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GENETIC VARIABILITY AND ASSOCIATION OF TRAITS FOR DESI TYPE CHICKPEA (Cicer arietinum L.) ADVANCED LINES UNDER POTENTIAL ENVIROMENT IN NORTH GONDAR, ETHIOPIA

Amare, Tsehaye

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BAHIR DAR UNIVERSITY

COLLEGE OF AGRICUTLURE AND ENVIRONMENTAL SCIENCES

GRADUATE PROGRAM IN PLANT BREEDING

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MSc. Thesis

By

Amare Tsehaye Kidea

June 2019

Bahir Dar, Ethiopia

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SUBMITTED IN PARTIAL FULFILLMENT OF THE REQUIREMENTS FOR THE DEGREE OF MASTER OF SCIENCE (MSc.) IN "PLANT BREEDING"

June 2019

Bahir Dar, Ethiopia

THESIS APPROVAL SHEET

As member of the Board of Examiners of the Master of Science (MSc.) thesis open defense examination, we have read and evaluated this thesis prepared by **Mr. Amare Tsehaye Kidea**, entitled **"Genetic variability and association of traits for Desi type chickpea** (*Cicer arietinum* L.) **advanced lines under potential environment in North Gondar, Ethiopia"**. We here by certify that, the thesis is accepted for fulfilling the requirements for the award of the degree of Master of Science (MSc.) in Plant Breeding.

Board of Examiners

Name of External Examiner_____

Signature_____ Date_____July 2019_____

Name of Internal Examiner_____

Signature  Date ___07 July 2019_____

Name of Chair Person_____

Signature_____ Date_____July 2019_____

DECLARATION

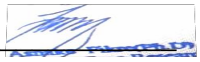
This is to certify that this thesis entitled **"Genetic variability and association of traits for Desi type chickpea** (*Cicer arietinum* L.) **advanced lines under potential environment in North Gondar, Ethiopia"** submitted in partial fulfillment of the requirements of for the award of the degree of Master of Science (MSc.) in **Plant Breeding** to the Graduate Program of College of Agriculture and Environmental Science, Bahir Dar University by **Mr. Amare Tsehaye Kidea,** ID (BDU1018495PR) is an authentic work carried out by him under our guidance. The matter embodied in this project work has not been submitted earlier for award of any degree or diploma to the best of our knowledge and belief.

Name of the Student Amare Tsehaye Kidea

Signature _____ Date 02 July 2019

Name of the supervisor

1) Asinake Fikre (PhD) (Major Supervisor)

Signature  Date 03 July 2019

2) Mr. Muluken Bantayhue (Co-Supervisor)

Signature_____ Date _____July 2019

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DEDICATION

This study is passionately dedicated to my beloved parents, who have been my source of inspiration and gave me strength when I thought of giving up, who frequently provide their moral, spiritual, emotional, and financial support. Lastly, I dedicated this thesis to the Almighty God, thanks for the guidance, strength, power of mind, protection and for giving me a healthy life.

ABBREVIATIONS/ACRONYMS

ANOVA	Analysis of variance
CSA	Central statistical agency
df	Degree of freedom
FAO	Food agricultural organization
g	gram
GA	Genetic advance
GAM	Genetic advance as percent of mean
ha	Hectares
hg	Hectogram
$kgha^{-1}$	Kilogram per hectare
NIRS	Near infra-red spectrometry
PCA	Principal Component analysis
SE	Standard error

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

Amare Tsehaye

Dr. Asinake Fikre (Major Supervisor**), Muluken Bantayhue (**Co-Supervisor**)**

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 data were recorded on days to 50 percent flowering, days to physiological maturity, seed filling period, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), above ground biomass ($kgha^{-1}$), harvest index, grain yield ($kgha^{-1}$) and protein content (%). 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 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 (D^2) 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. Generally the existence of huge variability infers no more need induced variation, 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.

***K*eywords**: Characters, Clustering, Chickpea, Genetic variability, Genotype

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Chapter 1. INTRODUCTION

1.1. Background and Justification

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 fallow lands through utilizing crop rotation system (Upadhyaya *et al.*, 2011).

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 (Jing, 2010). 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 (Halluer and 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 and Kidwell, 1998). Estimate the level of genetic variability and determine the significance of traits are important for further trait discovery, intercrossing 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 and Khan, 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 (Jakhar, 2014). 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 to estimate the total genotypic variability presented among germplasms under the study and to determine the association among traits.

1.2. Objective of the Study

1.3.1. General objective

To asses and quantify the level of genetic variability presented among tested chickpea germplasm lines and determine the significance of various economic traits.

1.3.2. Specific objectives

The study was proposed aiming at the following specific objectives

- To determine the level of genetic diversity among examined chickpea genotypes.
- To determine heritability and genetic advance of various traits
- To determine the correlation, direct and indirect effects of different traits on grain yield.
- To identify genotypes with higher/special level of significance for the breeding program.

Chapter 2. LITERATURE REVIEW

Ethiopia is endowed with diverse agro ecology, ecosystem, edaphic and climatic conditions. Consequently, the country is inhibited by amazingly great diversity of plants, animals and microbial genetic resources. Diversity in crop plants is conditioned by geographic, climatic and edaphic factors, cultural and ethnic differences, farming practices, and religious and cultural beliefs (Wordofa, 2015).

2.1. Origin

Chickpea *(Cicer arietinum* L.*)* is old legume crop believed to be originated in areas of southeast Turkey (7250 BC) and neighboring part of Syria (7260 BC) in the early Nilotic period and in Ethiopia since 290 BC around Lalibla cave during Iron age (Van Der Maesen, 1987). Vavilov (1926) suggested that South west Asia and Mediterranean are the two primary centers of origin and Ethiopia is the secondary center of diversity (Taleka *et al.*, 2017 and Rajeev *et al.*, 2019). Based on archeological evidence and written histories, scientists ratify that chickpea is most probably originated in an area of present-day south-eastern Turkey and adjoining part of Syria; because, different wild annual species of *Cicer*, closely related to the chickpea are found there (Van Der Maesen, 1976). During ancient time, food gatherers were attracted by wild species of chickpea with their seed size and shattering nature, then after artificial selection has been started for their large palatable seeds, reduced pod dehiscence, non-dormancy, synchronous ripening, earliness and their diversity. Apart from occasional escapes and volunteers from previous crops, *C. arietinum* does not occur in the wild state (Van Der Maesen, 1976).

2.2. Botany

Chickpea has diploid chromosome number (2n = 2x = 16) with a relatively small genome size of 740 mega base pair (ICRISAT and Group, 2010). Goa and Gezahagn (2018) referred chickpea grouped under Kingdom: Plantae, Division: Magnoliophyta, Class: Magnoliopsida, Order: Fabales, Family: Fabaceae, Subfamily: Faboide, Genus: Cicer and Species: C. arietinum. The name *Cicer* is derived from the Greek word 'kikus' meaning force or strength. The word arietinum

is also Latin, translated from the Greek word 'krios', an allusion for the shape of the seed which resembles the head of a ram. Chickpea crop received different name in different countries; garbanzo in Spanish, poischiche in French, kichar or chicher in German, chana in Hindi, gram or Bengal gram in English and shimbra in Ethiopia. In Turkey, Romania, Bulgaria, Afghanistan, and adjacent parts of Russia, chickpea is called nakhut or nohut (Skill, 1995).

2.3. Plant Habit

Chickpea is a cool season annual crop with a plant height ranging 20 cm to 1 m tall. The stems are branched with a semi erect to semi-spreading growth habit (Skill, 1995). There are two main commercial classes of seed: Kabuli and Desi (Corp *et al.*, 2004). Kabuli type chickpeas are round seed shape, cream-colored and large seeded. The plant height is medium to tall with large leaflets and white flowers. Desi type chickpeas are small seeded with angular shape. The seed color varies from cream, black, brown, yellow to green (Skill, 1995). Chickpea crops have a strong taproot system with 3 or 4 rows of lateral roots. The roots grow 1.5 to 2.0 meter deep while the stem is erect, branched, viscous, hairy, terete, herbaceous, green, and solid. There are primary, secondary, and tertiary branches (Skill, 1995). Chickpea leaves are petiolate, compound, and unimparipinnate (pseudoimparipinnate). The rachis is 3-7 cm long and each rachis supports 10-15 leaflets each with a small pedicel. The leaflets are 8-17 mm long and 5-14 mm wide (Skill, 1995).

Chickpea is a self-pollinated crop; cross pollination is less than 1% and the flowers are borne in an axillary raceme. Sometimes there are 2 or 3 flowers on the same node. Such flowers possess both a peduncle and a pedicel. At flowering, the floral and racemal portions of the peduncle form a straight line, giving the appearance that the flowers are placed on the leafy axil by a single peduncle. The bracts are 1-5 mm in length (Skill, 1995). Chickpea flowers are complete and bisexual, and have papilionaceous corolla. They are white, pink, purple or blue in color. In colored flowers, the peduncles may be of different colors, the floral part purplish and the racemal green. The axillary inflorescence is shorter than the subtending leaf (Skill, 1995).

Tadesse Megersa *et al*. (2016) referenced that the cultivated chickpea (*Cicer arietinum* L.) was one of the first grain legumes to be domesticated in the old world. The cultivation of chickpea in

central and Western Europe was extensive until the beginning of the 20th century. In Austria and Switzerland, chickpea was cultivated before 1914. Outside the Mediterranean area and Bulgaria, chickpea is typically a relict crop (Van Der Maesen, 1976). Moreover, according to Joshi *et al.* (2018) quoted chickpea (*Cicer arietinum* L.) is an important food legume, and is presently grown in more than 50 countries and imported by more than 150 countries.

2.4. Production

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 (Muhammad *et al.*, 2012). During 2011, about 80% of the chickpea area was from South and Southeast Asia (India 68%, Pakistan 8.9% and Myanmar 2.3%). The other major chickpea growing countries include Turkey, Australia, Ethiopia, Iran, Mexico, Canada and USA (Gaur *et al.,* 2013).

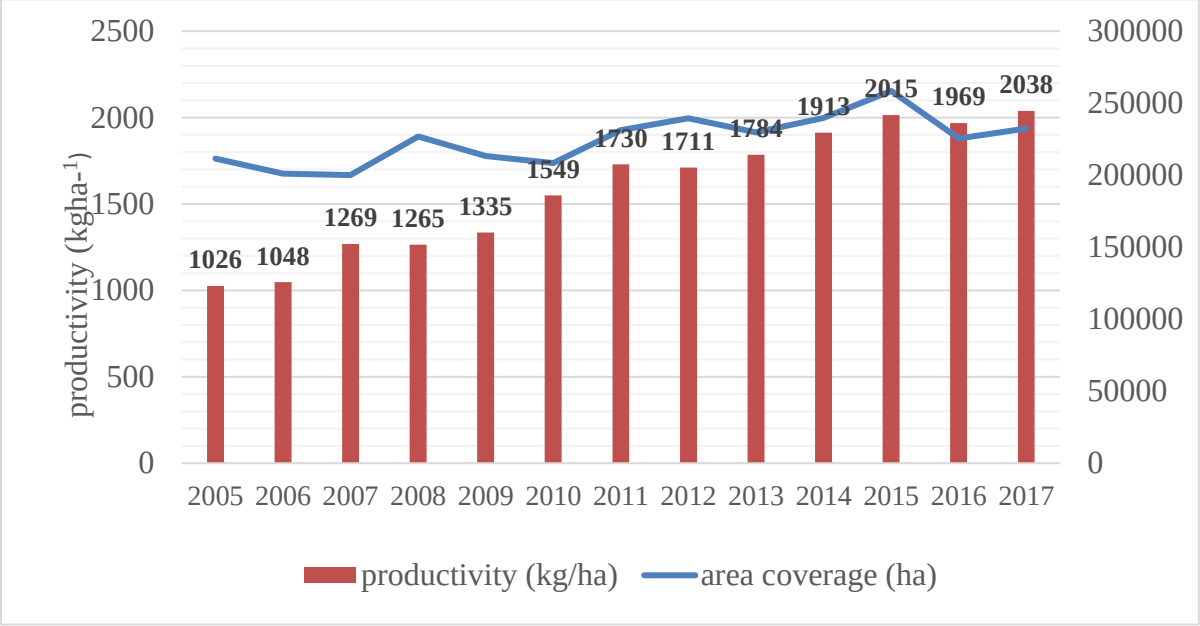
There are two different types of chickpea that are grown worldwide, Desi and Kabuli. Desi type chickpeas have colored and thick seed coat. The seed colors of Desi chickpeas are brown, yellow, green or black. The seeds are generally small and angular with a rough surface. The flowers are generally pink and the plants show various degrees of anthocyanin pigmentation, although some Desi types have white flowers and no anthocyanin pigmentation 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. The Kabuli type chickpeas are characterized by white or beige-colored seed with ram-head to rounded shape. The seed coat is thin with smooth seed surface. The flowers of Kabuli type are white and lack anthocyanin pigmentation on the stem. As compared to Desi type, the Kabuli type has higher levels of sucrose and lower levels of fiber. The Kabuli type generally has large seed size and receive higher market price than Desi type. The price premium in Kabuli type generally increases as the seed size increases.

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 (Minale Kassie *et al*., 2009 and Aliu *et al.*, 2016). Large seeded chickpea type called Kabuli, are well adapted to spring sowing

from Afghanistan westwards into Middle East, Southern Europe and North Africa, while small seeded cultivars of different colors called as Desi type chickpeas are mostly grown in winter from Pakistan, Eastward and also in Ethiopia, Sudan, Mexico, Chile (Jakhar, 2014).

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 (FAO, 2015). Ethiopia is the seventh largest producer worldwide and contributes about 2% to the total world chickpea production but it is among top ranked (1.913t/ha) in productivity, where as in Africa it is the largest producer accounting about (46%)of the continents production during 1994-2006 (Minale Kassie *et al.*, 2009). In Ethiopia chickpea cultivation has increased from about 211,490 ha in 2005 to about 232,341 ha in 2017 while yields jumped from about 1026 kg/ha to 2038 kg/ha, about 100% yield increment (FAO, 2017).

However Ethiopian chickpea production covered 242,000ha with yield surpassing 2t/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 (Asinake Fikre, 2014), however more than 25% percent of it is from North Gondar, Ethiopia (Minale Kassie, 2009)



(FAO, 2017)

Figure 1. Chickpea productivity and area coverage progress graph in Ethiopia

2.5. Climate Requirement

Chickpea is self-pollinated crop; cross pollination is less than 1% and it is usually grown as a rain fed cool weather and a dry climate crop in semi-arid regions. Climatic requirement of the crop is 18-26^{o}C day and 21-29^{o}C night temperatures with 21-41% of relative humidity and annual rainfall of 600-1000 mm on vertisol of pH 5.5-8.6 (Jakhar, 2014)**.** Chickpea seeds germinate at an optimum temperature (28-33°C) and moisture level in range of 5-6 days. Germination begins with absorption of moisture and swelling of the seed. The radicle emerges first followed by the plumule. The portion of the axis above the cotyledon called the epicotyl, elongates and pushes the plumule upward. The growth of the plumule produces an erect shoot and leaves, and the radicle grows to produce the roots (Corp *et al.*, 2004).

2.6. Use

Chickpea has now found to be into specialty health shops. Now a days exotic restaurants and culture foods come to spread all over the world, as a result widened the ease of understanding and occasional users of chickpea products. In North America, Kabuli chickpea is an indispensable item in bean salads and at salad bars (Maesen, 1976). Chickpea seeds contain protein, fiber, calcium, potassium, phosphorus, iron, zinc and magnesium along with appreciable quantities of selenium, sodium and copper, which make it one of the nutritionally best composed edible dry legumes, for human consumption (Upadhyaya *et al.*, 2011).

Chickpea provides 2-3 times more protein than cereals and it contains 20-24% protein, 4-10% fat, 52-71% carbohydrate, 10-23% fiber, minerals (Calcium, Phosphorus, and Iron) and vitamins (Wallace *et al.*, 2016). This makes the crop to be called as poor people's diet especially in arid and semi-arid regions of the world. Among essential amino acids lysine, methionine, threonine, valine, isoleucine and leucine are major components of seed protein (Gaur *et al*., 2013 and Jakhar, 2014). Beside rich in protein and some essential amino acids, it has an additional benefit through improving soil health and fertility (Jakhar, 2014). According to Gowda and Samineni (2016) reported that, it's tap root system enables to mine soil moisture from lower strata of the soil, ensued to be moisture stress tolerant crop.

Chickpea have many medicinal applications like for the control of aphrodisiac, bronchitis, catarrh, cutamenia, cholera, constipation, diarrhea, dyspepsia, flatulence, snakebite, sunstroke (Jakhar, 2014 and Wallace *et al.*, 2016), and in addition the glandular secretion of the leaves, stems, and pods contain malic and oxalic acid which are supposed to lower the cholesterol level of a blood and the sugar level (Wallace *et al*., 2016). Chickpea does not contain any anti- nutritional factors except the raffinose type oligosaccharides (easily neutralized by boiling or soaking in water) which cause flatulence (Upadhyaya *et al*., 2011).

2.7. Genetic Parameters

2.7.1. Genetic variability

Variability is the extent to which data points in a statistical distribution or data set diverge from the average value as well as the extent to which these data points differ from each other. Jivani and yadavendra (1989) studied genotypic and phenotypic coefficient of variation for yield and yield related traits in 42 genetically diverse genotypes of *Cicer arietinum* L., reported that, both genotypic and phenotypic coefficient of variation were high for number of pods per plant and 100-seed weight. Arora and Jeena (2001) evaluated forty genetically diverse genotypes of chickpea for genotypic and phenotypic variability, heritability and genetic advance in 18 quantitative characters and found the highest genetic variability for 100-seed weight, followed by primary branches per plant and seeds per plant. Kumar *et al*. (2001) studied 26 genotypes for genotypic and phenotypic variability, heritability and genetic advance in 12 quantitative characters, in which pods per plant exhibited the highest amount of genetic variability, followed by secondary branches per plant, grain yield and 100-seed weight. Ali *et al*. (2011) found maximum genetic variability for secondary branches per plant. Above ground biomass, number of pods per plant and grain yield which reflects that these traits respond to selection.

Singh and Yadava (2003) observed wide range of variability amongst genotypes for above ground biomass, grain yield and 100-seed weight. Usmani *et al*. (2005) evaluated thirty genotypes of chickpea and found that pod bearing length, grain yield, plant height, harvest index and number of pods per plant showed high genotypic coefficient of variation. Malik *et al*. (2010) recorded

maximum variation for pods per plant, followed by secondary branches per plant, biological yield, harvest index and grain yield. Parashi *et al.* (2013) reported that, variation among genotypes were highly significant for day to 50% flowering, day to maturity, plant height, number of primary branches per plant, number of secondary branches per plants, pods per plant, number of seed per pod, seed index, biological yield, economical yield and harvest index.

Mallu *et al.* (2014) tested 60 desi type chickpea lines under five environments and reported that days to flowering, plant height, maturity date, seed yield and hundred seed weight were highly significant for among genotype and GxE at 1% level of probability. Arshad and Ghafoor (2004) also reported that all the characters recorded display a considerable range of genetic variability. Hussain *et al.* (2016) investigate that relatively higher value of genotypic variances were found for number of pods per plant (94.93), biological yield per plant (75.30), grain yield per plant (34.27), plant height (30.71) and 100-grain weight (16.79), while the lower genotypic variances were found for number of seed per pod and number of primary branches per plant.

Muhammad *et al.* (2012) reported the highest genotypic, phenotypic and environmental variances were found for number of pods per plant and grain yield 48.148, 65.233, 17.045 and 21.723, 34.526, 12.804, respectively. The lowest genotypic, phenotypic and environmental variances were found for number of primary branches per plant 0.007, 0.013 and 0.06 followed by number seeds per pod 0.02, 0.04 and 0.02 respectively. The highest genotypic, phenotypic and environmental coefficients of variation were found for number of pods per plant 14.20, 16.52 and 8.45 followed by plant height 8.59, 9.28 and 4.53 respectively. Sirohi *et al.* (2008) reported that analysis of variance of the individual as well as combined over environments revealed significant differences among the genotypes for all the characters studied.

Jakhar (2014) reported that genotypic coefficient of variation (GCV) was highest for grain yield per plant (39.18%) followed by number of pods per plant (25.93%), 100 seed weight (24.84%), number of secondary branches (18.15%) and days to 50 percent flowering (13.18%). The maximum phenotypic coefficient of variation was recorded for seed yield per plant (40.19%) followed by number of pods per plant (26.64%), 100 seed weight (24.94 %) and number of secondary branches per plant (19.89%).

2.7.2. Heritability

Warner (1952) was the first person who gives a detailed method about estimation of heritability in crop plants. Parashi *et al*. (2013) reported that the highest broad sense heritability recorded was for economic yield (82%) followed by number of pods per plant (76%) and Harvest index (75%). (Mallu *et al.*, 2014) also reported that high broad sense heritability exhibited for days to 50% flowering, plant height, 100 seed weight, grain yield, number of secondary branches per plant, harvest index, days to maturity and number of pods plant. Estimates of heritability in broad sense varied from 23% for primary branches to 99% for above ground biomass (Arshad and Ghafoor, 2004). Muhammad *et al.* (2002) reported that high estimate of broad sense heritability for protein content reflected that selection could be effective for improving the trait. Smaller differences between genotypic and phenotypic coefficient of variability indicated that major proportion of phenotypic variance was due to genetic differences. From the foregoing results it may be concluded that the characters with high heritability i.e. 100-seed weight and protein content with small differences between genotypic and phenotypic coefficient of variability should be selected for constituting desirable genotypes of chickpea.

Muhammad *et al.* (2012) examined 20 genotypes and investigate the range of heritability between 0.47 and 0.86 while highest was for plant height and lowest for number of seeds per pod. The highest estimate of genetic advance was found for number of pods per plant. The higher heritability and genetic advance indicated that selection could be efficient to develop high yielder chickpea genotypes. Jakhar (2014) also reported that maximum percentage of heritability was observed for 100 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%), number of secondary branches (83.3%) and number of seeds per pod (65.1 %). High heritability (> 60%) was observed in the characters for, days to 50 percent flowering, number of secondary branches, number of pods per plant, number of seed per pod, 100 seed weight and seed yield per plant, indicating that those characters could require due attentions during selection of parental line for breeding programs.

Vijayaraje *et al*. (2015) reported the estimates of heritability in broad sense as follow. The maximum heritability estimate of 99.55 percent was recorded by number of grain yield followed

by plant height (96.00%), days to 50% flowering (91.35%), days to maturity (90.72%), biological yield per plant (89.99%), 100 seed weight (86.48%), number of pods per plant (82.81%), number of primary branches per plant (75.59%). The moderate heritability recorded by number of seeds per plant (61.85%). The lowest heritability of 36.49% was recorded by harvest index.

2.7.3. Genetic advance

The heritability estimates with genetic advance are more useful than the heritability value alone in selecting the best individuals. The estimates of Genetic Advance ranged from 0.62 to 51.07 with the highest estimate in case of biological yield (51.07%), number of pods per plant (18.41%), plant height (9.94%), days to maturity (2.61% (Parashi *et al.*, 2013). Arshad and Ghafoor (2004) reported genetic advance (5% selection intensity) was the highest for secondary branches (42.89), followed by primary branches (34.95), biological yield (30.24), pods per plant (27.08), and grain yield (26.65), while it was the lowest for days to maturity (2.48) and days to flowering (2.53).

Pratap *et al.* (2004) assessed thirty eight genetically diverse early maturing chickpea genotypes in four different environments and revealed that grain yield, 100-seed weight, reproductive phase and biological yield showed high heritability coupled with high genetic advance, while, these traits exerted moderate to high estimate of phenotypic and genotypic coefficient of variation but remaining traits exhibited moderate to low heritability. Hussain *et al.* (2016) test 15 different chickpea lines and they investigate high heritability coupled with high genetic advance as percent of mean were recorded for grain yield per plant (39.91), number of pods per plant (37.59), biological yield per plant (25.58) and 100-grain weight (22.62). This indicates that there was low environmental influence on the expression of these characters.

Singhal and Bharadwaj (2016) reported that the relative degree at which a character is transmitted to offspring is indicated by heritability. High heritability estimates coupled with high genetic advance as per cent of mean was seen in for days to fifty per cent flowering and 100 seed weight, while high heritability with moderate genetic advance was seen in days to maturity. Plant height and grain yield per plant showed low to moderate heritability coupled with low to moderate genetic advance as percent of mean. Traits having high heritability and high genetic advance as percent of

mean generally indicate that there is a predominance of additive gene action and are responsive to selection.

According to Jakhar (2014) the highest magnitude of genetic advance was observed for the character number of pods per plant (30.28) followed by days to 50% flowering (16.03), height of the plant (6.97), 100 seed weight (6.87), seed yield per plant (6.79) and days to maturity (6.31). The lowest genetic advance was exhibited by number of seeds per pod (0.28) followed by number of primary branches (0.51) and protein content (1.94).

Vijayaraje *et al.* (2015) reported genetic advance as per cent of mean ranged from 2.95 to 30.10 per cent. The maximum genetic advance as percent of mean (30.10%) was recorded by biological yield while minimum (2.95%) by harvest index. The characters, 100 seed weight (29.41%), number of seed per plant (27.31%) and plant height (22.57%) also recorded high genetic advance as percent of mean. The lowest genetic advance as percent of mean, 2.95 per cent was recorded by harvest index followed by days to maturity (10.24%), days to 50% flowering (15.83%) and number of pods per plant (16.52%).

2.8. Correlation Coefficient Analysis

The mathematical implications of correlation at genotypic, phenotypic and environmental levels were described by Searle (1961). Mishra (1988) studied sixteen genotypes and reported that grain yield per plant had positive association with days to flowering and days to maturity. Number of seeds per pod had significant positive association with seed yield per plant. Number of pods per plant had positive association with number of seeds per pod. Arshad and Ghafoor (2004) reported that grain yield per plant was positive and significantly correlated with plant height, pods per plant, 100 seed weight and biological yield but it was negatively correlated with days to flowering, primary branches and harvest index.

According to Ali *et al* (2010) reported, genotypic and phenotypic correlations coefficients of number of days taken to flowering with pods per plant and secondary branches per plant were positive however non-significant. The genotypic and phenotypic correlation coefficients between

number of secondary branches per plant, biomass per plant and grain yield per plant were positive and significant. Genotypic correlation between number of secondary branches per plant and seeds per pod was negative but significant. A positive and significant genotypic and phenotypic correlation was found for number of pods per plant with biomass per plant and grain yield per plant but highly significant genotypic correlation with biomass per plant (Ali *et al.,* 2010)

Thakur and Sirohi (2015), investigate that genotypic correlation coefficients were observed to be higher than that of phenotypic correlation coefficient indicating the strong inherent association for the various traits studied pointing out the possibility of effective phenotypic selection. Seed yield per plant exhibited stable positive association with biological yield per plant followed by pods per plant, primary branches per plant, plant height and harvest index at genotypic and phenotypic levels in both the individual as well as combined over seasons. Tadesse Megersa *et al.* (2016), reported that above ground biomass, plant height, number of pods per plant, number of seeds per pod, days to maturity and days to flowering exhibited significant and positive correlation with seed yield at genotypic level. The degree of association was highest between biomass and grain yield (0.83), followed by plant height and grain yield.

Muhammad *et al*. (2012), reported that genotypic and phenotypic correlation among plant height and number of primary branches per plant was positive however non-significant, but negative and highly significant with secondary branches per plant. Genotypic and phenotypic correlation coefficients of number of primary branches per plant with of number of pods per plant and seeds per pod were positive and significant A positive and non-significant association was noted for primary branches per plant with biomass per plant and number of grain per plant at genotypic levels but significant for number of grains per plant at phenotypic level. According to Ali *et al.* (2010), hundred seed weight were negatively correlated for observed traits of grain yield. A positive but non-significant association was noted between grain yield and 100-seed weight. The significant and positive association was found among days to flowering and number of grains per plant and grain yield per plant (Muhammad *et al.,* 2012).

2.9. Path Coefficient Analysis

Tadesse Megersa *et al.* (2016) reported that correlation and path coefficient analysis indicated that biomass, plant height, stand count at harvest and number of pods per plant were potent contributors to grain yield through direct effects. Although days to flowering, days to maturity and number of seeds per pod had significant association, these exhibited negative direct effects. Muhammad *et al.* (2012) concluded that from correlation and path coefficient studies that biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and 100-seed weight, number of days taken to flowering, number of days taken to maturity, primary branches per plant and secondary branches per plant can be used as selection criteria for higher yielding chickpea genotypes.

Ali *et al.* (2011) evaluated ten varieties of chickpea, which revealed that path coefficient showed that maximum direct effect on grain yield were found with pods per plant, seeds per pod, proteins and fats. According to Ali *et al.* (2010) investigation path coefficient showed that 100-seed weight had maximum direct effect on grain yield per plant followed by number of pods per plant, number of secondary branches per plant, seeds per pod, number of days taken to maturity and number of primary branches per plant. The number of days taken to flowering, plant height and biomass per plant had negative direct effects on grain yield. It was concluded that 100-seed weight, number of pods per plant, number of secondary branches per plant, seeds per pod, number of days taken to maturity and number of primary branches per plant are the characters which contribute largely to grain yield per plant.

Vijayaraje *et al.* (2015) reported that number of seeds per plant registered the maximum positive direct effect of 0.964 followed by Biological yield per plant (0.125), days to maturity (0.073). Number of pods per plant recorded highest negative direct effect of -0.181 followed by harvest index (-0.103), days to 50% flowering (-0.088), number of seeds per pod (-0.068), number primary branches per plant (-0.026) and plant height (-0.021). The traits like 100 seed weight exhibited low positive direct effects (0.023) on seed yield per plant.

2.10. Genetic Divergence (D^2) and Cluster Analysis

The concept of genetic divergence (D^2) statistics was originally developed by Mahalanobis (1936). The application of this technique is the assessment of genetic diversity in plant breeding. This is one of the potent techniques of measuring genetic divergence in various breeding materials. Vijayaraje *et al*. (2015) reported that genetic divergence studies are the vibrant tools for the evaluation of genotype and selection of parents for the breeding programme. Hence, the present study was mainly aimed at analysis of genetic divergence among the 100 genotypes and to identify the superior genotypes for formulating breeding programs. Inter-cluster distance is the main criterion for selection of genotypes using D^2 analysis. Genotypes belonging to the clusters with maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent clusters are likely to produce wide range of variability with desirable segregates. Syed *et al.* (2012) investigate cluster analysis on 27 genotypes of chickpea, and grouped into five clusters. Cluster II was the largest and consisted of 11 genotypes followed by cluster III which had 7 genotypes. The cluster V had 5 and cluster IV had 3 genotypes. Cluster I was unique in having only one genotype. According to Thakur *et al.* (2018) investigation the D^2 values of 100 genotypes were grouped into twelve clusters, which revealed that the genotypes varied significantly for all the characters studied indicating considerable variable in the germplasm. Cluster I consist of maximum 49 genotypes, followed by cluster III, cluster VII, cluster IX which had 16, 12 and 12 genotypes, respectively, while remaining all clusters possessed one genotype in each except cluster VIII which had 4 genotypes. Cluster I consisted maximum forty-nine genotypes indicating that the genotypes had narrow genetic divergent among them. The similarity in the base population, from which they had been evolved, might be the cause of genetic uniformity.

2.11. Principal Component Analysis

PCA is a statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables (entities each of which takes on various numerical values) into a set of values of linearly uncorrelated variables. Principal components have both direction and magnitude. The direction represents across which principal axes the data is mostly

spread out or has most variance and the magnitude signifies the amount of variance that Principal component captures of the data when projected onto that axis. The principal components are a straight line, and the first principal component holds the most variance in the data. Each subsequent principal component is orthogonal to the last and has a lesser variance. In this way, given a set of x correlated variables over y samples you achieve a set of uncorrelated principal components over the same y samples. Kumar (2015) examined 18 rice genotypes to assess the heritable diversity among the parent lines during Kharif 2013 and 2014, and reported the first five principal components exhibited more than one eigenvalues and accounted for 82 percent of total variation, comprised of 38.95 (PC I), 20.80 (PC II), 14.67 (PC III) and 10.69 (PC IV).

2.12. Protein content

In developing countries, grain legumes are next to cereals in human food dealing with the hunger and malnutrition. Chickpea *(Cicer arietinum* L.*)* is the nutritious legume crop providing ample amount of proteins, nutrients and vital amino acids to human body (Kahraman *et al.,* 2017). Chickpea *(Cicer arietinum* L.*)* grains are an excellent source of protein, carbohydrates, minerals, vitamins, dietary fiber, folate, β-carotene and health promoting fatty acids. Their consumption provides consumers with a variety of nutritional and health benefits. Limited breeding efforts have been made on nutritional quality traits of chickpea (Gaur *et al.,* 2015).

Chickpeas are an excellent source of proteins, carbohydrates, dietary fiber, minerals and vitamins. There is a growing interest in consumption of chickpea for promoting healthy diet and reducing risk of some diseases and other health problems. Chickpeas are rich in protein (20% - 22%) and the digestibility of chickpea protein is high as compared to several other legumes (Aliu *et al*., 2016). Singh *et al.* (1981) reported that Desi and Kabuli chickpea showed no noticeable difference in protein and amino acid content, however, Kabuli chickpea contains fewer anti-nutritional factors than Desi types. Awasthi *et al.* (1991) also recorded the protein content in chickpea, which ranged between 15.61 to 26.65 percent. Singh *et al.* (1991) tested protein in different genotypes of Desi and Kabuli chickpea and reported that biological value and utilizable protein are higher in Kabuli genotypes and they are also nutritionally better than the Desi variety.

Chapter 3. MATERIALS AND METHODS

3.1. 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 730mm. The average temperature of the areas is 21.65º C. The major crops grown widely are chickpea, tef, maize, spice crops (cumin, hot pepper, tomato), etc., under rain fed and irrigation but cereal mono cropping is the predominant crop grown in the study area (Tesifaye 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).

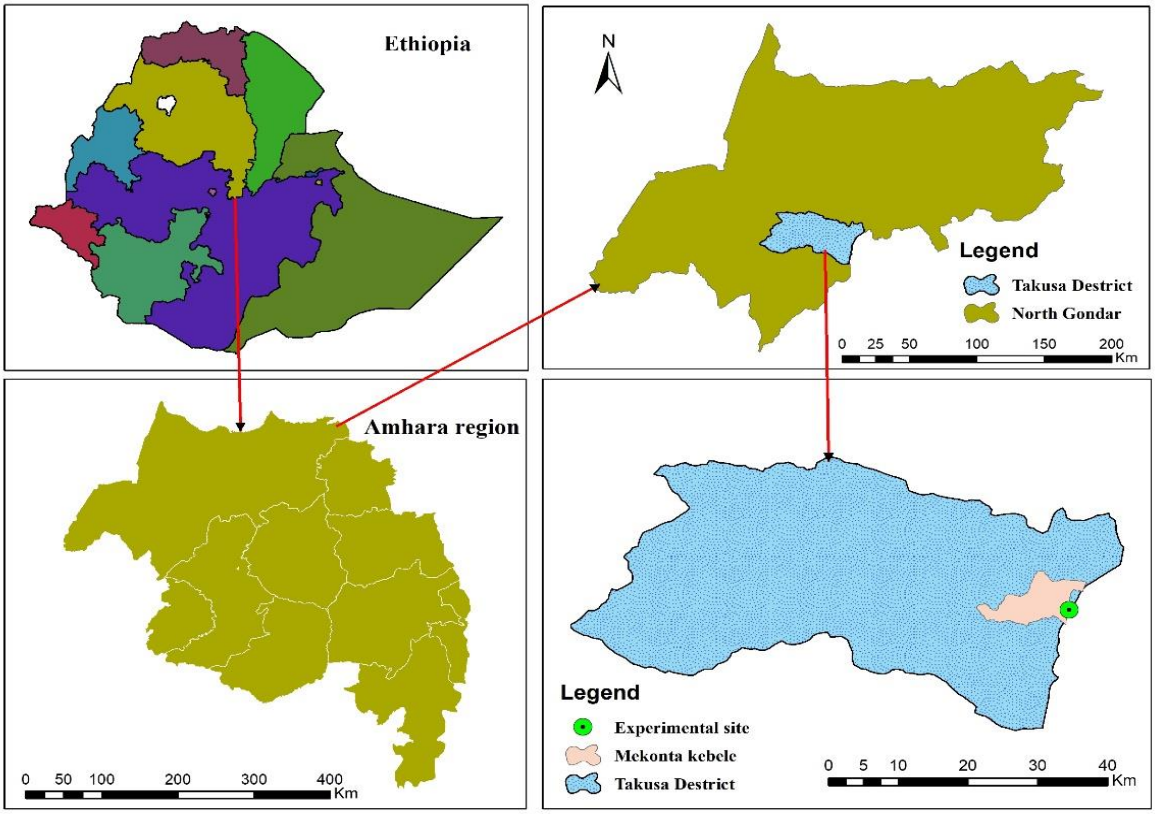


Figure 2. Study area map of experimental site Takusa district, North Gondar, Ethiopia

Climate data for the experimental area

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

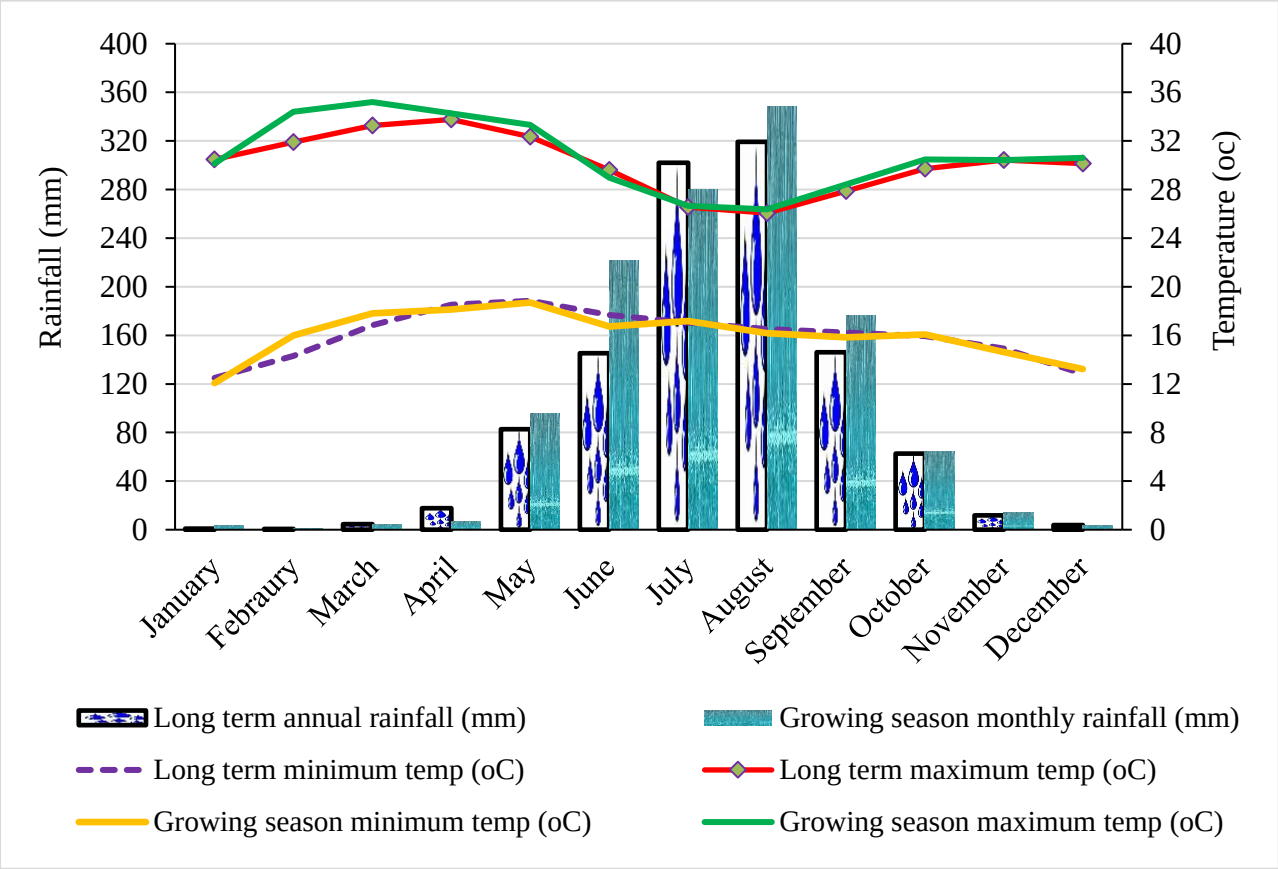


Figure 3. Graph showing long term (1987-2018) and growing season (2018) climate data

3.2. 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).

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-11108	G-51	icc-4958	G-76	iccx-060039-f3-p10-BP
G-2	Iccx-090013-f2-p147-BP	G-27	DZ-2012-CX-20115-0041	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-15762
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-20115-50045	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-14778	G-34	iccx-090013-f2-p145-BP	G-59	DZ-2012-CK-20115-16-0058	G-84	icc-13863
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-15888	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
G-15	Natoli	G-40	iccx-060039-f3-p173-BP	G-65	icc-15294	G-90	iccx-060045-f3-p197-BP
G-16	iccx060045-f3-p98-BP	G-41	iccu-115	G-66	iccx-060045-f3-p76-BP	G-91	DZ-2012-CX-0227
G-17	iccx060039-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-10673	G-95	icc-5135

Code	Genotype name/pedigree	Code	Genotype name/pedigree	Code	Genotype name/pedigree	Code	Genotype name/pedigree
G-21	DZ-2012-CK-0048	G-46	iccx-060039-f3-p131-BP	G-71	iccx-0900013-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-15614	G-100	iccu-94954

3.3. 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 2m 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 100kg/ha was used. 121kg NPS (23N, $46P_2O_5$, and 8.4S) fertilizer was applied. All the recommended crop management practices have been accomplished based on the recommendation.

3.4. Data Collected

Five plants per genotypes were selected randomly for recording plant based characters and net plot area for plot based characters following the descriptors of ICARDA (1985) .

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.
5. Grain yield (GY): Grain yield ($kgha^{-1}$) 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 (kgha^{-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.
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.
13. Protein content (%)

Quality parameter

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.

3.5. Data Analysis

3.5.1. 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 (Steel and Torrie, 1980). 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

$Yijl = \mu + rj + gi + Pl(j) + \varepsilon ijl$

Where: Yij is observed value of the trait of the Y for the i^{th} genotype in j^{th} replication

μ= the general mean of trait Y

rj = the effect of j^{th} replication

gi= the effect of i^{th} genotypes and

Pl (j) =block within replicate effect

εijl= the experimental error associated with the trait y for the i^{th} genotype in l^{th} block with in replication and j^{th} replication

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)(rk-k-1)	SSE	MSE	
Total	rk^2-1	SSTot		

(Gomez and Gomez, 1984)

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

3.5.2. 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 (1953) as follows:

Genotypic variance ($\sigma^2 g$) = (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 ($\sigma^2 e$) = error mean square=MS_e

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

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

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

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

Where: x = grand mean of character. The classification for genotypic coefficient of variation (Sivasuhramanian and Madhavamcnon, 1975) was as follows: Low (< 10%), Moderate (10-20%) and High (> 20%).

3.5.3. Estimation of heritability in broad sense (H^2)

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

Heritability (H^2) = ($\sigma^2 g/\sigma^2 p$)*100

Where, H^2=Heritability in broad sense, $\sigma^2 p$= Phenotypic variance, $\sigma^2 g$ =Genotypic variance

3.5.4. 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 x k x σp

Expected genetic advance as percentage of mean = (GAx100)/μ

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

3.5.5. 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) = $Pcovxy/\sqrt{(\sigma^2 px.\sigma^2 py)}$

Genotypic coefficient of correlation (rg) = $Gcovxy/\sqrt{(\sigma^2 gx.\ \sigma^2 gy)}$

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, $\sigma^2 g_x$=Genotypic variance for trait X, $\sigma^2 g_y$=Genotypic variance for trait Y, $\sigma^2 p_x$=Phenotypic variance for trait X, $\sigma^2 p_y$=Phenotypic variance for trait Y.

Phenotypic correlation coefficient was tested for their significance using the method suggested by Reeve & Rao (1981)

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

Significance genotypic correlation coefficient was tested with the following formula

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

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

3.5.6. 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 $\Sigma rik.pkj$ =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, $pr = 1 - rijPij$

3.5.7. Genetic distance and 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 inter-cluster 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

$D^2 = \lambda_{ij}. \sigma_i. \sigma_j$

Where, λ_{ij} = reciprocal matrix to the common dispersion matrix

σ_i = difference between the mean values of two populations for i^{th} character

σ_j = difference between the mean values of two populations for j^{th} character

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

   $D2= \sum Di^2/n$, where, $\sum D^2i$ is sum of distances between all possible combinations (n) is the population included in a cluster.

2) Average inter cluster D^2

   $D^2=\Sigma D^2i/n_i.n_j$

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

Cluster means

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included within the cluster.

3.5.8. 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 using SAS computer software based on formulas suggested by Holland (2016).

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.

Chapter 4. RESULTS AND DISCUSSION

4.1. Analysis of Variance of Studied Traits

The analysis of variance was carried out for 13 chickpea 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 days to flowering, days to maturity, plant height, number of primary branch, number of secondary branch, number of pod per plant, number of seed per pod, above ground biomass, harvest index, hundred seed weight and seed yield 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. Gudivada *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.

Table 3. Analysis of variance for the 13 traits of chickpea genotypes tested by triple lattice design in Takusa during 2018/19

	Source					
Traits	Replication Df=2	Block Df=27	Genotype Df=99	Error Df=171	CV (%)	R^2 Value
Days to flowering	3.6ns	2.4ns	131.2***	1.6	2.8	0.97
Days to maturity	7.6ns	3.36ns	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	0.003ns	0.06ns	1.11***	0.34	13.9	0.84
Number of secondary branch	0.017ns	0.049ns	16.79***	0.22	3.5	0.99
Number of pod per plant	1.1ns	3.2ns	1163.3***	1.7	7.7	0.99
Number of seed per pod	0.015ns	0.016ns	0.14***	0.12	10.5	0.85
Above ground biomass ($kgha^{-1}$)	15987ns	25549ns	1021547***	164.2	9.2	0.99
Grain yield ($kgha^{-1}$)	1616.2*	6896*	3599907***	90.1	13.4	0.99
Harvest index	0.0008ns	0.00046ns	0.00087**	0.007	1.7	0.98
Hundred seed weight (g)	22.07ns	3.4ns	114.03***	2.1	9.2	0.95
Protein content	0.01347ns	0.01521ns	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, $kgha^{-1}$: kilogram per hectare and g: gram.

4.2. 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 *et al*. (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 115 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-15294, 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 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 hade 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 icc-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 *et al.*, 2011; Kayan, 2012 and 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 23 to 108 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. Indicated that 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 , 2012; Gul *et al.*, 2013) in chickpea germplasm, Mishara (2009) in cowpea 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 kgha^{-1} to 10375 kgha^{-1} with a grand mean value of 5923kg/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 10.1g to 35.5g to 10g with a mean value of 0.43 and 22.6g respectively. The highest harvest index (0.52) was recorded from genotypes iccx-060045-f3-p98-BP, iccu-11108, 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 (35.5g) 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 (Qureshi *et al.*, 2004; Malik *et al.*, 2010; Khan *et al.*, 2011). 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 $kgha^{-1}$ to 4792$kgha^{-1}$ with a mean value of 2628 $kgha^{-1}$ (Table 4). In the present study, genotypes JV-11 (4792.2 $kgha^{-1}$), IE-16059/1 (4743.9 $kgha^{-1}$), 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 $kgha^{-1}$ (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 and 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.

4.3. 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 Megersa *et al.,* 2016). Genotypic and phenotypic variability (σ2g and σ2P), 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 (Tables 4).

4.3.1. 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 (3405267 and 3405103), followed by grain yield (1200029 and 1199938) 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 (205172.36 and 230991), followed by grain yield (104073.23 and 115361.96) 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 36.93) 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 Thakur 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 (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 (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 (- and 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 58.09), number of pod per plant (49.73 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. Gudivada *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).

4.3.2. 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).

4.3.3. 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. Gudivada *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). Saki *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.

Figure 4. Graph showing genotypic and phenotypic coefficient of variation (GCV and PCCV), heritability (H^2b) and genetic advance as percent of mean (GAM) for studied characters

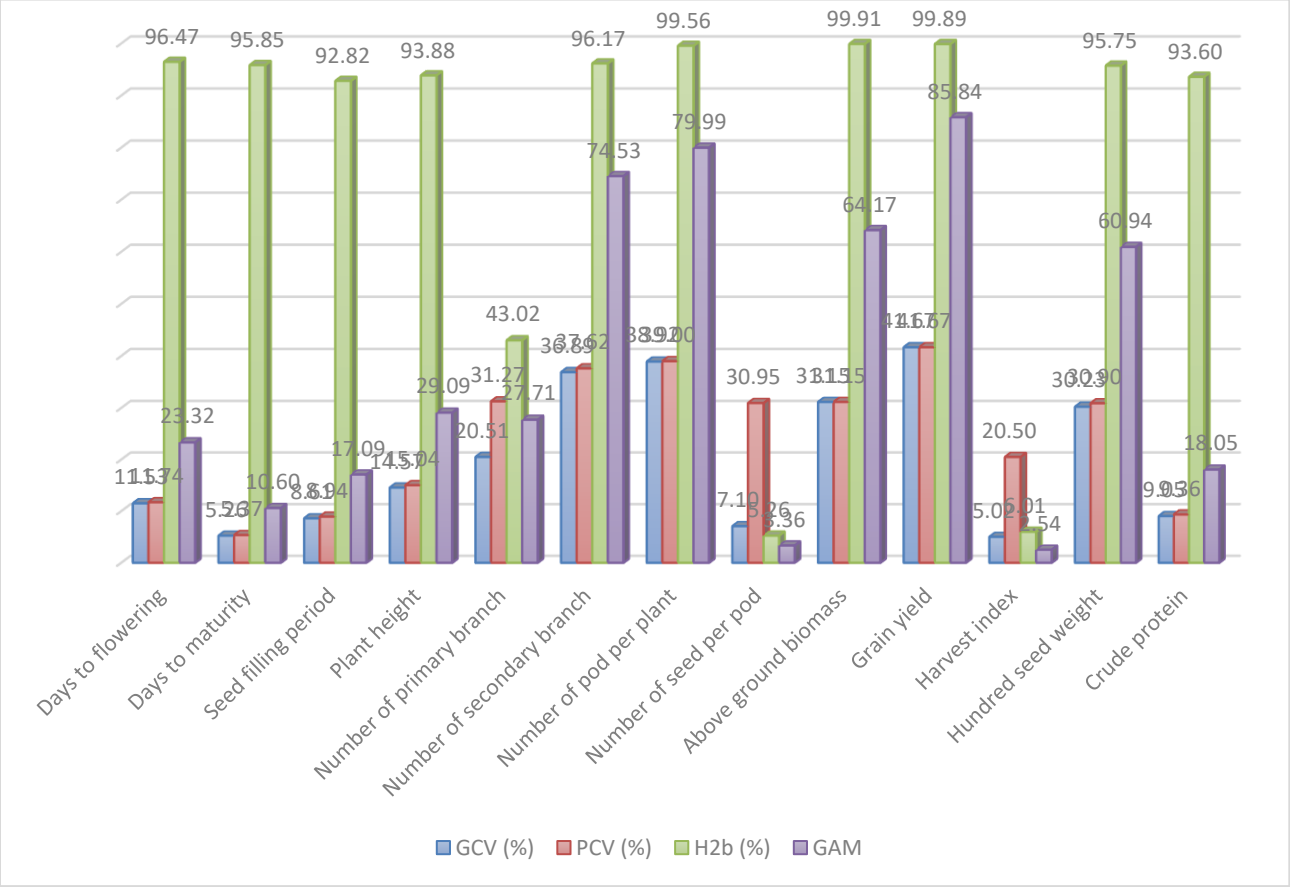


Table 4. Range, mean, variance, genotypic and phenotypic coefficient of variability, broad sense heritability, and genetic advance as of mean for the 13 characters of chickpea genotypes tested in Takusa district during 2018/19

	Range											
Character	Mean	max	min	MST	MSE	σ2e	σ2g	σ2P	GCV (%)	PCV (%)	H^2b (%)	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	10375	2344	10215474	164.2	164.2	3405103	3405267	31.15	31.16	99.9	3801	64.2
GY	2628	4792	975	3599907	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	49.41	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	2.7	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, $\sigma^2 g$: genotypic variance, $\sigma^2 p$: phenotypic variance H^2b: Broad sense heritability in percent, GCV (%): Coefficient of genotypic variance, PCV (%): coefficient of phenotypic variance, GA: genetic advance, GAM: genetic advance as percent of mean.

4.4. 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 traits, 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.

4.4.1. 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.* (2018) 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 Megersa *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 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 non-significant 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 indicated that there was moister stress during the growing season (figure 3).

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 non-significant correlation 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 showed non-significant correlation with traits of days to maturity, seed filling period and number of seed per pod though days to flowering which was 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. Number of seed per pod was the only character which showed non-significant correlation 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.

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 non-significant 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). Muhammad *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 non-significant 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 (Muhammad *et al.*, 2012; Yücel *et al*., 2006; Jakhar, 2014).

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 and Ambev, 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 non-significant 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 non-significant 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). Muhammad *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. 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). Muhammad *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 (Jukanti *et al.*, 2014).

Table 5. Genotypic (above diagonal) and phenotypic (below diagonal) correlations coefficients of the 13 traits chickpea genotypes

Chara-cters	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.

4.5. 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).

4.5.1. Genotypic direct and indirect effects of various characters on grain yield

The genotypic correlation coefficients is partitioned into direct and indirect effects by various yield contributing characters studied in this investigation (Table 6).

Direct effect

The direct effects exhibited by days to flowering, seed filling period, number of primary branches 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 and Padmavathi *et al.*, 2013). However, days to flowering and seed filling period and number of primary branch had significant correlation; it have 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.

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 Megersa *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 Megersa *et al*. (2016) investigated on some chickpea genotypes and found the similar results.

Table 6. Estimate of direct effect (bold face and diagonal) and indirect effects (off diagonal) at genotypic level in 100 chickpea genotypes

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

4.5.2. 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).

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.

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 *et al*. (2015), Pods per plant, primary branches per plant and plant height indirectly contributed to grain yield via above ground biomass. The indirect positive effects of pods per plant, primary branches per plant and plant height were resulted from their positive

correlation with grain yield. 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 *et al*. (2015)

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	rp
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	-0.145	0.097	0.046	0.0003	**-0.0076**	0.172	0.044	-0.0005	0.323	0.161	0.69***
NSB	-0.231	0.128	0.100	0.0004	-0.0053	**0.245**	0.065	-0.0005	0.455	0.234	0.98***
NPP	-0.213	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	-0.231	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.

4.6. Divergence (D^2) and Cluster 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 of D^2-statistics (Table 8 and Fig. 2).

4.6.1. Inter and intra cluster divergence D^2 analysis

The divergence (D^2) analysis revealed that the 100 chickpea genotypes were grouped into 9 significant clusters (Table 8). The intra-cluster 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 D^2 value, indicated that there were diversification within groups. The highest inter cluster distance were 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) were 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 D^2 statistics and classified in to 9 clusters. Parashi *et al.* (2013) evaluate 365 genotypes and found six significant clusters. Vijayaraje *et al.* (2015) investigated and found 16 clusters, indicating the presence of wide genetic diversity indicated that breeders can improve chickpea productivity only through simple selection.

Table 8. Intra (diagonal) and inter (off diagonal) cluster D2 values of 100 chickpea genotypes grown under potential environments of North Gondar.

Cluster	I	II	III	IV	V	VI	VII	VIII	IX
I	**61.6**	837.4	480.4	295.2	759.3	309.4	413.7	874.5	300.4
II		**76.5**	93.6	377.5	112.7	195.3	81.8	97.9	194.1
III			**48.9**	161.7	108.9	103.1	87.4	99.1	101.6
IV				**5.3**	287.2	90.6	183.6	390.9	98.2
V					**65.9**	168.2	97.6	119.9	166.4
VI						**21.9**	96.0	203.4	81.6
VII							**53.3**	104.7	95.4
VIII								**77.8**	202.2
IX									**21.2**

X^2=26.12 at 1% probability level and X^2 =21.03 at 5% probability level

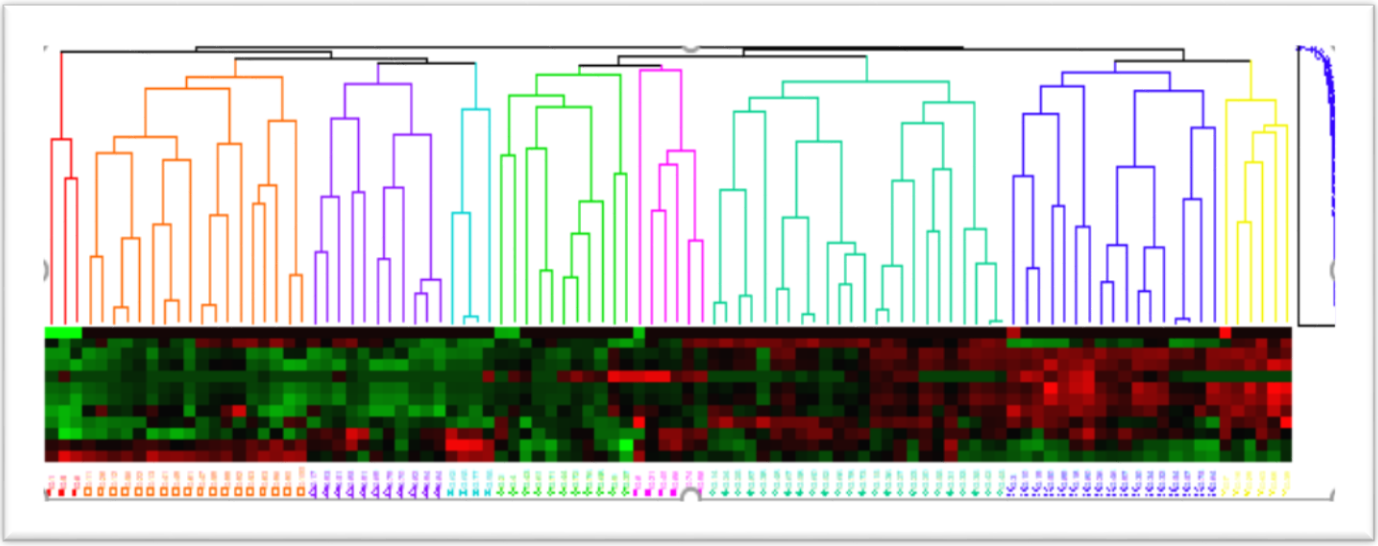


Figure 5. Dendrogram showing the genetic relationship among the 100 chickpea genotypes

4.6.2. 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 number were consisted in cluster I followed by cluster IV, VI, and IX (3 genotype, 4 genotype, 6 genotype and 6 genotype) respectively (Table 9).

Table 9. Distribution of 100 chickpea genotypes in different clusters

cluster number	number of cluster	Genotype included in the cluster
I	3	iccx-060045-f3-p12-BP, icc-1164, iccx-060039-f3-p39-BP
II	18	iccx-060039-f3-p174-BP, icc-15888, 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-20115-16-0058, 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-94954
III	11	iccx060039-f3-p21-BP, icc-4958, iccx-060039-f3-p270-BP, icc-10673, icc-15762, icc-4533, icc-13863, iccx-060045-f3-p130-BP, DZ-2012-CX-0227, iccx-060039, f3-p204-BP, iccx-060039-f3-p24-BP
IV	4	iccx-060045-f3-p173-BP, icc-15294, iccril-03-0167, icc-5135
V	11	Iccx-090013-f2-p147-BP, iccx-060039-f3-p196-BP, icc-14778, IE-16-109/2, JG-62, iccx-060039-f3-p57-BP, iccx-060039-f3-p178-BP, DZ-2012-CX-0048, iccx-0900013-f2-p107-BP, iccu-07103, iccx-060039-f3-p10-BP
VI	6	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	24	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-20115-0041, DZ-2012-ck-20115-50045, iccx-090013-f2-p3-BP, DZ-2012-CK-0040, iccx-090013-f2-p276-BP, iccx-090013-f2-p105-BP, DZ-2012-ck-0238, Dimtu, iccu-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, icc-14199xnatoli-p137, Dalota, iccx-090013-f2-p245-BP, iccx-0900013-f2-p115-BP
VIII	17	IE-16-012/2, IE-16-079/1, iccx-060039-f3-p182-BP, IE-16-059/2, iccu-11108, icc-1422, iccx-090013-f2-p120-BP, iccx-090013-f2-p145-BP, iccx-060039-f3-p131-BP, IE-16-059/1, IE-16-025/1, IE-16-003/1, icc-6279, icc-15614, DZ-2012-CX-0028, Local, iccril-03-0215
IX	6	IE-16-094/1, iccx060045-f3-p98-BP, iccx-060045-f3-p5-BP, iccx-090013-f2-p215-BP, iccx-090013-f2-p265-BP, JV-11

4.6.3. 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 (4429.3kgha^{-1}) and cluster I (1126.6kgha^{-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 (Baranwal, 2016).

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.

4.7. 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 PCA1 explained 49.5%, PCA2 showed 14.9%, PCA3 had 9.2%, PCA4 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.

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.

Table 11. Vector loadings and percentage explained variation by the first four PCs

	Eigenvectors			
characters	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.

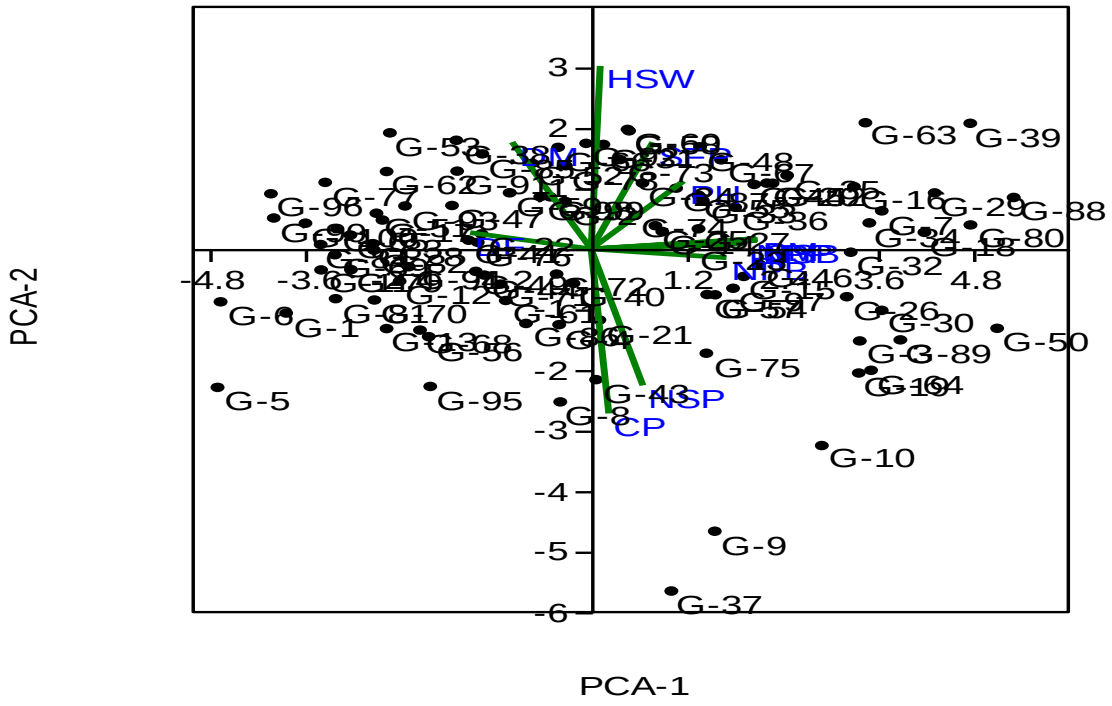


Figure 6. Biplot of PCA1 and PCA2 showing the overlay of 100 genotypes and the 13 studied traits

Principal component analysis (PCA) reduces a larger number of variables to a smaller number of factors and it is non-dependent 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 (Table 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).

Chapter 5. CONCLUSION AND RECOMENDATIONS

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 materials. 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 (D^2) analysis. Cluster VII and II were the largest with 24 and 18 genotypes followed by clusters XIII 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% 0f 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-15614, 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-14778, icc-510, DZ-2012-CK-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.

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7. APPENDICES

Appendix Table 1. Mean performance of 100 chickpea genotypes tested at in Takusa district during 2018/19 cropping season

Code	Genotype/pedigree	DF	DM	SFP	PH	NPB	NSB	NPP	NSP	BM	HI	HSW	GY	CP
1	iccx-060045-f3-p12-BP	62.7	118.0	55.3	31.5	1.4	3.2	28.3	1.00	3397.2	0.34	21.9	1165.3	17.39
2	Iccx-090013-f2-p147-BP	52.3	116.3	64.0	44.9	2.1	5.7	42.9	1.00	5622.2	0.41	20.7	2279.67	14.70
3	IE-16-012/2	51.0	109.7	58.7	46.5	3.8	8.9	65.0	1.40	7761.1	0.49	11.8	3818.53	15.45
4	iccx-060039-f3-p196-BP	56.3	112.3	56.0	37.9	2.7	5.6	42.4	1.33	5541.7	0.41	19.1	2251.37	15.53
5	icc-1164	74.3	119.7	45.3	27.5	1.2	3.5	29.8	1.30	3555.6	0.34	12.8	1214.6	15.54
6	iccx-060039-f3-p39-BP	70.3	117.0	46.7	29.9	1.3	2.0	23.8	1.00	2425.0	0.41	18.5	999.83	14.41
7	IE-16-094/1	52.3	117.7	65.3	47.5	3.3	9.9	79.0	1.00	8227.8	0.51	19.9	4204.07	16.13
8	DZ-2012-CK-0253	68.3	119.7	51.3	56.5	2.9	5.4	41.2	1.67	5388.9	0.40	14.5	2181.83	18.50
9	icc-14778	53.3	106.3	53.0	33.7	3.1	7.2	53.3	1.73	6802.8	0.46	11.9	3118.83	19.54
10	IE-16-079/1	49.7	106.7	57.0	42.9	3.2	8.2	61.0	1.60	7483.3	0.49	10.8	3637.1	17.82
11	iccx-060039-f3-p174-BP	67.3	118.7	51.3	32.4	2.4	3.8	31.5	1.00	3641.7	0.35	20.1	1258.73	14.54
12	icc-15888	62.7	116.3	53.7	32.2	2.3	4.7	38.5	1.00	4533.3	0.37	14.9	1683.63	14.01
13	iccril-04-0087	70.7	119.7	49.0	40.2	2.8	4.3	37.2	1.00	4305.6	0.36	18.1	1531.57	17.40
14	DZ-2012-CK-240	55.3	111.3	56.0	46.4	3.0	6.6	48.6	1.00	6480.6	0.44	30.5	2839.17	16.37
15	Natoli/ s.check	56.3	112.0	55.7	44.8	2.8	8.0	58.5	1.27	7194.4	0.49	26.1	3519.47	16.15
16	iccx060045-f3-p98-BP	54.0	112.7	58.7	43.6	3.5	9.5	72.9	1.00	8035.0	0.52	26.9	4159.97	14.27
17	iccx060039-f3-p21-BP	56.3	117.3	61.0	31.7	2.7	3.5	29.9	1.00	3533.3	0.34	28.0	1213.53	15.16
18	iccx-060039-f3-p182-BP	53.3	118.0	64.7	41.0	3.5	10.2	93.6	1.60	8708.4	0.51	19.7	4400.43	13.27
19	IE-16-059/2	52.7	106.0	53.3	47.9	3.3	9.2	68.7	1.53	7861.1	0.50	12.3	3932.8	15.11
20	iccx-060039-f3-p145-BP	58.0	119.3	61.3	46.5	2.9	8.9	65.5	1.00	7763.9	0.49	22.9	3832.1	14.98
21	DZ-2012-CK-0048	56.7	116.0	59.3	40.0	2.7	6.0	44.1	1.73	5891.7	0.41	23.9	2396.5	15.64
22	iccx-060039-f3-p188-BP	61.7	119.3	57.7	32.7	2.5	5.4	41.7	1.07	5422.2	0.41	19.1	2195.2	13.71
23	DZ-2012-CK-0030	50.0	110.3	60.3	44.7	2.5	6.9	51.2	1.33	6697.2	0.45	23.0	2988.5	14.07
24	iccx-090013-f2-p103-BP	55.3	109.7	54.3	50.3	2.9	6.2	46.3	1.00	6158.3	0.43	33.7	2674.0	14.68
25	DZ-2012-CK-0239	53.3	108.0	54.7	44.9	2.2	6.9	51.4	1.00	6716.7	0.45	30.0	2994.1	15.24
26	iccu-11108	53.0	115.0	62.0	41.7	3.2	9.4	70.5	1.27	7904.4	0.52	17.4	4082.0	16.46
27	DZ-2012-CX-20115-0041	60.3	118.7	58.3	45.1	2.7	7.5	55.2	1.33	6942.8	0.49	26.8	3387.6	15.33
28	iccx-060039-f3-p2015-BP	65.3	116.3	51.0	31.4	3.1	3.9	33.3	1.00	3755.6	0.36	26.2	1350.6	14.10

Code	Genotype/ pedigree	DF	DM	SFP	PH	NPB	NSB	NPP	NSP	BM	HI	HSW	GY	CP
29	iccx-060045-f3-p5-BP	48.7	107.0	58.3	44.8	3.2	10.3	95.9	1.00	8966.7	0.50	27.5	4512.8	14.00
30	icc-1422	52.0	113.3	61.3	37.9	3.0	10.1	89.3	1.27	8508.3	0.51	17.6	4312.2	16.52
31	DZ-2012-ck-20115-50045	64.3	126.0	61.7	45.3	2.9	6.7	49.9	1.00	6638.9	0.44	22.8	2946.2	13.97
32	iccx-090013-f2-p120-BP	51.7	111.0	59.3	42.6	2.7	9.7	74.6	1.27	8111.1	0.52	23.6	4177.7	14.91
33	iccx-090013-f2-p3-BP	51.0	112.7	61.7	34.6	2.5	7.7	56.9	1.00	7008.4	0.49	26.3	3436.2	14.23
34	iccx-090013-f2-p145-BP	50.0	111.0	61.0	38.3	3.1	10.0	81.2	1.17	8266.7	0.51	23.2	4217.0	13.85
35	DZ-2012-CK-0040	51.7	110.0	58.3	36.9	2.9	9.1	67.2	1.00	7836.1	0.50	30.8	3895.6	13.44
36	090013-f2-p276-BP	57.3	114.3	57.0	43.9	2.6	8.2	60.9	1.23	7433.3	0.49	29.8	3620.2	14.59
37	IE-16-109/2	45.0	96.3	51.3	37.1	2.5	6.2	45.4	1.67	5991.7	0.42	10.1	2514.0	20.47
38	iccx-090013-f2-p105-BP	59.3	116.7	57.3	50.9	2.6	4.1	35.7	1.00	4025.0	0.36	31.5	1447.5	13.62
39	iccx-090013-f2-p215-BP	54.3	113.0	58.7	57.5	3.1	11.2	104.4	1.00	9751.7	0.48	32.7	4720.0	14.41
40	iccx-060039-f3-p173-BP	56.3	122.7	66.3	38.1	2.5	5.6	43.0	1.73	5500.0	0.42	19.6	2309.1	15.03
41	iccu-115	67.0	118.0	51.0	38.9	2.5	5.4	41.2	1.00	5375.0	0.41	23.9	2176.2	14.78
42	DZ-2012-ck-0238	52.7	113.3	60.7	41.5	2.7	8.7	64.1	1.00	7738.9	0.49	32.4	3807.8	15.52
43	JG-62	46.7	105.0	58.3	28.7	2.3	6.2	44.7	1.23	5955.6	0.42	15.3	2472.1	16.07
44	iccx-060039-f3-p57-BP	54.0	111.0	57.0	37.6	2.4	4.8	38.3	1.33	4525.0	0.37	20.5	1686.7	13.36
45	Dimtu/s.check	52.3	114.0	61.7	41.7	2.7	8.2	60.4	1.07	7422.2	0.49	30.8	3617.4	15.07
46	iccx-060039-f3-p131-BP	53.7	114.3	60.7	39.3	2.7	8.4	62.9	1.27	7666.7	0.49	19.3	3742.8	14.77
47	iccx-060045-f3-p132-BP	64.3	118.3	54.0	34.0	2.4	5.2	40.2	1.00	5208.3	0.40	30.0	2101.4	14.57
48	iccu-090013-f2-p108-BP	53.3	117.0	63.7	46.0	2.4	7.2	54.0	1.00	6861.1	0.48	31.4	3315.4	15.02
49	iccril-03-0127	67.3	115.7	48.3	38.3	2.5	5.8	43.8	1.00	5736.1	0.40	18.2	2307.5	14.11
50	IE-16-059/1	48.3	110.0	61.7	45.7	3.1	11.5	108.5	1.33	9888.9	0.48	12.7	4743.9	16.39
51	icc-4958	59.0	120.0	61.0	38.1	2.2	2.9	26.7	1.23	2941.7	0.39	29.3	1126.4	15.03
52	iccx-060045-f3-p11-BP	51.7	116.7	65.0	41.9	2.1	5.2	40.1	1.00	5147.2	0.40	29.2	2079.8	14.71
53	iccx-060045-f3-p165-BP	64.3	122.0	57.7	41.2	2.2	4.2	36.8	1.00	4194.4	0.36	32.5	1493.5	13.57
54	IE-16-025/1	48.0	109.0	61.0	39.6	2.4	7.5	54.7	1.07	6900.0	0.48	12.0	3299.8	14.70
55	iccx-090013-f2-p129-BP	57.3	115.3	58.0	40.8	2.3	8.1	60.3	1.00	7408.3	0.49	24.5	3611.9	14.13
56	icc-67	65.0	117.0	52.0	32.5	2.2	5.1	39.5	1.07	4944.4	0.40	14.4	1991.3	16.03
57	IE-16-003/1	50.0	109.3	59.3	38.7	2.5	7.4	54.1	1.00	6897.2	0.49	12.6	3352.8	14.89
58	iccx-090013-f2-p234-BP	55.0	118.0	63.0	46.5	2.4	6.5	47.7	1.00	6397.2	0.44	31.7	2808.9	14.33
59	DZ-2012-CK-20115-16-0058	62.7	119.0	56.3	36.6	2.4	6.0	44.2	1.00	5913.9	0.41	28.0	2419.6	14.38
60	iccx-090013-f2-p107-BP	54.3	119.3	65.0	46.8	2.2	6.4	47.2	1.07	6363.9	0.44	34.2	2790.7	15.02

Code	Genotype/ pedigree	DF	DM	SFP	PH	NPB	NSB	NPP	NSP	BM	HI	HSW	GY	CP
61	iccx-060039-f3-p178-BP	54.7	107.3	52.7	36.9	2.3	5.0	39.4	1.00	4886.1	0.41	23.0	1989.6	15.57
62	iccx-060045-f3-p173-BP	63.7	133.0	69.3	33.9	2.3	4.5	37.9	1.00	4411.1	0.36	18.5	1590.8	15.17
63	iccx-090013-f2-p265-BP	52.0	117.7	65.7	46.2	3.1	9.7	76.0	1.00	8166.7	0.51	35.5	4186.6	15.52
64	icc-6279	47.0	105.0	58.0	30.9	2.8	10.1	88.7	1.00	8488.9	0.51	15.5	4308.6	17.65
65	icc-15294	69.3	133.0	63.7	31.1	2.0	4.6	38.2	1.00	4441.7	0.36	13.7	1615.9	15.61
66	iccx-060045-f3-p76-BP	57.7	117.7	60.0	42.7	2.2	6.2	45.0	1.00	5966.6	0.42	29.1	2499.7	13.56
67	icc-14199xnatoli-p137	57.3	118.0	60.7	46.4	2.7	7.9	57.7	1.07	7111.1	0.49	29.2	3489.1	14.53
68	DZ-2012-CX-0048	57.7	110.7	53.0	33.3	2.1	4.3	37.4	1.27	4325.0	0.36	20.3	1556.4	15.04
69	iccx-060039-f3-p270-BP	60.0	114.0	54.0	38.3	1.4	2.9	26.3	1.00	2722.2	0.41	25.6	1112.9	15.35
70	icc-10673	53.7	108.3	54.7	34.3	1.9	2.9	26.1	1.00	2675.0	0.41	17.3	1105.5	14.26
71	iccx-0900013-f2-p107-BP	48.3	104.3	56.0	36.9	2.0	4.8	39.0	1.00	4650.0	0.38	25.0	1780.5	15.25
72	iccu-07103	55.0	114.0	59.0	37.7	2.3	5.7	43.4	1.47	5666.7	0.41	19.5	2294.6	13.36
73	Dalota/s.check	52.7	115.7	63.0	38.0	2.3	6.5	48.2	1.13	6430.6	0.44	32.4	2825.9	13.90
74	iccx-060045-f3-p232-BP	56.3	119.3	63.0	38.9	2.2	6.9	51.2	1.40	6686.1	0.45	29.1	2985.1	15.03
75	icc-15614	48.0	105.3	57.3	35.7	3.2	7.1	52.7	1.00	6755.6	0.45	15.6	3042.2	16.80
76	iccx-060039-f3-p10-BP	58.7	117.7	59.0	34.7	1.9	5.3	40.7	1.33	5291.6	0.40	19.5	2137.6	12.97
77	iccril-03-0167	67.7	132.0	64.3	32.2	1.7	4.4	37.5	1.00	4341.7	0.36	13.0	1558.8	13.39
78	iccx-090013-f2-p245-BP	55.7	117.7	62.0	41.7	2.5	6.0	44.0	1.20	5797.2	0.40	29.9	2334.6	13.64
79	icc-15762	56.0	115.7	59.7	37.1	1.4	3.0	27.1	1.00	2938.9	0.39	22.1	1131.8	16.30
80	DZ-2012-CX-0028	51.3	120.7	69.3	45.5	3.3	10.8	98.2	1.67	9369.4	0.49	26.4	4577.1	15.75
81	iccx-060045-f3-p157-BP	66.3	116.3	50.0	40.6	1.5	4.0	34.6	1.00	3911.1	0.36	15.0	1418.2	15.08
82	icc-4533	57.7	115.0	57.3	36.1	1.4	4.2	36.3	1.00	4108.3	0.36	17.0	1467.3	13.82
83	iccx-060039-f3-p107-BP	68.0	120.0	52.0	37.8	1.5	4.6	38.1	1.07	4422.2	0.36	26.9	1610.0	15.18
84	icc-13863	57.0	118.3	61.3	36.9	1.2	3.2	28.5	1.00	3391.7	0.35	12.8	1170.7	13.78
85	iccx-060045-f3-p130-BP	55.0	126.3	71.3	35.3	1.9	4.9	39.1	1.07	4777.8	0.41	31.7	1948.6	16.40
86	icc-510	59.0	125.3	66.3	37.4	2.4	5.5	41.7	1.33	5455.6	0.40	18.1	2202.9	19.00
87	iccx-0900013-f2-p115-BP	50.7	110.0	59.3	44.7	2.3	6.9	52.1	1.00	6736.1	0.45	32.3	3050.1	15.07
88	JV-11	49.0	111.0	62.0	41.6	3.8	12.5	113.5	1.00	10375.0	0.46	25.2	4792.2	14.75
89	Local/check	50.7	110.7	60.0	44.3	3.1	10.0	82.3	1.47	8300.0	0.51	12.7	4223.5	15.64
90	iccx-060045-f3-p197-BP	69.0	119.3	50.3	44.0	1.4	1.7	22.1	1.00	2344.4	0.42	28.5	975.9	15.12
91	DZ-2012-CX-0227	49.3	118.0	68.7	34.6	1.7	4.7	38.3	1.00	4483.3	0.37	24.5	1660.2	14.04
92	iccx-060045-f3-p91-BP	60.3	118.7	58.3	34.7	3.9	6.1	44.7	1.00	5955.5	0.42	31.8	2476.5	12.88
93	iccx-060039-f3-p204-BP	55.0	117.7	62.7	36.3	2.1	3.9	33.7	1.00	3788.9	0.36	23.2	1360.4	14.37

Code	Genotype/ pedigree	DF	DM	SFP	PH	NPB	NSB	NPP	NSP	BM	HI	HSW	GY	CP
94	iccx-060039-f3-p24-BP	55.3	116.3	61.0	37.2	1.6	4.3	37.5	1.00	4336.1	0.36	12.5	1560.5	14.48
95	icc-5135	68.3	126.0	57.7	30.3	2.3	5.1	39.7	1.47	5016.7	0.40	12.4	2014.4	17.90
96	iccx-060045-f3-p253-BP	66.7	125.0	58.3	31.8	1.3	3.6	30.0	1.00	3550.0	0.34	33.1	1217.2	16.15
97	iccril-03-0215	53.3	118.3	65.0	37.6	2.8	7.9	57.6	1.33	7094.5	0.49	16.6	3477.4	16.04
98	iccx-060045-f3-p126-BP	53.3	117.7	64.3	35.0	2.1	5.5	41.6	1.47	5402.8	0.41	31.7	2193.0	13.71
99	iccx-060045-f3-p102-BP	65.0	119.7	54.7	41.8	3.0	6.2	45.7	1.00	6018.3	0.42	25.2	2517.2	14.29
100	iccu-94954	68.3	123.0	54.7	42.7	1.7	2.5	25.5	1.00	2505.5	0.42	23.7	1045.4	15.48
Coefficient of variation (%)		2.8	1.4	3.4	5.5	13.9	3.5	7.7	10.50	9.2	1.70	9.2	13.0	0.86
Grand Mean of characters		57.0	115.6	58.6	39.5	2.5	6.4	50.6	1.14	5923.0	0.43	22.7	2628.7	15.13
Critical value (Tukey (%))		5.6**	5.8**	7**	7.7**	1.2**	1.4**	6.2**	0.43**	589.**	0.3**	7.6**	323.5**	0.46**

Note: DF: days to flowering, DM: days to maturity, SFP: seed filling period, PH: 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: above ground biomass in kilogram per hectare, HI: harvest index, GY; grain yield in kilogram per hectare, HSW: hundred seed weight in gram and CP: crude protein.

AUTHOR BIOGRAPHY

The Author was born on 03, October 1990 in Gondar Zuria district, North Gondar of Amhara Regional State, Ethiopia. As soon as he reached the age for education, he attend his elementary school in Chinchaye elementary school, and his junior, secondary and preparatory school in Maksegnit junior, secondary and preparatory school. Having passed the Ethiopian school leaving certificate examination (ESLCE), he joined Debre Birehan University since 2010 and graduate in 2012 with BSc. degree in plant science.

Soon after graduation, the Author was employed in the Ministry of Trade and Transport, at Genda Wuha and W/belesa office, North Gondar, Ethiopia for 3 and 10 months respectively as quality control expert from 2013 to January 2014, and he was employed Amhara Agricultural Research Institute (AARI) at Gondar agricultural research center, North Gondar, Ethiopia, for about three years (2014-2017) as crop assistant researcher. During his stay he had generated five research proposals and he was running two ongoing research activities. Moreover he has written two of the completed lowland and mid land research activities.