea evaluated for 10 quantitative traits [36].

Ghafoor *et al.*, [37] reported characters with largest absolute values closer to unity with in the first principal component influenced the clustering more than those lower absolute values closer to zero. Traits having relatively higher value in the first principal component (PC1) (which showed 61.1% of the total variation) like days to maturity, hundred seed weight, biological yield, grain yield and harvest index had more contribution to the total diversity and they were the ones that most differentiated the clusters. Plant height, number of pod, days to maturity, hundred seed weight and harvest index were the main traits that explains the variation in the second principal component (PC2). Days to flowering, hundred seed weight, plant height, and days to maturity explain much of the variation in the third principal component (PC3). Similarly previous works reported by researchers [38-40] (Table 6).

Table 5: Correlation coefficients between grain yield and yield-related traits.

	PH	PB	SB	FD	PPP	SPP	DM	HSW	BY	GY
PB	-0.202	-								
SB	0.142	0.445**	-							
DF	0.371*	0.079	0.091	-						
PPP	0.003	0.179	0.039	0.169	-					
SPP	-0.005	-0.259	0.156*	0.095	0.138*	-				
DM	0.369*	-0.012*	0.202**	0.218	-0.046**	0.117***	-			
HSW	-0.13	0.445**	-0.112*	0.088	0.062*	0.075	0.316*	-		
BY	0.04	0.296*	0.138*	0.247*	0.553***	0.263***	0.325***	0.48*	-	
GY	-0.146	0.372	0.068*	0.268*	0.499***	0.189***	0.379***	0.597***	0.92***	-
HI	-0.019	-0.148*	0.377*	-0.07	0.041	0.003	0.26	0.238	0.098	0.3

Table 6: Principal component analysis of quantitative traits.

Character	Eigenvectors			
	PCA 1	PCA 2	PCA 3	PCA 4
Plant height	0.003787	-0.321281	0.501249	0.398226
Number of primary branch plant ¹	0.004213	0.005902	-0.000753	-0.033855
Number of secondary branch plant ¹	0.030987	-0.02502	-0.043251	-0.022033
Days to flowering plot ¹	0.050145	0.053302	-0.41354	-0.519739
Number of pod plant ¹	0.176303	-0.028212	0.017011	0.072292
Number of seed pod ¹	0.01471	0.003263	-0.018559	-0.00262
Days to maturity plot ¹	0.14749	0.194215	-0.103151	-0.222416
Hundred seed weight	0.250338	0.437909	0.715937	-0.454419
Biological yield plant ¹	0.822763	0.046187	-0.173717	0.267942
Grain yield plant ¹	0.33563	0.196982	-0.104686	0.211686
Harvest index ¹	-0.30197	0.788702	-0.104337	0.43801
Eigen value	74.228555	32.391373	8.6117659	3.891131
Percent of total variance explained	61.1	26.7	7.1	3.2
Cumulative of total variance (%)	61.19	87.89	94.9	98.2

CONCLUSION

In the analysis of variance, the mean square was highly significant for all traits studied. This pointed out the existence of adequate genetic variability among the experimental chickpea indicating the suitability of these materials to achieve the objectives outlined. The mean and range of the character considered in this study showed also wide variation. Based on the yield there was a significant yield difference among the studied chickpea genotypes. The coefficient of variation in majority of the character is less than indicated the precision of the study.

High heritability in broad sense and high genetic advance were obtained for the character studied, which showed that there was the possibility of selection to improve yield and yield related traits in chickpea genotype. Most of character studied depicted narrow difference in values of PCV and GCV and showed high value of PCV and GCV. In this study both PCV and GCV displayed a wide range of value for characters considered.

Majority of characters showed positive and high inter-character correlations to yield that indicated the possibility of correlated response to selection. Then with increase in one, there is a possibility of increment in the other characters. The dendrogram obtained from the hierarchical cluster analysis grouped into four clusters and two solitary accessions based on similarity and dissimilarity of accessions through studied traits. Released varieties are better than landraces in yield product compared to landrace accessions. The principal component analysis revealed principal components PC1 to PC4 with Eigen values 74.2, 32.3, 8.6 and 3.2 respectively, have accounted for 98.2% of the total variation. The first two principal components PC1 and PC2 with values of 61.1% and 26.1% respectively contributed more to the total variation. Generally, further studies of chickpea genotypes with larger sample size in broad environments and seasons can give additional information on chickpea variability in order to improve yield product.

REFERENCES

- Geervani P. Utilization of chickpea in India and scope for novel and alternative uses. *Uses of Tropical Grain Legumes: Proceedings of Consultants' Meeting*. 1991;27-30.
- Van der Maesen LJ. Origin, history and taxonomy of chickpea. *The chickpea* 1987;11-34.
- Zeeshan M, Arshad W, Ali S, Owais M, Zulkiffal M, Hussain M. Genetic divergence and character association in chickpea (*Cicer arietinum*) under rainfed conditions. *Wudpecker J Agric Res*. 2013;2(1):28-32.
- Chaudhary DP, Kumar A, Mandhania SS, Srivastava P, Kumar RS. Maize as fodder? An alternative approach. *Dir Maize Res Bull*. 2012;04-32.
- Christodoulou V, Bampidis VA, Hucko B, Ploumi K, Iliadis C, Robinson PH, et al. Nutritional value of chickpeas in rations of lactating ewes and growing lambs. *Anim Feed Sci Tech*. 2005;118(3-4):229-241.
- Food and Agricultural Organization Crop Production Index. Rome, Italy. 2010.
- Central Statistics Authority. Crop Report Data. 2013.
- Tabikew D, Asnake F, Kibebew A, Lijalem K. Improved chickpea (*Cicer arietinum* L.) technologies and seed production in Ethiopia. Ethiopia Agricultural Research Center Institute (EIARC), Research bulletin, Debre Zeit, Ethiopia. 2009.
- Huluka M, Tadesse N. Chickpea and lentil disease research in Ethiopia. *Proceedings of the First National Cool-Season Food Legumes Review Conference, Ababa, Ethiopia: ICARDA*. 1993-1994;346-366.
- Jing R, Vershinin A, Grzebyta J, Shaw P, Smykal P, Marshall D, et al. The genetic diversity and evolution of field pea (*Pisum*) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis. *BMC Evol Biol* 2010;10(1):1-20.
- Allard RW. Principles of plant breeding. John Wiley and Sons inc, New York. 1960.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. *Agron*. 1955;47(7):314-318.
- Rao VR, Hodgkin T. Genetic diversity and conservation and utilization of plant genetic resources. *PCTOC*. 2002;68(1):1-9.
- Noor F, Ashaf M, Ghafoor A. Path analysis and relationship among quantitative traits in chickpea (*Cicer arietinum* L.). *Pak J Biol Sci* 2003;6(6):551-555.
- Board JE, Kang MS, Harville BG. Path analyses of the yield formation process for late planted soybean. *Agron J*. 1999;91:128-135.
- Welsh RJ. Fundamentals of plant genetics and breeding. John Wiley & Sons, New York. 1990.
- Bejiga G, Anbessa Y, Gaur PM, Jagdish K, Rao BV. Chefe (ICC92318) A New Kabuli Chickpea Variety for Ethiopia. *SAT e-Journal*. 2005;1:1-2.
- SAS. SAS/STAT Institute Enterprise guide, version 9.1 edition. Cary, NC, USA: SAS Institute Inc. 2004.
- Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. 1977.
- Talebi R, Rokhzadi A. Genetic diversity and interrelationships between agronomic traits in landrace chickpea accessions collected from 'Kurdistan' province, north-west of Iran. *Int J Agric Crop Sci*. 2013;5(19):2203-2209.
- Dadi M. Morphological and random amplified polymorphic DNA (RAPD) marker variation analysis in some Ethiopian drought tolerant and susceptible chickpea (*Cicer arietinum*L.) genotypes Addis Ababa University, Ethiopian. 2005.
- Sakar D. The effect of irrigation on spring-sown chickpea. *Pakistan Agric J*. 2006.
- Dasgupta T, Islam MO, Gayen S. Genetic variability and analysis of yield components in chickpea (*Cicer arietinum* L.). *Ann Agric Res*. 1992;13:157-160.
- Mather K, Jinks JL. (The study of continuous variation(3rd ed), London: Chapman and Hall; Biometrical genetics. 1982.
- Arshad M, Bakhsh A, Bashir M, Haqqani M. Determining the heritability and relationship between yield and yield components in chickpea (*Cicer arietinum* L.). *Pak J Bot*. 2002;34:237-245.
- Deshmukh SN, Basul MS, Reddy PS. Genetic variability, character, association and path coefficients of traits in virginia bunch varieties of groundnuts. *India J Agric Sci*. 1992;56: 816-821.
- Padmavathi PV, Murthy SS, Rao VS, Ahamed ML. Correlation and path coefficient analysis in Kabuli chickpea (*Cicer arietinum* L.). *Int J App Biol & Pharm*. 2013;4(3):107-110.
- Saleem M, Shahzad K, Abdul-ur-Rauf S. Heritability estimates for grain yield and quality characters in chickpea (*Cicer arietinum*). *Int J Agri Biol*. 2002;4(2):275-276.
- Usman S, Qurban A, Naveed MT, Muhammad S. Correlation analysis of seed yield and its components in chickpea (*Cicer arietinum* L.) genotypes. *IJAVMS*. 2012;6(4):269-276.
- Tulu A. Correlation and variation studies on yield and some plant

- characters in some indigenous and exotic chickpea varieties. Addis Ababa University, Addis Ababa. 1985.
31. Shanko D, Andargie M, Zelleke H. Interrelationship and path coefficient analysis of some growth and yield characteristics in cowpea (*Vigna unguiculata* L. Walp.) genotypes. *J Plant Sci.* 2014;2(2):97-101.
 32. Keneni G, Bekele E, Assefa F, Imtiaz M, Debele T, Dagne K, et al. Phenotypic diversity for symbio-agronomic characters in Ethiopia chickpea (*Cicer arietinum* L.). Germplasm accessions. *Afr J Biotechnol.* 2012;11(63):12634-12651.
 33. Ba FS, Pasquet RS, Gepts P. Genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.] as revealed by RAPD markers. *Genet Resour Crop Evol.* 2004;51(5):539-550.
 34. Qurban A, Muhammad A. Estimation of Variability and correlation analysis for quantitative traits in chickpea (*Cicer arietinum* L.). *IJAVMS.* 2011;6(4):241-249.
 35. Naveed MT, Ali Q, Saeed U, Hussain B. Combining ability analysis for various quantitative traits in chickpea (*Cicer arietinum* L.). *IJBPAS.* 2012;1(4): 503-511.
 36. Talebi R, Karami E. Morphological and physiological traits associated with seed yield in different chickpea (*Cicer arietinum* L.) genotypes under irrigated and water- deficit environments. *SAJEB.* 2011;1(6):260-267.
 37. Ghafoor A, Gulbaaz FN, Afzal M, Ashraf M, Arshad M. Inter-relationship between SDS-PAGE markers and agronomic traits in chickpea (*Cicer arietinum* L.). *Pak J Bot.* 2003;35(4):613-624.
 38. Noirot M, Hamon S, Anthony F. The principal component scoring: A new method of constituting a core collection using quantitative data. *Genet Resour Crop Evol.* 1996;43(1):1-6.
 39. Muniraja C, Satish RG, Raju C, Manjunath H. Principal component analysis among genotypes of chickpea (*Cicer arietinum* L.). *Int J Agric Sci.* 2011;7(2):382-386.
 40. Gomez AK, Gomez AA. Statistical procedures for agricultural research. John Willey and Sons, New York. 1984;657.