GENETIC VARIABILITY AND ASSOCIATION AMONG SEED YIELD AND YIELD RELATED TRAITS IN DESI CHICKPEA (*Cicer arietinum* L.) GENOTYPES

MSc THESIS

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Genetic Variability and Association among Seed Yield and Yield Related Traits in Desi Chickpea (*Cicer arietinum* L.) Genotypes

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We hereby certify that we have read and evaluated this Thesis entitled '**Genetic Variability and Association among Seed Yield and Yield Related Traits in Desi Chickpea (***Cicer arietinum* L.) **Genotypes**' prepared under our guidance by **Birhanu Gizaw.** We recommend that it be submitted as fulfilling the thesis requirement.

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DEDICATION

Dedicated to my father Mr. Gizaw Lemma and my mother Mrs. Mestewat Ayalew.

STATEMENT OF AUTHOR

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BIOGRAPHICAL SKETCH

The author was born on May 9, 1984 in Meta District, Eastern Hararghe Zone, Oromia Regional State, from his father Gizaw Lemma and his mother Mestewat Ayalew. He attended elementary school at Bekiye, Chalanko and Karamile and high school at Dire Dawa Comprehensive Secondary School at Dire Dawa. After the completion of his high school education, he joined Mekele University and graduated with BSc Degree in Dry Land Crop and Horticultural Sciences in 2007. Soon after graduation, he was employed by the Gorogotu Wareda Agricultural Office of east Hararghe Zone, Oromia region as Agronomist, where he has been serving from December 2007 until he joined the School of Graduate Studies at Haramaya University in September 2017.

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LIST OF ABBREVIATIONS

AGRA	Alliance for Green Revolution in Africa
ARARI	Amhara Regional Agricultural Research Institute
CSA	Central Statistics Agency
GCV	Genotypic Coefficient Of Variation
GAM	Genetic Advance as Percent of Mean
ICARDA	International Center for Agricultural Research in the Dry areas
ICRISAT	International Crop Research Institute for the Semi-arid Tropics
PCV	Phenotypic Coefficient of Variation
SAS	Statistical Analysis System
USD	United States dollar

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ABSTRACT

Evaluation of genotypes for the existence of variations and generation of genetic information is the key step in plant breeding to develop varieties for the targeted area of production. Twenty desi chickpea genotypes were tested in randomized complete block design with three replications. The objectives of the study were to estimate the extent of genotypic and phenotypic variability, estimate the genotypic and phenotypic associations among characters and to estimate the direct and indirect contribution of traits on seed yield. Data were collected for eleven traits and subjected to analysis of variance. There were significant differences among genotypes for eleven quantitative traits including grain yield which ranged from 1844.3 kg/ha (DZ-2012-CK-0029) to 3742.3kg/ha (DZ-2012-CK-0034) with mean value of 2804.24kg/ha. Out of the total genotypes tested, 45% of them had yielded above the grand mean (2804.24kg/ha). The range for phenotypic coefficient of variation (PCV) was from 3.38% to 21.99%, while the genotypic coefficient of variation (GCV) ranged from 1.6% to 20.28%. Heritability in broad sense was ranged from 51.95(number of secondary branches per plant) to 95.00% (number of primary branches per plant). Genetic advance as percent of mean ranged from 3.36 % to 40.79. In this study, plant height, number of primary branches per plant and seeds per plant had higher heritability estimates coupled with higher genetic advance as percent of mean. GCV and PCV values had low magnitude of differences for plant height, primary branches per plant and number of seeds per plant. Hence, the traits are highly heritable indicating the influence of environment was less. Seed yield had positive and highly significant correlation coefficients with primary branches per plant, pods per plant, seeds per pod and seeds per plant at both phenotypic and genotypic levels. The association between yield, and yield related characters through phenotypic and genotypic path coefficients revealed that number of pods per plant, seeds per pod and number of seeds per plant exerted moderate to high positive direct effect on seed yield. The 20 desi chickpea genotypes were grouped into eight distinct clusters. Clusters I, II and III consisted of 8(40%), 5(25%) and 6(30%) genotypes, respectively. In addition, Cluster IV has consisted one genotype. Generally, this study revealed the presence of variability among the tested genotypes and the possibility of increasing grain yield. Yet, this study was conducted for one season and at one location which needs to be tested in subsequent trials at different locations and seasons to develop high yielding varieties.

Keywords: Correlation, Genetic Advance, Genotypes, Heritability, Path analysis, Seed yield.

1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinating crop believed to be first domesticated in the Middle East. It is a diploid (2n = 2x = 16) crop which belongs to the family Leguminoseae, subfamily Papilionacea and genus cicer (Van der Maesen, 1987). It is grown all over the five continents around 50 countries with, 90 % of its cultivated area around 1.3×10^7 ha in developing countries (Jagadish and Jayalakshmi, 2014). India ranks first in the world with respect to the cultivated area (68.5%) followed by Pakistan (8.7%). Interims of production India accounts for 68% of the total world production followed by Australia (5.9%). The other major chickpea producing countries are Pakistan, Iran, Australia, Turkey, Myanmar and Ethiopia. The crop is mainly grown under rain fed conditions with a world average yield of 931 kg/ ha (FAOSTAT, 2015).

Ethiopia is the leading producer, consumer and exporter of chickpea in Africa. The country shares 4.5% of the global chickpea market and more than 60% of Africa's global chickpea market (FAOSTAT, 2015). In Africa, Ethiopia stands third in productivity after Egypt and Sudan (FAOSTAT, 2012). The country is also a second center of diversity for chickpea. It was cultivated on an area of 242,703.73 hectares during 2017/2018 with a total production of 499,425.55 tons giving an average national productivity of 2.058 tons/ha (CSA, 2018). The area coverage for chickpea cultivation in Oromia Regional State during 2017/2018 growing season was 92,829.49 ha with production of 216,583.72 tons and an average productivity of 2.333 tons/ha (CSA, 2018).

The two types of chickpea are known, desi and kabuli depending on size, shape, and color of the seeds. The former type is shorter, with smaller leaf, pink or blue flowers, pigmented seeds, whereas the later type is taller, with longer leaf, white flowers, and more rounded and cream colored seeds (Jukanti *et al*., 2012). It is believed that the desi type originates first and the kabuli type originated latter through natural mutation (Shiferaw *et al*., 2007). Although both types differ in many traits, they cross easily with each other and the transfer of genes from one type to another is easy (Gaur *et al*., 2010).

In today's world, parallel to population growth, nutrition problem is also growing increasingly, especially productions of high-range protein foods have been important for solving nutritional problem. Legumes play an important role in agriculture and diet of many developing countries and are a major source of dietary nutrients for many people (Dejene , 2010). In 2050, global demand for chickpea is projected to be 18.3 million tones and the low income food deficit countries are expected to suffer the widest supply demand gap. Most of this deficit can be met through breeding for drought tolerance and yield stability (Nedumaran and Bantilan, 2013).

Improvement of yield in crops the primary objective of a plant breeder. Selection of superior genotypes is the basis of crop improvement. The efficiency of selection depends on the identification of genetic variability from the phenotypic expression of the characters. Variability means difference among the individuals of the same or different species. The variability may be due to environment or genotypes or interaction of both the components. Assessment of genetic variability in the base population is the first step in any breeding programme (Sarker *et al*., 2013).

The success of good breeding programme usually depends upon the genetic variability present in the breeding materials. Thus knowledge on genetic variability, heritability and genetic advance is essentials for a breeder to choose better genotypes for crop improvement. Selection is an integral part of breeding processes by which genotypes with high productivity in a given environment are selected. The polygenic inheritance of yield components makes selection more difficult. Moreover, these complex traits are highly influenced by environment, which reduces the progress to be achieved through selection (Dan, 2014).

Desi chickpea types are dominating the production over 80% in Ethiopia in terms of both area coverage and volume of production (Kinfe *et al*., 2015). It is mainly grown in the central, northern and eastern highland areas of the country (Shiferaw *et al.,* 2007). The area under chickpea cultivation has increased by 57% from about 154,281 ha in 2003 to about 242,703.73 ha in 2017 while yields jumped from about 0.881tons/ha to 2.058 tons/ha during the same period (CSA, 2018). Although this growth is impressive, chickpea productivity in Ethiopia is still below the potential yield of 4-5 tons/ha (Fikre, 2016) and 6 t/ha was reported in Israel in 2012 (FAOSTAT, 2013). The reason for this chickpea production constraints gap mainly

limited availability and adoption of high yielding varieties with abiotic and biotic stress resistance.

Knowledge on the extent and pattern of genetic variability present in a population is absolutely essential for further improvement of the crop. Similarly, information on the extent and nature of interrelationship among character help in formulating efficient scheme of multiple trait selection. Even though some works have been done on desi type chickpea (Fikru, 2004) and on kabuli type chickpea (Temesgen, 2007) in other parts of Ethiopia, there is a need to study the variability and identity of genotypes form eastern Ethiopia. Therefore, this study was carried out with the following objectives:-

Objectives

- to assess the genetic variability for seed yield and yield related traits in desi chickpea genotypes;
- to estimate the genotypic and phenotypic associations among characters, and
- to assess the direct and indirect effects of yield related traits on seed yield of chickpea

2. LITRETURE REVIEW

2.1. Biology of Chickpea

Chickpea is an annual crop that can complete its life cycle depending on the prevailing meteorological conditions. The desi type chickpea reaches physiological maturity within 95-105 days and kabuli type within 100-110 days. Plants are shrubby and rarely grow more than one meter high. Roots are robust and long. Desi-type chickpeas are bushy plants with relatively small leaflets and flowers. Stems are branched, straight, erect to prostrate, and more or less ribbed (Bharadwaj *et al*., 2010). Desi chickpea has a thick, colored seed coat. The common seed colors include various shades and combinations of brown, yellow, green and black. The seeds are generally small and angular with a rough surface. The flowers are generally pink; however, some desi types have white flowers. The kabuli type chickpeas are characterized by white-colored seed with ram's head shape, thin seed coat, smooth seed surface, white flowers, and lack of anthocyanin pigmentation on the stem. The plant is medium to tall in height, with large leaflets and white flowers (Gaur *et al*., 2010).

Chickpea is an herbaceous annual and the plant height generally ranges from 30-70 cm. It has tap root system, which is usually deep and strong. The lateral roots develop nodules with the symbiotic rhizobium bacteria, capable of fixing atmospheric nitrogen in plant usable form. The nodules are visible about one month after plant emergence and generally confined to the top 15 cm of the surface. The number of leaflets varies from 5 to 17(Gaur *et al*., 2010).

The entire surface of the plant shoot is densely covered with fine hairs and it secretes a highly acidic substance containing malic, oxalic and citric acids. These acids play an important role in protecting the plant against insect pests. The plants have primary generally 1-8, secondary and tertiary branches. Five growth habits, based on angle of branches from the vertical, are classified as erect, semi erect, semi spreading, spreading and prostrate. The erect and semi-erect varieties enable mechanical harvesting (ICRISAT, 2010).

2.2. Origin and Geographic Distribution

Chickpea is an important cool-season food legume having extensive geographical distribution. South Eastern Turkey and neighboring areas of Syria were considered as the center of origin for cultivated chickpea (Van der Maesen, 1972; Marien *et al*., 2015). The earliest remains of

chickpea seeds date back to around 7000 BC in Syria and Turkey. However, Ethiopia is also considered by some authors as the secondary center of origin and diversity for chickpea. Related wild species of chickpea have been found in northern Ethiopia (Geletu *et al*., 1996). In Ethiopia, archaeological evidences from Lalibela caves indicated seed samples over 2500 years of age (Mitiku, 2011).

It is an annual crop that grows best on heavy soil, rough seed bed and requires moderately high temperature (Singh and Diwakar, 1995). Soils need to be well drained, with pH 5–7 to achieve optimum growth (Kassa *et al*., 2009). It is generally a long-day plant. Several factors, including the length of growing period, mean air temperature, soil drainage, soil reaction, soil depth, occurrence of soil borne diseases etc, determine the adaptation and performance of chickpea (Yadeta, 2003). It is widely grown in different agro-ecological zones falling between 1500 to 2600 meters above sea level where the annual average rain fall ranges between 700 to 1300 mm (Tabikew *et al*., 2009).

The geographic distribution differs for kabuli and desi chickpea types, with the kabuli chickpea tending to be restricted to the western Mediterranean where the desi chickpea are mainly absent. The desi chickpea range more widely from the eastern Mediterranean to central Asia and the Indian subcontinent. The desi type covers about 80-85% chickpea area and is predominantly grown in South and East Asia, Iran, Ethiopia and Australia, while kabuli type is grown in the countries of Mediterranean region, West Asia, North Africa and North America (Gaur *et al*., 2010). Ninety two percent of the area and 89% of the production of chickpea grain are concentrated in semi-arid tropical countries (Ali *et al.,* 2011).

Although chickpea is widely grown in Ethiopia, the major producing areas are concentrated in the two regional states of Amhara and Oromia. These two regions cover more than 92% of the entire chickpea area and constitute about 93% of the total chickpea production. Other regions contribute 8% average cultivated chickpea area and chickpea production share of 7%, during 2009 (CSA, 2017).

2.3. Importance of Chickpea

In Ethiopia, chickpea is widely grown across the country and serves as a multi-purpose crop (Shiferaw and Teklewold, 2007). Among pulses, chickpea is the fourth leading grain legume primarily grown for food and feed as well as soil fertility amendment in Ethiopia. Besides

providing the essential components of human dietary and health requirements, they fix atmospheric nitrogen and enrich the soil fertility. It fits well in rotation with cereal crops and helps prevent build up of diseases, insect pests and weeds (Geletu *et al*., 1996).

Among the cool season food legumes, chickpea is believed to be the most drought resistant crop and is able to produce reasonable yields in low rainfall conditions. Chickpea has ability to withstand drought stress. It provides a source of cash for smallholder producers. As a nutritious legume crop, chickpea has the potential to improve both soil health and human nutrition. It reduces malnutrition and improves human health especially for the poor who cannot afford animal products. Chickpea is cholesterol free and a good source of high quality protein, carbohydrates. Chickpea used as medicinal value for people with diabetes because of its high nutritional value and near absence of anti-nutritive components (Williams and Singh, 1987).

Chickpea is cultivated for different values it provides, whether in nutrition, food and environmental rehabilitation, or in cash generation. Its nutritional value, medicinal value and market value, as compared to other annual crops, are some of the most important merits for which the crop is grown in Ethiopia. Nutritionally, the chickpea seed has 38-59% carbohydrate, 18–24% protein, 3% fiber, 4.8-5.5% oil, 3% ash, 0.2% calcium and 0.3% phosphorus. Digestibility varies from 76-78% for its protein and 57-60% for its carbohydrate (Kumar *et al*., 2016).

Medicinally, a cooked chickpea-milk (4:1) mixture has been found beneficial for infants, effectively controlling diarrhea. In addition, chickpea has been reported as an important means in controlling bronchitis, cholera and constipation; acids in chickpea seed are supposed to lower blood cholesterol levels. Chickpea is cholesterol free and its regular consumption prevents diabetes and reduces risk of heart disease (Jukanti *et al*., 2012).

2.4. Production and Utilization of Chickpea in Ethiopia

In Ethiopia, chickpea holds third place as a grain legume both by area coverage and volume of production, next to faba bean and haricot bean (CSA, 2016). The diverse biophysical and agro-climatic condition in Ethiopia is suitable for growing a number of pulses and legume

crops. Chickpea is one of the main annual crops in Ethiopia both in terms of its share of the total cultivated area of pulse crops and its role in direct human consumption. It is the second most important crop in volume of production after bean, in the country (CSA, 2017).

The crop has a major role in the daily diet of the rural community and poor sectors of urban population (Menale *et al*., 2009). The local consumption of chickpea in different forms for household use and local market has increased with time (CSA, 2016). Virtually all domestic pulse crop production is marketed through processors for export but the majority is sold on the local market and consumed locally. However, the quantity and quality of the product produced limit the ability of domestic producers to influence world markets and to consistently produce sufficient quantities to be a reliable supplier for large users. Though most of the production of the crop in Ethiopia is restricted to rainfed fields, chickpea is assumed to be the most adaptive to drought, and responds better to small irrigation than other legume crops (Nigusie. 2017).

The crop provides an important source of food and nutritional security for the rural poor, especially those who cannot produce or cannot afford costly livestock products as source of essential proteins. The consumption of chickpea is also increasing among the urban population mainly because of the growing recognition of its health benefits and affordable source of proteins (Shiferaw *et al*., 2007). In Ethiopia chickpea is consumed in different ways: as green, cooked (*nifro*), roasted (*kollo*) or germinated seeds are served as snacks. Split seeds (*kik*) and flour of chickpea seeds (*shiro*) are used to make *wot* (sauce) taken with *injera* (bread). The flour of chickpea is also used to make '*shimbra asa*', popular dish for fasting days. Its straw is used as animal feed and stalk and roots as fuel (Senait, 2015).

In the export market, chickpea contributes a significant portion of the total value of pulse exports. For example, chickpea constituted about 25.02% of the pulse export volumes in 2016. Due to the improvement of production in the country and new markets demand, Ethiopian chickpeas have gained an important place in India and Pakistan. The country exported 48,739 tons of chickpeas valued at 22.56 million USD. Moreover, the crop is being exported mainly to Asia and Europe contributing positively to the country's foreign exchange earnings (FAOSTA.2016).

2.5. Phenotypic and Genotypic Variability

The amount of variation present in any population is measured and expressed in terms of variance (Singh, 2001). Variability is defined as the occurrence of differences among individuals due to differences in their genetic composition and environment in which they are raised (Allard, 1960; Falconer *et al*., 1996). The amount of variation present in any population is measured and expressed in terms of variance (Falconer *et al*., 1996). Information regarding genetic variability present in a population is prerequisite for planning effective breeding programme for improvement of any crop. The genetic variability is determined with the help of certain genetic parameters, such as, genetic coefficient of variation, phenotypic coefficient of variation (Yucel *et al.*, 2006).

Phenotypic variability is the observable variation present in a character in a population; it includes both genotypic and environmental variation and, as a result, its magnitude differs under different environmental conditions. Genotypic variability, on the other hand, is the component of variation, which is due to the genotypic differences among individuals within a population, and is the main concern of plant breeders (Qureshi *et al*., 2004). Estimates of genotypic coefficients of variations (GCV) and phenotypic coefficients of variations (PCV) are used to study the variability that exists in a given population (Kalloo, 1988).

Hasan and Deb (2014) observed highly significant difference among chickpea genotypes for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among the experimental material and advocated that enough scope was present for the selection of good performing genotypes in relation to seed yield. Sewak *et al*. (2012) found that wide range of variability was observed for both qualitative and quantitative traits. Getachew *et al*. (2015) reported phenotypic variance for number of days taken to 50% flowering, number of days taken to 90% maturity, plant height, and number of pod per plant, 100 seed weight, number of seed per pod and seed yield was higher than genotypic variance indicating the influence of environmental factors.

Aarif *et al*. (2014) revealed high phenotypic coefficient of variation for hundered seed weight, followed by seed yield per plant and secondary branches per plant. Fikru (2004) reported the presence of sufficient variability for days to 50% flowering, days to 50% maturity, number of pods per plant, number of secondary branches per plant, plant height, hundred seed weight,

harvest index and seed yield. Dev *et al (*2017) reported the relative magnitude of difference between phenotypic coefficient of variation and genotypic coefficient of variation was low for number of pods per plant, number of seeds per pod, 100 seed weight and days to 50% flowering indicating that these characters were less influenced by the environments.

Abebe (1985) in studying correlation and variation of some indigenous and exotic chickpea varieties and reported that there was a wide range of variation for plant height, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield. According to Temesgen (2007), PCV values ranged from 6.63% for days to maturity to 43.29% for number of seeds per plant, where as the GCV ranged from 6.49% for days to maturity to 39.57% for number of seeds per plant. According to the study of Raju *et al.* (2017) plant height and number of primary branches per plant expressed moderate levels of GCV as well as PCV. In addition, days to 50% flowering had low levels of PCV and GCV.

According to Yucel *et al*. (2006), there are GCV for number of seeds per plant, number of secondary branches per plant and number of pods per plant. Similarly, high PCV are recorded for number of seeds per plant, number of secondary branches per plant, number of pods per plant and seed yield per plant. Yadav *et al*. (2015) observed high PCV and GCV for plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, hundred seed weight and seed yield per plant. Desai *et al*. (2015) observed highest GCV for hundered seed weight, followed by number of pods per plant, seed yield per plant and number of seeds per pod.

Thakur *et al*. (2018) reported moderate PCV and GCV for plant height and days to 50 % flowering, where as lowest PCV and GCV were recorded for harvest index and days to maturity. Demissew (2010) reported biomass yield, harvest index and number of branches per plant were traits which contributed to the variation in grain yield of soybean. Nizama *et al*. (2013) evaluated 50 genotypes of chickpea and found high PCV and GCV for pods per plant, seed yield per plant and secondary branches per plant. The low value of a genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was noted for characters such as days to 50% flowering and days to maturity (Parida *et al*., 2018).

2. 6. Heritability

In a broad sense, heritability can be defined as the proportion of the genotypic variation to the total variance (Allard, 1960). It is a measure of the degree to which a phenotype is genetically influenced and can be modified by selection (Schlegel, 2010). Heritability of a trait is important in determining its response to selection. It was found out earlier that genetic improvement of plants for quantitative traits requires reliable estimates of heritability in order to plan an efficient breeding program (Akinwale *et al*., 2011). Generally, heritability indicates the effectiveness with which selection of genotypes could be based on phenotypic performance (Songsri *et al*., 2008).

According to the study of Getachew *et al*., 2015 heritability estimates were found to be high for hundred seed weight (98.7 %), seeds per pod (93.5%), pods per plant (84.01%), plant height (83.8.%), days to 90% physiological maturity(82.5%) and 50% days to flowering (89.8%) for kabuli type chickpea, whereas low estimates of heritability was recorded for grain yield (47.7%). These results indicated the influence of dominant and epistatic genes for these characters.

Zali *et al*. (2011) reported that heritability estimates were greater for number of days to 50% flowering, days to maturity, plant height, number of secondary branches, number of primary branches and number of seeds per plant. Misra (1991) found high heritability estimates for days to 50% flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and hundred seed weight; low for seed yield and number of branches per plant. Highest heritability was recorded for days to 50 per cent flowering followed by biological yield per plant, plant height, hundred seed weight, grain yield per plant and days to maturity (Ullah *et al*., 2011).

Dev *et al.* (2017) reported high estimates of heritability in broad sense were recorded for hundred seed weight (97.69 %), days to 50 % flowering (93.45 %), and days to maturity (92.12 %). High to moderate values were recorded for seed yield per plant (78.05 %), plant height (75.39 %) and harvest index (73.90 %). Yadav *et al.* (2015) found high heritability for number of primary branches per plant, number of secondary branches per plant, plant height, pod length, and pods per plant indicating the influence of environment was low for these traits.

2.7. Genetic Advance

Improvement in the mean genotypic value of selected families over the mean of the base population is commonly termed as genetic advance under selection. Genetic advance expected from selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001). Genetic advance gives clear picture and precise view of segregating generations for possible selection.

Kumar *et al*. (2014) reported high genetic advance as percentage of mean for seed yield per plant, followed by hundred seed weight, harvest index, number of effective pods per plant, total number of pods per plant and number of secondary branches. Nizama *et al*. (2013) observed that high genetic advance as percentage of mean for 100-seed weight, followed by pods per plant and seed yield per plant. Zali *et al*. (2011) found genetic advance at 5% selection intensity was highest for number of secondary branches, number of seeds per plant and seed yield and lowest for number of days to 50% flowering and number of days to 50% maturity. This implies that progress on improving seed yield could be achieved through simple selection of the number of secondary branches and number of seeds per plant.

Biru *et al.* (2017) found that number of seeds per pod and hundred seed weight have high genetic advance as a percent of mean, whereas number of pods per plant and grain yield showed moderate genetic advance as a percent of the mean. Therefore, selection based on traits with a high-level genetic advance as a percent of the mean will result in the improvement of the performance of the genotypes. Hagos *et al*. (2018) reported that genetic advance was high for number of seeds per pod (64.2%) followed by number of secondary branches per plant (59.4%), number of pods per plant (48.9%) and hundred seed weight (46.1%).

Heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties since high heritability does not always indicate high genetic gain (Ali *et al*., 2010). Higher estimates of heritability coupled with better genetic advance confirms the scope of selection in developing new genotypes with desirable characteristics (Ajmal *et al*., 2009).

2.8. Correlation and path analysis

2.8.1. Correlation coefficient analysis

Correlation coefficient measures the relationship between two variables (Dabholkar, 1999). The various characteristics of crop plants are generally interrelated or correlated. Phenotypic and genetic correlations are commonly used in plant breeding. Phenotypic correlations involve both genetic and environmental effects (Singh, 2001). Genetic correlation is the association of breeding values of the two characters. Genetic correlation is a measure of the extent to which the same gene or closely linked genes cause simultaneous variation in two different traits (Halluer and Miranda, 1988). Genotypic and phenotypic correlation coefficients tell us the association between and among two or more characters (Sharma, 1998).

Fikru (2004) reported strong positive genotypic and phenotypic correlations of seed yield with number of pods per plant, number of secondary branches per plant and hundered seed weight across environments. Ali *et al*. (2011) found that correlation studies showed biomass per plant, number of pods per plant, number of secondary branches per plant, number of seeds per pod and hundred seed weight were positive and significant at genotypic level but positive and highly significant at phenotypic level.

Megersa *et al*. (2016) found that hundred seed weight shows significant and negative correlation with days to 50% flowering, day to maturity, plant height, number of pods per plant, number of seeds per plant except biomass, seed yield and harvest index. Tesfamichael *et al*. (2015) found that number of pods per plant showed positive and highly significant correlation with days to 50% flowering, days to 50% podding, plant height, number of primary branches per plant, number of secondary branches per plant, days to 75% maturity and negative and significant correlation with hundred seed weight.

Srivastava *et al*. (2017) reported positive and significant correlation of biological yield per plant, harvest index and number of pods per plant with seed yield per plant. Number of seeds per plant, number of secondary branches, hundred seed weight, number of pods per plant, number of primary branches and plant height also had positive and highly significant phenotypic correlations with seed yield (Zali *et al*., 2011).

Kumar (2016) found that plant height revealed highly significant and positive correlation with days to 50% flowering and days to maturity. Thakur *et al*. (2018) showed that seed yield per plant has highly significant and positive correlation with seed weight, harvest index, total

number of pods per plant, number of secondary branches, number of primary branches and total number of seeds per plant. Thus, those characters considered as selection criteria, while selecting superior genotypes under rain fed condition. Temesgen (2007) reported days to flowering showed negative and highly significant correlation with grain filling period, number of pods per plant, number of seeds per pod and number of seeds per plant.

Getachew *et al*. (2015) reported that number of seeds per plant had negative and highly significant genotypic correlation with hundred seed weight and number of pods per plant had positive and highly significant genotypic correlation with number of seeds per plant. Salgotra (2016) showed the association of number of pods per plant was also highly significant and positively correlated with plant height, number of primary branches per plant, number of secondary branches per plant and seeds per plant. Singh *et al*. (2017) reported hundred seed weight possessed significant and positive phenotypic correlation with primary branches per plant, plant height and secondary branches per plant.

2.8.2. Path coefficient analysis

Path coefficient analysis is very important statistical tools that indicate which variables exert influence on other variables, while recognizing the impacts of multicolinearity (Akanda and Mundt, 1996). Path coefficient analysis separates the direct effects from the indirect effects through other related traits by partitioning the correlation coefficient. It requires a cause and effect situation among variables. The estimates of correlation coefficients revealed only the relationship between yield and yield associated traits, but did not show the direct and indirect effects of different traits on yield. This is because the attributes that are in association do not exist by themselves, but are linked to other components traits (Mulugeta et *al.*, 2012).

Path analysis applied in chickpea revealed that biological yield had high direct and positive effect followed by harvest index, confirming highly significant association of these traits with seed yield (Vaghela *et al*., 2009). Singh (2007) reported hundred seed weight, plant height, days to flowering and days to maturity contributed to seed yield mainly through indirect effect via biological yield and harvest index. Plant height and number of pods per plant had the highest direct effect on biomass yield. Yucel *et al*. (2006) reported that number of seeds per plant and number of pods per plant had highest direct influence on seed yield. Conversely, days to flowering had a negative and small direct effect on seed yield.

Thakur and Sirohi (2009) reported that number of pods per plant, number of secondary branches per plant and hundred seed weight had exerted positive direct effect on seed yield. The path coefficient analysis revealed that harvest index, days to 50 % flowering, number of seeds per pod and number of pods per plant exhibited high and positive direct effects on seed yield per plant. All these characters turned out to be the major component of seed yield. Positive and moderate direct effect was observed for number of primary branches per plant whereas, negative was observed for days to maturity (Jivani *et al.*, 2013).

Mohammadi and Talebi (2015) found that number of seeds per plant and hundered seed weight had a positive direct effect on seed yield. Jhadav *et al*. (2014) found that the high positive direct effect exhibited by numbers of branches per plant followed by hundred seed weight and number of pods per plant on grain yield at both genotypic and phenotypic level. Maximum positive effect of biomass yield on seed yield coupled with relatively strong and positive value of genotypic correlation (Megersa *et al*., 2016). Number of seeds per pod had negative direct effect but number of pods per plant and biomass produced positive indirect effects through this trait.

3. MATERIALS AND METHODS

3.1. Description of Experimental Site

The experiment was conducted at Haramaya University main campus during the 2017 cropping season. Haramaya University is located 25 km northwest of Harar town in eastern Hararge Zone, Oromia region, Ethiopia. The research site is located at an altitude of 2026 meters above sea level, 9°24'59" N latitude and 42°02'14" E longitude. Haramaya has a bimodal rainfall distribution pattern. The short rainy season extends from April to June and whereas the long rainy season extends from July to September. The total rainfall during the crop season was 452.6mm, with the mean maximum and minimum temperature of 21.3^{O}C and 7.4^{O}C respectively. Monthly rainfall distribution during the cropping season, maximum and minimum temperature data were shown on Appendix Table 1. The soil type of Haramaya is fluvisol with sandy clay loam texture (Kebene and Jones, 2017).

3.2. Experimental Materials

A total of 20 desi chickpea genotypes obtained from High Land Pulse Research Program of Debre Zeit listed in Table 1.

Table 1. Descriptions of 20 desi chickpea genotypes

Sr. No.	Genotypes	Pedigree

1	DZ-2012-CK-0027	ICCV - 030037- F4 – P13 –BP-BP
2	DZ-2012-CK-0028	ICCV - 10 X ICCV - 87322
3	DZ-2012-CK-0029	ICCV - 04112 X ICCV-93954
4	DZ-2012-CK-0030	ICCV - 04112 X ICCV-93954
5	DZ-2012-CK-0032	ICCV-08111
6	DZ-2012-CK-0033	ICCV-12-03-0208
7	DZ-2012-CK-0034	ICCV-04112 X ICCV-93954
8	DZ-2012-CK-0035	ICCV-04112 X ICCV-93954
9	DZ-2012-CK-0036	DO-58
10	DZ-2012-CK-0037	DO-51
11	DZ-2012-CK-0040	ICCV-0811
12	DZ-2012-CK-0227	ICCV-93954 X ICCV-6914
13	DZ-2012-CK-0232	ICCV-39 X ICCV-6679
14	DZ-2012-CK-0235	ICCV-93954 X ICCV-5003
15	DZ-2012-CK-0236	ICCV-93954 X ICCV-4552
16	DZ-2012-CK-0239	JG-11 X ICCV-4958
17	DZ-2012-CK-0241	JG-11 X ICCV-4958
18	DZ-2012-CK-0248	VOITH41KFUP 98-52C X EUP-48-47C) X SEZ-15063
19	DZ-2012-CK-0253	ICCV-96836
20	Local check	Local variety

3.3. Experimental Design and Field Management

The experimental was laid out using randomized complete block design (RCBD) with three replication. Four rows were used per plot for each genotype. The row lengths, between row and within row spacing were 2 m, 30 cm and 10 cm, respectivily. The outer two rows were served as border row and the two middle rows were used for data collection. The distance between plots and replications were 0.5 and 1.5 m respectively.

The experimental field history showed that sorghum had been harvested in the previous copping season. Experimental field ploughed two times using farm tractor plough and third manually using labor worker during planting. Planting was done at the end of august, 2017. Weeds were removed by hand hoeing three times. Fertilizer was not applied. The crop was harvested when leaves reached senescence and more than 90% of the stems and pods lost their green colour turning to yellow, seeds in the pods feel hard and rattle within the pod.

3.4. Data Collection

The data on the following attributes was collected on the basis of the central two rows in each plot/replication. Data was collected on 11 parameters, on plot and plant basis, as shown below:

Data recorded on plot basis

Days to flowering: It was recorded as number of days from planting to the stage when 50% of the plants in a plot produced flower.

Days to maturity: It was recorded as the number of days from planting to the stage when 90% of the plants in a plot produced a matured pod, implying the stage at which pods lose their pigmentation and begin to dry.

Grain filling period: The number of days from flowering to maturity.

Hundred seed weight: Weight of 100 seeds in gram that was sampled from each plot after the moisture level was adjusted to 10%.

Seed yield per hectare: Seed yield in kilogram of plants obtained from the two middle rows adjusted to 10% moisture level and converted to kg/ha.

The data for the following characters were recorded from five randomly taken plants from each experimental plot and the average value was considered per plant basis.

Plant height: The height in centimeters was measured from the ground level to the tip of the plant at maturity.

Number of primary branches per plant: Number of primary branches counted at maturity.

Number of secondary branches per plant: The average number of secondary branches formed on the primary branches per plant counted from five randomly taken plants at maturity in each plot.

Number of pods per plant: The mean number of pods taken from random plants at harvest.

Number of seeds per pod: The mean number of seeds per pod taken from the random plants at harvest.

Number of seeds per plant: The mean number of seeds per plant obtained from randomly taken plants.

3.5. Data Analysis

3.5.1. Analysis of variance

The data collected were subjected to analysis of variance following the procedures outlined by Gomez and Gomez (1984) and using SAS software version 9.0, (SAS, 2002). Mean separation was carried out using Duncan's Multiple Range Test (DMRT).

Table 2. Analysis of variance in randomized complete block design and expected mean square for single location

Source of variation	DF	Mean square	Expected mean square
Replication	r-1	MS_r	$\sigma^2e + g\sigma^2r$
Genotypes	g-1	MSg	$\sigma^2e + r\sigma^2g$
Error	(r-1)(g-1)	MSe	σ^2e

Where, r = number of replications; g = number of genotypes; MSr = mean square due to replications; MSg = mean square due to genotypes; MSe = mean square of error; σ^2g, σ^2r and σ^2e are variances due to genotype, replication and error, respectively.

Analysis of variance in randomized complete block design was computed using the following model: $Yij = \mu + rj + gi + \varepsilon ij$

Where, Y_{ij} = the response of trait Y in the i^{th} genotype and the j^{th} replication

μ= the grand mean of trait rj = the effect of the j^{th} replication

g_i = the effect of the i^{th} genotype ε_{ij} = experimental error effect

3.5.2. Estimation of genetic parameters

3.5.2.1. Variance components

Different genetic parameters including genotypic variance (δ^2g), phenotypic variance (δ^2p), phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were estimated using the formula, adopted from Burton and Devane (1953) and Johnson *et al.* (1955).

Genotypic variance $\left(\sigma_g^2\right) = \frac{MSg - MSe}{r}$

Where: σ_g^2= genotypic variance MSe = mean square due to genotypes.

MSg = environmental variance r = number of replication

Phenotypic variance (σ_{ph}^2) = $\sigma_g^2 + \sigma_e^2$

Where: σ_p^2 = phenotypic variance and σ_e^2 = Environmental variance

Coefficient of variation at phenotypic and genotypic levels was estimated using following formula.

Genotypic Coefficient of Variation GCV (%) = $\frac{\sqrt{\sigma_g^2}}{\text{grand mean}} x\ 100$

Phenotypic Coefficient of Variation PCV (%) = $\frac{\sqrt{\sigma_p^2}}{\text{grand mean}} x\ 100$

3.5.2.2. Estimation of broad sense heritability

Heritability (H) in broad sense for all characters were computed using the formula of Falconer *et al*. (1996) as follows:

$H^2 = \frac{\sigma_g^2}{\sigma_p^2} x\ 100$ Where, σ_p^2 = phenotypic variance and σ_g^2 = Genotypic variance

3.5.2.3. Genetic advance

The genetic advance for selection intensity (k) at 5% (k=2.063) was estimated by the following formula (Johnson *et al*., 1955):

$GA = k * \sigma_{ph} * H_b^2$

Where, GA represents the expected genetic advance under selection; σ_{ph} is the phenotypic standard deviation; H_b^2 is heritability in broad sense and k is selection intensity. The genetic

advance as percent of population mean was also estimated following the procedure of (Johnson *et al*., 1955).

Genetic advance as percent of mean = x100

3.5.3. Association of characters

3.5.3.1. Estimation of correlation coefficients (r)

The phenotypic and genotypic correlation coefficients between two variables were estimated from the covariance two traits as described by Singh and Chaudhary (1985).

$$COV_{gxy} = \frac{MSP_g - MSP_e}{r}$$

Where: COV_{gxy} = genotypic covariance between traits x and y.

MSP_g = genotypic mean sum product of traits x and y

MSP_e = environmental mean sum product of traits x and y

r = number of replication.

$$COV_{pxy} = COV_{gxy} + COV_{exy}$$

Where: Cov_{pxy} = phenotypic covariance between traits x and y.

Cov_{gxy} = genotypic covariance between traits x and y.

Cov_{exy} = environmental covariance between traits x and y

Correlation coefficients at genotypic level (rg_{xy}) were calculated as:

$$rg_{xy} = \frac{COV_{gxy}}{\sqrt{\sigma^2_{gx} X \sigma^2_{gy}}}$$

Where: rg_{xy} = genotypic correlation coefficient between traits x and y

Cov_{gxy} = genotypic covariance between traits x and y.

δ^2_{gx} = genotypic variance of trait x

δ^2_{gy} = genotypic variance of trait y

Correlation coefficients at phenotypic level (rp_{xy}) were calculated as;

$$rp_{xy} = \frac{COV_{pxy}}{\sqrt{\sigma^2_{px} X \sigma^2_{py}}}$$

Where:

rp_{xy} = phenotypic correlation coefficient between traits x and y

Cov_{pxy} = phenotypic covariance between traits x and y.

σ^2_{px} = phenotypic variance of trait x.

σ^2_{py} = phenotypic variance of trait y.

The calculated phenotypic correlation value was tested for its significance using t-test:

$$t = \frac{r_{ph}}{SE(r_{ph})}$$

Where:

r_{ph} = Phenotypic correlation

$SE(r_{ph})$ = Standard error of phenotypic correlation was obtained using the following formula (Sharma, 1998).

$$SE(r_{ph}) = \frac{\sqrt{1 - r^2_{ph}}}{n - 2}$$

Where, n is the number of genotypes tested, r_{ph} is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = \frac{r_{gxy}}{SEr_{gxy}}$$

Where: SEr_{gxy} = Standard error of genotypic correlation coefficient between character X and Y

The calculated "t" value was compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SEr_{gxy} = \frac{\sqrt{(1 - r_{gxy}^2)2}}{2h_x^2 * h_y^2}$$

Where: h^2x = Heritability of trait x

h^2y = Heritability of trait y

3.5.3.2. Path Coefficient analysis

Path coefficient analysis was calculated as suggested by Dewey and Lu (1959) to determine direct and indirect effect of different variables on seed yield as:

$r_{ij} = P_{ij} + \sum r_{ik}P_{kj}$

Where:

r_{ij} = is mutual association between the independent trait (i) and dependent trait (j) as measured by the correlation coefficient.

Pij = is component of direct effects of the independent trait (i) on the dependent variable (j);

$\sum r_{ik}p_{kj}$ = summation of components of indirect of a given independent character (i) on a given dependent character (j) via all other independent characters (k).

The contribution of the remaining unknown factor was measured as the residual factor (P_R), which is calculated as: $P_R = \sqrt{(1 - \sum r_{ij}p_{ij})}$

The magnitude of P_R indicates how best the causal factors account for the variability of the dependent factor (Singh and Chaudhary, 1999). That is, if P_R value is small (for instance, nearly zero) the dependent character considered (seed yield) fully explained by the variability in the independent characters, whereas higher P_R value indicates that some other factors which have not been considered, need to be included in the analysis to account fully the variation in the dependent character (seed yield).

4. RESULTS AND DISCUSSION

4.1. Analysis of Variance and mean performance of genotypes

4.1.1. Analysis variance

The result of analysis of variance (ANOVA) of eleven quantitative characters for the twenty genotypes was presented in Table 3. Mean squares genotype of 11 characters showed highly significant difference ($P< 0.01$) among the tested desi chickpea genotypes. The result suggested the presence of considerable variations among desi chickpea genotypes for all traits measured, which justifies the possibility of carrying out further genetic analysis. Biru *et al*. (2017), Fikru (2004), Hasan and Deb (2014), Temesgen (2007) and Tebebu (2011) reported that highly significant differences ($P\leq0.01$) among genotypes indicating, indicating the presence of adequate variability.

Table 3. Mean squares from Anova for 11 traits of 20 desi chickpea genotypes evaluated at Haramaya University in 2017.

Traits	Replication (2)	Genotype (19)	Error (38)	CV (%)
Days to 50% flowering	45.17	78.8**	7.1	5.4
Days to maturity	36.32	44.69**	3.11	1.57
Grain filling period	1.52	18.42**	4.01	3.21
Plant height (cm)	9.31	75.01**	5.49	6.58
Number of primary branches per plant	0.04	1.16**	0.02	4.65
Number of secondary branches per plant	0.33	11.26**	2.65	11.41
Number of pods per plant	19.19	225.62**	45.47	13.38
Number of seeds per pod	0.001	0.02**	0.004	5.46
Number of seeds per plant	32.31	462.01**	17.94	6.35
Hundred seed weight (g)	106.30	28.59**	4.90	10.54

Seed yield per hectar (kg/ha)	49667.1	670892.2**	146978.9	13.67

** Highly significant difference at P<0.01. Numbers in parenthesis refers to degrees of freedom. CV (%) =coefficient of variation in percent

4.1.2. Range and mean performance of genotypes

4.1.2.1. Crop phonology

The range and mean values for 11 traits of 20 desi chickpea genotypes evaluated in this study are presented in Table 3. Genotypes showed variation for days to flowering ranging from 42 to 68 days with mean of 50 days, and days to maturity ranging from 109 to 128 days with the mean of 112 days. The tested genotypes had mean value of 62 days for grain filling period and the range was from 57 to 68 days. DZ-2012-CK-0035 was early to mature followed by DZ-2012-CK-0036, DZ-2012-CK-0034, DZ-2012-CK-0236, DZ-2012-CK-0027 and DZ-2012-CK-0037 while, DZ-2012-CK-0253, DZ-2012-CK-0232 and DZ-2012-CK-00029 were late to mature in Table 5. The mean value of the genotypes for grain filling period was 62 days and ranged from 57 to 68 days. In general, the present result showed that there is a wide range of variations among the genotypes in crop penology traits. Similarly, previous studies conducted on chickpea genotypes showed high genetic variation for days to flowering ,days to maturity and plant height (Getachew *et al.*, 2015, Thakur *et al.*, 2015) and days to flowering, , plant height (Temesgen ,2007).

Among the tested genotypes, DZ-2012-CK-0035, DZ-2012-CK-0036, DZ-2012-CK-0236 and DZ-2012-CK-0037 were early to flower and mature while DZ-2012-CK-0253, DZ-2012-CK-0232 and DZ-2012-CK-0033 were late to days to flower and mature. The genotype DZ-2012-CK-0035, DZ-2012-CK-0227 and DZ-2012-CK-0030 were flowered earlier with the mean of 42, 46 and 46 day, respectively. However, the genotype DZ-2012-CK-0232, DZ-2012-CK-0029 and DZ-2012-CK-0253 reached 50 percent flowering in 53, 55 and 68 days, respectivily, and were relatively late. However, genotypes that delayed to flower and mature had shown relatively lower grain filling period.

Among 20 genotypes, 65% exhibited days to flowering lower than the genotypes mean indicating those genotypes were early flowering as compared to the others. This suggests that the higher chance of selecting early maturing genotypes which can escape the terminal moisture stress in the study area. In this experiment, genotypes with early flowering also shown early maturity and late maturing coincided with late days of flowering. The findings are agree with

the result of Getachew *et al.* (2015) who indicated the two (days to heading and maturity) coincide with each other and reports also flowering time plays an important role in its selection and has a direct relationship with earliness or lateness of a genotype, because this indicates early flowering genotype usually mature early.

4.1.2.2. Growth characters and yield components

The plant height ranged from 31 cm for DZ-2012-CK-0236 to 54 cm for DZ-2012-CK-0253 with mean of 36 days. DZ-2012-CK-0253 was taller followed by DZ-2012-CK-0028 and DZ-2012-CK-0034 DZ-2012-CK-0232 and the height of the other genotypes were similar and short. This result indicated that most of desi chickpea genotypes are short. Agreed with the finding of Jukanti *et al*. (2012) that the height of desi chickpea is short. Number of primary branches per plant ranged from 2.2 for DZ-2012-CK-0035 to 4.23 for DZ-2012-CK-0030 with a mean of 3.04. Number of secondary branches per plant ranged from 10.9 for DZ-2012-CK-0253 to 18 for DZ-2012-CK-0036 with a mean of 14.28.

Table 4. Estimates of range and mean of the eleven characters studied at Haramaya University.

Traits	Range	Mean± SE
Days to 50% flowering	42-68	49.62±1.54
Days to maturity	109.3-127.7	111.97±1.02
Grain filling period	57-68	62.33±1.16
Plant height (cm)	31.07-53.83	35.63±1.40
Number of primary branches per plant	2.2-4.23	3.04±0.30
Number of secondary branches per plant	10.9-18	14.28±0.94
Number of pods per plant	40.1-69.4	50.38±3.86
Number of seeds per pod	1.02-1.32	1.18±0.04
Number of seeds per plant	45.67-84.7	66.66±4.60
Hundred seed weight (g)	16.57-26.37	21.01±1.28
Seed yield per hectar (kg/ha)	1844.3-3742.3	2804.24±221.31

SE= standard error of the mean

Number of pods per plants ranged from 40.1 to 69.4 for DZ-2012-CK-0253 and DZ-2012-CK-0227 respectively with a mean of 50 pods per plant. Number of seeds per plant varied from 45.67 to 84.7 with mean of 66.66 seeds per plant. Minimum and maximum seeds per plant were noted in genotype DZ-2012-CK-0029 and DZ-2012-CK-0034 respectively. Wide ranges of performances were recorded for both number of seeds per plant and pods per plant. Among the tested genotypes, DZ-2012-CK-0034, DZ-2012-CK-0227,

DZ-2012-CK-0239 and DZ-2012-CK-0032 were recorded the higher number of pods per plants coincided with number of seeds per plant.

The largest hundred seed weight was recorded from DZ-2012-CK-0034 is 26.4g and the smallest from DZ-2012-CK-0253 is 16.6g. Most of the genotypes had hundred seed weight values above that of the local check and hence in the target of improving this trait is possible. Hence, selection strategy could be more focused on those genotypes when the improvement of this trait is desired. Malik *et al.* (1988) and Getachew *et al.* (2015) observed number of pods per plant is an important selection criterion for the development of high yielding genotypes. Singh and Bains (1984) showed hundred seed weight is highly variable character and can be influences a seed yield.

The maximum yield was obtained from DZ-2012-CK-0034 (3742.3 kg/ha) followed by DZ-2012-CK-0227 (3345.0 kg), DZ-2012-CK-0032 (3319.0 kg) and DZ-2012-CK-0239 (3277.7 kg). The minimum yields were obtained from DZ-2012-CK-0029 (1844.3 kg), DZ-2012-CK-0253 (2255.7 kg), Local check (2285 kg) and DZ-2012-CK-0035 (2439.0 kg) presented in Table 5. Seed yield per hectare ranged from 1844.3 kg/ha to 3742.3 kg/ha which showed wide variation with a mean value of 2804.24kg/ha. This showed that there is huge variation within the test entries for grain yield.

The high yielding genotype DZ-2012-CK-0034 (3742.3 kg/ha) had a yield advantage of 63 % compared with that of the local checks. Similarly, the second and third high yielding genotype DZ-2012-CK-0227 and DZ-2012-CK-0032 had yield advantages of 46% and 45% over the local check, respectively. Out of the total genotypes tested, 45% of them had yielded above the grand mean (2804.24kg/ha), which intern indicates the existence of high yielding genotypes and the possibility of improving grain yield via direct selection of those genotypes with high yield potential for the study area.

Table 5. Mean performance of twenty desi chickpea genotypes for eleven yield and yield attributing traits tested at Haramaya University main campus in 2017/18

Trt	DF	DM	GFP	PH	NPB	NSB	PPt	SPo	SPt	HSW	SYPha
DZ-2012-CK-0029	55.3b	112.7b-d	57h	32.07d-f	2.7e-h	12g-i	47.3i	1.02h	45.67g	18.6g-h	1844.3g
DZ-2012-CK-0236	47.3d-f	110c-e	62.7b-f	31.2f	3.2b-f	14.7b-f	58.1b-g	1.19b-f	68.8b-d	18.8g-h	2877.7b-f
DZ-2012-CK-0227	46.3fg	111c-e	64.7b	34.3d-f	3.7ab	16.6ab	69.4a	1.27ab	78.1ab	24.7b-c	3345.0ab
DZ-2012-CK-0033	51.7b-d	111c-e	59.3gh	33.9d-f	2.6gh	11.9hi	47.0g-i	1.08ab	52.8fg	21.6e-c	2258.3fg
DZ-2012-CK-0028	48d-f	112b-e	64b-d	41.2b	3.5a-c	16.1a-c	64.5ab	1.25a-c	75.8ab	17.4h	3201a-c
DZ-2012-CK-0030	46.3fg	110.3c-e	64b-d	36.2cd	4.23a	15.7a-d	63.4a-c	1.23a-d	75.4ab	25.1b-c	3151a-c
DZ-2012-CK-0027	48.3d-f	110.3c-e	62b-g	34.6d-f	3.3b-g	14.1b-h	56.1b-h	1.16b-g	65.9b-f	23.1a-e	2782.3b-f
DZ-2012-CK-0035	42g	109.3e	60.7e-g	32.0ef	2.2h	12.7f-i	49.8e-i	1.11f-h	58.6d-g	19.6e-h	2439e-g
DZ-2012-CK-0040	49.3 c-f	111.7b-e	62.3b-f	34.2d-f	3.1c-h	13.9c-h	55.9bc-h	1.16c-g	66.7b-e	24.8b-c	2790.7b-f
DZ-2012-CK-0032	47ef	112e	65ab	35.1de	3.7ab	16.4a-c	65.5ab	1.26a-c	77.4ab	17.6hg	3319ab
DZ-2012-CK-0239	48.3d-f	112.7bc	64.3bc	35.7c-e	3.6a-c	16.5a-c	65.8ab	1.26a-c	77.7ab	21.2e-f	3277.7ab
DZ-2012-CK-0248	50c-f	111c-e	61d-g	33.1d-f	2.9c-h	12.9f-i	50.9de-i	1.12e-h	60.1d-f	22.1b-f	2485.7d-f
DZ-2012-CK-0034	48.7c-f	110c-e	68a	34.1d-f	3.5b-d	13e-i	65.7ab	1.32a	84.7a	26.4a	3742.3a
DZ-2012-CK-0241	48d-f	111.7b-e	63.7b-e	32.5d-f	3.4b-e	15.7a-e	61.9a-d	1.22a-e	73.4a-c	21.4e-f	3100b-d
DZ-2012-CK-0235	48d-f	111.3b-e	63.3b-e	33.2d-f	3.3b-f	14.7b-g	58.4a-f	1.19b-f	68.6b-d	25.6ab	2947b-e
DZ-2012-CK-0036	48.3d-f	109.7de	61.3c-g	34.5d-f	2.9c-h	18a	53.3c-h	1.13d-g	61.6c-f	19.2g-h	2568.7c-f
DZ-2012-CK-0253	68a	127.7a	59.7f-h	53.83a	2.6f-h	10i	40.1i	1.07gh	55.3e-g	16.6h	2255.7fg
DZ-2012-CK-0037	47.3d-f	110.3c-e	63.0b-e	34.5d-f	3.3b-f	14.8b-f	59.9a-e	1.19b-f	70.5b-d	19.3g-h	2927b-e
DZ-2012-CK-0232	53d	114b	61.0d-g	39.7bc	2.8d-h	13d-i	53.0c-h	1.13d-g	61.2c-f	20.2e-h	2487.3d-f
Local check	51b-e	110.7c-e	59.7f-h	36.1cd	2.5gh	12.1f-i	46.6hi	1.09f-h	54.9e-g	17h	2285fg

DF = Days to 50% flowering, DM = Days to maturity, GFP = Grain filling period, PH = Plant height (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, PPt = Number of pods per plant, SPo = Number of seeds per pod, SPt = Number of seeds per plant, HSW = Hundred seed weight (g), SYPha = seed yield per hectar (kg/ha). NB: Means followed by the same letter are not significantly different at 1% of DMRT level significance.

4.2. Estimates of Variance Component

4.2.1. Phenotypic and genotypic variations

Estimates of phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) of the traits studied are presented in Table 6. The GCV ranged from 1.6 (grain filling period) to 20.28% (number of primary branches per plant), while PCV ranged from 3.68 (day to maturity) to 21.99% (number of seed per plant).

According to Deshmukh *et al*. (1986), PCV and GCV can be categorized as low (<10%), moderate (10-20%) and high (>20%). Accordingly, PCV values were considered as high for number of primary branches per plant, number of pods per plant, number of seeds per plant and seed yield per hectar. However, day to flowering, plant height, number of secondary branches per plant and hundred seed weight can be considered as moderate PCV values. Other characters, days to maturity, grain filling period and number of seed per pod had low PCV values.

The present result agrees with the findings of several investigators. Temesgen (2007) that high PCV for number of primary branches per plant, number of pods per plant and number of seeds per plant; medium for day to flowering, plant height and hundered seed weight; low PCV for day to maturity in kabuli type chickpea genotypes. In addition, Nizama *et al*. (2013) and Parida *et al*. (2018) reported days to maturity, grain filling period and number of seeds per pod had low PCV values. Thakur *et al*. (2018) reported moderate PCV for day to flowering and plant height; high PCV for number of primary branches per plant, number of pod per plant and number of seeds per plant. Ali *et al*. (2011) reported high PCV for number of primary branches per plant, number of pods per plant and number of seeds per plant. Biru *et al*. (2017) reported low PCV for days to maturity while Astereki *et al*. (2015) reported high PCV for number of pods per plant. Hagos *et al.* (2018) reported high PCV for number of pods per plant, number of seeds per plant and seed yield per hectar. However, the present finding disagrees with those of Nizama *et al.* (2013), Aarif *et al*. (2014) and Biru *et al*. (2017) that reported medium PCV for seed yield per hectar.

Table 6. Estimates of variance components and coefficients of variability, heritability and genetic advance of the eleven characters studied at Haramaya University.

Traits	σ^2_p	σ^2_g	σ^2_e	PCV (%)	GCV (%)	H^2 (%)	GA (5%)	GAM (5%)
Days to 50% flowering	31.00	24.89	6.11	11.22	10.05	80.61	9.26	18.66
Days to maturity	16.97	13.86	3.11	3.68	3.33	81.69	6.94	6.19
Grain filling period	8.81	4.80	4.01	4.76	1.60	54.52	3.34	3.36
Plant height (cm)	28.44	23.04	5.49	14.96	13.48	81.01	8.91	25.00
Number of primary branches per plant	0.40	0.38	0.02	20.08	20.28	95.00	1.24	40.79
Number of secondary branches per plant	5.52	2.87	2.65	16.46	11.86	51.95	2.52	17.65
Number of pods per plant	105.52	60.05	45.47	20.39	15.40	56.91	12.06	23.94
Number of seeds per pod	0.009	0.005	0.004	7.98	5.82	53.15	10.29	18.17
Number of seeds per plant	195.96	178.02	17.94	21.99	20.02	90.85	26.24	39.36
Hundred seed weight (g)	12.80	7.89	4.90	17.03	13.38	61.69	4.55	21.68
Seed yield per hectar (kg/ha)	321616.6	174637.8	146978.9	20.22	14.9	54.29	635.17	22.65

σ^2_g= genotypic variance, σ^2_p= phenotypic variance, σ^2_e= phenotypic variance, PCV= phenotypic coefficient of varience, GCV= genotypic coefficient of varience, H^2= broad sense heritability, GA= Genetic advance, GAM= genetic advance as as percent of mean

High values of GCV were recorded for number of primary branches per plant and number of seeds per plant, while medium GCV values were computed for days to 50% flowering, plant height, number of secondary branches per plant, number of pods per plant, hundred seed weight and seed yield. Other characters such as days to maturity, grain filling period, number of seeds per pod had low GCV values. High GCV values of some of the traits suggested that the possibility of improving the trait through selection.

Similar results were previously reported by Fikru (2004) that high GCV values for number of seeds per plant in desi type chickpea genotypes. Temesgen (2007) also reported low GCV values for days to maturity and grain filling period and medium GCV for day to flowering, plant height and 100 seed weight and high GCV for number of seeds per plant. Ali *et al*. (2011) and Thakur *et al*. (2018) reported high GCV for number of primary branches per plant and number of seeds per plant. Biru *et al*. (2017) and Parida *et al*. (2018) reported low GCV values for day to flowering and grain filling period. Hagos *et al.* (2018) and Sharma and Saini (2010) reported high GCV for number of seed per plant and Raju *et al*. (2017) reported plant height had medium GCV values.

The PCV was greater than GCV for all these traits, except for number of primary branches per plant. The magnitude of difference between PVC and GCV values was relatively high for grain filling period, number of secondary branches per plant, number of pods per plant and hundred seed weight,. This implies greater influence of environmental factors for the phenotypic expression of these characters that make difficult to exercise selection based on phenotypic performance of the genotypes to improve the characters. These results agree with Temesgen (2007) who reported high magnitude difference between PVC and GCV values for number of pods per plant and number of seeds per plant.

The difference in magnitude between PVC and GCV values were low for days to flowering, days to maturity, plant height, primary branches per plant, number of seed per pod, number of

seeds per plant and seed yield per hectar. These indicated the observed variations for these traits were mostly due to genetic factors with little environmental factors. These results agree with Yucel *et al*. (2006) who reported low magnitudinal difference between PVC and GCV values for days to flowering and plant height. Dev *et al*. (2017) reported low values for days to flowering and number of seeds per pod. Temesgen (2007) reported low magnitude for days to flowering, days to maturity and seeds per pod and Borate *et al.* (2010) reported low magnitude for days to flowering and number of seeds per pod.

4.2.2. Estimates of broad sense heritability

The estimated heritability values for the studied traits are presented in Table 6. The heritability values ranged from 51.95% for number of secondary branches per plant to 95.00% for number of primary branches per plant.

According to Singh (2001), if heritability of a character is very high (80% or more) selection for such characters could be fairly easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. He also intended that heritability for the studied traits is moderate if it is 40-80%. But, for characters with low heritability (40% or less) selection may be considerably difficult or virtually impractical due to the masking effect of the environment.

Considering the categories of heritability values, high heritability (>80%) was computed for days to 50% flowering, days to maturity, plant height, number of primary branches per plant and number of seeds per plant. Moderate heritability (40-80%) was computed for grain filling period, number of secondary branches per plant, number of pods per plant, number of seeds per pod and hundred seed weight and seed yield per hectar.

The present result is in agreement with the works of Hagos *et al.* (2018) and Sharma and Saini (2010) who reported high heritability for days to 50% flowering, plant height, number of seeds per plant; Getachew *et al.* (2015) who reported high heritability for days to 50% flowering, day

to maturity, plant height, number of pods per plant, number of seeds per plant; Dev *et al.* (2017), Khan *et al.* (2011), Mushtaq *et al.* (2013), Zali *et al*. (2011), Hagos *et al*. (2018) reported high heritability for days to maturity. This result agree with Astereki *et al*. (2015) who reported moderate heritability for number of pods per plant; Dev *et al*. (2017) who reported moderate heritability for number of secondary branches per plant. Mushtaq *et al*. (2013) who reported moderate heritability for number of seeds per pod.

4.2.3. Estimates of genetic advance

The genetic advance as the percentage of the mean (GAM) at 5% selection intensity is presented in Table 6. Genetic advance as percent of mean ranged from 3.36 % for grain filling period to 40.79% for number of primary branches per plant. Genetic advance under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Singh, 2001).

According to Johnson *et al.* (1955), genetic advance as a percent of the mean was categorized as high (>20%), moderate (10-20%) and low (0-10%). Based on this classification, plant height, number of primary branches per plant, pods per plant, seeds per plant, hundred seed weight and seed yield had the high genetic advance as percent of mean in the current study. This study agree with the findings of Getachew *et al.* (2015) and Hagos *et al*. (2018) who reported high genetic advance for pods per plant and hundred seed weight. In addition, Ali *et al*. (2011) and Gul *et al.* (2013) reported high genetic advance for plant height and primary branches per plant respectively. Ali *et al.* (2011) and Hagos *et al.* (2018) also reported high genetic advance for plant height and hundred seed weight.

Accordingly, genetic advance as percent of mean was moderate for days to flowering, number of secondary branches per plant and seeds per pod. However, it was low for days to maturity and grain filling period. Similarly, Babbar *et al.* (2012) reported medium genetic advance for

days to 50% flowering; Raju *et al.* (2017) reported medium genetic advance for days to flowering and number of secondary branches per plant. Likewise, Zali *et al*. (2011) reported low genetic advance for days to maturity.

Johnson *et al.* (1955) suggested the importance of considering both the genetic advance and heritability of traits rather than considering separately in determining how much progress can be made through selection. In this study, high heritability accompanied with high genetic advance was observed in case of plant height, number of primary branches per plant and seeds per plant. High heritability accompanied with high genetic advance indicated that these traits were highly heritable and selection of high performing genotypes is possible to the improvement of the characters. Similarly, Biru *et al*. (2017) reported that traits having high heritability combined with high genetic advance for seeds per plant.

4.3. Character associations

4.3.1. Phenotypic and genotypic correlations of seed yield and yield related traits

Genotypic and phenotypic correlation coefficient estimates between each pairs of characters are presented in Table 7. The analysis of the relationship among characters and their association with seed yield is essential to establish selection criteria (Singh *et al*., 1990). The magnitudes of genotypic correlation coefficients for most of the characters were higher than their corresponding phenotypic correlation coefficients, except few cases, which indicate the presence of inherent association among various characters. These present results agree with Kumar and Arora (1991), Fikru (2004) and Hagos *et al.* (2018).

Seed yield showed positive and highly significant phenotypic and genotypic correlation coefficients with grain filling period, number of primary branches per plant, number of secondary branches per plant, number of seeds per pod, number of seeds per plant and number of pods per plant. Seed yield had positive and significant genotypic correlation with hundred seed weight. Besides, it had positive and highly significant phenotypic correlation with number

of pods per plant. Days to flowering showed highly significant negative correlation with seed yield at both phenotype and genotype while negative and non-significant also for days to maturity.

Ali *et al.* (2010) and Chopdar *et al*. (2017) also reported that seed yield have positive and highly significant phenotypic and genotypic correlation with number of primary branches per plant, number of seeds per pod and number of seeds per plant. Getachew *et al*. (2015) and Hagos *et al*. (2018) observed positive and significant genotypic correlation with number of pods per plant and hundred seed weight. Demissew reported (2010) pointed out number of pods per plant and number of seeds per pod show association with grain yield on soybean Fikru (2004) and Temesgen (2007) also reported that number of pods per plant, number of secondary branch per plant and 100 seed weight were positively associated with seed yield.

Table 7. Estimation of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients between yields and yield component traits in twenty desi chickpea genotypes.

Variable	DF	DM	GFP	PH	NPB	NSB	PPt	SPo	SPt	HSW	SYPha
DF	1	0.836**	-0.653**	0.756**	-0.636**	-0.641**	-0.635**	-0.658**	-0.637**	-0.511ns	-0.644**
DM	0.811**	1	-0.246ns	0.863**	-0.231ns	-0.246ns	-0.242ns	-0.268ns	-0.238ns	-0.301ns	-0.242ns
GFP	-0.646**	-0.190ns	1	-0.214ns	0.940**	0.929**	0.926**	0.933**	0.935**	0.577**	0.942**
PH	0.622**	0.730**	-0.140ns	1	-0.208ns	-0.206ns	-0.171ns	-0.205ns	-0.179ns	-0.345ns	-0.199ns
NPB	-0.623**	-0.181ns	0.923**	-0.141ns	1	0.941**	0.934**	0.941**	0.939**	0.556ns	0.945**
NSB	-0.624**	-0.189ns	0.914**	-0.151ns	0.938**	1	0.940**	0.947**	0.943**	0.498ns	0.944**
PPt	-0.630**	-0.199ns	0.914**	-0.118ns	0.928**	0.930**	1	0.944**	0.947**	0.515ns	0.942**
SPo	-0.638**	-0.205ns	0.920**	-0.142ns	0.938**	0.941**	0.938**	1	0.945**	0.514ns	0.945**
SPt	-0.634**	-0.196ns	0.923**	-0.118ns	0.932**	0.930**	0.936**	0.932**	1	0.527ns	0.944**

HSW	-0.315**	-0.125ns	0.421*	-0.227ns	0.386*	0.359*	0.360*	0.354ns	0.378*	1	0.550*
SYPha	-0.638**	-0.192ns	0.932**	-0.137ns	0.940**	0.942**	0.937**	0.941**	0.939**	0.386*	1

DF = Days to 50% flowering, DM = Days to maturity, GFP = Grain filling period, PH = Plant height (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, PPt = Number of pods per plant, SPo = Number of seeds per pod, SPt = Number of seeds per plant, HSW = Hundred seed weight (g), SYPha = seed yield per hectar (kg/ha).
*, ** = Significant a 5% and 1% probability level, respectively. ns = non significant

4.3.2. Estimate of correlation coefficients among other characters

Day to maturity had positive and highly significant phenotypic and genotypic association with days to flowering (Table 8). Arshad *et al*. (2004) and Megersa *et al*. (2016) also reported days to maturity showed positive significant genotypic correlation with days to 50% flowering; Temesgen (2007) and Kumar (2016) reported days to maturity showed positive phenotypic significant correlation with days to 50% flowering.

Grain filling period had also negetive and highly significant phenotypic and genotypic correlation with days to flowering. Similarly, Ali *et al.* (2010) reported grain filling period had negetive and highly significant genotypic and phenotypic correlation with days to flowering. But the present flinging disagrees with that of Getachew *et al.* (2015) who reported grain filling period had positive significant correlation with days to 50% flowering.

Plant height had positive and highly significant phenotypic and genotypic correlation with days to 50% flowering and day to maturity. In harmony to this investigation, Megersa *et al*. (2016) who reported plant height had positive significant genotypic correlation with days to 50% flowering and day to maturity; Kumar (2016) reported plant height had positive significant phenotypic correlation with days to 50% flowering and days to maturity and Jha *et al*. (2012) reported plant height had positive significant genotypic correlation with days to maturity.

Number of primary branches per plant had positive and highly significant phenotypic and genotypic association with grain filling period. It had negetive and highly significant genotypic correlation with days to flowering. Similar results were reported by Ali *et al.* (2010) who reported numbers of primary branches per plant have significant and positive correlation with grain filling period. But disagree with Singh *et al*. (1990) and Temesgen (2007) who reported significant and positive correlation of number of primary branches per plant with day to maturity.

Number of secondary branch had positive and highly significant phenotypic and genotypic correlation with grain filling period and number of primary branch per plant. It also showed negative and significant genotypic correlation with day to flowering. Similarly, Singh *et al*. (1990), Temesgen (2007) and Zali *et al.* (2011) reported positive association of number of secondary branches per plant with number of primary branches per plant. In contrast, Hagos *et al.* (2018) reported positive and significant correlation of number of secondary branches per plant with number of pods per plant and number of seeds per plant.

Number of pods per plant had positive and highly significant phenotypic and genotypic correlation with grain filling period, number of primary branches per plant and number of secondary branches per plant. However, It had negetive and highly significant phenotypic and genotypic correlation with day to flowering. This result agree with the previous findings Ali *et al.* (2011), Hagos *et al*. (2018) and Kumar (2016) reported that number of pods per plant have positive and highly significant genotypic correlation with number of primary branch per plant and number of secondary branches per plant. Tesfa *et al*. (2015) observed that number of pods per plant showed positive and highly significant correlation with number of secondary branches per plant. Srivastava *et al*. (2017) reported number of pods per plant showed positive and significant correlation with number of primary branches per plant. Temesgen (2007) reported number of pods per pant had negative significant phenotypic correlation with days to 50% flowering.

Number of seeds per pod had positive and highly significant phenotypic and genotypic correlation with grain filling period, number of primary branches per plant, number of secondary branches per plant and number of pods per pant. It had negetive and highly significant phenotypic and genotypic correlation with day to 50% flowering and day to maturity. The present result agree with Megersa *et al.* (2016) and Getachew *et al.* (2015) who reported who reported seeds per pod was positively correlated with number of pod per plant;

Singh *et al*. (1990) who reported negative and significant phenotypic correlations between numbers of seeds per pod with days to 50% flowering; Kumar and Arora (1991) who reported the positive correlation of number of seeds per pod with number of pods per plant and also negative significant genotypic correlation with days to 50% flowering.

Number of seeds per plant exhibited positive and highly significant phenotypic and genotypic correlation with grain filling period, number of primary branches per plant number of secondary branches per plant, number of pods per plant and number of seeds per pod. It had also negative and significant phenotypic and genotypic correlation with day to flowering. Positive correlation of number of seeds per plant with these trait and among each other indicates that the possibility of simultaneous improvement of these characters through selection.

The present result is in agreement with the work of Yucel *et al*. (2006) and Hasan and Deb (2014) which showed positive and highly significant phenotypic and genotypic correlation between number of seeds per plant and number of pods per plant. Hagos *et al.* (2018) reported number of seeds per plant had positive and highly significant phenotypic and genotypic correlation with for number of secondary branches per plant, number of pods per plant and seeds per pod. Temesgen (2007), Salgotra (2016), Kumar (2016) and Thakur *et al.* (2018) who reported number of seeds per plant exhibited a positive and highly significant phenotypic correlation with number of pods per plant and number of seeds per pod. Getachew *et al.* (2015) reported also reported number of seeds per plant exhibited a positive and highly significant genotypic correlation with number of pods per plant. Positive correlation of number of seeds per plant with number of pods per plant, number of seeds per pod and among each other indicates that the possibility of simultaneous improvement of these characters through selection.

Hundred seed weight had positive and highly significant genotypic correlation with grain filling period. It had positive and significant phenotypic correlation with grain filling period, number of

primary branches per plant, number of secondary branches per plant, number of pod per plant, number of seeds per plant. The present result is agreement with Singh *et al*. (2017) who reported 100 seed weight was positive and significant phenotypic correlation with number of primary branches per plant and number of secondary branches per plant; Hagos *et al*. (2018) who reported 100 seed weight was positive and significant correlation with number of pod per plant.

4.4. Path Coefficient Analysis

This analysis was conducted using seed yield as dependent variable and all other traits studied as independent variables. The phenotypic and genotypic direct and indirect effect of different characters on seed yield is presented in (Tables 8 and 9). Dewey and Lu (1959) suggesting the scale of path coefficient in rice as: 0.00 to 0.09 is negligible, 0.10 to 0.19 is low, 0.20 to 0.29 is moderate and 0.30 to 0.99 is high and more than 1 very high. Both phenotypic and genotypic correlations were analyzed by path coefficient analysis technique to identify the important yield attributes by estimating the direct effects of traits contributing to grain yield and separating the direct from the indirect effects through other related traits by partitioning the correlation coefficient and finding out the relative importance of different characters as selection criteria.

4.4.1. Phenotypic path coefficient analysis of seed yield with other traits

The phenotypic path coefficient analysis (Table 8) showed that number of seed per pod, number of pod per plant and number seed per plant exerted moderate and positive direct effect on seed yield. Hundred seed weight, number of primary branches per plant and grain filling period had positive and low to negeligible positive direct effect on seed yield. Day to flowering and number of secondary branches per plant exerted negative and negeligible direct effect on the yield.

Table.8. Estimates of direct (bold diagonal) and indirect effect (off diagonal) at phenotypic level for eleven different characters on seed yield of 20 desi chickpea genotypes evaluated at Haramaya University main campus in 2017/18.

Variable	DF	GFP	NPB	NSB	PPt	SPo	SPt	HSW	r_p
DF	**-0.001**	-0.187	-0.149	-0.150	-0.121	0.009	-0.037	-0.002	-0.638
GFP	0.001	**0.002**	0.175	0.219	0.219	-0.012	0.054	0.275	0.932
NPB	-0.012	0.177	**0.055**	0.225	0.268	0.001	0.224	0.002	0.940
NSB	0.055	0.001	0.227	**-0.013**	0.227	0.002	0.265	0.178	0.942
PPt	0.001	-0.013	0.181	0.223	**0.265**	0.055	0.222	0.001	0.937
SPo	0.055	0.001	0.001	0.226	0.179	**0.267**	0.225	-0.013	0.941
SPt	0.002	0.179	-0.013	0.056	0.268	0.223	**0.223**	0.001	0.939
HSW	0.000	0.005	0.086	0.086	0.068	-0.005	0.022	**0.122**	0.386

Residual =0.062

Where: DF = Days to 50% flowering, GFP = Grain filling period, HSW = hundred seed weight (g). NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, PPt = Number of pods per plant, r_p = phenotypic correlation with seed yield, SPo = Number of seeds per pod, SPt = Number of seeds per plant.

The indirect effect of grain filling period via other characters was positive and moderate to negeligible effect on seed yield except number of seeds per pod (Table 8). The indirect effect number of primary branches per plant via number of secondary branches per plant, number of pods per plant and number of seeds per plant was positive and moderate. However, the indirect effect of number of secondary branches per plant via number of primary branches per plant, number of pods per plant and number of seeds per plant on seed yield was positive and moderate. The result is agree with Hagos *et al*. (2018) who reported the indirect effect of grain filling period via all character except day to flowering was negeligible effect on seed yield. But disagree with Agrawal *et al.* (2018) who reported the indirect effect of number of secondary branches via number of primary branches per plant had negligible values.

Number of pods per plant had positive and moderate direct effect on seed yield. The phenotypic correlation with seed yield was positive and highly significant. The indirect effect of number of pods per plant through number of secondary branches per plant and number of seed per plant was positive and moderate values. The current result is similar with Fikru (2004), Thakur and Sirohi (2009) who reported positive direct effect of number of pods per plant on seed yield in

desi type chickpea. Similarly, Temesgen (2007) reported number of pods per plant have positive direct effect on seed yield in kabuli chickpea genotypes. Singh *et al*. (2017) reported number of pods per plant had positive direct effect on seed yield. Hagos *et al*. (2018) reported the indirect effect of number of pods per plant via number of seeds per plant had positive effect on seed yield.

Number of seeds per pod had positive and moderate direct effect on seed yield. Their indirect effects via other traits were all positive and moderate to negeligible value on seed yield (Table 7). Similarly, Kumar (2016) reported number of seeds per pod exerts positive direct effect on seed yield. The result disagree with the findings of Padmavathi *et al.* (2013), Megersa *et al*. (2016), Thakur *et al.* (2018), who reported negative direct effect of number of seeds per pod and Temesgen (2007) who reported negative indirect effect of number of seeds per pod via secondary branches per plant on seed yield.

Number of seed per plant had positive and moderate direct effect on seed yield. The indirect effects of number of seeds per plant through number of pods per plant and number seeds per pod were positive and moderate values. The indirect effect of number of seeds per plant via other characters was weak to negligible value on seed yield (Table 8). The result agrees with Hagos *et al*. (2018), Zali *et al* (2011) and Mohammadi and Talebi (2015) who reported positive direct effect of number of seeds per plant on seed yield. Thakur *et al.* (2018) reported the positive indirect effect of number of seeds per plant on seed yield via number of pods per plant. Hagos *et al*. (2018) also reported indirect effect of number of seeds per plant on seed yield is positive and moderate.

Hundred seed weight exerted positive and weak direct effect on seed yield and it had positive and significant phenotypic correlation. The indirect effect of hundred seed weight on seed yield via number of pods per plant, seeds per pod and seeds per plant is negeligible (Table 8). Similarly, Fikru (2004), Mushtaq *et al.* (2013), Megersa *et al.* (2016), Mushtaq *et al.* (2013),

Singh *et al*. (2017) and Zali *et al* (2011 reported positive direct effects on seed yield and its indirect effects hundred seed weight on seed yield via other traits are weak to negeligible.

The results of residual effects (R=0.062) revealed that 93.8% of the yield of chickpea was contributed by the characters studied in this experiment. The role of other independent variables on seed yield related components which had not been included in this analysis were expected to influence yield only by 6.2%. The residual effect measures the role of other possible independent variables which were not included in the study on the dependent variable. Therefore the present result indicates the independent variables included in the study had sufficiently captured the variation in yield.

4.4.2. Genotypic path coefficient analysis of seed yield with other traits

The results of genotypic path coefficient analysis of grain yield with other traits are presented in Table 9. The highest positive genotypic direct effect on seed yield was exerted by number of pod per plant followed by number of seeds per plant. Grain filling period, number of primary branches per plant, number of seeds per pod and hundred seed weight exerted positive and negligible direct effect on seed yield. However, day to flowering and number of secondary branches per plant had negetive and negligible direct effects on seed yield.

The genotypic path coefficient analysis also revealed that grain filling period had high and positive indirect effects on seed yield through number of secondary branches per plant and hundred seed weight. The indirect effect of grain filling period via number of pod per plant was positive and modarete effect on seed yield. Therefore, their positive genotypic correlation coefficient with seed yield was mainly due to indirect effect. Similarly, Hagos *et al.* (2018) reported the indirect effect of grain filling period via number of seeds per pod and number of seed per plant was negetive value on seed yield. But disagree with the indirect effects of grain filling period via number of secondary branches per plant and hundred seed weight was negetive value on seed yield.

Variable	DF	GFP	NPB	NSB	PPt	SPo	SPt	HSW	r_g
DF	**-0.013**	-0.214	-0.058	-0.246	-0.169	0.033	0.013	0.009	-0.644
GFP	-0.007	**0.015**	0.086	0.356	0.246	-0.047	-0.018	0.311	0.942
NPB	0.014	-0.047	**0.087**	0.360	0.308	-0.006	0.249	-0.019	0.945
NSB	0.012	-0.019	0.250	**-0.047**	0.364	0.086	0.304	-0.007	0.944
PPt	0.086	-0.019	-0.006	0.253	**0.360**	-0.047	0.303	0.013	0.942
SPo	-0.007	0.013	-0.047	0.305	0.251	**0.086**	0.363	-0.019	0.945
SPt	0.013	-0.019	0.086	0.252	0.361	-0.047	**0.306**	-0.008	0.944
HSW	-0.005	0.188	0.051	0.190	0.137	-0.026	-0.010	0.025	0.550

Table 9. Estimates of direct (bold diagonal) and indirect effect (off diagonal) at genotypic level for eight different characters on seed yield in twenty desi chickpea genotypes tested at Haramaya University main campus in 2017/18.

Residual=0.035

Where: DF = Days to 50% flowering, GFP = Grain filling period, HSW = hundred seed weight (g). NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, PPt = Number of pods per plant, r_p = phenotypic correlation with seed yield, SPo = Number of seeds per pod, SPt = Number of seeds per plant, HSW=Hundred seed weight

The indirect of number of primary branches per plant had positive and high effects through number of secondary branches per plant and number of pods per plant on seed yield. However, the indirect effects of number of primary branches per plant had positive and moderate via number of seeds per plant was positive and moderate. Similarly, Hagos *et al*. (2018) reported that indirect effects exerted by number of primary branches per plant on seed yield via grain filling period, number of seeds per pod and number of seeds per plant were negetive and negeligible.

The indirect effect of number of secondary branches per plant on seed yield through number of pods per plant and number of seeds per plant was positive and high. The indirect effect of number of secondary branches per plant via number of primary branches per plant was positive and moderate on seed yield (Table 9). Therefore, the positive genotypic correlation coefficient with seed yield was mainly due to indirect effect. Thus it is important to consider indirect effect to select the traits. The present result agrees with the reports of Temesgen (2007) who found

negetive direct effect of number of secondary branches per plant on seed yield. Hagos *et al.* (2018) reported number of secondary branches per plant had positive and high indirect effects via number of seeds per plant on seed yield. In contrary Mushtaq *et al.* (2013) reported number of secondary branches per plant had positive and high direct effect on seed yield.

Number of pods per plant had positive and high direct effects on seed yield. The genotypic correlations between these traits were positive and significant. The indirect effect of number of pods per plant on seed yield through number of seeds per plant was positive and high. The indirect effect of number of pods per plant on seed yield via number of secondary branches per plant was positive and moderate. Similarly, Agrawal *et al.* (2018), Singh *et al*. (2017), Megersa *et al*. (2016), Padmavathi *et al.* (2013) and Dev *et al.* (2017) reported positive and high direct effect of number of pods per plant on seed yield.

Number of seeds per pod exerted negative and negligible direct effect on seed yield. The indirect effect of number of seeds per pod via number of secondary branches per plant and number of seeds per plant was positive and high value on seed yield. However, the indirect effect of number of seeds per pod via number of pods per plant was positive and modarete. The genotypic correlation it had with seed yield was positive and highly significant mainly due to their indirect effect. The present result is agree with Kumar (2016), Singh *et al*. (2017) who reported number of seeds per pod had positive and moderate direct effect. Dev *et al.* (2018) reported number of seeds per pod exerted positive and high direct effect on seed yield in desi chickpea genotypes. Hagos *et al.* (2018) reported the indirect effect of number of seeds per pod via number of pods per plant and number of seeds per plant was positive and moderate and high effect respectively on seed yield in desi and kabuli chickpea genotypes.

Number of seeds per plant had positive and high direct effects on seed yield. The indirect effect of number of seeds per plant via number of secondary branches per plant and number of pod per plant was positive and moderate and high value respectively on seed yield. Therefore, both

direct and indirect selection through these traits might be helpful in yield improvement. The present result agree with Zali *et al* (2011), Hagos *et al*. (2018) who reported number of seeds per plant had positive direct effects on seed yield. Hagos *et al*. (2018) who reported the indirect effects of seeds per plant via number of seeds per pod and hundred seed weight was negetive value. But disagree with Hasan and Deb (2014) number of seeds per plant had negative direct effect on seed yield.

The indirect effect of hundred seed weight via all characters was moderate to negeligible effect on seed yield (Table 9). Singh *et al*. (2017) reported hundred seed weight to have positive direct effects and also reported the indirect effects of hundred seed weight via all other characters was moderate to negeligible on seed yield. Mushtaq *et al.* (2013) and Megersa *et al. (*2016) reported hundred seed weight to have positive direct effects. Contrary with Temesgen (2007) reported the indirect effects of hundered seed weight via number of pods per plant and number of secondary branches per plant exerted negetive value on seed yield.

The results of residual effects (R=0.035) revealed that 96.5% of the yield of chickpea was contributed by the characters studied in this experiment. The role of other independent variables or seed yield related components which had not been included in this analysis were expected to influence yield only by 3.5%. This shows total variation in seed yield in which the numbers of characters chosen for the study were appropriate for yield improvement in chickpea. Similarly, Temesgen (2007) reported (0.0384) effects of genotypic path analysis on kabuli chickpea genotypes.

4.5. Clustering of Genotypes

The Euclidean dissimilarity distance of genotypes estimated from 11 quantitative traits was used to construct dendrograms based on the Unweighted Pair-Group with Arithmetic Means (UPGMA). Accordingly, the 20 desi chickpea genotypes were grouped into four distant clusters (Figure 1 and Table 9). Cluster I was the largest cluster that contained eight genotypes

(40%) including local check. Cluster II consisted of five genotypes (25%) and Cluster III contained six genotypes (30%). Cluster IV was the least with only one genotype (5%). This indicates that the presence of genetic divergence among the tested genotypes. The previous finding reported the presence of diversity among the chickpea genotypes classifying in different number of distinct clusters. Previous findings reported the presence of divergence among chickpea genotypes. Temesgen (2007) classified 49 kabuli chickpea genotypes in to 8 distinct clusters and Dumber and Deshmukh (1984) grouped 17 chickpea genotypes into nine clusters.

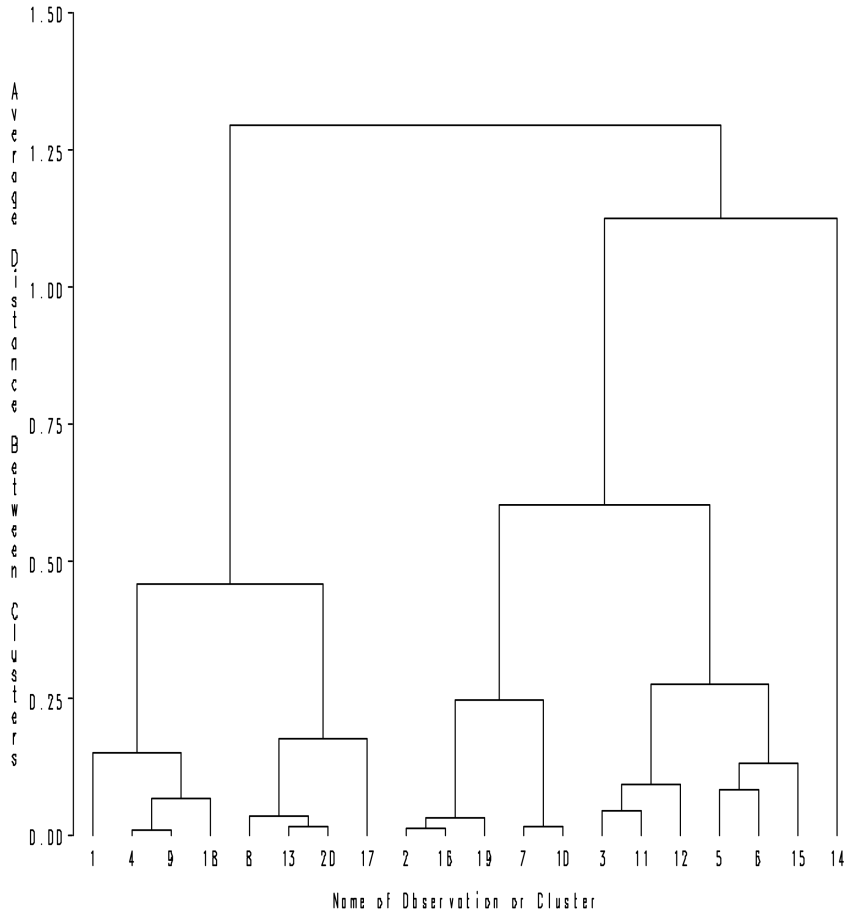
1.50
1.25
1.00
0.75
0.50
0.25
0.00
Average Distance Between Clusters
1 4 9 18 8 13 20 17 2 16 19 7 10 3 11 12 5 6 15 14
Name of Observation or Cluster

Figure 1. Tree diagram of 20 desi chickpea genotypes for 11 studied variables based on Euclidean dissimilarity distance using Unweighted Pair-Group with Arithmetic Means (UPGMA).

Note: 1= DZ-2012-CK-0029, 2= DZ-2012-CK-0029, 3= DZ-2012-CK-0029, 4= DZ-2012-CK-0029, 5= DZ-2012-CK-0029, 6= DZ-2012-CK-0029, 7= DZ-2012-CK-0029, 8= DZ-2012-CK-0029 , 9= DZ-2012-CK-0029, 10= DZ-2012-CK-0029, 11= DZ-2012-CK-0029, 12= DZ-2012-CK-0029, 13= DZ-2012-CK-0029, 14= DZ-2012-CK-0029,15= DZ-2012-CK-0029, 16= DZ-2012-CK-0029, 17= DZ-2012-CK-0029, 18= DZ-2012-CK-0029, 19= DZ-2012-CK-0029, 20= DZ-2012-CK-0029

Cluster	Number of Genotypes and (%)	Genotype lists
I	8(40%)	DZ-2012-CK-0033, DZ-2012-CK-0248, DZ-2012-CK-0232, DZ-2012-CK-0035, DZ-2012-CK-0253, DZ-2012-CK-0029, DZ-2012-CK-0036. Local variety
II	5(25%)	DZ-2012-CK-0236, DZ-2012-CK-0235, DZ-2012-CK-0027, DZ-2012-CK-0037
III	6(30%)	DZ-2012-CK-0227. DZ-2012-CK-0032. DZ-2012-CK-0028, DZ-2012-CK-0030, DZ-2012-CK-0239, DZ-2012-CK-0241
IV	1(5%)	DZ-2012-CK-0034

Table 10. Distribution of 20 desi chickpea genotypes in to four clusters based on D^2 analysis

4.5.1. Cluster mean analysis

Table 11. Mean value of 11 quantitative characters of the four clusters for 20 desi chickpea genotypes.

Traits	Clusters I	II	III	IV	Overall Mean
DF	53.25	48.07	47.33	42.00	49.62
DM	113.21	110.73	111.61	110.33	111.97
GFP	59.96	62.67	64.28	68.00	62.33
PH	36.99	34.11	35.83	31.07	35.63
NPB	2.64	3.18	3.58	4.23	3.04

Note: 1= DZ-2012-CK-0029, 2= DZ-2012-CK-0029, 3= DZ-2012-CK-0029, 4= DZ-2012-CK-0029, 5= DZ-2012-CK-0029, 6= DZ-2012-CK-0029, 7= DZ-2012-CK-0029, 8= DZ-2012-CK-0029 , 9= DZ-2012-CK-0029, 10= DZ-2012-CK-0029, 11= DZ-2012-CK-0029, 12= DZ-2012-CK-0029, 13= DZ-2012-CK-0029, 14=

NSB	12.31	18.44	16.15	18.00	14.28
PPt	48.51	57.68	64.44	69.4	50.38
SPo	1.09	1.18	1.25	1.32	1.18
SPt	56.28	68.09	76.30	84.7	66.66
HSW	19.34	22.31	21.23	26.37	21.01
SYPha	2382.17	2878.27	3232.28	3742.33	2804.24

DF = Days to 50% flowering, DM = Days to maturity, GFP = Grain filling period, PH = Plant height (cm), NPB = Number of primary branches per plant, NSB = Number of secondary branches per plant, PPt = Number of pods per plant, SPo = Number of seeds per pod, SPt = Number of seeds per plant, HSW = Hundred seed weight, NPB= number of primary branches per plant, NSB= number of secondary branches per plant, PPt= number of pods per plant, SPo = number of seeds per pod, SPt= number of seeds per plant , SYPha = seed yield per hectar

Clusters I had mean values greater than overall mean values of genotypes for days to flowering, days to maturity and plant height. However, the other remaining traits had low values than overall mean. Clusters II, III and IV had mean values greater than overall mean values of genotypes for grain filling period, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight and seed yield. Clusters II, III and IV had mean values lower than overall mean values of genotypes for days to flowering and days to maturity and plant height for cluster II and IV (Table 11). Clusters I consists of eight genotypes with low mean seed yield. However, the groups of these clusters were late maturing than the average crop maturity of genotypes. Therefore, genotypes included in these clusters might not be considered for selection. Clusters II, III and IV consists of five, six and one genotypes having late grain filling period but higher mean values for number of number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, hundred seed weight and seed yield.

Clusters III and IV had identified as higher mean values for seed yield and most of desirable traits that could be used for selection of genotypes and further evaluation of members of these

clusters is possible to develop varieties. Relatively maximum number of pods per plant and number of seeds per plant were recorded for Clusters III and IV. This implying that genotypes of Cluster-III and Cluster-IV could be used when directs selection for increment on seed yield and yield components are desired. Results indicated that the crossing between superior genetic divergences of clusters may provide desirable recombinants for developing high yielding desi chickpea genotypes. The genotypes falling in the same cluster are more closely related (less divergent) than those belonging to another cluster and the genotypes falling in different cluster are more divergent.

The more distant the genotypes crossed, might end up with obtaining heterotic hybrids and result in varieties with a broad genetic base. Hence, crossing of genotypes between clusters I with and clusters III and IV will produce wide range of variability and high heterotic expression in F2 generation for parameters: days to 50% flowering, grain filling period, plant height, number of primary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant because the mean difference of these traits on the two classes is wide in Table 11. Crossing Cluster II with cluster IV can be improved traits such as days to flowering, grain filling period, plant height, number of primary branches per plant, number of pods per plant, number of seeds per plant and hundred seed weight.

5. SUMMARY AND CONCLUSIONS

The success of a crop improvement program depends upon the genetic variability present in the genotypes of the crop. Thus assessing genetic variability and knowledge of the association among traits is essential. In order to generate such information in desi chickpea, a total of 20 genotypes including local check were tested at Haramaya University main campus in 2017. The specific objective of the study were to assess the genetic variability for yield and yield related traits, to estimate the genotypic and phenotypic associations among characters, and to assess the direct and indirect effects of yield related traits on yield. The genotypes were evaluated

using randomized complete block design with three replications. Data were collected for 11 traits. The data generated from the experiment were subjected to analysis of variance and subsequent estimation of genotypic and phenotypic coefficients of variations, estimations of heritability in broad sense and expected genetic advance, correlation and path analysis studies.

The analysis of variance revealed that there were sufficient variations among desi chickpea genotypes for seed yield and yield related traits. There were highly significant variations among genotypes for most traits. The highest mean performance for seed yield was obtained from genotypes DZ-2012-CK-0034 and lowest mean performance for seed yield was obtained from genotype DZ-2012-CK-0029. Among twenty genotypes tested ten of them had higher mean yield than the grand mean, and this gives an opportunity for plant breeders for new variety release of the crop.

Phenotypic coefficient of variation (PCV) was high for number of primary branches per plant, pods per plant, seeds per plant and seed yield per hectar. However, day to flowering, plant height, and number of secondary branches per plant and hundred seed weight had moderate PCV value. Number of primary branches per plant and seed per plant categorized as high GCV value. Moderate GCV computed for days to 50% flowering, plant height, number of secondary branches per plant, pod per plant, hundred seed weight and seed yield per hectar. High heritability estimates were recorded for days to flowering, days to maturity, plant height, number of primary branches per plant and number of seeds per plant. Grain filling period, number of secondary branches per plant, number of pods per plant, number of seeds per pod, hundred seed weight and seed yield per hectar observed medium heritability. In this study, plant height, number of primary branches per plant and seeds per plant had high heritability estimates coupled with higher genetic advance as percent of mean. This indicated that these traits were highly heritable and selection of high performing genotypes is possible.

Seed yield had shown highly significant and positive phenotypic and genotypic correlation with grain filling period, number of primary branches per plant, number of secondary branches per plant, number of seeds per pod, number of seeds per plant and hundred seed weight. Thus implies that the genetic influence on these traits was similar. Phenotypic path coefficients revealed that number of seeds per pod, number of pod per plant and number seed per plant exerted moderate and positive direct effect on seed yield. Genotypic path coefficients indicated that number of pod per plant and number of seed per plant exerted highly positive direct effect on seed yield. Hence, direct selection of these traits could improve the grain yield. The residual effects were 0.037 and 0.065 at genotypic and at phenotypic levels respectively. Generally, the present findings revealed adequate existence of variability for most of the traits in the studied genotypes which need to be exploited in future desi chickpea breeding in the study area.

Based on Euclidean dissimilarity distance analysis 20 desi chickpea genotypes classified in to four classes. Cluster I was the largest cluster that contained 8 genotypes including local check. Cluster II and III contained five and six genotypes respectively. Cluster analysis showed the presence of genetic distance between clusters III and IV. The present study generally implied the presence of significant genetic variability among the tested genotypes for all the eleven traits studied. These conditions indicated that there is good opportunity to improve these traits through selection. However, the findings of this study can be of preliminary as the data was obtained from one location and one year only, further multi location and multiyear work is required. The genotypes used were also over focus.

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7. APPENDIX

Appendix Table 1. Monthly rainfall distribution, maximum and minimum temperature at Haramaya University main campus during the crop growing season of 2017 years.

Month	Temperature (C^o)			Rainfall (mm)
	Maximum	minimum	average	
July	24.6	14.4	19.50	147
August	14.3	4.2	9.25	130.9

September	22.4	12.6	17.50	160
October	24.9	8.1	16.50	14.7
November	23.9	4.3	14.10	0.0
December	17.8	1.0	9.40	0.0
Mean T^{o}	21.3	7.4	14.38	---
Total rainfall	---	---	----	452.6

Source: Jigjiga Meteorological Station (2017)