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Evaluation of genetic variability and association of traits in Kabuli chickpea (*Cicer arietinum* L.) genotypes in East Gojjam Zone, Northwestern, Ethiopia

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ABSTRACT

Genetic variability study is an important task for generating genetic information on variability and association of important traits of Kabuli chickpea for further improvement through selection and/or hybridization. In this regard, the study aimed to estimate the magnitude of genetic variation and association of traits among 36 Kabuli chickpea genotypes for 13 traits by using 6 × 6 simple lattice design for two consecutive years at East Gojjam Zone. Analysis of variance indicated that there were highly significant genotypic differences for all studied trait. Over years, most studied traits showed highly significant differences except 100 seed weight and plant height, which were not significant. The analysis indicated highly significant (p ≤ 0.01) difference were observed for the interaction effects of genotypes by years in most studied traits, such as seed yield, biomass yield. Both PCV and GCV value were high for traits like days to flowering, number of primary branch, number of pod per plant, number of seed per plant, biomass yield, hundred seed weight, seed yield and harvest index. High heritability coupled with high genetic advance was observed for key trait, such as seed yield, biomass yield, 100 seed weight, number of pods and seeds per plant, indicated that high heritability is due to additive gene effects and therefore, making selection an effective strategy for improving Kabuli chickpea. Seed yield had a highly significant and positive genotypic as well as phenotypic association with the number of seeds per pod, number of seeds and pods per plant and biomass yield. The path coefficient analysis revealed that biomass yield; the number of seeds per pods and seeds plant^{-1} had a positive direct effect on seed yield at both genotypic and phenotypic levels. Overall, the results of the study showed the presence of sufficient genetic variation among Kabuli chickpea genotypes. The variability of traits, which were exhibited among the genotypes, can serve in planning selection and crossing programs for the future chickpea improvement. However, it requires multi location and year trails among a larger

set of candidate genotypes to verify the stability and develop high yielding varieties.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is grown all over the world in about 57 (fifty-seven) countries including Ethiopia. India is the leading producer [1]. Chickpea is also the third most important annual cool season food grain legumes in the world after common bean (*Phaseolus vulgaris* L.) and field pea [2,3]. This crop has a small genome size of 740 Mbp and is self-pollinated. Further, chromosomal constitution reveals chickpea as a diploid species with 2n=2x=16chromosomes [4]. The crop is grown under wide agro ecological conditions in midlands with an altitude of 1500 2300 mASL and rainfall of 7001 up to 300mm in Ethiopia [5]. It is commonly cultivated in vertisol type using residual moisture offers to the farmers for double cropping. Chickpeas do have multiple roles in the farming systems of many developing countries including Ethiopia ranging from human food, animal feed, export commodities and provide environmental services [1,6,7]. Nutritionally, chickpea is the cheapest and most radially available source of protein, fat, carbohydrate, fiber and minerals and vitamins [8]. Ethiopia is the sixth largest chickpea producing country sharing 3.15% of the world's total production, first in Africa shares about (63%) of the total production, 4.5% of the global chickpea market and more than 60% of Africa's market [9]. The crop is the third food grain legume in Ethiopia in terms of area and production [10]. Its productivity was (2.18), next to soya bean (2.49) and fababean (2.22) tha^{-1}. Chickpea cultivation in Amhara Region was 0.1 million hectares in production of 0.2 million tons with productivity of 1.96 tha^{-1}. East Gojjam Zone accounts 0.008 million ha of cultivated area and 0.02 million tons of production with productivity of 2.3 tha^{-1}. Awabel district covers 200 hectares of land [11].

However, the national average seed yield in Ethiopia is low, 2.18 tons ha^{-1} far below its genetic potential yield of 2.9 tons ha^{-1} [12,13], because the production of the crop nationally constrained by many factors such as usage of inappropriate improved varieties, use of inherent low productive farmers varieties, biotic and abiotic factors [6,14,15]. To alleviate some of these problems, many chickpea breeding efforts have been done since its beginning in the 1970's in Ethiopia to improve production and productivity. In its age of breeding approximately, 29 super performing varieties were released in both types; most of these were developed from the breeding material supplied by ICRISAT and ICARDA [6]. Nevertheless, most of the developed verities were Desi type. For a successful improvement of kabuli type chickpea fairly, the presence of genetic variability plays vital role. The selection of superior genotypes depends on the variability of genotypes [10]. The success of improvement in crop breeding depends upon the magnitude of genetic variability available in breeding material and the extent of heritability of desirable traits [16-18].

Yield is a complex quantitative trait that is dependent on associations and direct and indirect effects of many yield contributing traits [19]. Thus, it helps in the determination of the selection criteria for simultaneous improvement of various traits along with economic yield [20]. Therefore, correlation in combination with path coefficient analysis will be an important tool to realize the association and quantify the direct and indirect influence of one trait upon another [21]. Understanding the genetic source of yield and yield traits in addition to genetic variation and relationships between genotypes is vital to exploit the existing genetic variability and its potential use in breeding programs [22]. The demand for a variety with high yield over a range of production environments is very high among chickpea growers. Hence, genetic improvement to develop varieties with high yield potential, wider adaptability and resistance/tolerance to biotic and abiotic stresses, with acceptable end use quality, is the most viable and environment friendly option to sustainably increase chickpea yield [6].

Such improvement of crops requires the creation and introduction of genetic variability, in breeding coupled with selection, and extensive evaluation of breeding materials at multiple locations/ seasons to identify adapted and stable genotypes with desirable agronomic traits [23,24]. Still, variability of the quantitative traits of crops is the great interest to researchers to develop a new variety [25]. Previous studies were carried out on genetic variability of chickpeas with the help of genetic parameters, correlation coefficient and path analysis to determine the important traits and improvement of various traits along with economic yield for a different location in Ethiopia. But, little information is available in northwestern parts of the country [11,26-28]. Besides, the availability of genetically improved Kabuli chickpea varieties has little enough and limited efforts have been made to improve the crop through the study of Kabuli chickpea genetic variability for major traits such as yield [29]. Even though different research efforts have been done for the development of improved varieties across the country in Ethiopia, there is a limitation

of Kabuli chickpea variety development work and popularization efforts from the national research system in East Gojjam Zone for selecting well-adapted and high yielding genotypes [30]. Therefore, it is important to estimate the magnitude of genetic variability for yield, yield related traits of Kabuli chickpea genotypes, association among traits, and determine the direct and indirect effect of yield related traits on seed yield.

MATERIALS AND METHODS

Description of the study area

The experiment was conducted in East Gojam Zone, Northwestern Ethiopia during two seasons the 2019/2020 and 2020/2021 main cropping season. The study area was found at a distance of 258 km northwest of Addis Ababa. Geographically, the site lies at 10° 29' latitude north and 37° 44' longitude east with an altitude of 2104 mAMSL. It receives a mean annual rainfall of about 1090 mm. The mean minimum and maximum annual temperatures are 15°C and 24°C, respectively. The soil type of the site is predominantly black vertisols with a pH value of 6.45 (Figure 1).
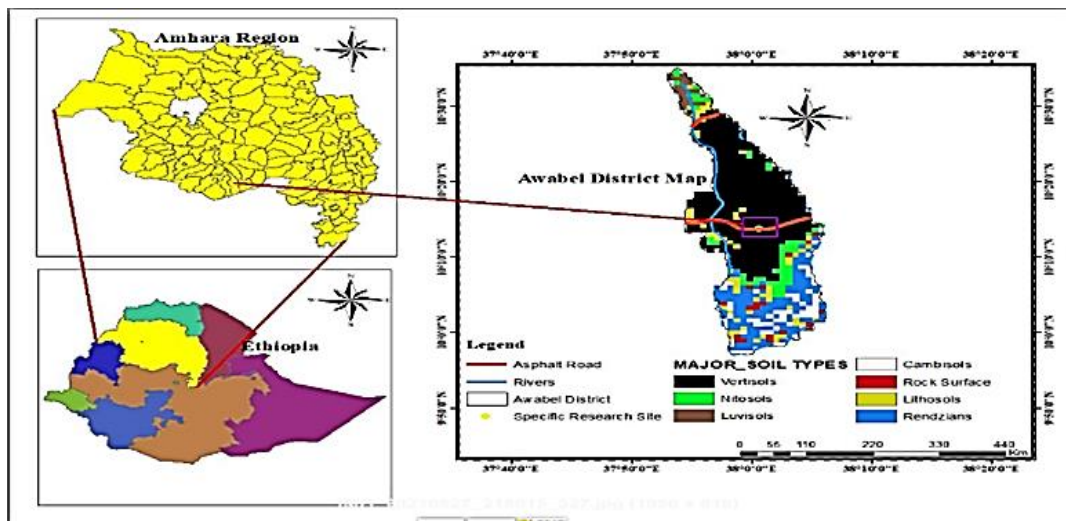

Figure 1. Schematic map of the study area.

Experimental materials

Thirty-six Kabuli chickpea genotypes including two standard check varieties (Arerti and Habru) were included in the study. These experimental materials were obtained from the highland pulse research program, Debre Zeit Agricultural Research Center (DZARC) (Table 1).

Table 1. List of Kabuli chickpea genotypes used in the experiment.

Code	Genotype pedigree	Code	Genotype pedigree	Code	Genotype pedigree
G-1	FLIP-93-93C	G-13	Arerti	G-25	FLIP-12-343C
G-2	FLIP-12-53C	G-14	FLIP-12-60C	G-26	FLIP-12-311C
G-3	FLIP-12-110C	G-15	FLIP-12-57C	G-27	FLIP-12-176C
G-4	FLIP-12-37C	G-16	FLIP-12-86C	G-28	FLIP-12-40C
G-5	Habru	G-17	FLIP-12-342C	G-29	FLIP-12-01C
G-6	FLIP-12-198C	G-18	FLIP-12-263C	G-30	FLIP-12-331C
G-7	FLIP-12-107C	G-19	FLIP-82-150C	G-31	FLIP-12-265C
G-8	FLIP-12-287C	G-20	FLIP-88-85C	G-32	FLIP-12-55C
G-9	FLIP-12-06C	G-21	FLIP-12-108C	G-33	FLIP-12-197C
G-10	FLIP-12-18C	G-22	FLIP-12-322C	G-34	FLIP-12-210C
G-11	FLIP-12-79C	G-23	FLIP-12-310C	G-35	FLIP-12-75C
G-12	FLIP-12-61C	G-24	FLIP-12-109C	G-36	FLIP-12-192

Experimental design, procedures and trial management

The experiment was carried out in a 6 × 6 simple lattice design during the 2019/2020 and 2020/2021 two cropping seasons. The total plot size was 2.25 m^2 (1.5 m length × 1.5 m width) with a net plot size of 1.35 m^2. Each genotype was planted with a spacing of 30 cm between rows and 10 cm between plants. NPS fertilizers were applied as recommended (121 kg ha^{-1}) and all other agronomic practices were done as per the recommendation for chickpea production.

Data collection

The data were collected from the net plot area at randomly selected and tagged five individual plants by adopting [31,32]. The data were collected on plot basis are days to 50% flowering (DF), days to 90% physiological maturity (DM), Pod Filling Period (PFP), Hundred Seed Weight (HSW) (g), Biomass Yield (BY), Seed Yield (SY) and Harvest Index (HI). While the data collected on plant basis were Plant Height (PH) (cm), Number of Primary Branches (NBP), Number of Secondary Branches (NSB), Number of Pods per Plant (NPP), Number of Seeds Per Pod (NSP) and Number of Seeds Per Plant (NSPP).

Data analysis

Analysis of variance: All measured traits were subjected to Analysis of Variance (ANOVA) using PROC GLM of SAS statistical software version 9.4 to assess the difference among the tested genotypes. Comparison of treatment means were tested using Least Significant Difference test (LSD) at 5% of probability level [33]. The relationship between traits with yield and yield components were correlated using the Proc-Corr Pearson's correlation procedures.

Estimation of genetic parameters

Estimation of variances components: The phenotypic variance, genotypic variance and coefficients of variations were estimated by the procedure suggested by Burton GW et al. [34].

Environmental variance $(\sigma^2 e) = MSe$

Genotypic variance $(\sigma^2 g) = \dfrac{MSg - msgy}{ry}$

Phenotypic variance $(\sigma^2 p) = \sigma^2 g + \dfrac{\sigma^2 gy}{y} + \dfrac{\sigma^2 e}{ry}$

Genotype × Environment variances $(\sigma^2 gy) = \dfrac{MSg - mse}{r}$

Phenotypic Coefficient of Variation (PCV) $= \dfrac{\sqrt{\delta^2 p}}{\bar{x}}$

Genotypic Coefficient of Variation (GCV) $= \dfrac{\sqrt{\delta^2 g}}{\bar{x}}$

Where, $\bar{X}$=grand mean of a character, r=replication, msgy=genotypic x year mean square, MSg=genotypic mean square and MSe=mean square of error

PCV and GCV values ranging from >20% are regarded as high, values 10% to 20% as a medium,<10% are considered as suggested by Deshmukh S et al. [35].

Heritability in a broad sense: Heritability (H2) is expressed as a percentage of the ratio of the genotypic variance $(\sigma^2 g)$ to the phenotypic variance $(\sigma^2 p)$ as follows [36]:

Broad sense heritability (H2) $= \left[\dfrac{\sigma^2{}_g}{\sigma^2{}_p} \right] x100$

Where,

H2=heritability in a broad sense, $\sigma^2 p$=phenotypic variance, $\sigma^2 g$=Genotypic variance. According to Singh, heritability values were categorized as high greater than 60 moderate 40-59% and less than 40% is engaged as low.

Genetic Advance (GA): According to Allard [36], selection intensity (K) at 5% was computed as follows:

GA= K × δP × H^2 = K$\sqrt{\delta^2 p}$ *H2

Expected genetic advance as percentage of mean=GA/$\bar{X}$ ×100

Where, ($\sqrt{\delta^2 p}$=Square root of phenotypic variance), H2=Heritability in a broad sense x=grand populations mean for the trait under considerations, K=is a constant value at Standardized selection differential (where k=2.06 at

5% selection intensity) σp=phenotypic variance

Genetic advance as a percent of the mean range was categorized as low (<10%), moderate (10 up to 20%) and high (>20%) as suggested by Johnson P, et al. [37].

Association of traits

Estimation of phenotypic and genotypic associations: Phenotypic and genotypic correlations were estimated using the formula suggested by Miller P, et al. [38].

Path coefficient analysis: Path coefficient analysis was computed by using the suggested formula by Wright [39] and worked out by Dewey and Lu [21] using the phenotypic correlations to determine the direct and indirect effect of yield components on seed yield [20,38]. The residual effect (U) is the unexplained variation of the trait that is not accounted for by the path coefficient and is calculated using the formula of Dewey DR, et al., Singh RK, et al. [21,40].

RESULTS AND DISCUSSION

Analysis of variance

The homogeneity test of variances over two years showed the f-ratio was <3 for all traits. ANOVA has shown a highly significant difference among traits of all studied genotypes (Table 2). ANOVA has also shown significant difference among traits over years, except the trait plant height and 100-seed weight. Combined ANOVA indicated that the interaction effects of genotype and year were significant for most traits such number of pods per plant, number of seeds per plant, number of seeds per pod, biomass yield, hundred seed weight and seed yield. This indicates the existence of high genetic variability that endowed the breeder for future improvement. Our result was corroborated with the results of many agronomic traits and in chickpea genetic variability and association study [2,40-43,27].

Table 2. Combined analysis of variance for 13 traits of tested genotypes over years.

Traits	Replication	Block	Genotype (G)	Year (Y)	G*Y	Error	CV	R^2
	DF=1	DF=5	DF= 35	DF=1	DF=35	DF=143		
DF	44.4	6.87	133.77[**]	250.69[**]	11.22	12.34	6.13	0.87
PFP	12.25	106.78[**]	194.24[**]	8130.03[**]	18.32	27.33	7.06	0.89
DM	5.06	144.37[**]	340.22[**]	15149.5[**]	11.52	35.57	4.58	0.92
PH	0.095	59.85[**]	63.50[**]	0.0034	63.92[**]	18.62	9.06	0.79
NPB	0.33	0.112	7.21[**]	5.56[**]	0.95[**]	0.21	11.56	0.95
NSB	47.61[**]	0.49	3.19[*]	26.01[**]	4.25[**]	2	20.95	0.72
NPP	13.93	39.68	554.49[**]	30531.73[**]	310.06[**]	19.8	9.23	0.97
NSP	0.0015	0.0049	0.046[**]	0.067[**]	0.0126[**]	0.0041	5.55	0.88
NSPP	8.507	75.68[*]	521.66[**]	2789.6[**]	83.23[**]	27.2	15.04	0.93
HSW	55	76.33	146.69[**]	8.5	81.88[**]	34.19	18.35	0.78
SY	465487.8	171230.7	4553790.5[**]	3989873.1[**]	335634.0[*]	209955.6	15.57	0.93
BY	1544736	4483217	19611924.7[**]	29606376.3[**]	10414631.4[**]	2829656	21.13	0.86
HI	0.037	0.023	0.032[**]	0.00075[**]	0.035	0.01088	26.49	0.78

Note:[*]: significant at ($p \leq 0.05$) and [**]: Highly significant ($p \leq 0.01$) probability level. CV: Coefficient of variation; DF: Days to 50% Flowering; DM: Days to 90% Maturity; PFP: Pod Filling Period; PH: Plant Height; NPB: Number of Primary Branches; NSB:Number of Secondary Branches; NPP: Number of Pods Per Plant; NSPP: Number of Seeds per Plant; NSP: Number of Seeds per Pod; BY: Biomass Yield; HSW: Hundred Seed Weight; SY: Seed Yield and HI: Harvest Index.

Mean and range values

Seed yield ranged from 929.5-5530.4 kgha[-1] with a mean value of 2948.69 kgha[-1]. The highest seed yield was

recorded from genotype FLIP-93-93C (5530.4 kgha^{-1}) followed by FLIP-12-198C (5033.4 kgha^{-1}) and FLIP-12-343C (4406.8 kgha^{-1}). Genotype FLIP-93-93C it could be most promising for seed yield improvement of the Kabuli chickpea. The highest biomass yield was recorded for FLIP-12-37C and FLIP-12-57C (133001 kgha^{-1}). Chickpea straw has important role for animal feed and soil improvement. Hence, genotype FLIP-12-37C and FLIP-12-57C will be considered in biological yield improvement of Kabuli chickpea to address farmers need and improve animal production fairly. Similar results were noted in the previous study on Kabuli chickpea genotypes (Tables 3 and 4) [27,42,44,45].

Table 3. Mean performance of 36 Kabuli chickpea genotypes for yield components and yield evaluated over years at Awabel district.

	Traits						
Gen	**DF**	**PFP**	**DM**	**PH**	**NPB**	**NSB**	**NPP**
1	60[b-e]	80.5[a-f]	140.25[bc]	50.62[b-g]	5.47[a-e]	7.37[a-f]	70.75[a]
2	53[f-j]	66.5[lmn]	118.25[no]	51.92bcd	4.6[e-g]	6.15[c-i]	45.05[j-n]
3	53[f-j]	73[j-l]	124.75[i-n]	49.12[c-g]	5[e-g]	6.57[b-]	53.77[efg]
4	44.75[k]	66.75[lmn]	110.25[lmn]	49.17[c-g]	3.55[hij]	7.07[a-h]	47.52[g-m]
5	50.75[ij]	74.25[d-k]	123.75[j-n]	42.47[ijk]	2.2[pq]	5.87[d-i]	34.57[qrs]
6	48.25[jk]	70.5[i-l]	118.5[mno]	46.97[c-j]	5.77[abc]	8.42[ab]	57.77[de]
7	54.75[f-i]	81.25[a-e]	135.25[c-j]	48.25[c-i]	5.1[d-f]	7.42[a-f]	51.47[f-i]
8	49.75[j]	73.25[f-l]	121.75[lmn]	52[bcd]	3.37[h-k]	6.57[b-h]	50.77[f-i]
9	57.75[c-f]	69.75[j-m]	126.25[i-n]	46.85[c-j]	4.37[g]	7.2[a-h]	43.6l[-p]
10	55[f-i]	72[h-l]	125.75[i-n]	47.07[c-j]	2.02[pq]	5.55[f-i]	50.6[f-k]
11	64.75[ab]	62.75[mno]	126.25[i-n]	46.6[c-j]	6[a]	8[abc]	65.82[abc]
12	55.75[e-h]	74.75 [d-k]	129[f-l]	45.82[e-k]	1.77[q]	6.1[c-i]	28.9[s]
13	53[f-j]	60.5[no]	112.25[o]	42.82[h-k]	2.4l[-q]	6.32[c-h]	33.82[rs]
14	56.75[e-h]	73.75[e-l]	130.25[e-k]	46.25[d-k]	2.82[k-o]	7.12[a-h]	32.65[rs]
15	66.5[a]	83.5[ab]	148.75[a]	50.27[b-g]	3[i-l]	7.45[a-f]	44.42[k-n]
16	50.5[ij]	78.25[a-h]	127.5[g-l]	42.5[ijk]	5.92[ab]	7.27[a-h]	68.47[abc]
17	66.25[a]	83.75[ab]	148.75[a]	44.57[g-k]	2.32[n-q]	5.35[ghi]	42.82[m-p]
18	65.75[a]	81.25[a-d]	145.75[ab]	49.55[b-g]	1.75[q]	5.7[e-i]	30.75[s]
19	66[a]	89[o]	123.75[j-n]	44.9[f-k]	5.32[b-e]	6.725[b-h]	52.4[e-h]
20	57.5[d-g]	82.5[abc]	138.75[bcd]	49.9[b-g]	5.7[a-d]	7.32[a-g]	50.57[f-k]
21	63.5[ab]	77[b-j]	140.25[bc]	50.95[b-d]	3.15[h-l]	6.725[b-h]	33.47[rs]
22	62[a-d]	61.25[no]	122[k-n]	55.62[ab]	3.7[h]	5.3[hi]	53.77[efg]
23	57[e-h]	76.5b[-j]	132.25c[-i]	45.45[e-k]	5.75[a-d]	8[abc]	62.4[cd]
24	62[a-d]	75.5[c-k]	136.25[c-f]	46.47[d-j]	6[a]	7.2[a-h]	68.07[bc]
25	52.75[g-j]	69.75[j-m]	121.21[mn]	44.82[g-k]	4.97[e-g]	6.72[b-h]	45.27[i-n]
26	60.25[b-e]	77.25[b-i]	136.25c[-f]	52.62[bc]	5.42a[-e]	8.8[a]	63.87[bcd]
27	52.75[hij]	77.75[a-i]	130.25[e-k]	44.55[g-k]	3.17[h-l]	6.175[c-i]	38.05[o-r]
28	50.25[ij]	83.25[ab]	132.25[c-i]	51.27[b-e]	4.97[e-g]	6.95[a-h]	42.1[m-p]
29	60[b-e]	66.51[mn]	125.25[i-n]	60.875[a]	2.6l[-p]	4.275[i]	37.15[pqr]
30	56.7[e-h]	82.75[abc]	138.25[b-e]	46.85[c-j]	2.7[l-o]	5.6[e-i]	41.9[m-p]
31	64.5[ab]	71.5[h-l]	134.75[c-h]	46.4[d-k]	4.875[e-g]	7.75[a-d]	54.12[ef]
32	52.5[hij]	79.5[a-g]	130.75[d-j]	42.92[h-k]	2.9[j-n]	6.7[b-h]	33.52[rs]
33	56[e-h]	72[h-l]	126.75[h-m]	40.32[k]	3.52[hij]	6.775[b-h]	70.75[a]
34	64.75[ab]	72.5[g-l]	136[c-f]	48.77[c-h]	5.22[c-f]	6.6[b-h]	40.42[n-q]
35	62.5[abc]	69[klm]	130.25[e-k]	42.12[jk]	2.8[k-o]	6.775[b-h]	46.37[h-n]
36	52.25[hij]	84.75[a]	135.75[c-g]	45.55[e-k]	3.6[hi]	7.6[a-e]	49.15[f-l]

Range	44.75-66.5	61.25-89	110.25-148.75	42.12-60.87	1.77-6	4.27-8.42	28.9-70.75
Mean	57.2	74	130.11	47.59	3.99	6.76	48.2
LSD	4.96	7.38	8.47	6.09	0.65	2	6.28

Table 4. Mean performance of 36 Kabuli chickpea genotypes.

Gen	Traits					
	NSP	NSPP	HSW(g)	SY (Kg/ha)	BY (Kg/ha)	HI
1	1.31[a-d]	50.3[b]	26.75[i-l]	5530.4[a]	13301[a]	0.437[b-g]
2	1.14[g-k]	33.67[d-h]	33.75[d-i]	3522.2[d-g]	9319[d-h]	0.383[c-l]
3	1.1[i-l]	41.8[c]	43.75[ab]	3346.5[e-h]	9270[d-h]	0.365[d-l]
4	1.22[-g]	28.42[h-k]	32[e-k]	4328[c]	11773[abc]	0.409[b-j]
5	1.25[c-f]	34.2[d-h]	30.25[f-l]	3817.6[cde]	11078[a-d]	0.386[b-k]
6	1.4[a]	70.47[a]	29[f-l]	5033.4[ab]	11573[a-d]	0.433[b-g]
7	1.04[lm]	28.7[h-k]	30.75[f-l]	1661.3[opq]	7828[f-j]	0.270[i-l]
8	1.035[lm]	22.4[jk]	35.5[b-g]	2437.1[j-n]	9704[c-f]	0.256[kl]
9	1.03[lm]	22[k]	24.75[jkl]	929.5[r]	3581[n]	0.268[jkl]
10	1.2[e-h]	33.1[e-i]	44[a]	3611.6[def]	7463[f-l]	0.502[a-d]
11	1.18[f-i]	29.67[f-j]	31[f-l]	2757[h-k]	6830[i-l]	0.421[b-h]
12	1.18[f-i]	22.45[jk]	40[a-e]	948.5[r]	3760[mn]	0.296[g-l]
13	1.14[g-k]	49.22[b]	27.25[g-l]	4328[c]	7868[f-j]	0.641[a]
14	1.14[g-k]	26[ijk]	34.5[c-h]	3029.4[f-j]	6438[i-m]	0.521[abc]
15	1.21[e-h]	24.4[jk]	29.5[f-l]	3872[cde]	13301[a]	0.293[g-l]
16	1.16[f-j]	49.2[b]	26.75[i-l]	3365.6[e-h]	7857[f-j]	0.435[b-g]
17	1.14[g-k]	33.42[d-h]	34.5[c-h]	3844.8[cde]	7460[f-l]	0.525[abc]
18	1.06[kl]	22.3[k]	29.75[f-l]	3347.6[e-h]	7310[g-l]	0.468[b-f]
19	1.12[h-l]	22.6[jk]	26[ijkl]	1361.1[pqr]	4332[mn]	0.416[b-i]
20	0.96[m]	22.6[jk]	27.5[g-l]	2418.4[j-n]	5184[lmn]	0.477[b-e]
21	1.16[f-j]	28.27[h-k]	41.5[a-d]	3863.4[cde]	10774[b-e]	0.36[d-l]
22	1.05[klm]	35.8[c-f]	24[kl]	3366.2[e-h]	8399[e-j]	0.402[b-k]
23	1.12[h-l]	49.575[b]	24.5[kl]	2625.3[j-m]	5397[k-n]	0.491[b-e]
24	1.05[klm]	25[jk]	23[l]	2248.5[k-o]	6790[i-l]	0.389[b-k]
25	1.32[abc]	64.4[a]	24[kl]	4406.8[bc]	8289[f-j]	0.533[ab]
26	1.12[h-l]	24.8[jk]	35[c-h]	2010[mno]	5342[k-n]	0.41[b-j]
27	1.16[f-j]	40[cde]	30[f-l]	2263.2[k-o]	7855[f-j]	0.357[d-l]
28	1.18[f-i]	37[c-f]	42.75[abc]	2698.6[i-l]	8510[e-j]	0.321[f-l]
29	1.4[a]	38.85[cde]	35.25[b-g]	3558.6[d-g]	7533[f-l]	0.48[b-e]
30	1.03[lm]	23.55[jk]	33.75[d-i]	1928.5[nop]	7025[h-l]	0.280[h-l]
31	1.04[lm]	33.17[d-i]	26[ijkl]	2103.3[l-o]	678[li-l]	0.363[d-l]
32	1.14[g-k]	32.75[e-i]	36[a-f]	1238[qr]	6266[j-m]	0.238[l]
33	1.35[ab]	40.52[d]	33[e-j]	2950.9[g-j]	7610[f-k]	0.389[b-k]
34	1.28[bcde]	35.85[c-f]	30.5[f-l]	1877[n-q]	6892[i-l]	0.309[g-l]
35	1.2[e-h]	33.15[e-i]	29[f-l]	2248.2[k-o]	8671[e-i]	0.29[g-l]
36	1.08[jkl]	38.7[cde]	41.75[a-d]	3276.5[e-h]	9433[c-f]	0.353[e-l]
Range	0.96-1.35	22-70.47	23-43.75	929.5-5530.4	3581-13301	0.238-0.641
Mean	1.16	34.67	31.86	2948.69	7966.58	0.39
LSD	0.09	7.36	8.25	646.89	2374.8	0.147

Estimates of genetic parameters

Phenotypic and genotypic variance components and coefficients of variation: The value of phenotypic variance was higher than a genotypic variance for most traits studied, indicates the highest contribution of the environmental effects to the phenotypic variance in these traits and selection on phenotypic bases of these traits may not be effective for genetic improvement unless the environmental conditions are optimize. However, the difference is not high for number of seeds per pod and harvest index, indicates that the phenotypic expression of these traits was less influenced by environmental factors, and selection on phenotypic bases of these traits may be effective for genetic improvement. Dev et al., and Fasil reported similar results in Kabuli chickpea genetic variability studies [23,27].

The PCV value ranged from 5% to 71.7% for number of secondary branch and seed yield and GCV also ranged from 5.9 to 73 % for number of secondary branch and seed yield. High GCV and PCV values were observed for days to flowering, biomass yield, the number of seeds per plant, seed yield, number of primary branches, harvest index, hundred seed weight, and number of pod per plant, indicate the existence of wide genetic variation among the genotypes and had a possibility of genetic improvement through selection for these traits. The remaining studied traits except number of secondary branches exhibited moderate GCV values. The difference between GCV and PCV values was very low for most traits, indicating these traits are highly controlled by additive gene action and less influenced by the environment. In line with the present result, Joshi et al., reported high GCV and PCV values for biomass yield, seed yield, harvest index and 100 seed weight. Similarly, Awol et al., noted high GCV and PCV for seed yield, biomass yield, days to flowering, and days to maturity, number of pods per plant, number of seeds per pod and number of seeds per plant [2,41]. Mohan and Thiyagarajan [17] reported high GCV and PCV values for biomass yield, seed yield, and hundred seed weight. Zerfu et al., also reported high GCV and PCV for hundred seed weight, seed yield and biomass yield [46].

Broad sense heritability: The highest estimate of heritability values were observed for all studied traits, indicates selection based on phenotypic appearance of individual genotypes for such trait might be calm which infers these traits competency of replying to selection compression due to relatively small contribution of the environment to the phenotype. However, choosing superior individuals based on heritability evaluations alone may not be indication for genetic improvement. Similar findings reported by Dev et al., [23] Shengu et al., [47] and Fasil [27] for hundred seed weight, days to maturity, above ground biomass yield, harvest index, plant height, and number of primary branches, number of seed per plant and seed yield. Joshi et al., [2] reported high estimate of heritability for seed yield, biomass yield and hundred seed weight. However, the selection of superior individuals based on heritability estimates alone may not be an indication of genetic improvement. High heritability alone is not enough to make sufficient improvement through selection generally in advance generations unless accompanied by substantial amount of genetic advance [48]. The efficacy of heritability is increasing with the estimation of genetic advance, which indicates the degree of gain in a trait obtained under a particular selection pressure [49].

Genetic advance: Biomass yield (106.6), seed yield (147.7), number of primary branches (136.4), harvest index (80), hundred seed weight (72.6), number of seed per plant (34.5), number of pod per plant (93.3), number of seeds per plant (133), days to maturity (29.1), pod filling period (37.9), days to flowering (41.2) and plant height (29.8) had high GAM (Table 5). This indicates selection of genotype based on this trait might result in a high response in the new population. A genetic advance exceeding 100 percent for some studied traits indicates a substantial improvement in the trait and suggests that the selection process has been effective in promoting desirable genetic characteristics. Similarly, these results were agreed by Awol et al., [41] reported high GAM values for seed yield, biomass yield, number of pods per plant, and hundred seed weight. In the same way, Mohan and Thiyagarajan [17] reported high GAM for the number of secondary branches and number of pods per plant. In addition Zerfu et al., [46] reported high GAM values for the number of secondary branches, seed yield, biomass yield, hundred seed weight and harvest index. Higher heritability coupled with high GAM suggests that the traits are controlled by additive gene action. Days to flowering, biomass yield, and the number of seeds per plant, seed yield, and number of primary branches, harvest index, hundred seed weight, and number of pod per plant had high values of GCV, heritability and genetic advance as percentages of the mean. Such situations are the greatest potential initiated by additive genetic

factors, there by imitating the effectiveness of selection for the enhancement of these traits. Therefore, these traits are significant for the genetic improvement of the Kabuli chickpea. Similar to this result high heritability coupled with high GAM values were reported for traits hundred seed weight, number of pods per plant, number of secondary branches, number of seeds per plant, seed yield and harvest index [27]. Thus, genetic advance is yet another important selection parameter that aids breeder in a selection programs. It has been emphasized that without genetic advance, the heritability values would not be of practical importance in selection based on phenotypic appearance. So, the genetic advance should be considered along with heritability in coherent selection breeding programs [50].

Table 5. Estimates of genetic parameters for 13 traits of 36 Kabuli chickpea genotypes.

Trait	Min-Max	Mean	$\sigma^2 e$	$\sigma^2 g$	$\sigma^2 gy$	$\sigma^2 P$	GCV	PCV	H2	GA	GAM
DF	44.75-66.5	57.2	12.33	130.97	5.06	136.58	20	20.4	97.9	23.6	41.2
PFP	61.25-89	74.85	27.33	189.66	4.66	198.82	18.4	18.8	97.7	28.4	37.9
DM	110.25-148.75	130.11	35.56	337.34	6.26	349.36	14.1	14.4	98.3	37.8	29.1
PH	42.12-60.87	47.59	18.62	47.52	54.61	79.48	14.5	18.7	77.3	14.2	29.8
NPB	1.77-6	3.99	0.21	6.97	0.85	7.45	66.2	68.4	96.8	5.4	136.4
NSB	42.12-60.87	47.59	2	5.7	3.25	7.82	5	5.9	85.3	4.9	10.3
NPP	28.9-70.75	48.24	19.8	476.98	300.16	632.01	45.3	52.1	86.9	45	93.3
NSP	0.96-1.35	1.16	0.0041	0.04	0.01	0.05	17.8	19.1	93.4	0.4	34.5
NSPP	22-70.47	34.67	27.2	500.85	69.63	542.47	64.6	67.2	96.1	46.1	133
HSW	23-43.75	31.86	34.19	126.22	64.79	167.16	35.3	40.6	86.9	23.1	72.6
SY	929.5-5530.4	2948.69	209955.6	4469882	230656.2	4637699	71.7	73	98.2	4355.3	147.7
BY	3581-13301	7966.58	2829656	17008267	8999803	22215583	51.8	59.2	87.5	8495.7	106.6
HI	0.238-0.641	0.39	0.0108	0.02	0.03	0.04	39.1	51.8	75.5	0.3	80

Note:*: significant at ($p \leq 0.05$) and **: highly significant ($p \leq 0.01$) probability level. CV: Coefficient of Variation, DF: Days to 50% Flowering; DM : Days to 90% Maturity; PFP: Pod Filling Period; PH: Plant Height; NPB: Number of Primary Branches; NSB: Number of Secondary Branches; NPP : Number of Pods Per Plant; NSPP: Number of Seeds Per Plant; NSP: Number of Seeds Per pod; BY: Biomass Yield; HSW: Hundred Seed Weight; SY: Seed Yield and HI: Harvest Index.

Association of traits

The degree of association between pairs of trait at the genotypic and phenotypic levels was estimated and results are presented in Table 5.

Genotypic correlation coefficients of seed yield with other traits: Designing, evaluating and setting selection criteria for the ideal characters in breeding program of crop plants are proceed from studies of correlation at the genotypic and phenotypic levels [51]. Genotypic correlation study provides the direction, strength and the point of association between the traits beyond the environmental effect. Seed yield showed positive and significant (P $\leq$ 0.05) genotypic association with the number of seeds per pod (r=0.41) and number of seed per plant (r=0.35). In agreement with this finding Tesfamichael, et al., [52] reported positive and significant (p<0.05) correlation of seed yield kg ha^{-1} with biomass yield kgha[-1](r=0.85), number of pods plant-1 (r=0.57), but non-significantly correlated with other traits such as days to 50% flowering, plant height, number of primary branches plant[-1] [50]. Similarly, significant and positive association was reported among seed yield with number of pods plant[-1], number of seed plant[-1] by Fiaz S, et al. [53]. Tadesse, et al., [54] also reported significant and positive correlation of seed yield with biomass yield, plant height, number of pods per plant and number of seeds per pod, while other traits showed non-significant association with seed yield. Fasil, [27] reported highly significant and positive association of number of seeds per plant, hundred seed weight, and number of pods per plant with seed yield kgha[-1].

Genotypic correlation coefficients of among other traits: Genotypic correlation coefficient among other

related traits are shown in Table 5. Days to flowering had positive association with days to maturity (r=0.63), while highly and negatively significant genotypic correlation with number of seed per plant (r=-0.34). The result indicates genotypes that exhibited prolonged flowering period may result delaying of maturity, reducing number of seed per plant. Positive and highly significant association exhibited for days to maturity with pod filling period (r=0.76), this indicates early matured genotype took the shortest pod filling period. Similar to the present findings [17,27,55] reported positive and significant association of days to maturity with days to flowering and pod filling period. Number of primary branch showed positive and significant genotypic correlation with number of secondary branch (r=0.64), number of pod per plant (r=0.72) and negative significant association with biomass yield (r=-0.39). Number of Hasan and Deb [56] reported the same result for association of number of primary branch with number of pod per plant, number of seed per plant and number of secondary branch. Ali et al., [57] also reported positive and significant association of number of primary branches per plant with number of pods per plant and seeds per pod. Zerafu et al., [46] reported high and significant association between number of primary branch and secondary branch.

Number of seed per pod showed significant and positive genotypic association with number of number of seed per plant (r=0.599), 100 seed weight (r=0.51) and seed yield (r=0.41). Positive and significant association was recorded for number of seed per plant with seed yield (r=0.6), biomass yield(r=0.34) and harvest index (r= 0.41). Similarly, noted that highly significant and positive associations for number of seed per pod with number of pod per plant [42,51]. Above ground biomass yield showed significant and positive genotypic association with seed yield (r=0.51) and harvest index (r=0.48). Getachew et al., [42] and Awol and Asnake [58] revealed positive and significant association for above ground dry biomass yield with seed yield, while negative and significant association with harvest index. Tesfamichael et al., [52] also noted that biomass yield kgha^{-1} showed positive and significant (p<0.05) association with number of pods per plant-1 (r=0.75) and it was negatively and highly significant (p<0.01) association with 100 seed weight (r=-0.53).

Phenotypic correlation coefficients of seed yield with other traits: Correlation analysis indicated that seed yield exhibited significant and positive phenotypic associations with the pod filling period (r=0.16), number of pods per plant (r=0.17), number of seeds per pod (r=0.22), number of seeds per plant (r=0.16) and biomass yield (r= 0.52), indicates these traits are important for seed yield improvement. Yield is a polygenic traits controlled by several simply inherited traits. The correlation coefficients highlight the pattern of association among these yield components and helps in determining the important trait to improve the crop. In line with the present findings, similar results are reported in chickpea study [11,27,59].

Phenotypic correlation coefficients among other traits: Positive and significant association was recorded between days to flowering with days to maturity (r=0.54), while negative and highly significant association with number of seed per plant (r=-0.32) and hundred seed weight (r=-0.22). Positive and highly significant association exhibited for pod filing period with days to maturity (r=0.88), number of secondary branches (r=0.18), number of pods per plant (r=0.43). While, negative and significant association were observed pod filling period with number of seeds per pod and number of seed per plant, this indicates early pod filling genotypes were expected to be low number of seeds per pod and plant. Positive and significant correlation was recorded with number of pod per plant (r=0.48) and negative and significant association with number of seed per pod and plant. [37,56] and [27] reported similar association between traits.

Highly and positive phenotypic associations were recorded for number of seed per pod with number of seed per plant (r= 0.5), above ground biomass yield (r=0.34) and seed yield (r=0.22). Number of seed per plant showed significant and positive phenotypic association with seed yield (r=0.46), biomass yield (r=0.16), number of primary branches(r=0.17) and harvest index (r=0.25), while highly and negative significant association with days to flowering (r=-0.35), pod filling period (r=-0.28) and days to maturity (r=-0.39). Above ground biomass yield showed significant and positive phenotypic association with number of pod per plant (r=0.18), number of seed per pod (r=0.34), number of seed per plant (r=0.46) and seed yield (r=0.52) and harvest index (r=0.48). Similarly Tadesse et al. [54] and Amare [60] reported positive and significant association for above ground biomass yield with number of pod per plant, seed yield, number of seed per plant and number of seed per pod. Hundred seed weight showed negative and significant phenotypic correlation with days to flowering (r=-0.22), number of primary branches (r=-0.20). Positive and significant associations were recorded with plant height (r=0.186). Positive and significant association were observed for harvest index with number of seed per plant (r=0.25) and biomass yield(r=-0.48), but negative and significant association with seed yield (r=-0.41). Plant height showed non-significant phenotypic association with all traits. Fasil [27] reported positive and significant correlation for harvest index with number of primary branch and number of seed per plant, contrary to the present result, plant height had significant phenotypic correlation with 100 seed weight [26].

Selection of genotypes for high yield alone is difficult because yield is the end product of components of several characteristics and has a polygenic inheritance. There might be component interactions in which a gene conditioning an increase in one trait will influence another provided other conditions are kept constant. Therefore, the selection of genotypes with high mean values for these traits along with high seed yield seems more important rather than selection for yield per se alone. Understanding the association of other traits with seed yield and the selection of genotypes for yield and for traits that have a significant correlation with yield is important. From the present result among 13 traits, the number of pods per plant, number of seeds per pod, number of seeds per plant and biomass yield had positive and significantly associated with seed yield at both genotypic and phenotypic levels. Therefore, these traits might be important selection criteria for further yield improvement of Kabuli chickpea.

Path coefficient analysis

In the present study seed yield was considered as a resultant variable and number of pods per plant, number of seeds per pod, number of seeds per plant and biomass yield, were causal (independent) variables in both genotypic and phenotypic (Tables 6 and 7).

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlations coefficients of the 13 traits over years.

Variable	DF	PFP	DM	PH	NPB	NSB	NPP	NSP	NSPP	BY	HSW	GY	HI
DF	1	0.02	0.63**	0.15	-0.002	-0.075	0.035	-0.145	0	-0.24	-0.18	-0.24	0.031
PFP	0.081	1	0.76**	-0.055	-0.069	0.14	-0.062	-0.21	-0.13	0.28	-0.042	0.129	-0.27
DM	0.54**	0.88**	1	0.059	-0.049	0.072	-0.024	-0.2524	-0.34*	0.065	-0.138	-0.04	-0.19
PH	0.076	0.029	0.06	1	0.0628	-0.22	-0.053	-0.0064	-0.19	0.17	0.148	0.172	-0.038
NPB	0.0108	0.04	0.0485	0.0451	1	0.68**	0.72**	-0.0551	0.2898	-0.387**	-0.041	-0.08	0.0017
NSB	-0.059	0.184*	0.15	-0.133	0.36**	1	0.155	-0.087	-0.031	-0.038	-0.045	-0.054	0 .053
NPP	0.174	0.433**	0.48**	-0.085	0.47**	0.155	1	0.042	0.26	-0.316	0.13	0.074	0.072
NSP	-0.15	-0.20**	-0.24**	0.015	-0.035	-0.087	-0.1	1	0.599**	0.062	0.51**	0.41**	0.21
NSPP	-0.35**	-0.28**	-0.39**	-0.054	0.17*	-0.031	-0.097	0.509**	1	-0.18	0.60**	0.34*	0.41**
HSW	-0.22**	0.12	-0.015	0.186*	-0.20**	-0.038	-0.135	0.045	-0.12	1	-0.013	0.106	-0.205
BY	-0.1	0.05	0.013	0.1	-0.055	-0.044	0.18*	0.34**	0.46**	-0.027	1	0.51**	0.48**
SY	-0.13	0.16*	0.082	0.12	-0.016	-0.05	0.17*	0.22**	0.16*	0.13	0.52**	1	-0.03
HI	0.012	-0.14	-0.1	-0.011	-0.057	0.053	-0.037	0.095	0.25**	-0.16	0.48**	-0.41**	1

Note: ***, **, * indicate very highly significant at 0.1%, highly significant at 1%, and significant at 5% probability levels, respectively. DF: Days to 50% Flowering; DM: Days to 90% Maturity; PFP: POD Filling Period; PH: Plant Height; NPB: Number of Primary Branches; NSB: Number of Secondary Branches; NPP: Number of Pods per Plant; NSP: Number of Seeds per Pod; NSPP: Number of Seeds Per Plant; BY: Biomass Yield; HI: Harvest Index; HSW: Hundred Seed Weight; SY: Seed Yield.

Table 7. Genotypic direct (bold and diagonal) and indirect effects of traits on seed yield for studied. Genotypes.

	NSP	NSPP	BY	Rg
NSP	0.44	-0.57	-0.25	0.27
NSPP	-0.6	0.61	-0.69	-0.05
BY	-0.14	-0.65	0.79	0.64

Note: Residual = 0.46, NPP=Number of pods per plant, NSP=Number of seeds per pod, NSPP=number of seeds per plant and BY= biomass yield, rg=genotypic correlation coefficient

Genotypic direct and indirect effects of various characters on seed yield: Biomass yield (0.79), number of seeds per plant (0.61) and number of seed per pod (0.44) had a positive direct effect on seed yield. Therefore, these

traits should be included in selection parameters for obtaining the maximum seed yield of Kabuli chickpea would be quite effective for the breeding program for yield improvement rather than for yield per se alone. The indirect effect of number of seeds per plant and number of seeds per pod on yield was negative *via* biomass yield. The indirect effect of biomass yield and number of seed per pod *via* number of seeds per plant exerted a negative effect on seed yield. In the same way, Tadesse et al. [54] reported the number of pods per plant increased seed yield indirectly through biomass yield. Agrawal et al., [55] and Fasil [27] also reported biomass yield and pods per plant had a high positive direct effect on seed yield. Shafique et al., [61] noted the positive direct effect of the number of pods per plant and the number of seeds per plant on seed yield. The residual effect of (0.46) indicates that the trait, which is included in the genotypic path analysis, explained 54 % of the total variations in seed yield.

Phenotypic direct and indirect effects of various traits on seed yield: Biomass yield showed a strong positive direct effect on seed yield (1.14). The number of seed per pod had positive direct effect on seed yield. While, negative direct effect had observed in number of seed per plant on seed yield. The indirect effect of number of seeds per pod had *via* number of seed per plant had been positive and negative for biomass yield. The direct effect of number of seeds per plant, biomass yield and number of seed per pod was positive. This indicates the importance of the traits to be used as direct selection criteria to improve seed yield. Similarly, Tadesse et al., [54] reported that the number of pods per plant increased seed yield indirectly through above ground biomass at the phenotypic level. Gizachew [11] reported days to maturity, number of pods per plant, number of seeds per plant, hundred seed weight and plant height had a positive direct effect on seed yield. The residual effect of (0.15) indicates that the trait, which is included in the phenotypic path analysis, explained 85 % of the total variation in seed yield. The remaining 15 % variation was the contribution of other factors, which is due to low environmental effects on the expression of the phenotypes (Table 8).

Table 8. Phenotypic direct (bold and diagonal) and indirect effects of traits on seed yield for studied genotypes

	NSP	NSPP	BY	Rg
NSP	0.39	0.03	-0.16	0.27
NSPP	-0.16	-0.08	0.03	-0.05
BY	-0.04	0.03	0.14	0.64

Note: Residual = 0.15, NPP=Number of Pods per Plant, NSP= Number of Seeds per Pod, NSPP=Number of Seeds Per Plant and BY=Biomass Yield and rp=phenotypic correlation coefficient

CONCLUSION

In conclusion, the analysis of variance showed the existence of high genetic diversity among the studied Kabuli chickpea genotypes. Combined analysis of variance showed significant variations for most traits. The role of gene action was high for the expression of most traits such as biomass yield, number of seeds per plant, seed yield, indicating the existence of wide genetic variation among the genotypes and had a possibility of genetic improvement through selection for these traits. High heritability coupled with high genetic advance as a percent of mean was observed for traits biomass yield, seed yield, number of seeds per pod, number of pods per plant showing that the high heritability is most likely due to additive gene effects; and the importance of selection for the improvement of Kabuli chickpea for these traits. Seed yield showed a highly significant and positive association at both genotypic and phenotypic levels with the number of seeds per pod, number of seeds per plant and biomass yield. Therefore, the association of these traits with seed yield is important for further Kabuli chickpea improvement. The number of seeds per pod, number of seeds per plant and biomass yield had a direct effect on seed yield increment. Hence, from the present results, it has been observed adequate existence of variability for most of the traits in the studied genotypes, which need to be, exploited in future Kabuli chickpea breeding. However, this study was conducted for two seasons and at one location which needs to be conducted in subsequent breeding trials considering more locations to develop high yielding varieties. It would be worthwhile to study qualitative traits among genotypes to identify accessions having high quality and marketable produce for progress improvement *via* the selection and/or hybridization program of Kabuli chickpea.

DATA AVAILABILITY

The original data used for data analysis and presented in the text. Further, inquiries can be directed to the corresponding author.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest.

ACKNOWLEDGMENTS

FUNDING

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