SOIL & CROP SCIENCES | RESEARCH ARTICLE

Genetic variability and association analysis of Desi-type chickpea (*Cicer arietinum* L.) advanced lines under potential environment in North Gondar, Ethiopia

Amare Tsehaye1*, Asnake Fikre2 and Muluken Bantayhu3

**Abstract:** The success of good breeding program usually depends upon the genetic variability present in the breeding materials, however, spatial and temporal studying on the amount, kind and magnitude of variability as well as genetic relationship of traits are not efficiently exploited yet. The present investigation was designed to assess the extent of variability, genetic advance, heritability and interrelation of different traits of 100 chickpea genotypes using triple lattice design in Takusa district, North Gondar, Ethiopia, during 2018/19 main cropping season. The examined genotypes were highly significant for all studied traits. The magnitude of genotypic and phenotypic coefficient of variation indicated the presence of variability among advanced lines. The trait above ground biomass exhibited the highest range of variability followed by grain yield, number of pods per plant, hundred seed weight, days to flowering and days to maturity. The highest estimates of genotypic and phenotypic coefficient of variation were exhibited grain yield followed by number of pods per plant, number of secondary branches per plant, above ground biomass, and harvest index. The highest broad sense heritability coupled with high

---

**Additional information is available at the end of the article**

---

**ABOUT THE AUTHOR**

The Author was born on 03, October 1988 in North Gondar of Amhara Regional State, Ethiopia. As soon as he reached the age for schooling, he attend his education and joined Debre Birhan University and graduate with B.Sc. degree in plant science. Soon after, the Author was employed at Amhara Agricultural Research Institute (AARI), Gondar agricultural research center, North Gondar, Ethiopia, as sorghum and chickpea breeder. Now he completed his master of science in plant breeding at Bahir Dar University and working as chickpea breeder at Amhara Agricultural Research Institute, Ethiopia. During his stay he had generated more than 10 research proposals and published more than 3 research activities in Known journals.

---

**PUBLIC INTEREST STATEMENT**

Chickpea is the second most important legume crop, contributing significantly in securing nutritional and food security particularly in poor and developing countries. However, it could not get the due attention from researchers and breeders across the world. Despite research and breeding activities of last five decades in chickpea improvement, yield increase is relatively not satisfactory. To hasten chickpea production and productivity knowing Informations on the relative magnitude of different sources of variation among different genotypes for several traits to know their range of genetic diversity. Because the genetically diverse genotypes are likely to produce heterotic effect and superior segregate when incorporated in hybridization in crop improvement program. Therefore, the success of good breeding program usually depends upon the genetic variability present in the breeding materials, so assessment of genetic variability in the base population should have to be prior action in breeding program.
genetic advance were observed for grain yield, number of pods per plant, number of secondary branches per plant, above ground biomass and hundred seed weight. In the present investigation inter distance (D²) values were ranged from 81.6 to 874.5 with a total of 9 significant clusters. The first four principal components, whose Eigenvalues greater than one, accounted more than 81.5% of the total variation. Hence, the existence of huge variability infers, exploiting the existing variation is enough to improve chickpea grain yield only thorough simple selection by giving due attention for above ground biomass, number of secondary branch per plant, number of pod per plant and harvest index.

**Subjects:** Agriculture & Environmental Sciences; Botany; Plant & Animal Ecology; African Studies

**Keywords:** PCA; path coefficient analysis; clustering; chickpea; genetic variability

1. **Introduction**

Pulse crops play as a driver in the home of agriculture for economic growth and food security. It occupies approximately 13% of cultivated land and account for approximately 10% of the agricultural value addition. They are also contribute much more for smallholder in income generation, since high value crop than cereals, and it is a cost effective source of protein that accounts for approximately 15% of protein intake (CGIAR, 2010). Pulses, such as chickpea (Cicer arietinum L.), as dry seeds of leguminous, are an important sources of human regimen throughout the world. Chickpea is the most important pulse crop in Ethiopia. The bulk of the crop variety in the country is dominated by the sweet Desi type and the Kabuli type is also grown in limited areas. In Ethiopia chickpeas are consumed widely fresh as green vegetables, sprouted, fried roasted and boiled. It is also ground into flour to make baby feed mixed with other cereals, soup bread and meat. It is also used to rehabilitate depleted follow lands through utilizing crop rotation system (Upadhyaya et al., 2011).

Globally chickpea is cultivated on over 13.2 million hectare with an annual production of 13.1 million tons and productivity less than 1 t/ha, much less than estimated potential of 6 t/ha under optimum growing conditions. There are two different types of chickpea that are grown worldwide, Desi and Kabuli. Desi-type chickpeas have colored and thick seed coat. The seed colors of Desi chickpeas are brown, yellow, green or black. The seeds are generally small and angular with a rough surface. The flowers are generally pink and the plants show various degrees of anthocyanin pigmentation, although some Desi types have white flowers and no anthocyanin pigmentation.

![Figure 1. Chickpea productivity and area coverage progress graph in Ethiopia.](image-url)
on the stem. The Desi-types account for 80–85% of world’s chickpea area. The splits (dal) and flour (besan) are invariably made from Desi type. Among the two chickpea types, the Desi type is dominantly grown in Ethiopia. The major chickpea growing zones include: East Shewa, West Shewa and North Gondar (Kassie et al., 2009; Aliu et al., 2016).

Ethiopia is the leading 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 (Foostat, 2015). Ethiopia is the seventh largest producer worldwide and contributes about 2% to the total world chickpea production but it is among top ranked (1.913 t/ha) in productivity, where as in Africa it is the largest producer accounting about (46%)of the continents production (Kassie et al., 2009). However Ethiopian chickpea production covered 242,000 ha with yield surpassing 2 t/ha (CSA, 2017/18), more than 90% of the entire chickpea area and 92% of the total chickpea production is from Amhara and Oromia regional states, with 52.5% and 40.5% respectively, however more than 25% percent of it is from North Gondar, Ethiopia (Minale, 2009).

The genetic diversity of genotypes makes them an important resource of genes for breeding programs, developing new farming systems, diversification of production and new quality products. Information about genetic diversity helps the selection of parental genotypes from random populations. Accurate estimation of the levels and patterns of genetic diversity is useful to estimate the potential of heterotic combinations before attempting crosses and hence saving time and resources (Hollauer & Miranda, 1988). Such information can serve for introgression of desirable genes from wild germplasm to the high yielding germplasm resource, analysis of genetic variability in germplasm and identification of different combinations for creating segregating progenies with greatest genetic variability (Barrett & Kidwell, 1998). Estimate the level of genetic variability and determine the significance of traits are important for further trait discovery, inter-crossing design, economic trait detection and good parental lines establishment.

Genetic variability refers the genetic differences within or among genotypes. Genetic variability has great importance for the survival of a species. When a population of an organism contains a large gene pool, the genetic blueprints of individuals in the population vary significantly and the group has a greater chance of surviving and flourishing than a population with limited genetic variability because some of the individuals may have inherited traits making them particularly resistant to biotic and abiotic factors. The more genetic variability present within species or populations, the higher the likelihood that at least some of the individuals will be resistant to biotic and abiotic factor, high yielder, and most economical like in nutrient use efficiency.

The major constraints to chickpea productivity are biotic stresses like ascochyta blight, pod borer, cut worm and fusarium wilt, abiotic stresses like drought, extreme temperatures and salinity. Chickpea has high variation for various qualitative and quantitative traits i.e. grain color and shape, color of flower, pod number, seed coat color, earliness, insect pest resistance, that can help breeders to develop or select superior lines and varieties. For maintenance and efficient utilization of germplasm, it is important to investigate the extent of genetic variability and its magnitude for the determination of the success of a breeding program (Khan & Farhatullah, 2011). The efficiency of selection depends on the identification of genetic variability from the phenotypic expression of the characters.

The success of good breeding program usually depends upon the genetic variability present in the breeding materials, so assessment of genetic variability in the base population should have to be prior action in breeding program. Information on the relative magnitude of different sources of variation among different genotypes for several traits helps in measurement of their range of genetic diversity. The genetically diverse genotypes are likely to produce heterotic effect and superior segregate when incorporated in hybridization to hasten crop improvement program. Thus, knowledge on genetic variability, heritability and genetic advance is essential for a breeder to choose and for efficient utilization of better genotypes for crop improvement programs.
However, spatial and temporal studies on the amount, kind and magnitude of variability as well as genetic relationship of traits are not efficiently exploited. Thus, the purposes of this study were estimate the total genotypic variability presented among germplasms under the study and to determine the correlations among traits. Therefore the present study aimed to assess and quantify the level of genetic variability present among tested chickpea germplasm lines and determine the significance of various economic traits.

2. Materials and methods

2.1. Description of the study area
The experiment was conducted at Mekonta farm site in Takusa district, North Gondar, Ethiopia. The area is located at 12º 0’ 50” to 12º 23’ 40” northern latitude and 36º 24’ 28” to 37º 6’ 58” east longitude with an altitude of 1780 meter above sea level with annual rainfall of 730 mm. The average temperature of the areas is 21.65°C. The major crops grown widely are chickpea, tef, maize, spice crops (cumin, hot pepper, tomato), etc., under rainfed and irrigation but cereal mono cropping is the predominant crop grown in the study area (Tesfaye Wossen, 2017). The soil type of the area is light vertisol with a pH ranging from 6.5 to 8.0. The field was loose tilt and well drained. The stubble and debris from the previous crop was removed. A rough seedbed was prepared to avoid packing of the cloddy surface due to winter rains and to facilitate soil aeration and for easy seedling emergence (Aliu et al., 2016).

2.2. Climate data for the experimental area
Takusa district is the key growing areas of chickpea in Ethiopia (Kassie, 2009). The area received a long term mean annual rainfall of 1097 mm with a mean annual temperate of 23°C (min 16°C and max 30°C). The experimental area received 1217 mm mean annual rain fall with 22°C (min 13.27°C and max 30.6°C) mean annual temperature during the growing season in 2018.

2.3. Experimental materials
A total of 100 advanced lines of Desi-type chickpea germplasms were evaluated in 2018/19 main cropping season at Mekonta farm site, Takusa district, North Gondar, Ethiopia The genotypes were acquired from Debre Zeit agricultural Research Center, Ethiopia. The list of genotypes is given below (Table 1).

2.4. Experimental design and field management
The experiment was laid out in triple lattice design with three replications. Each genotype had 2 rows in a plot of 2 m length with a row to row and plant to plant spacing of 30 cm and 10 cm, respectively. Each genotype was assigned to each plot randomly. A seed of 100 kg/ha was used. 121 kg NPS (23 N, 46P₂O₅, and 8.4S) fertilizer was applied. All the recommended crop management practices have been accomplished based on the recommendation

2.5. Data collected
Five plants per genotypes were selected randomly for recording plant based characters and net plot area for plot based characters:

2.6. The data collected on plot basis and their descriptions are indicated as follow
   (1) Days to flowering (DF): Number of days from planting to 50% of plants bears flower.
   (2) Days to physiological maturity (DM): The number of days from sowing to the stage when 90% of the plants in a plot have reached physiological maturity.
   (3) Seed filling period (SFP): The number of days from flowering to maturity (i.e. the number of days to maturity minus the number of days to flowering).
   (4) Hundred seed weight (HSW) (g): The weight of hundred seeds taken randomly from the harvest seed lots of each plot.
Table 1. List of genotypes used in the present investigation

| Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree |
|------|-------------------------|------|-------------------------|------|-------------------------|------|-------------------------|
| G-1  | iccx-060045-f3-p12-BP   | G-26 | iccu-11,108             | G-51 | icc-4958                | G-76 | iccx-060039-f3-p10-BP   |
| G-2  | iccx-090013-f2-p147-BP  | G-27 | DZ-2012-CX-20,115-0041 | G-52 | iccx-060045-f3-p11-BP   | G-77 | iccril-03-0167          |
| G-3  | IE-16-012/2             | G-28 | iccx-060039-f3-p2015-BP | G-53 | iccx-060045-f3-p165-BP  | G-78 | iccx-090013-f2-p245-BP  |
| G-4  | iccx-060039-f3-p196-BP  | G-29 | iccx-060045-f3-p5-BP    | G-54 | IE-16-025/1             | G-79 | icc-15,762              |
| G-5  | icc-1164                | G-30 | icc-1422                | G-55 | iccx-090013-f2-p129-BP  | G-80 | DZ-2012-CX-0028         |
| G-6  | iccx-060039-f3-p39-BP   | G-31 | DZ-2012-ck-20,115-50,045 | G-56 | icc-67                  | G-81 | iccx-060045-f3-p157-BP  |
| G-7  | IE-16-094/1             | G-32 | iccx-090013-f2-p120-BP  | G-57 | IE-16-003/1             | G-82 | icc-4533                |
| G-8  | DZ-2012-CK-0253         | G-33 | iccx-090013-f2-p3-BP    | G-58 | iccx-090013-f2-p234-BP  | G-83 | iccx-060039-f3-p107-BP  |
| G-9  | icc-14,778              | G-34 | iccx-090013-f2-p145-BP  | G-59 | DZ-2012-CK-20,115-16-0058 | G-84 | icc-13,863              |
| G-10 | IE-16-079/1             | G-35 | DZ-2012-CK-0040         | G-60 | iccx-090013-f2-p107-BP  | G-85 | iccx-060045-f3-p130-BP  |
| G-11 | iccx-060039-f3-p174-BP  | G-36 | 090013-f2-p276-BP       | G-61 | iccx-060039-f3-p178-BP  | G-86 | icc-510                 |
| G-12 | icc-15,888              | G-37 | IE-16-109/2             | G-62 | iccx-060045-f3-p173-BP  | G-87 | iccx-0900013-f2-p115-BP |
| G-13 | iccril-04-0087          | G-38 | iccx-090013-f2-p105-BP  | G-63 | iccx-090013-f2-p265-BP  | G-88 | JV-11                   |
| G-14 | DZ-2012-CK-240          | G-39 | iccx-090013-f2-p215-BP  | G-64 | icc-6279                | G-89 | Local                   |
| Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree | Code | Genotype Name/ pedigree |
|------|-------------------------|------|-------------------------|------|-------------------------|------|-------------------------|
| G-15 | Natoli                  | G-40 | iccx-060039-f3-p173-BP  | G-65 | icc-15,294              | G-90 | iccx-060045-f3-p197-BP  |
| G-16 | iccx-060045-f3-p98-BP   | G-41 | iccu-115                | G-66 | iccx-060045-f3-p76-BP   | G-91 | DZ-2012-CX-0227         |
| G-17 | iccx-060039-f3-p21-BP   | G-42 | DZ-2012-ck-0238         |      | icc-14199xnatoli-p137  | G-92 | iccx-060045-f3-p91-BP   |
| G-18 | iccx-060039-f3-p182-BP  | G-43 | JG-62                   | G-68 | DZ-2012-CX-0048         | G-93 | iccx-060039-f3-p204-BP  |
| G-19 | IE-16-059/2             | G-44 | iccx-060039-f3-p57-BP   | G-69 | iccx-060039-f3-p270-BP  | G-94 | iccx-060039-f3-p24-BP   |
| G-20 | iccx-060039-f3-p145-BP  | G-45 | Dimtu                   | G-70 | icc-10,673              | G-95 | icc-5135                |
| G-21 | DZ-2012-CK-0048         | G-46 | iccx-060039-f3-p131-BP  | G-71 | iccx-090013-f2-p107-BP  | G-96 | iccx-060045-f3-p253-BP  |
| G-22 | iccx-060039-f3-p188-BP  | G-47 | iccx-060045-f3-p132-BP  | G-72 | iccu-07103              | G-97 | iccril-03-0215          |
| G-23 | DZ-2012-CK-0030         | G-48 | iccu-090013-f2-p108-BP  | G-73 | Dalota                  | G-98 | iccx-060045-f3-p126-BP  |
| G-24 | iccx-090013-f2-p103-BP  | G-49 | iccril-03-0127          | G-74 | iccx-060045-f3-p232-BP  | G-99 | iccx-060045-f3-p102-BP  |
| G-25 | DZ-2012-CK-0239         | G-50 | IE-16-059/1             | G-75 | icc-15,614              | G-100| iccu-94,954             |
Table 2. Structure of analysis of variance (ANOVA) for triple lattice design (TLD)

| Source                  | Df     | SS    | MS    | Computed F |
|-------------------------|--------|-------|-------|------------|
| Replication (adj)       | r-1    | SSR   | MSR   | MSR/MSE    |
| Treatment (unadj)       | k^2-1  | SST   | MST   | MST/MSE    |
| Block in rep (adj)      | r(k-1) | SSB   | MSB   | MSB/MSE    |
| Intra block error       | (k-1)(r-k-1) | SSE | | |
| Total                   | rk^2-1 | SSTot | | |

(5) Grain yield (GY): Grain yield (kg ha^{-1}) from the specified net plot area and adjusted to its recommended (10%) moisture content.

(6) Above ground biomass (BM): the weight of the above ground mass including seed (kg ha^{-1}) of chickpea in specified net plot area as soon as harvesting.

(7) Harvest index (HI): calculated as the ratio of grain yield to above ground biological yield.

2.7. Data collected on plant basis and their descriptions are indicated as follow

(8) Number of pods per plant (NPP): Average of actual count of five plants pod.

(9) Number of seeds per pod (NSP): five random pods were crushed for each five random plants, counting the total seed and divided for number of pod and number of plant.

(10) Plant height (PH) (cm): The average height of five plants taken randomly from each plot measured at physiological maturity starting from ground to tip of the shoot.

(11) Number of primary branches (NPB): Average of actual count of primary branches on the main stem per plant.

(12) Number of secondary branches (NSB): Average of number of branches arising directly from primary branches.

2.8. Quality parameter

(13) Protein content (%)

The determination of the composition of chickpea seed was performed at Ethiopia Institute of Agricultural Research (EIAR), food research lab using the Near-infra-red spectrometry (NIRS) facility. The approach of protein analysis was done through measuring the crude protein (CP) content of samples of chickpea by NIRS of the 100 working samples. NIR spectral data were collected using NIR Analyzer (Brimrose) in the reflectance mode. Each sample was scanned twice in the 1100-2300 nm spectral range. Partial least squares (PLS) regression was applied to the spectral data through Unscramble software (version 8.0.5) to develop a calibration model capable of estimating the CP content of the samples. As a result, correlation coefficients of 0.95, 0.86 and 0.88 were obtained for calibration, cross validation and external validation respectively. Moreover, low standard errors were achieved. The standard error of calibration (SEC) was 0.52, the standard error of cross validation (SECV) was 0.88 and the standard error of prediction was 0.75.

2.9. Data analysis

2.9.1. Analysis of variance (ANOVA)

The data were subjected to analysis of variance using SAS software 9.0 computer package to test the level of significance among the genotypes for different characters under study. Tukey was used for comparison of genotypic means at 5% and 1% significance levels. The ANOVA was computed using the following mathematical model:

Model of triple lattice design
\[ Y_{ijl} = \mu + r_j + g_i + P(lj) + \epsilon_{ijl} \]

Where: \( Y_{ij} \) is observed value of the trait of the \( Y \) for the \( i \)th genotype in \( j \)th replication

\( \mu \)= the general mean of trait \( Y \)

\( r_j \)= the effect of \( j \)th replication

\( g_i \)= the effect of \( i \)th genotypes and

\( P(lj) \)= block within replicate effect

\( \epsilon_{ijl} \)= the experimental error associated with the trait \( Y \) for the \( i \)th genotype in \( l \)th block with \( j \)th replication

Where, \( r \): Number of replication, \( k^2 \): Number of treatment, \( k \): Number of treatments in a block

**2.10. Estimation of phenotypic and genotypic parameters**

The genotypic and phenotypic variance components and coefficient of phenotypic and genotypic variability was estimated according to statistical procedure, by using the formula, adopted by Burton and De vane as follows:

Genotypic variance (\( \sigma^2g \)) = (\( MS_g-MS_e \))/\( r \), where: \( MS_g \) = mean square due to genotypes

\( MS_e \)= error mean square, \( r \)= the number of replication

Environmental variance (\( \sigma^2e \)) = error mean square = \( MS_e \)

Phenotypic variance (\( \sigma^2p \)) = (\( \sigma^2g \)) + (\( \sigma^2e \))

Coefficient of variation at phenotypic and genotypic levels was estimated using the following formula and interpreted using the guidelines given by Subramanian and Sivasubramanian (1975).

Phenotypic coefficient of variation (PCV) = (\( \sqrt{\sigma^2p/X} \) *100

Genotypic Coefficient of variation (GCV) = GCV = (\( \sqrt{\sigma^2g/X} \) *100

Where: \( X \)= grand mean of character. The classification for genotypic coefficient of variation (Subramanian & Sivasubramanian, 1975) was as follows: Low (< 10%), Moderate (10–20%) and High (> 20%).

**2.11. Estimation of heritability in broad sense (H²)**

Heritability in broad sense is expressed as a percentage of the ratio of the genotypic variance (\( \sigma^2g \)) to the phenotypic variance (\( \sigma^2p \)) estimated on genotype mean using method proposed by Allard (1960). It was computed by adopting the formulae presented by Allard as:

\[ \text{Heritability (H²)} = (\sigma^2g/\sigma^2p) \times 100 \]

Where, \( H² \)=Heritability in broad sense, \( \sigma^2p \)= Phenotypic variance, \( \sigma^2g \)=Genotypic variance

**2.12. Estimate of genetic advance**

Genetic advance for all characters was computed by adopting on the formulae presented by Allard (1960) and GA as percentage of the mean expected from selection of the best 5% of the genotypes were estimated as:
Expected genetic advance (GA) = $H^2 \times k \times \sigma_p$

Expected genetic advance as percentage of mean = (GAx100)/$\mu$

Where, $k$ is a constant value at selection intensity of 5% ($k = 2.06$), $\sigma_p$ is the phenotypic standard deviation; $H^2$ is broad sense heritability; and $\mu$ is the grand populations mean for the trait under considerations.

### 2.13. Correlation

Correlation ($r$) was calculated based on the following formula

$$
\frac{\sum xy - \frac{\sum x \sum y}{n}}{\sqrt{\left(\sum x^2 - \frac{(\sum x)^2}{n}\right) \left(\sum y^2 - \frac{(\sum y)^2}{n}\right)}}
$$

Testing correlation for significant = $(r\sqrt{n}-2)/(1-r^2)$

The phenotypic and genotypic correlation coefficients was computed using the formula suggested by Singh and Chaudhury (1985).

Phenotypic coefficient of correlation ($rp$) = $Pcov_{xy}/\sqrt{(\sigma^2x, \sigma^2y)}$

Genotypic coefficient of correlation ($rg$) = $Gcov_{xy}/\sqrt{(\sigma^2x, \sigma^2y)}$

Where, $rp$ = Phenotypic correlation coefficient, $rg$ = Genotypic correlation coefficient, $Pcov_{xy}$ = Phenotypic covariance between variables $x$ and $y$, $Gcov_{xy}$ = Genotypic covariance between variables $x$ and $y$, $\sigma^2x$ = Genotypic variance for trait $X$, $\sigma^2y$ = Genotypic variance for trait $Y$, $\sigma^2p_x$ = Phenotypic variance for trait $X$, $\sigma^2p_y$ = Phenotypic variance for trait $Y$.

Phenotypic correlation coefficient was tested for their significance.

t = $r/SE_{rp}$ where, $SE_{rp} =\sqrt{(1-r^2)/(n-2)}$

Significance genotypic correlation coefficient was tested with the following formula

t = $rg_{xy}/SE_{rg_{xy}}$ where, $SE_{rg_{xy}} =\sqrt{(1-2rg_{xy})/(2H_x^*H_y)}$

$SE_{rg_{xy}}$ = Standard error of genotypic correlation coefficient between character $X$ and $Y$

### 2.14. Path coefficient analysis

The path coefficients was obtained using the general formula of Dewey and Lu (1959) by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient. $rij = pij + \sum rik.pkj$

Where, $rij$ = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficient.

$pij$ components of direct effects of the independent character

(i) On the dependent variable

(j) As measured by the genotypic path coefficient; and $\sum rik.pkj$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent character (k).
The contribution of the remaining unknown factor was measured as the residual factor (Pr), which is calculated as, \( pr = 1 - rij \).

### 2.15. Cluster analysis

Cluster analysis is a group of multivariate techniques whose primary purpose is to group objects (e.g., respondents, products, or other entries) based on the characteristics they possess. It is a means of grouping genotypes based upon attributes that make them similar. Data of five plants from each genotype was averaged replication wise and mean data was used for statistical analysis. Clustering pattern among 100 chickpea genotypes was assessed by using Tocher's method (Rao, 1952). Average intra- (diagonal) and intercluster distance was estimated by using Tocher’s method representing Euclidean distances considering yield and its ten contributing traits in chickpea genotypes.

The generalize distance between two population is defined by Mahalanobis (1936) as

\[
D^2 = \lambda_{ij} \cdot \sigma_i \cdot \sigma_j
\]

Where, \( \lambda_{ij} \) = reciprocal matrix to the common dispersion matrix
\( \sigma_i \) = difference between the mean values of two populations for \( i \)th character
\( \sigma_j \) = difference between the mean values of two populations for \( j \)th character

### 2.16. Determination of genetic distance

Formal rules can't be laid down for finding the clusters because a cluster is not a well-defined term the only criteria appears to be that any two groups belonging to the same cluster should at least on an average show a smaller \( D^2 \) than those belonging to the two different clusters. Tocher method described by Rao (1952) is to start with the two closely associated groups and find a third group which has the smallest \( D^2 \) from the two. Similarly the fourth is chosen to have the smallest \( D^2 \) from the first three and so on if at any stage the average \( D^2 \) of the group from those already listed appears to be high, then this group does not fit in the former groups and is therefore taken outside the former cluster. The group of first cluster are then omitted and rest are treated similarly it is also useful to calculate the change in average \( D^2 \) within a cluster due to inclusion of an additional group if the changes are appreciable, then the newly added group has to be considered as outside the cluster.

Average intra and inter cluster \( D^2 \) and \( D \) values

1. Average intra cluster \( D^2 \)

\[
D^2 = \frac{\sum D^2}{n}, \text{ where, } \sum D^2 \text{ is sum of distances between all possible combinations (n) is the population included in a cluster.}
\]

2. Average inter cluster \( D^2 \)

\[
D^2 = \frac{\sum D^2}{n_i n_j}
\]

Where, \( n_i = \) number of population in cluster \( i \), \( n_j = \) number of population in cluster \( j \)

### 2.17. Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included within the cluster.
2.18. Principal component analysis
Principal component analysis (PCA) was used to find out the characters, which accounted more to the total variation. The data were standardized to mean zero and variance of one before computing principal component analysis. Principal components were calculated.

The first PCA value (Y1) is given by the linear combination of the variables X1, X2 … Xp

\[ Y1 = a11X1 + a12X2 + ... + a1pXp \]

The second principal component is calculated in the same way,

\[ Y2 = a21X1 + a22X2 + ... + a2pXp \]

This continues until a total of p principal components have been calculated, equal to the original number of variables. At this point, the sum of the variances of all of the principal components will equal the sum of the variances of all of the variables.

3. Results and discussion

3.1. Analysis of variance of studied traits
The analysis of variance was carried out for 13 traits. The analysis of variance showed highly significant difference among the genotypes for all traits (Table 3). Several authors, Arshad and Ghafoor (2004), Parashi et al. (2013), Mallu et al. (2014), and Joshi et al. (2018) reported that there was considerable genetic variability for all yield and yield related traits under their independent investigation. Sirohi (2008) confirmed the analysis of variance of the individual as well as combined over environments revealed significant differences among the genotypes for all the characters studied. The present investigation indicated that the presence of considerable genetic variability for the studied genotypes, which empowers the breeder to improve chickpea production only through simple selection.

Thirteen most important quantitative traits were subjected for analysis of variance (Table 3), significant blocking and replication effects were observed for seed filling period, plant height and grain yield, while the remaining observed characters showed non-significant difference, indicating that except for a few traits, block and replication was not a factor the imminent genotype difference. Parida et al. (2018) investigated on some chickpea genotypes and reported that genotypes were grain yield, primary branch per plant and plant height showed significant block and replication effect. Indicating that the present experimental plot was showed uniform error variance for studied traits and genotypes.

3.2. Mean and range of traits under the study
The mean and range values for different characters studied in the present investigation are given below (Table 4), while mean performance of the 100 chickpea genotypes for 13 observed traits are presented in the Appendix Table 1.

The genotype mean for days to 50% flowering was 57 days. The variation of this trait ranged from 45 to 74 days. Genotype IE-16-109/2 took the minimum days for 50% flowering while the maximum was by genotype icc-1164. About 39% of the genotypes tested in the study need greater than 57 days (grand mean) for flowering (Table 4). Mallu et al. (2014) examined sixty Desi genotypes and reported wide genetic variability for days to flowering. Khan and Farhatullah (2011) and Gul et al. (2013) also reported significant genetic variability for days to 50% flowering. The noted wide genotypic variation for days to 50% flowering could be due to variations in their genetic makeup, environmental influences and genotype by environment interactions. This critical stage is highly sensitive and may be influenced by oscillation of temperatures which adversely disturb viability of pollen and pollination that could results poor fertilization and low seed set.
Days to maturity was ranged from 96 days to 133 days, with a grand mean value of 116 days, indicating that the tested genotypes were under the category of early to medium maturing genotypes. The longest maturity date was recorded by genotype icc-15,294, while the shortest was from genotype IE-16-109/2. Jakhar (2014) also found a wide variation ranged from 51.67 to 82.67 days variability (Table 4). Chauhan (2011) reported similar result for observed character of days taken to maturity. In the present investigation a wide variation was existed among tested germplasms, indicating that early maturing to medium maturing genotypes that enables the breeder to select the best genotype for different agro ecologies was identified. Crop phenology (flowering and maturity) contributes a vital role in increasing grain yield and yield related characters of chickpea. Breeding for earliness is one of the breeding objectives of chickpea as most end users and farmers usually seek for early maturing varieties. Early maturity could give consecutive merit like excess nitrogen fixation and enhancement of soil organic matter (Mallu et al., 2014).

Seed filling period varied from 45.3 to 71.3 days with a genotype mean value of 59. This showed that genotypes were different in seed filling period. The shortest seed filling period was from genotype icc-1164, while the longest seed filling period was from genotype iccx-060045-f3-p130-BP (Table 4). Seed filling duration greatly affects major yield contributing traits and quality

| Traits                          | Replication Df =2 | Block Df =27 | Genotype Df =99 | Error Df =171 | CV ( %) | R² Value |
|---------------------------------|-------------------|--------------|-----------------|---------------|---------|----------|
| Days to flowering               | 3.6 ns            | 2.4 ns       | 131.2***        | 1.6           | 2.8     | 0.97     |
| Days to maturity                | 7.6 ns            | 3.36 ns      | 112.4***        | 1.6           | 1.4     | 0.96     |
| Seed filling period             | 21.4*             | 5.04*        | 78.5**          | 1.9           | 3.4     | 0.92     |
| Plant height (cm)               | 20.5*             | 7.9*         | 101.55***       | 2.15          | 5.5     | 0.93     |
| Number of primary branch        | 0.003 ns          | 0.06 ns      | 1.11***         | 0.34          | 13.9    | 0.84     |
| Number of secondary branch      | 0.017 ns          | 0.049 ns     | 16.79***        | 0.22          | 3.5     | 0.99     |
| Number of pod per plant         | 1.1 ns            | 3.2 ns       | 1163.3***       | 1.7           | 7.7     | 0.99     |
| Number of seed per pod          | 0.015 ns          | 0.016 ns     | 0.14***         | 0.12          | 10.5    | 0.85     |
| Above ground biomass (kg ha⁻¹)  | 15987 ns          | 25549 ns     | 1,021,547***    | 164.2         | 9.2     | 0.99     |
| Grain yield (kg ha⁻¹)           | 1616.2*           | 6896*        | 3,599,907***    | 90.1          | 13.4    | 0.99     |
| Harvest index                   | 0.0008 ns         | 0.00046 ns   | 0.00087**       | 0.007         | 1.7     | 0.98     |
| Hundred seed weight (g)         | 22.07 ns          | 3.4 ns       | 114.03***       | 2.1           | 9.2     | 0.95     |
| Protein content                 | 0.01347 ns        | 0.01521 ns   | 5.757**         | 0.1274        | 0.84    | 0.99     |

Note: ***, **, * and ns indicates highly significant at 0.1%, highly significant at 1%, significant at 5% and non-significant respectively. CV: Coefficient of variations and Df: degree of freedom, cm: centimeter, kg ha⁻¹: kilogram per hectare and g: gram.
### Table 4. Range, mean, variance, genotypic and phenotypic coefficient of variability, broad sense heritability, and genetic advance as of mean for the 13 characters of chickpea genotypes tested in Takusa district during 2018/19

| Character | Range | Mean | max | min | MST | MSE | a\textsuperscript{2}e | a\textsuperscript{2}g | a\textsuperscript{2}P | GCV (%) | PCV (%) | H\textsuperscript{2}b (% | GA | GAM |
|-----------|-------|------|-----|-----|-----|-----|----------|--------|--------|--------|--------|-----------|-----|------|
| DF        | 57    |74.3 | 45  | 131.2|1.58 |1.58 |43.21     |44.79   |11.53   |11.74   |96.5    |13.30     |23.3 |
| DM        | 116   |133  |96   |112.4|1.60 |1.60 |36.93     |38.53   |5.26    |5.37    |95.8    |12.26     |10.6 |
| SFP       | 59    |71.3 |45.3 |78.4 |1.97 |1.97 |25.48     |27.45   |8.61    |8.94    |92.8    |10.02     |17   |
| PH        | 39.5  |57.5 |27.5 |101.6|2.16 |2.16 |33.13     |35.29   |14.57   |15.04   |93.8    |11.49     |29   |
| NPB       | 2.47  |3.9  |1.2  |1.11 |0.34 |0.34 |0.26      |0.60    |20.51   |31.27   |43      |0.68      |27.7 |
| NSB       | 6.37  |12.6 |1.7  |16.79|0.22 |0.22 |5.52      |5.74    |36.89   |37.62   |96.2    |4.75      |74.5 |
| NPP       | 51    |113.5|22.1 |1163.3|1.72 |1.72 |387.19    |388.91  |38.92   |39.00   |99.6    |40.45     |79.9 |
| NSP       | 1.15  |1.73 |1    |0.14 |0.12 |0.12 |0.01      |0.13    |7.10    |30.95   |5.26    |0.04      |3.4  |
| BM        | 5923  |10.375|2344 |10215.474|164.2|164.2 |3405.103  |3405.267|31.15   |31.16   |99.9    |3801      |64.2 |
| GY        | 2628  |4792 |975  |35999.907|90.1 |90.1 |1199938   |1200029 |41.67   |41.68   |99.8    |2256      |85.8 |
| HI        | 0.43  |0.52 |0.34 |0.01 |0.01 |0.01 |0.0005    |0.0078  |5.02    |20.50   |6.01    |0.01      |2.54 |
| HSW       | 22.7  |35.5 |10.10|144.03|2.10 |2.10 |47.31     |49.61   |30.23   |30.90   |95.7    |13.8      |60.9 |
| CP        | 15.13 |20.47|12.88|5.757|0.127|0.127|1.877     |2.004   |9.054   |9.356   |93.6    |2.6       |18.05|

Note: DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH: plant height, NPB: number of primary branch, NSB: number of secondary branch, NPP: number of pod per plant, NSP: number of seed per pod, BM: above ground biomass, HI: harvest index, HSW: hundred seed weight, GY: grain yield, max: maximum, min: minimum, MST: mean square of treatments, MSE: mean square of error, a\textsuperscript{2}g: genotypic variance, a\textsuperscript{2}P: phenotypic variance H\textsuperscript{2}b: Broad sense heritability in percent, GCV (%): Coefficient of genotypic variance, PCV (%): coefficient of phenotypic variance, GA: genetic advance, GAM: genetic advance as percent of means.
characters through influencing the nutrient uptake efficiency and source sink relationship. In the present investigation genotypes that took about 60 days of seed filling period exhibit the highest yield. This idea is strongly agreed with the investigation of Mallu et al. (2014) i.e. medium maturing genotypes which have medium seed filling period provide the highest yield, resulted from genetic makeup, environment (availability of moisture and nutrient uptake efficiency) and genotype by environment interaction.

Plant height was varied from 27.5 cm to 57.5 cm with a genotype mean height of 39.5 cm. The shortest plant height was recorded from genotype iccx-1164 and the longest plant height was recorded from genotype iccx-090013-f2-p215-BP (Table 4). Similar results were reported in previous studies by many authors (Khan & Farhatullah, 2011; Kayan & Adak, 2012; Mallu et al., 2014) in chickpea and Imani et al. (2013) in lentil. The wide range of variation for plant height could be due to genetic, environment and genotype by environment interactions. Plant height is one of the desirable characters in chickpea which reduces lodging effect and enhance ultimate seed yield. The results detected the potential of evaluated germplasm in obtaining genotypes with modest plant height along with other yield traits. Hence genotypes with modest plant height and reasonable yield traits could be used for genetic enhancement of chickpea varieties.

Number of primary and secondary branch was ranged from 1.2 to 3.9 and 1.7 to 12.6 with a grand mean of 2.47 and 6.37, respectively. Among the tested genotypes the maximum number of primary branch was recorded from genotype iccx-060045-f3-p91-BP, while the most branched and spreading habit were recorded from genotype JV-11 while the lowest branched were recorded from genotype iccx-060045-f3-p197-BP (Table 4). The present investigation showed the higher primary and secondary branch the higher the grain yield, indicating that breeders can boost chickpea yield through improvement of those characters which is directly influencing number of pod per plant. Chauhan (2011) and Jakhar (2014) investigated the highest grain yield from genotypes that afford maximum number of secondary branch.

Number of pod per plant greatly varied from 22.1 to 113.5 with a mean value of 50.8 (Table 4), which implies genotypes were respond differently for this character. Number of pod per plant is direct contributor for increment of chickpea economic yield. The highest pod number per plant was recorded from genotypes JV-11. Chickpea yield could be determined by the number of pods plant^{-1}. Genotypes varied with respect to number of pods per plant and showed existence of genetic variation. Similar results have been reported by many researcher Qureshi et al. (2004), Malik et al. (2010), Kayan and Adak (2012), Gul et al. (2013), and Latief et al. (2011) in lentil germplasm. The differences for number of pods per plant could be due to genotypes, environment and the interaction of both genotype and environment (GxE). This variation is resulted from the genetic makeup of the genotypes, environmental factor or the combined effect of both genotype and environment.

Number of seed per pod was also varied from 1 to 1.7 with 1.15 grand mean. In the present investigation genotype iccx-060039-f3-p173-BP exhibited the highest seed number per pod, while major genotypes especially large seeded type exhibit one seed per pod (Table 4). The observed trait of seed per pod was one of the yield attributing trait. Jakhar (2014) suggest that number of seed per pod varied significantly between genotypes and was one of the yield attributing character for grain yield of chickpea.

Above ground biomass showed a wide range of variation ranging 2344 kg ha^{-1} to 10,375 kg ha^{-1} with a grand mean value of 5923 kg/ha. The highest biomass was recorded from genotypes JV-11 and IE-16-059/1, while the lowest biomass was from genotype iccx-060045-f3-p197-BP (Table 4). In the present investigation genotypes that had maximum above ground biomass provides the highest grain yield, indicating that biomass were the major yield attributing trait. Ali et al. (2010) and Jakhar (2014) reported similar result. The highest significant variability could be attributed from the use of different genotypes which differed in number of branches, plant height, which all affect the biological yield.
Harvest index and hundred seed weight were also ranged from 34% to 52% and 10.1 g to 35.5 g to 10 g with a mean value of 0.43 and 22.6 g respectively. The highest harvest index (0.52) was recorded from genotypes iccx-060045-f3-p98-BP, iccu-11,108, and iccx-090013-f2-p265-BP; while the lowest harvest index (0.34) was recorded from genotype icc-1164 which is early maturing genotype. The largest and smallest hundred seed weight was recorded from genotype iccx-090013-f2-p265-BP (35.5 g) and IE-16-109/2 (10.1) respectively (Table 4). Malik et al. (2010) conduct a research on genetic variability and interrelationship among some agronomic traits in chickpea and investigate a significant variation in all studied agronomic traits including harvest index. Seed weight is one of the most important traits in seed consumed pulse crops including. The findings exhibited highly significant differences for 100 seed weight among studied genotypes (Table 3), which indicated the existence of considerable diversity. Significant and wide range of variations for 100 seed weight were reported by many authors (Khan & Farhatullah, 2011; Malik et al., 2010; Qureshi et al., 2004). The substantial variability could be attributed to the use of diverse genotypes, differed in pod size, pod filling period which affect the seed weight for the reason that late occurring biotic and abiotic stresses.

Crude protein were ranged from 12.88 to 20.47 with a mean value of 15.13 (Table 4), indicating that genotypes under this investigation showed significant difference for protein content. The highest protein content were recorded from the early genotype, which might suggest that the early maturing genotypes are better in soil nutrient uptake efficiency and additional nitrogen fixation than late maturing genotypes. Mallu et al. (2014), reported breeding for earliness is one of the chief breeding objectives of chickpea to have early maturing varieties in order to enable the crop to mature within the rainy periods and utilize the available moisture and nutrients, moreover early maturity could give consecutive merit like excess nitrogen fixation and enhancement of seed quality traits.

Grain yield showed a wide range of variation from 975 kg ha⁻¹ to 4792 kg ha⁻¹ with a mean value of 2628 kg ha⁻¹ (Table 4). In the present study, genotypes JV-11 (4792.2 kg ha⁻¹), IE-16,059/1 (4743.9 kg ha⁻¹), and iccx-090013f2-p215-BP (4720) exhibited the maximum grain yield among the tested genotypes, while genotype iccx-060045-f3-p197-BP and iccx090039-f3-p39-BP found to be low yielder less than 1000 kg ha⁻¹ (Appendix Table 1). Generally grain yield is dependent on yield attributing traits chiefly on number of secondary branch, number of pod per plant, above ground biomass and harvest index. Yield is a quantitative character, the result of various physiological and biochemical processes. Yield and yield contributing traits could have dynamic correlation with environmental effects. The investigation displayed wide genetic variability among studied genotypes for seed yield (Table 4). Significantly high variation for seed yield indicated the potential of the germplasm to determine the best genotypes for specific and broad adaptation across environments. In chickpea germplasm, previous studies have reported substantial variation for seed yield (Farshadfar & Farshadfar, 2008; Malik et al., 2010). High seed yield might be indicative of effectiveness of genotypes in utilization of the available moisture and nutrients and converted into economic yields. The presence of significant variation among evaluated genotypes for seed yield could be due to genetic, environment and genetic makeup combined with environmental effect. Best performance and high seed yield is one of the basic criteria for identifying and selecting superior varieties for end users and farmers. Besides, the presence of wide variation for seed yield could be attributed to high number of pods plant⁻¹, high biomass yield enables to converted final seed yield and heavier 100 seed weight. A crossover genotype by environment interaction indicated inconsistent performance of genotypes across environments for seed yield. Hence promising, high yielding potential genotypes can concurrently be combined with enhancement of diverse traits such as flowering, maturity and yield related traits for better economic yield.

3.3. Estimates of genetic parameters

The amount of genotypic and phenotypic variability that exists among genotypes is critically important in determining the success of breeding programs. Genotypic and phenotypic coefficients of variation are used to measure the variability that exists in a given genotypes (Tadesse et al.,
Genotypic and phenotypic variability (a2g and a2P), estimated genotypic and phenotypic coefficient of variability (GCV and PCV), broad sense heritability as well as genetic advance and genetic advance as percent of mean are presented below “Table 4”.

3.4. Variance components and coefficients of variation

In the present study the highest phenotypic and genotypic variance were observed from character of above ground biomass yield (3,405,267 and 3,405,103), followed by grain yield (1,200,029 and 1,199,938) respectively. The smallest phenotypic and genotypic variance were observed from harvest index (0.01 and 0.0078), followed by seed per pod (0.13 and 0.01) and number of primary branch (0.60 and 0.26) respectively (Table 4). Tesfay Belay (2018) found the highest phenotypic and genotypic variance from above ground biomass yield (205,172.36 and 230,991), followed by grain yield (104,073.23 and 115,361.96) respectively; while the lowest were from seed per pod and number of primary branch (0.01 and 0.02: 0.01 and 0.05) respectively. Parashi et al. (2013) also investigated the highest genotypic variance from above ground biological yield and grain yield. In addition to above ground biomass yield and grain yield, wide phenotypic and genotypic variability were recorded from number of pod per plant 9388.91), hundred seed weight (49.41), days to flowering (44.79 and 43.21), days to maturity (38.53 and 38.93) and plant height (35.29 and 33.13). This indicates that the genotype could be less influenced by the environmental factors and expressed by the phenotype. Hence the effectiveness of selection based on phenotypic performance could be possible for those traits. The present result agrees with the investigation of Ali et al. (2010) and Thokur and Sirohi (2015) for pods per plant, above ground biomass, grain yield, and plant height. Similar findings was also repeated by Chauhan (2011), for number of pod per plant, plant height, biomass yield, harvest index, days to flowering and days to maturity. The result of all characters in the present investigation showed that the phenotypic variance were higher in magnitude than that of genotypic variance (Table 4). Chauhan (2011) also reported similar results.

Estimates of the phenotypic coefficient of variation in this study were higher than their corresponding genotypic coefficient of variation, this implies that there was the influence of environment on the expression of these characters even though the differences were small. The smaller difference between the values of GCV and PCV, the smaller the influence of the environment for the expression of these characters. According to Deshmukh et al. (1986) PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10% and 20% to be moderate.

The present investigation confirm that GCV ranged from 5.02% (harvest index) to 41.67% (Grain yield). Phenotypic coefficient of variation (PCV) ranged from 5.37% (days to maturity) to 41.68% (Grain yield). Based on Deshmukh et al. (1986) classification among all characters the highest GCV and PCV values (>20%) were observed for grain yield (41.67% and 41.68%), number of pod per plant (38.92% and 39%), number of secondary branch (36.89% and 37.62%), above ground biomass yield (31.15% and 31.16%), hundred seed weight (30.23% and 30.90%), number of primary branch (20.51% and 31.27%), number of seed per pod (< 30.95%), and harvest index (and 20.5%), respectively. Moderate GCV and PCV were recorded from plant height (14.57% and 15.04%) and days to flowering (11.53% and 11.74%) respectively. The remaining characters showed low (<10%) GCV and PCV values. Saki et al. (2009) also investigate the highest genotypic and phenotypic coefficient values from grain yield (52.53% and 57.40%), and number of branch per plant (39.43% and 46.17%), respectively.

The present investigation showed, the existence of sufficient variability subsequently the scope of genetic improvement could be achieved through simple selection for these traits. Parida et al. (2018) reported higher magnitude of GCV and PCV for grain yield per plant, number of pod per plant, hundred seed weight and lowest for days to maturity which strongly support this finding. Chauhan (2011) also reported that grain yield, above ground biomass, number of pod per plant, and hundred seed weight showed highest GCV and PCV values while the lowest was from days to maturity which is close-fitted with the present investigation. The rest of the characters grouped...
under low genotypic coefficients of variation i.e. seed feeling period and number of seed per pod indicating less scope of selection as they were under huge influence of environment. Similar results of highest GCV and PCV for grain yield (39.8 and 40.9), number of pod per plant (25.93 and 26.64) and hundred seed weight (24.8 and 24.9) respectively were found for chickpea (Jakhar, 2014).

3.5. Estimates of heritability

The estimated heritability for the studied characters (Table 4) showed the heritability values varied from 5.26% for number of seed per pod to 99.9 % for above ground biomass and 99.8% for grain yield. In addition to grain yield and above ground biomass maximum heritability (>80%) were computed for number of pod per plant (99.6%), days to flowering (96.5%), number of secondary branch (96.2%) days to maturity (95.8%), protein content (93.6%), seed filling period (92.8%), plant height (93.8%), and hundred seed weight (95.7%) indicating selection could be fairly easy and improvement is possible using these traits in breeding program. Similar results were also reported by Jakhar (2014), for hundred seed weight (99.20 %) followed by grain yield (95.00 %), number of pods per plant (94.7 %), days to 50 per cent flowering (87.3 %), and number of secondary branches (83.3 %). According to Ali et al. (2010) and Joshi et al. (2018) high heritability value for grain yield (99.81%), above ground biomass (99.84%), number of pod per plant (99.27%) and hundred seed weight (99.71%) have been reported. Hussain et al. (2016) also reported high heritability for grain yield (96.40%), number of pods per plant (93.19%), 100-grain weight (89.67%), biological yield (83.83%) and plant height (78.83%). Generally for high heritable traits, selection could be the first option in breeding program but may be considerably difficult or virtually impractical for less heritable due to the influence of environment on the gene expression (Tesfay Belay, 2018).

3.6. Estimates of expected genetic advance

The highest magnitude of genetic advance was observed for the character above ground biomass (3801) followed by grain yield (2256), number of pod per plant (40.45), hundred seed weight (13.8), days to flowering (13.3), days to maturity (12.26), plant height (11.49) and seed filling period (10.02). The lowest genetic advance were exhibited by harvest index (0.01) followed by number of seed per pod (0.04), number of primary branch (0.68), protein content (2.7) and number of secondary branches (4.75) (Table 4). Tesfay Belay (2018) reported the high genetic advance from above ground biological yield (879.31) and grain yield (631.01); while the lowest were from number of primary branch and number of seed per pod (0.1 and 0.21) respectively. Johnson et al. (1995) and Vimal and Vishwakarma (1998) identified characters which have high heritability and genetic advance. Parida et al. (2018), also investigated hundred seed weight, pods per plant, seed per pod and grain yield showed high heritability combined with high genetic advance which could be used as a powerful tool in phenotypic selection as such characters could be controlled by additive gene action and less influenced by the environment.

Genetic advance as percent mean was categorized as low (0–10%), moderate (10–20%) and high (≥20%) (Johnson et al., 1955). Therefore, the expected genetic advance as the percent of means ranged from 2.54% for harvest index to 85.8% for gain yield (Table 4). In addition to grain yield, high GAM was observed for number of pod per plant (79.9), number of secondary branch (74.5), hundred seed weight (60.9), above ground biomass yield 64.2), plant height (29), number of primary branch (27.7) and days to flowering (23.3); while moderate GAM was observed for protein content (18.05), seed filling period (17), and days to maturity (10.6). The lowest GAM was obtained for harvest index and number of seed per pod (Table 4). Soki et al. (2009) investigate the highest genetic advance as percent of mean from grain yield (97.83), number of pod per plant (88.97) and number of branch per plant (69.39). Chauhan (2011) reported high expected genetic advance for observed characters of grain yield, above ground biomass, hundred seed weight and total pod per plant that coincide with the present investigation.

3.7. Correlation of traits

The correlation coefficient is an index of the proportion of causes common in the genesis of two variables to the total (Bowley, 1920). Estimates of genotypic and phenotypic correlation
coefficients between each pair of characters were studied (Table 5). In most cases, the genotypic correlation coefficients were greater in magnitude than the phenotypic correlation coefficients, displayed that strong inherent genetic relationships among various characters were offered, indicating less influenced by environment (Jakhar, 2014). In this study, genotypic correlation coefficients were found to be higher in magnitude than that of phenotypic correlation coefficients in most of the characters, which clearly indicated the presence of inherent association among various characters. The current investigation revealed that each studied parameters were associated negatively and positively, indicating that the traits under the study were influenced and supported one on another.

3.8. Correlation of grain yield and yield related traits

In the present study, grain yield showed highly significant positive genotypic correlation with seed filling period (0.335), plant height (0.5), number of primary branches (0.757), number of secondary branch (0.99), number of pods per plant (0.945), above ground biomass yield (0.987) and harvest index (0.924), while significant positive correlation at 5% were showed for number of seed per pod (0.244). Highly negative significant genotypic correlation were observed for days to flowering (−0.615), and days to maturity (−0.385), indicating that the longer the maturity date the lower the grain yield delivered. Ali and Ahsan (2012) who evaluated 20 genotypes of chickpea and reported that negative and highly significant association occurred among days to maturity and total dry weight per plant, number of pods per plant, number of grain per plant and grain yield. Sohail et al. also reported that grain yield was highly and positively correlated with number of pod per plant (0.959) and secondary branch (0.835) at genotypic level. Yücel et al. (2006) also evaluate 40 chickpea genotypes and found similar result. At phenotypic level, grain yield showed highly positive significant correlation with seed filling period (0.319), plant height (0.475), number of primary branch (0.690), number of secondary branch (0.989), number of pod per plant (0.944), number of seed per pod (0.222), above ground biomass yield (0.987) and harvest index (0.92), while days to flowering (−0.603) and days to maturity (−0.374) demonstrated highly negative significant phenotypic correlation. The remaining observed traits, hundred seed weight and protein content did not show any significant genotypic or phenotypic correlations for grain yield (Table 5). Ali et al. (2010) examine some chickpea genotypes and noted maximum positive highly significant genotypic and phenotypic correlation for grain yield were detected for number of pod per plant, seed per plant, above ground biomass and number of secondary branch, while negative significant genotypic and phenotypic correlation were observed with hundred seed weight and days to flowering. Tadesse et al. (2016) reported high degree of association between biomass and grain yield (0.83) and plant height and grain yield. Hamdi et al. (2003) also reported that grain yield was positively and significantly correlated with pod numbers, harvest index and negatively with flowering duration. Gupta and Krishna (1989) carried out correlation and path analysis in segregating population of chickpea and found that seed yield was positively correlated with pods per plant, seeds per plant and branches per plant. They further reported that correlation of these characters among themselves were also positive and significant. Sadhu and Mandal (1989) reported genetic analysis of seed yield and its components in one hundred twenty three varieties of chickpea. They noted that seed yield was positively correlated with pods per plant, seeds per pod and secondary branches. Lal et al. (1993) studied correlation and path analysis for seven yield components in 59 genotypes of chickpea and reported that seed yield was significantly and positively correlated with pod number and plant height and revealed significantly negative correlation with 100 seed weight. Malik et al. (2010) observed highly significant and positive correlation of grain yield with biological yield, secondary branches and number of pods per plant. Secondary branches were positively correlated with number of pods per plant and grain yield per plant, whereas it was negatively associated with 100 grain weight.

Days to flowering showed highly positive significant genotypic correlation only with days to maturity but negatively and highly correlated with seed filling period, number of primary branch, number of secondary branch, number of pod per plant, above ground biomass, grain yield, and harvest index. Plant height and number of seed per pod showed negative significant genotypic
### Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlations coefficients of the 13 traits chickpea genotypes

| Characters | DF   | DM   | SFP  | PH   | NPB  | NSB  | NPP  | NSP  | BM   | GY   | HI   | HSW  | CP   |
|------------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| DF         | 1    | 0.680*** | −0.479*** | −0.246* | −0.414*** | −0.611*** | −0.564*** | −0.199* | −0.610*** | −0.615*** | −0.582*** | −0.030ns | −0.069ns |
| DM         | 0.660*** | 1    | 0.318*** | −0.147ns | −0.307**  | −0.371*** | −0.336**  | −0.156ns | −0.369**  | −0.385*** | −0.404*** | 0.147ns  | −0.184ns |
| SFP        | −0.483*** | 0.339*** | 1    | 0.142ns | 0.169ns  | 0.346***  | 0.327***  | 0.070ns | 0.347***  | 0.335***  | 0.270**  | 0.215*  | −0.131ns |
| PH         | −0.223*** | −0.126* | 0.133* | 1    | 0.427*** | 0.471***  | 0.447***  | 0.083ns | 0.492***  | 0.500***  | 0.495*** | 0.319*  | −0.023ns |
| NPB        | −0.376*** | −0.275*** | 0.150* | 0.378*** | 1    | 0.770***  | 0.720***  | 0.281** | 0.771***  | 0.757***  | 0.656*** | 0.030ns | 0.092ns |
| NSB        | −0.598*** | −0.361*** | 0.328*** | 0.448*** | 0.704*** | 1    | 0.968***  | 0.242* | 0.991***  | 0.990***  | 0.871*** | 0.033ns | 0.064ns |
| NPP        | −0.553*** | −0.328*** | 0.310*** | 0.425*** | 0.657*** | 0.967*** | 1    | 0.212* | 0.944***  | 0.945***  | 0.801*** | 0.011ns | 0.052ns |
| NSP        | −0.178**  | −0.134* | 0.067ns | 0.094ns | 0.228*** | 0.220*** | 0.194*** | 1    | 0.259**  | 0.2440*  | 0.214*  | −0.362*** | 0.380*** |
| BM         | −0.598*** | −0.359*** | 0.331*** | 0.468*** | 0.703*** | 0.990*** | 0.944*** | 0.236*** | 1    | 0.987***  | 0.862*** | 0.056ns | 0.065ns |
| GY         | −0.603*** | −0.374*** | 0.319*** | 0.475*** | 0.690*** | 0.989*** | 0.944*** | 0.222*** | 0.987*** | 1    | 0.924*** | 0.054ns | 0.072ns |
| HI         | −0.568*** | −0.389*** | 0.257*** | 0.466*** | 0.597*** | 0.866*** | 0.796*** | 0.192** | 0.855*** | 0.920*** | 1    | 0.073ns | 0.089ns |
| HSW        | −0.037ns | 0.135* | 0.203*** | 0.290*** | 0.019ns | 0.032ns  | 0.011ns  | −0.324*** | 0.055ns  | 0.052ns  | 0.068ns | 1    | −0.371*** |
| CP         | −0.066ns | −0.180** | −0.126* | −0.025ns | 0.085ns | 0.063ns  | 0.052ns  | 0.344*** | 0.064ns  | 0.072   | 0.088ns | −0.360*** | 1    |

Note, *** and ** indicates very highly significant at 0.1%, highly significant at 1% and significant at 5% probability levels, respectively. DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH: plant height, NPB: number of primary branch, NSB: number of secondary branch, NPP: number of pod per plant, NSP: number of seed per pod, BM: above ground biomass, HI: harvest index, HSW: hundred seed weight, GY: grain yield.
correlation with days to flowering. At phenotypic level, only days to maturity showed positive and highly significant correlation but the remaining observed traits except hundred seed weight showed negative and highly significant phenotypic correlation. The maximum genotypic and phenotypic correlation of days to flowering was observed for days to maturity (0.680 and 0.660) respectively while the highest negative genotypic correlation was for grain yield (−0.615 and −0.603), respectively (Table 5). According to Chauhan (2011), days to 50% flowering had significant positive association with days to pod initiation (0.9138) and days to maturity (0.3973); while significant negative correlation were with biological yield (−0.4638), grain yield per plant (−0.3767), plant height (−0.3492), harvest index (−0.2882) and number of seeds per pod (−0.2292). Genotypes that exhibit longer flowering period results wastage of critical pod setting periods and exposing for stress conditions.

Days to maturity showed positive and highly significant genotypic and phenotypic correlation for observed traits of days to flowering (0.680 and 0.660) and seed filling period (0.318 and 0.339) respectively. Negative and highly significant genotypic correlation were exhibited for number of primary branch, number secondary branch, number of pod per plant, above ground biomass, grain yield and harvest index. Plant height, number of seed per pod and hundred seed weight showed nonsignificant genotypic correlation for days to maturity. Negative and highly significant phenotypic correlation were showed for traits of number of primary branch, number of secondary branch, number of pod per plant, above ground biomass, grain yield and harvest index while plant height, number of seed per pod and hundred seed weight were showed negative significant phenotypic correlation. The maximum genotypic and phenotypic correlation of days to maturity was for days to flowering (0.680 and 0.660) respectively. Yaqoob et al. (1990) studied the inter-relationship between grain yield and other important characters in twelve genotypes of chickpea and reported negative correlation between grain yield and days to maturity.

Seed filling period showed positive and highly significant genotypic correlation for days to maturity, number of secondary branch, and number of pod per plant, above ground biomass, grain yield and harvest index while hundred seed weight was showed positive significant genotypic correlation. Plant height, number of primary branch and number of seed per pod showed nonsignificant correlated for seed filling period at genotypic level, chickpea partially possess indeterminate growth habit, indicating that as the number of branch and pod number increase the time period for maturity will increase. Highly and negative genotypic and phenotypic correlation were observed only from days to flowering. Positive and highly significant phenotypic correlation were observed for days to maturity, number of primary branch, number of secondary branch, number of pod per plant, above ground biomass, grain yield, harvest index and hundred seed weight. Plant height showed positive significance phenotypic correlation at 95% level of confidence whereas number of seed per pod was not correlated. The maximum positive genotypic and phenotypic correlation was observed for above ground biomass (0.3473) and days to maturity (0.3393) respectively “Table 5”.

At genotypic level plant height was not correlated with traits of days to maturity, seed filling period and number of seed per pod though days to flowering correlated significantly however negative. positive highly significant genotypic correlation were observed for number of primary branch, number of secondary branch, number of pod per plant, above ground biomass, harvest index, hundred seed weight and grain yield. Days to flowering was showed negative high significant phenotypic correlation for plant height. At phenotypic level observed traits, number of primary branch, number of secondary branch, number of pod per plant, above ground biomass, harvest index, hundred seed weight and grain yield were showed positive highly significant correlation. Seed filling period and days to maturity was showed positive significant phenotypic correlation for plant height at 5%. Number of seed per pod was the only character which is not correlated phenotypically with plant height. The strong positive genotypic and phenotypic correlation for plant height were observed with grain yield (0.5 and 0.475), respectively “Table 5”.
Primary branch showed positive highly significant genotypic correlation with plant height, number of secondary branch, number of pod per plant, number of seed per pod, above ground biomass and harvest index but seed filling period and hundred seed weight showed positive significant genotypic correlation. At genotypic level days to flowering and days to maturity were negatively correlated with number of primary branch at 1% level of significance and at phenotypic level all studied traits except hundred seed weight, days to flowering and days to maturity were showed positive highly significant phenotypic correlation. Days to flowering and days to maturity were showed strong negative significant phenotypic correlation for primary branch while hundred seed weight was not significant. The highest positive genotypic and phenotypic correlation with number primary branch were observed for above ground biomass (0.7706 and 0.7028) and number of secondary branch (0.7704 and 0.7044), respectively “Table 5” Jakhar (2014); Chauhan (2011) found similar investigation with the present investigation.

Secondary branch was showed positive highly significant genotypic correlation for all studied traits except for days to flowering, days to maturity, number of seed per pod and hundred seed weight while number of seed per pod was positive significant at 5% and hundred seed weight which was nonsignificant for genotypic correlation. At phenotypic level all observed traits except hundred seed weight, days to flowering and days to maturity, showed positive highly significant phenotypic correlation. Days to flowering and days to maturity were showed negative and highly significant genotypic and phenotypic correlation for secondary branch. The highest positive genotypic and phenotypic correlation with number of secondary were observed for traits of above ground biomass (0.9912 and 0.9903) and grain yield (0.9903 and 0.9894) respectively (Table-4.3). Naveed et al. (2012) also investigate similar results.

Number of pod per plant was showed positive highly significant genotypic correlation for traits, plant height, number of primary branch, number of secondary branch, above ground biomass, grain yield and harvest index while number of seed per pod was significant at 95% confidence level. Days to flowering and days to maturity was showed strong negative significant genotypic and phenotypic correlation at 1% level of significance. Hundred seed weight was showed nonsignificant genotypic and phenotypic correlation for number of pod per plant. The maximum positive correlation with number of pod per plant was showed for the trait of number of secondary branch 0.968 at genotypic and 0.967 at phenotypic level (Table-4.3). similar results were also repeated by many authors (Jakhar, 2014; Naveed et al., 2012; Yücel et al., 2006).

Seed per pod was showed positive highly significant genotypic correlation for number primary branch and above ground biomass yield, while grain yield, number of secondary branch, number of pod per plant, and harvest index was positively significant at 5%. Hundred seed weight at 1% and days to flowering 5% were correlated negatively with seed per pod at genotypic level. At phenotypic correlation level all observed traits under this investigation except hundred seed weight, days to flowering and days to maturity, were highly significant. Hundred seed weight and days to flowering were highly significant for phenotypic correlation, however days to maturity were showed negative significant phenotypic correlation at 5%. In genotypic and phenotypic correlation the maximum relationship with number of seed per pod was brought from hundred seed weight (−0.3617 and −0.3241) which is negatively “Table 5”. (Chauhan, 2011; Zhou & Ambew, 2012) agreed with the present investigation.

Above ground biomass was showed highly significant genotypic and phenotypic correlation for all traits except hundred seed weight, which showed nonsignificant correlation for genotype and phenotype. Seed filling period, plant height, number of primary branch, number of secondary branch, number of pod per plant, number of seed per pod, grain yield and harvest index were showed positive highly significant genotypic and phenotypic correlation for observed traits of above ground biomass yield, while days to flowering and days to maturity were showed negative and highly significant genotypic and phenotypic correlation. In genotypic and phenotypic correlation the maximum relationship with above ground biomass were observed for traits of number of secondary branch (0.9912
and 0.9903) respectively, “Table 5”. According to Ali et al. (2010) investigation genotypic and phenotypic correlation for trait of above ground biomass was highly positively significant with plant height, grain yield, primary and secondary branch, number of pod per plant, while negative significant correlation were showed with days to flowering, number of seed per pod and hundred seed weight.

Harvest index was showed positive highly significant genotypic correlation for traits of seed filling period, plant height, number of primary branch, number of secondary branch, number of pod per plant above ground biomass and yield, grain yield, while number of seed per pod were significant at 5%. Days to flowering and days to maturity were highly but negatively correlated for trait of harvest index at genotypic level. At phenotypic level all studied traits except hundred seed weight were showed highly significant correlation with harvest index, however days to flowering and days to maturity were showed negative correlation. Hundred seed weight were the only character which was showed nonsignificant correlation at phenotypic and genotypic level of for the trait of harvest index. The maximum genotypic and phenotypic relationship with harvest index was showed from grain yield (0.9240 and 0.92020 respectively, “Table 5”. Naveed et al. (2012) also found similar result.

Hundred seed weight was showed positive highly significant genotypic and phenotypic correlation for plant height (0.3185 and 0.2900), respectively, while seed filling period were significantly correlated at 5%. The only trait that was highly and negatively correlated with hundred seed weight at genotypic and phenotypic was number of seed per pod and protein content (−0.361 and −0.371) and (−0.324 and −0.360) respectively. All the remaining studied trait under the present investigation were not showed statistically significant genotypic and phenotypic correlation with hundred seed weight. The principal association for hundred seed weight were brought from number of seed per pod which is negative correlation “Table 5”. Naveed et al. (2012) found and report the same result with this investigation.

At genotypic level protein content showed highly positive significant correlation only for the trait of number of seed per pod (0.380) while highly negative significant correlation were observed with hundred seed weight, indicating that the smaller the seed size the higher the protein level. Phenotypically number of seed per pod was the only trait which showed positive highly significant correlation for the trait of protein content, while hundred seed weight and days taken to maturity were showed negative highly significant correlation with protein content. Seed filling period were showed negative significant phenotypic correlation for observed trait of protein content. The remaining observed traits, days to flowering, plant height, number of primary branch, number of secondary branch, number of pod per plant, above ground bio mass, harvest index and grain yield were not showed significantly genotypic and phenotypic correlation for the character of protein content. It has often been observed that seeds with smaller size have more protein when compared with those with larger size because total carbohydrates in pulse seeds contribute 50–70% of the seed weight and Proteins 25–35% of the seed weight. Protein is negatively correlated with hundred seed weight and carbohydrate.

3.9 Path coefficient analysis

Phenotypic and genotypic correlations were partitioned in to direct and indirect effects to identify importance of different traits for grain yield under the study. In most cases, the magnitudes of the phenotypic direct and indirect effects were slightly greater than the genotypic effects. Path analysis was carried out at phenotypic and genotypic level by taking grain yield as dependent variable in order to see the causal factors and to identify the common components responsible for producing grain yield (Tables 6 and 7).

3.10 Genotypic direct and indirect effects of various characters on grain yield

The genotypic correlation coefficients are partitioned into direct and indirect effects by various yield contributing characters studied in this investigation (Table 6).
| Character | DF   | DM   | SFP  | PH   | NPB  | NSB  | NPP  | NSP  | BM   | HI   | rg   |
|-----------|------|------|------|------|------|------|------|------|------|------|------|
| DF        | -0.79| 0.507| 0.299| -0.0005| 0.004| -0.193| -0.028| 0.0003| -0.25| -0.155| -0.62*** |
| DM        | -0.54| 0.746| -0.198| -0.0003| 0.003| -0.117| -0.017| 0.0002| -0.15| -0.107| -0.38*** |
| SFP       | 0.38 | 0.237| -0.624| 0.0003| -0.002| 0.109| 0.016| -0.0001| 0.14 | 0.072 | 0.33*** |
| PH        | 0.19 | -0.109| -0.089| 0.0021| -0.004| 0.149| 0.022| -0.0001| 0.20 | 0.131 | 0.50*** |
| NPB       | 0.33 | -0.229| -0.105| 0.0009| -0.010| 0.243| 0.035| -0.0004| 0.32 | 0.174 | 0.75*** |
| NSB       | 0.49 | -0.277| -0.216| 0.0010| -0.008| 0.316| 0.048| -0.0003| 0.41 | 0.231 | 0.99*** |
| NPP       | 0.45 | -0.251| -0.204| 0.0010| -0.007| 0.306| 0.049| -0.0003| 0.39 | 0.213 | 0.94*** |
| NSP       | 0.16 | -0.117| -0.044| 0.0002| -0.003| 0.077| 0.010| -0.0014| 0.11 | 0.057 | 0.24* |
| BM        | 0.49 | -0.275| -0.217| 0.0011| -0.008| 0.313| 0.046| -0.0004| 0.41 | 0.229 | 0.98*** |
| HI        | 0.47 | -0.301| -0.168| 0.0011| -0.007| 0.275| 0.039| -0.0003| 0.35 | 0.265 | 0.92*** |

Residual value 0.03577

Note, ***indicates very highly significant at 0.1% and * indicates significant at 5% probability levels, DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH: plant height, NPB: number of primary branch, NSB: number of secondary branch, NPP: number of pod per plant, NSP: number of seed per pod, BM: above ground biomass, HI: harvest index, rg: genotypic correlation.
Table 7. Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at phenotypic level in 100 chickpea genotypes

| Characters | DF   | DM   | SFP  | PH   | NPB  | NSB  | NPP  | NSP  | BM   | HI   |
|------------|------|------|------|------|------|------|------|------|------|------|
| DF         | 0.386| −0.234| −0.147| −0.0002| 0.0029| −0.146| −0.037| 0.0004| −0.275| −0.153| −0.61*** |
| DM         | 0.254| −0.354| 0.103| −0.0001| −0.0021| −0.088| −0.022| 0.0003| −0.165| −0.105| −0.37*** |
| SFP        | −0.186| −0.120| 0.305| 0.0001| −0.0011| 0.080| 0.021| −0.0001| 0.152| 0.069| 0.32*** |
| PH         | −0.086| 0.045| 0.040| 0.0008| −0.0029| 0.110| 0.028| −0.0002| 0.215| 0.126| 0.47*** |
| NPB        | −0.144| 0.097| 0.046| 0.0003| −0.0076| 0.172| 0.044| −0.0005| 0.323| 0.161| 0.69*** |
| NSB        | −0.237| 0.128| 0.100| 0.0004| −0.0053| 0.245| 0.065| −0.0005| 0.455| 0.234| 0.98*** |
| NPP        | −0.211| 0.116| 0.094| 0.0003| −0.0050| 0.237| 0.067| −0.0004| 0.433| 0.215| 0.94*** |
| NSP        | −0.069| 0.047| 0.020| 0.0001| −0.0017| 0.054| 0.013| −0.0022| 0.108| 0.052| 0.22*** |
| BM         | −0.236| 0.127| 0.101| 0.0004| −0.0053| 0.242| 0.063| −0.0005| 0.459| 0.231| 0.99*** |
| HI         | −0.219| 0.138| 0.078| 0.0004| −0.0045| 0.212| 0.053| −0.0004| 0.393| 0.270| 0.92*** |

Residual value 0.0393

Note, ***indicates highly significant at 0.1%, DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH: plant height, NPB: number of primary branch, NSB: number of secondary branch, NPP: number of pod per plant, NSP: number of seed per pod, BM: above ground biomass, HI: harvest index, rp: phenotypic correlation.
3.11. Direct effect
The direct effects exhibited by days to flowering, seed filling period, number of primary branch and number of seed per pod were negative, whereas days to maturity, plant height, number of secondary branch, number of pod per plant, above ground biomass and harvest index gave positive direct effects on grain yield (Table 6). The highest positive direct effect of 0.746 was exhibited by days to maturity and followed by above ground biomass (0.41), number of secondary branch (0.316), harvest index (0.265), number of pod per plant (0.049) and plant height (0.0021). Significant positive high correlation and considerable positive direct effects were observed for days to maturity, above ground biomass, number of secondary branch and harvest index. The present investigation is supported by many authors (Jatasra et al., 1978; Padmavathi et al., 2013). However, days to flowering and seed filling period and number of primary branch had significant correlation; it has high negative direct effect (−0.79) and −0.624 (−0.01) on grain yield respectively, indicating that they are bad contributors to grain yield (Table 6). Arshad and Ghafoor (2004) reported a negative direct effect from traits of number of primary branches, plant height and days to maturity. Yücel et al. (2006) also reported a high negative direct effect days taken to flowering for grain yield. Hence these traits could be considered as chief components of selection in a breeding program for obtaining higher grain yield.

3.12. Indirect effect
Number of pod per plant contributed indirectly to grain yield via above ground biomass and harvest index, however it has low positive direct effect. Days to flowering exhibit high negative direct effect to grain yield, but indirectly it increase economic yield through improving days to maturity (0.507). Even though number of primary branch had a small negative direct effect on grain yield, indirectly improve grain yield through biological yield, harvest index and number of secondary branches. Tadesse et al. (2016), reported that plant height and number of pod per plant increase grain yield indirectly through above ground biomass and harvest index. Biological yield had highest positive indirect effect on grain yield through harvest index, number of secondary branch, days to flowering and negatively through influencing seed filling period. Thakur and Sirohi (2015); Tadesse et al. (2016) investigated on some chickpea genotypes and found the similar results.

3.13. Phenotypic direct and indirect effects of various traits on grain yield
The phenotypic correlation coefficients were partitioned into direct and indirect effects by various yield contributing traits (Table 7).

3.14. Direct effects
Above ground biomass (0.459) showed highest positive direct effect on grain yield followed by days to flowering (0.386), seed filling period (0.305), harvest index (0.270), number of secondary branch (0.245), number of pod per plant (0.067), and plant height (0.0008), while highest negative direct effect for grain yield were showed for days to maturity (−0.354) followed by number of primary branch (−0.0076), and number of seed per pod (−0.0022). Chauhan (2011) investigated and reported similar results with the existing investigation.

3.15. Indirect effects
Plant height, number of primary branch, number of secondary branch, number of pod per plant, and number of seed per pod exerted highest positive indirect effect on grain yield via above ground biomass and harvest index (0.215 and 0.126; 0.323 and 0.161; 0.455 and 0.234; 0.433 and 0.215) respectively. In addition number of primary branch via number of secondary branch (0.172), days to maturity through days to flowering (0.254), above ground biomass through harvest index (0.231) and harvest index through above ground biomass (0.393) indirectly showed positive contribution for grain yield. While days to flowering showed highest negative indirect effect on grain yield via above ground biomass (−0.231) followed by number of secondary branch (−0.231), harvest index (−0.219), number of pod per plant (−0.213), seed filling period (−0.186), and number of number of primary branch (−0.145). Days to maturity also showed
highest negative indirect effect on grain yield through days to flowering (~0.234) and seed filling period (~0.120). Seed filling period showed highest negative indirect effect on grain yield via days to flowering (~0.147). According to Thakur and Sirohi (2015), Pods per plant, primary branches per plant and plant height indirectly contributed to grain yield via above ground biomass. The contribution of residual factors that influenced grain yield was very low at both genotypic and phenotypic levels indicating that the most important traits are recorded in this investigation. The results indicated that biological yield is most noticeable trait contributing directly to grain yield and most other traits were correlated to grain yield indirectly through above ground biomass as reported by Thakur and Sirohi (2015).

### 3.16. Divergence (D²) analysis

Genetic divergence in 100 genotypes of chickpea were measured following the procedure of Mahalanobis (1936) D² statistic (Table 8). The genotypes were categorized into nine distinct significant clusters using Tocher’s method using D²-statistics (Table 8 and Figure 2).

### 3.17. Inter- and intracluster divergence D² analysis

The divergence (D²) analysis revealed that the 100 chickpea genotypes were grouped into 9 significant clusters (Table 8). The intracluster distance values were ranged from 5.3 (cluster IV) to 77.8 (cluster VIII). More than 66% of the intra cluster distance were greater than 53.5 D² value, indicated diversification. The highest inter cluster divergence was observed between genotypes of cluster I and cluster VIII (874.5) followed by cluster I and cluster II (837.4), cluster I and cluster V (759.3), cluster I and cluster III (480.4), cluster I and cluster VII (413.7), cluster IV and cluster VIII (390.9), cluster II and cluster IV (377.5) and Cluster II and cluster VI (309.4). Cluster I and cluster IX (300.4), Cluster I and cluster IV (295.2), cluster IV and cluster V (287.2). The lowest inter cluster distance (81.6) was found between cluster VI and cluster IX followed by cluster II and cluster VII (81.8), cluster III and cluster VII (87.4), cluster IV and cluster VI (90.6), cluster II and cluster III (93.6), indicating existence of closer proximity between these clusters (Table 4.6). Farshadfar and Farshadfar (2008) analyzed 360 chickpea lines in D² statistics and classified in to 9 clusters. Parashi et al. (2013) evaluate 365 genotypes and found six significant clusters. Vijayaraje et al. investigated and found 16 clusters, indicating the presence of wide genetic diversity indicated that breeders can improve chickpea productivity only through simple selection.

### 3.18. Grouping of genotypes in to different clusters

Composition of the clusters revealed that cluster VII has the largest cluster consisting of 24 genotypes, followed by cluster II consisting of 18 genotypes, cluster VIII consisting of 17 genotypes, cluster III and V consisting about 11 genotypes. While the smallest numbers were consisted
Figure 2. Study area map of experimental site Takusa district, North Gondar, Ethiopia.

Figure 3. Graph showing long term (1987–2018) and growing season (2018) climate data.
Figure 4. Graph showing genotypic and phenotypic coefficient of variation (GCV and PCCV), heritability ($H^2_b$) and genetic advance as percent of mean (GAM) for studied characters.

Figure 5. Dendrogram showing the genetic relationship among the 100 chickpea genotypes.
in cluster I followed by cluster IV, VI, and IX (3 genotype, 4 genotype, 6 genotype and 6 genotype) respectively (Table 9).

3.19. Cluster mean analysis
The cluster mean for different traits (Table 10), indicated wide range of variation for all the characters under the study. The highest and lowest mean value for grain yield were recorded from cluster IX (4429.3kg ha$^{-1}$) and cluster I (1126.6kg ha$^{-1}$) respectively. The genotype found in cluster IX showed the highest above ground biomass, number of pod per plant, number of secondary branch, number of primary branch, plant height and harvest index, while the lowest were from genotypes in cluster I, however they were protein rich genotypes. The lowest and highest mean value for days to flowering were recorded from genotypes in cluster IX and I respectively. The maximum maturity days were recorded from genotypes in cluster IV, while the minimum was from cluster V. The longest and shortest grain filling period were recorded from genotypes in cluster IV and I respectively. The maximum plant height was from cluster IX and the lowest was from genotypes in cluster I. The maximum number of primary branch, secondary branch and number of pod per plant were recorded from genotypes in cluster IX, while all the reverse were from genotypes in cluster I. The largest mean value of hundred seed weight were registered from genotypes in cluster VII, while the smallest mean value were from cluster IV. Therefore, hybridization between genotypes accounted wide genetic variance is likely to be effective for developing extreme divergent heterotic cross combination. Therefore chickpea genotypes has to be earnestly exploited spatially and temporarily in breeding programs.

3.20. Principal components analysis
The principal component analysis (PCA) is important for the reflection of the highest contributor to the total variation at each axis of differentiation. The Eigen values from PCA are used for determination of how many factors to retain. In the present investigation, only the first four principal components with Eigen values greater than one based on methods proposed by Kaiser (1960) were used and cumulatively they explained 81.5% variability. The first PC1 explained 49.5%, PC2 showed 14.9%, PC3 had 9.2%, PC4 7.8 (Table 11). Zhou and Ambev (2012) reported the first principal component was considered which explained 57.4% of the variation observed. Ghafoor et al. (2003) reported that 88.6% of the total variability of 62 chickpea genotypes evaluate for 11 quantitative traits was explained by the first three principal components.
Table 9. Distribution of 100 chickpea genotypes in different clusters

| Cluster | Number of Genotype included in the cluster |
|---------|--------------------------------------------|
| I       | iccx-060045-f3-p12-BP, iccc-1164, iccx-060039-f3-p39-BP |
| II      | iccx-060039-f3-p174-BP, iccc-15,888, iccril-04-0087, iccx-060039-f3-p188-BP, iccx-060039-f3-p2015-BP, iccu-115, iccx-060045-f3-p132-BP, iccril-03-0127, iccx-060045-f3-p165-BP, icc-67, DZ-2012-Ck-20,115-16-0058, iccx-060045-f3-p157-BP, iccx-060039-f3-p107-BP, iccx-060045-f3-p197-BP, iccx-060045-f3-p91-BP, iccx-060045-f3-p253-BP, iccx-060045-f3-p102-BP, iccu-94,954 |
| III     | iccx060039-f3-p21-BP, iccc-4958, iccx-060039-f3-p270-BP, icc-10,673, icc-15,762, icc-4533, iccc-13,863, iccx-060045-f3-p130-BP, DZ-2012-CX-0027, iccx-060039, f3-p204-BP, iccx-060039-f3-p24-BP |
| IV      | iccx-060045-f3-p173-BP, iccc-15,294, iccril-03-0167, icc-5135 |
| V       | iccx-090013-f2-p147-BP, iccx-060039-f3-p196-BP, icc-14,778, IE-16-109/2, JG-62, iccx-060039-f3-p57-BP, iccx-060039-f3-p178-BP, DZ-2012-CX-0048, iccx-090013-f2-p107-BP, iccu-07103, iccx-060039-f3-p10-BP |
| VI      | DZ-2012-CK-0253, DZ-2012-CK-0048, iccx-060039-f3-p173-BP, iccx-060045-f3-p232-BP, icc-510, iccx-060045-f3-p126-BP |
| VII     | DZ-2012-CK-240, Natoli, iccx-060039-f3-p145-BP, DZ-2012-CK-0030, iccx-090013-f2-p103-BP, DZ-2012-CK-0239, DZ-2012-CX-20,115-0041, DZ-2012-ck-20,115-50,045, iccx-090013-f2-p3-BP, DZ-2012-CK-0040, iccx-090013-f2-p276-BP, iccx-090013-f2-p105-BP, DZ-2012-ck-0238, Dimtu, iccx-090013-f2-p108-BP, iccx-060045-f3-p11-BP, iccx-090013-f2-p129-BP, iccx-090013-f2-p234-BP, iccx-090013-f2-p107-BP, iccx-060045-f3-p76-BP, iccx-16199xnatoli-p137, Dalota, iccx-090013-f2-p245-BP, iccx-0900013-f2-p115-BP |
| VIII    | IE-16-012/2, IE-16-079/1, iccx-060039-f3-p182-BP, IE-16-059/2, iccu-11,108, icc-1422, iccx-090013-f2-p120-BP, iccx-090013-f2-p145-BP, iccx-060039-f3-p311-BP, IE-16-059/1, IE-16-025/1, IE-16-003/1, icc-6279, icc-15,614, DZ-2012-CX-0028, Local, iccril-03-0215 |
| IX      | IE-16-094/1, iccx060045-f3-p98-BP, iccx-060045-f3-p55-BP, iccx-090013-f2-p215-BP, iccx-090013-f2-p265-BP, JV-11 |

Above ground biomass, number of secondary branches, number pod per plant and harvest index explained the highest variation on PCA1 (Table 11). Days to maturity, seed filling period, hundred seed weight and grain yield explain the highest variation on PCA2. Highest contributors for explained variance in PCA3 include days to maturity, seed filling period and number of secondary branch, while in PCA4, days to flowering, days to maturity, plant height, number of primary branch and number of seed per pod. Days to flowering was loaded negatively on PCA1, while number of seed per pod on PCA2. Hundred seed weight and seed filling period loaded negatively on PCAA3 and PC4 respectively. Hence due attention should be provided for traits responsible for the highest explained variance primarily on PCA1.

Principal component analysis (PCA) reduces a larger number of variables to a smaller number of factors and it is nondependent procedure. The goal is dimension reduction. In this new reference frame, note that variance is greater along the x axis than it is on the y axis. Also note that the spatial relationships of the points are unchanged; this process has merely rotated the data. Finally, note that our new vectors, or axes, are uncorrelated. To select a subset of variables from a larger set, based on which original variables have the highest correlations with the principal component. The characters contributing the maximum to the divergence (Tables 8 and 10) should be given greater emphasis for deciding the type of cluster for purpose of further selection and the choice of parental lines in hybridization (Jagadev et al., 1991).

4. Conclusion and recommendations

The present analysis of variance revealed highly significant differences among genotypes for all observed traits, which indicated a considerable amount of variability present under examined
### Table 10. Cluster means for yield and its contributing traits of chickpea genotypes grown under potential growing areas

| Characters | DF  | DM  | SFP | PH (cm) | NPB | NSB | NPP | NSP | BM (kg/ha) | HI  | HSW (g) | GY (kg/ha) | CP |
|------------|-----|-----|-----|---------|-----|-----|-----|-----|------------|-----|---------|------------|----|
| Cluster I  | 69.1| 118.2| 49.1| 29.6    | 1.3 | 2.9 | 27.3| 1.1 | 3125.9     | 0.37| 17.7    | 1126.6     | 16 |
| Cluster II | 65.7| 119.0| 53.4| 36.9    | 2.3 | 4.6 | 37.1| 1.0 | 4541.0     | 0.39| 23.9    | 1765.0     | 15 |
| Cluster III| 55.8| 117.0| 61.2| 36.0    | 1.8 | 3.7 | 31.8| 1.0 | 3608.8     | 0.38| 22.2    | 1350.7     | 15 |
| Cluster IV | 67.3| 131.0| 63.8| 31.9    | 2.1 | 4.7 | 38.3| 1.1 | 4552.8     | 0.37| 14.4    | 1695.0     | 15 |
| Cluster V  | 52.9| 109.2| 56.3| 36.3    | 2.3 | 5.5 | 42.5| 1.3 | 5387.1     | 0.40| 18.6    | 2189.2     | 16 |
| Cluster VI | 58.3| 120.1| 61.8| 41.0    | 2.5 | 5.8 | 43.8| 1.6 | 5720.9     | 0.41| 22.8    | 2378.1     | 16 |
| Cluster VII| 55.1| 115.1| 59.9| 43.9    | 2.6 | 7.1 | 52.8| 1.1 | 6678.2     | 0.46| 29.2    | 3075.5     | 16 |
| Cluster VIII| 50.8| 111.4| 60.6| 41.0    | 3.0 | 9.2 | 74.3| 1.3 | 7998.0     | 0.49| 16.5    | 3961.5     | 15.6|
| Cluster IX | 51.7| 113.2| 61.4| 46.9    | 3.3 | 10.5| 90.3| 1.0 | 8920.5     | 0.50| 27.9    | 4429.3     | 14.8|

Note: DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH(cm): plant height in centimeter, NPB: number of primary branch, NSB: number of secondary branch, NPP: number of pod per plant, NSP: number of seed per pod, BM(kg/ha): above ground biomass in kilogram per hectare, HI: harvest index, GY(kg/ha): grain yield in kilogram per hectare, HSW(g): hundred seed weight in gram and CP: crude protein.
Table 11. Vector loadings and percentage explained variation by the first four PCs

| Eigenvectors | PCA 1     | PCA 2     | PCA 3     | PCA 4     |
|--------------|-----------|-----------|-----------|-----------|
| Days to flowering | -0.28075  | 0.04999   | 0.12578   | 0.63391   |
| Days to maturity | -0.18339  | 0.32644   | 0.62095   | 0.30031   |
| Seed filling period | 0.14316   | 0.32619   | 0.57997   | -0.46201  |
| Plant height | 0.21446   | 0.20712   | -0.12539  | 0.42723   |
| Number of primary branch | 0.31426   | -0.02652  | 0.00829   | 0.25527   |
| Number of secondary branch | 0.38464   | 0.02581   | 0.03960   | 0.05348   |
| Number of pod per plant | 0.36746   | 0.02992   | 0.04833   | 0.06441   |
| Number of seed per plant | 0.12032   | -0.41611  | 0.40159   | 0.08335   |
| Biomass | 0.38357   | 0.03203   | 0.04034   | 0.06323   |
| Harvest index | 0.35498   | 0.01542   | -0.04762  | 0.04875   |
| Hundred seed weight | 0.02097   | 0.55884   | -0.20404  | 0.06172   |
| Grain yield | 0.38678   | 0.02935   | 0.01844   | 0.06368   |
| Protein content | 0.04099   | -0.50181  | 0.18815   | 0.13651   |
| Eigen value | 6.43      | 1.93      | 1.2       | 1.02      |
| proportion | 49.5      | 14.9      | 9.2       | 7.8       |
| cumulative | 49.5      | 64.5      | 73.7      | 81.5      |

Note: PCA- principal component analysis.

Estimates of genotype mean exhibited wide range together with large value for most of the characters. The trend of variability at genotypic level was similar to that of at phenotypic for some of the characters.

High estimate of genotypic and phenotypic coefficient of variation were observed for grain yield, number of pods per plant, number of secondary branches per plant, above ground biomass and hundred seed weight. High heritability estimates coupled with high genetic advance as percent of mean was observed for characters of grain yield, number of pods per plant, number of secondary branches per plant, above ground biomass and harvest index.

Number of secondary branches per plant, number of pods per plant, above ground biomass, harvest index and number of primary branches per plant had showed positive and highly significant correlation with grain yield of chickpea both at genotypic and phenotypic levels.

Path analysis revealed that above ground biomass followed by number of secondary branch, and harvest index, which showed strong positive association with grain yield also exhibited positive direct effects on grain yield. All the 100 genotypes were grouped into 9 clusters based on genetic divergence (D2) analysis. Cluster VII and II were the largest with 24 and 18 genotypes followed by clusters VIII containing, 17 genotypes. The principal components are linear combinations of the original variables weighted by their contribution to explaining the variance in a particular orthogonal dimension. Consequently the total variance of 81.5% of PCA value was brought from 4 PCs, however the largest variation (49.5%) brought from PCA-1.

Estimation of genetic variability in the base population should to be the primary action in breeding program, since the success of good breeding program usually depends upon the genetic variability present in the breeding materials. Information on the relative magnitude of different
sources of variation among different genotypes for several traits helps in the measurements of their range of genetic diversity. The genetically diverse genotypes are likely to produce heterotic effect and superior segregate when incorporated in hybridization to hasten crop improvement program. In general, knowledge on genetic variability, heritability and genetic advance is essential for a breeder to choose and efficient utilization of better genotypes for crop improvement programs. Therefore, the present study used multivariate techniques to evaluate the measure of genetic variation, heritability, genetic advance and association for different traits of 100 chickpea genotypes under the study.

The characters, grain yield, number of pods per plant, number of secondary branches per plant, above ground biomass and harvest index undergo high heritability coupled with high genetic advance as percent of mean; indicating grain yield could be improved via simple selection by giving due attention for traits having better heritability and genetic advance as percent of mean. So, while making selection, maximum weight should be given to number of pods per plant, number of secondary branches per plant, biological yield and 100 seed weight for attaining higher grain yield in future breeding programs.

The cluster analysis classified the 100 chickpea genotypes into nine separate clusters, exhibiting that hybridization of genotypes across clusters could lead to increase in heterosis in cross progenies. Cluster IX comprise higher grain yield, above ground biomass, number of pod per plant and plant height, while the highest flowering date and maturity date was from cluster I and cluster IV respectively. Cluster VII had genotypes that contain the largest seed weight, while the largest seed filling period was from cluster IV. Hybridization among the genotypes from these clusters which showed maximum distance might produce high yielding varieties having broad genetic base. In general the genotypes JV-11, IE-16-059/1, iccx-090013-f2-p215-BP, DZ-2012-CX-0028, iccx-060045-f3-p5-BP, iccx-060039-f3-p182-BP may serve as potential parents for grain yield. IE-16-109/2, iccx-0900013-f2-p107-BP, icc-6279, JG-62, icc-15,614, IE-16-059/2 can be also a parental line for earliness, while iccx-090013-f2-p265-BP, iccx-090013-f2-p107-BP, iccx-090013-f2-p103-BP, iccx-090013-f2-p215-BP for hundred seed weight. IE-16-109/2, icc-14,778, icc-510, DZ-2012-CX-0253, icc-5135 also be a potential parental line for quality character of crude protein. Generally genotypes listed above may serve as a parental lines for hybridization program in the improvement of chickpea grain yield and its contributing trait.

Looking the genetic variability and association of studied characters in the target genotypes of chickpea in the present study together with literatures, following suggestions were made;

The genetic variability for different characters should be exploited further using much more genotypes to know more about the existing level of diversity. The characters showing high heritability along with high GA should be given due attention in the development of desirable genotypes through simple selection. Genotypes from different clusters, identified for a specific character may be used as parent for breeding program with an objective to improve the specific traits.

Funding
The authors received no direct funding for this research.

Competing Interests
The authors declares no competing interests.

Author details
Amare Tsehay1
E-mail: amaretsehay1@gmail.com
Asnake Fikre2
Muluklen Bantayhu3
E-mail: oragawamore268@gmail.com
1 Amhara Agricultural Research Institute, Bahir Dar, Ethiopia.
2 Ethiopia Institute of Agricultural Research, Addis Ababa, Ethiopia.
3 Bahir Dar University College of Agriculture, Bahir Dar, Ethiopia.

Citation information
Cite this article as: Genetic variability and association analysis of Desi-type chickpea (Cicer arietinum L.) advanced lines under potential environment in North Gondar, Ethiopia, Amare Tsehay, Asnake Fikre & Muluklen Bantayhu, Cogent Food & Agriculture (2020), 6: 1806668.

References
Ali, Q., & Ahsan, M. (2012). Estimation of genetic variability and correlation analysis for quantitative traits in chickpea (Cicer arietinum L.). International Research Journal of Plant Science, 2(6), 166-169. https://doi.org/10.5455/ijavms.20110601090444
Ali, Q., Ahsan, M., & Saleem, M. (2010, January). Genetic variability and trait association in chickpea (Cicer arietinum L.) Genetic variability and trait association in chickpea (Cicer arietinum L.). African Journal of Agricultural Research, 7(23), 3403-3412.
Aliu, S., Kouli, H. P., Rusinovci, L., Shala-Mayrhofer, V., Fetahu, S., & Zeka, D. (2016). Genetic diversity for some nutritive traits of chickpea (Cicer arietinum L.) from different regions in Kosovo. Turkish Journal of Field Crops, 21(1), 156–161. https://doi.org/10.17557/tjfc.57905

Allard, R. W. (1960). Selection under self-fertilization. *Proceedings of plant breeding. John Wiley & Sons, Inc.*

Arshad, M., & Ghafoor, A. (2004). Path coefficient analysis in chickpea (Cicer arietinum L.) under rainfed conditions. Pakistan Journal of Botany, 36(1), 75–82.

Barrett, B. A., & Kidwell, K. K. (1998). AFLP-based genetic diversity assessment among wheat cultivars from the Pacific Northwest. Crop Science, 38(5), 1261–1271. https://doi.org/10.2135/cropsci1998.0011183X030800050025x

Belay, T. (2012, September). Genetic variability, correlation and path analysis for quantitative traits of seed yield, and yield components in chickpea (Cicer arietinum L.). African Journal of Plant Science, 12(3), 58-64. https://doi.org/10.5897/AJPS2014.1242

Bowlley, A. L. (1920). Elements of Statistics. *Indian Journal of Agricultural Sciences,* 3(12), 44.

CGIAR. (2010). Pulse value chain in Ethiopia. Sustainable Solution for Ending Hunger and Poverty, 1–44.

Chauhan, H. N. A. S. (1911). Studies on genetic variability for yield and quality traits of chickpea. *Springer.*

Deshmukh, S. N. S., Basu, M. S., & Reddy, P. S. (1986). Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of ground nut. *Indian Journal of Agricultural Science, 56,* 515–518.

Dewey, D. I., & Lu, K. H. (1959). A correlation and path-coefficient analysis of components of casted wheatgrass seed production. *Agronomy Journal, 51*(9), 515–518. https://doi.org/10.2134/agronj1959.00021962005100900002x

Feestast, F. (2015). Agriculture organization of the United Nations statistics division 2014. *Acessado Em, 9.*

Farshadfar, M., & Farshadfar, E. (2008, December). Genetic variability and path analysis of chickpea (Cicer arietinum L.) landraces and Lines. *Journal of applied sciences, 8*(21), 3951-3956. https://doi.org/10.3923/ jas.2008.3951.3956

Ghafoor, A., Gulboaz, F. N., & Arshad, M. (2003). Interrelationship between SOD-Page markers and agronomic characters in chickpea (Cicer arietinum L.). *Pakistan Journal of Botany, 35*(2), 613–624.

Gul, R., Khan, H., Bibi, M., Ain, Q. U., & Imran, B. (2013). Genetic analysis and interrelationship of yield attributing traits of chickpea (Cicer arietinum L.). *The Journal of Animal and Plant Sciences, 23*(2), 521–526.

Gupta, S. K., & Krishno, R. (1989). Genetic variability and heritability for quality traits in Bengal gram. *Indian Journal of Agricultural Biochemistry, 8,* 66–67.

Hallauer, A. R., & Miranda, J. B. (1988). Quantitative genetics in maize breeding. *Iowa State Univ. Press.*

Hamdi, A., El-Ghareib, A., Shoafy, A., & Ibrahim, M. (2003). Direct and indirect relationships among lentil characters. *Indian Journal Of Agricultural Research, 37*(11), 224–229.

Hussain, N., Ghaffar, A., Aslam, M., & Hussain, K. (2016). Assessment of genetic variation and mode of inheritance of some quantitative traits in chickpea (Cicer arietinum L.). *Journal of Animal and Plant Sciences, 26*(3), 1334–1338.

Imani, A., Moosavi, S. S., & Kamar, A. (2013). Evaluation of morphological and phenological traits of 25 lentil cultivars under rainfed and irrigated conditions. *Global Journal of Plant Eco-Physiology, 3*(2), 83–86.

Jagadev, P. N., Samal, K. M., & Lenka, D. (1991). Genetic divergence in rape mustard. *The Indian Journal of Genetics and Plant Breeding, 465–467.*

Jahoor, D. A. N. S. (2014). Genetic diversity studies in chickpea (Cicer arietinum L.)“master of science (agriculture). *Bangladesh Journal of Botany, 45*(3), 459-464.

Jatasa, D. S., Ram, C., Chandra, S., & Singh, A. (1978). Correlation and path analysis in segregating population of chickpea (Cicer arietinum L). *Indian Journal of Agricultural Research, 12*(4), 219–222.

Johnson, H. W., Robinson, H. F., & Comstock, R. E. (1995). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal, 47*(7), 314–318. https://doi.org/10.2134/agronj1995.00021962004700070009x

Johnson, H. W., Robinson, H. F., & Comstock, R. F. (1955). Genotypic and Phenotypic Correlations in Soybeans and Their Implications in Selection 1. *Agronomy Journal, 47*(10), 477–483. https://doi.org/10.2134/ agronj1955.00021962004701000008x

Joshi, P., Yasin, M., & Sundaram, P. (2018). Genetic variability, heritability and genetic advance study for seed yield and yield component traits in a chickpea recurrent parent inbred line (RIL) population. *International Journal of Pure and Applied Bioscience, 6*(2), 136–141.

Kaiser, H. F. (1960). The application of electronic computers to factor analysis. *Educational and Psychological Measurement* Karoz, 2011, 141–151. https://doi.org/10.1177/016204701102901116

Kassie, M., Shiferaw, B., Asfaw, S., Abate, T., Mursico, G., Ferede, S., & Asfesse, K. (2009, June). Current situation and future outlooks of the chickpea sub-sector in Ethiopia. *Pakistan Journal of Botany, 43*(1), 273-298.

Kayan, N., & Adak, M. S. (2012). Association of some characters with grain yield in chickpea (Cicer arietinum L.). *Pakistan Journal of Botany, 44*(1), 267–272.

Khan, R., & Farhatullah, K. H. (2011). Dissection of genetic variability and heritability estimates of chickpea germplasm for various morphological markers and quantitative traits. *Sarhad Journal of Agriculture, 27*(3), 67–72.

Lal, R. K., Bhoung, B. K., Gupta, V. P., & Loll, R. (1993). Variability correlation and path analysis in gram. *Haryana Agricultural University Journal Of Research, 23*(1).

Latief, A., Ghzawi, A. A., Bsoul, E., Aukour, F., Al- Ajlouni, Z., Al- Azzam, Z., & Al- Ajlouni, M. M. (2011). Genetic variation and quantitative traits in jordanian lentil landraces. *Advances in Environmental Biology, 5*(11), 3676–3680.

Mahalanobis, P. (1936). On the generalised distance in statistics. *Proceedings national institute of science (Vol. 2, pp. 49–55).* India. *http://iitr. isical. ac. in/ DispaceHandle1/1268

Malk, S. R., Bakhsh, A., Asif, M. A., Iqbal, U., & Iqbal, S. M. (2010). Assessment of genetic variability and interrelationship among some agronomic traits in chickpea. *International Journal of Agriculture and Biology, 12*(1), 81-85.

Mallu, T. S., Mwongi, S. G., Nyende, A. B., Rao, N. V. P. R. G., Odeny, D. A., Rathore, A., & Kumar, A. (2014). Assessment of genetic variation and heritability of agronomic traits in chickpea (Cicer arietinum L.). *International Journal of Agronomy and Agricultural Research, 3*(4), 76-88.

Naveed, M. T., Qurban Ali, M. A., & Hussain, B. (2012). Correlation and path coefficient analysis for various quantitative traits in chickpea (Cicer arietinum L.). *Journal of Life Sciences, 6*(2), 97–106. https://doi.org/10.5455/jlvs.137
Padmavathi, V., Sreemanarayana, S., Satyanarayana, V., & Loi, A. (2013). Correlation and path coefficient analysis in kabuli chickpea (Cicer arietinum L.). International Journal of Applied Biology and Pharmaceutical Technology, 4(3), 107–110.

Parash, V., Lod, D., & Mohse, L. (2013). Genetic diversity studies in chickpea (Cicer arietinum L.). A Quarterly Journal, 7(9), 2757–2763. http://ijpq.indianjournals.com/ijqir.aspx?Target=ijqir&Vol=10&Issue=1&Article=047

Parida, G., Saghfi, S., Elvazi, A., Akbarzadeh, A., Kavetkky, T., Aliyeva, I., & Khollolv, R. (2018). Study of genetic advance and broad sense heritability. 3(1), 5–12.

Qureshi, A. S., Shaukat, A., Baksh, A., & Arshad, M. G. A. (2006). An assessment of variability for economically important traits in chickpea (Cicer arietinum L.). Pakistan Journal of Botany, 36(4), 779–785.

Rao, C. R. (1952). Advanced statistical methods in biometrical research. Johan Willy and Sons.

Sadhu, S. K., & Mandal, A. K. (1989). Genetic variability and characters association in chickpea (Vol. 21). Genetika.

Seki, A. I., Zaman, M. A., Kamal, M. M., & Begum, H. (2009). Genetic variability, correlation and path co-efficient analysis for agronomic traits in chickpea (Cicer arietinum L. 7, 12–21.

Singh, R. K., & Chaudhury, B. D. (1985). Biometrical methods of quantitative genetic analysis. Haryana Journal of Horticultural Sciences, 12(1), 151–156.

Sirohi, S. K. T. A. A. (2009, January). Studies on genetic variability, heritability and genetic advance in chickpea (Cicer arietinum L.) under different environments. Indian Journal of Agricultural Sciences, 4(1), 242–245.

Subramanian, M., & Sivasubramanian, P. (1975). X-ray induced fused perianth in ricinus communis (L.). Radiation Botany, 15(3), 307–308. https://doi.org/10.1016/S0033-7560(75)80030-5

Tadesse, M., Fikre, A., Esthete, M., Girma, N., Korb, L., & Mohamed, R. (2016). Correlation and path coefficient analysis for various quantitative traits in desi chickpea genotypes under rainfall conditions in Ethiopia. Journal of Agricultural Science, 8(12), 112–118. https://doi.org/10.5539/jas.v8n12p112

Thakur, S. K., & Sirohi, A. (2015). Correlation and path coefficient analysis in chickpea (Cicer arietinum L.) under different seasons (CICER ARIETINUM L.) UNDER DIFFERENT SEASONS. Indian Journal of Pulses Research, (January 2009).

Upadhyaya, H. D., Thudi, M., Dronavalli, N., Gujaria, N., Singh, S., Sharma, S., & Varshney, R. K. (2011). Genomic tools and germplasm diversity for chickpea improvement (Vol. 9). Plant Genetic Resources: Characterisation and Utilisation. https://doi.org/10.1017/S1479262111000048

Vimal, S. C., & Vishwakarma, S. R. (1998). Heritability and genetic advance in barley under partially reclaimed saline-sodic soil. Barley and Wheat Newsletter.

Wossen, T. (2017). Determination of optimum rates of nitrogen and phosphorus fertilization for white cumin. Plant Genetic Resources, 7(2), 460–463.

Yaqoob, M., Jan, H., & Ahmad, M. B. (1995). Inter-relationship between grain yield and other important characters in chickpea. Sarhad Journal of Agriculture, 6, 159–164.

Yücel, D. Ö., Anlarsal, A. E., & Yücel, C. (2008). Genetic variability, correlation and path analysis of yield, and yield components in chickpea (Cicer arietinum L. Turkish Journal of Agriculture and Forestry, 30, 183–188.

Zhou, M., & Ambev, K. I. (2012). Determine how chickpea genotypes react to high temperatures and how they can be used in the improvement program for elevated temperatures. 26(4), 1–82. https://doi.org/10.16528/j.cnki.22-1054/f.2015.05.004

Page 35 of 36
