

Genetic Diversity Analysis of Kabuli Chickpea (*Cicer arietinum* L.) Genotypes at Arsi-Robe, Southeastern Ethiopia

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Abstract: Chickpea is an important pulse crop in Ethiopia; however, the production of the crop is not at its potential due to many constraints of which limited availability of high yielding varieties. Thus the main objectives of this study were to assess the magnitude of genetic diversity among kabuli chickpea genotypes for yield and yield related traits. Forty nine kabuli chickpea genotypes were evaluated for 11 traits in 2019/20 at Arsi Robe using 7 x 7 simple lattice designs with two replications. The analysis of variance result showed significant differences among genotypes. Cluster analysis showed the existence of wide variability among genotypes and grouped into six clusters. Maximum inter cluster distances were observed from cluster-IV and III followed by cluster IV and V, and cluster II and IV, while minimum inter cluster distances were found between cluster II and VI followed by cluster III and VI. The first three principal components explained about 66.1% of the total variations among the 49 kabuli chickpea genotypes. The first component accounts 34.58% of the total variation. It provides better opportunity for plant breeders to select parental materials to use for crossing in the breeding program. However, it requires multi-location and year trials to verify the consistency of existing genotypic variability.

Keywords: Cluster Analysis, Genetic Distance, Genetic Diversity, Inter Cluster Distance

1. Introduction

Chickpea (*Cicer arietinum* L.) belongs to the family leguminosae. It is one of the most important cool season food grain legumes in the world after common bean (*Phaseolus vulgaris* L.) and field pea (*Pisum sativum* L.) [1]. Chickpea is annual, self-pollinated and diploid species with $2n=2x=16$ chromosomes [2]. It is grown in 54 countries with nearly 90% of its area covered in developing countries [3]. Chickpea covered 242,703 ha, which is 15.2% of the pulse area, with 499, 426 tons of grain production (16.8% of pulses) [4]. Ethiopia is the largest producer, consumer and exporter of chickpea in Africa and shares about 4.5% of global and more than 60% of Africa's global chickpea market [5].

Two types of chickpea are known, namely kabuli and desi type. Kabuli type chickpea is one of the major pulses grown in Ethiopia, mainly grown under residual moisture which can

also contribute for the low productivity and production. It has good sources of carbohydrate (54 to 71%), protein (12.6 to 29%), lipid (3.4 to 8.8%), and energy (357 to 447 kcal/100g). Chickpea also contain fiber, minerals (calcium and phosphorus), vitamins and health beneficial phytochemicals and it is low in sodium, fat and cholesterol free [6]. Despite the significant economic importance of chickpea, the productivity remains low with national average yield of 2.05 t ha⁻¹ [4].

Increased the number of genotypes in plant genetic resource require tools for analyzing and classifying genetic variations for further utilization in crop breeding program. Genetic diversity among the parents is a prerequisite for the improvement and selecting better sergeant's materials for various traits. The more diverse parents have the more the chances of improving the characters under consideration. Cluster analysis refers to a multivariate statistical analysis technique used to partition a set of genotypes into groups

based on the uniformity of traits they possess. Each cluster within a group is more similar among individual genotypes and more diverse from the individual in other cluster.

Chickpea is adapted to black soils in the cool semi-arid areas of the tropic, sub tropics as well as temperate areas. Arsi zone is one of the strategic areas for production of chickpea in Ethiopia. However, the production of the crop is constrained by many factors including the use of low productive farmers' varieties, together with unimproved traditional practices, biotic (Root rot, *Ascochyta* blight, Fusarium wilt, weed and pod borer) and abiotic (drought, soil salinity and water logging) factors [7].

The major problem of chickpea improvement program in Ethiopia has been lack of genotypes that consistently perform well across different chickpea growing environments and resistance to biotic factors. To improve those chickpea production problems, chickpea research was started before four decades in Ethiopia. Therefore, developing high yielding and disease resistant genotypes is very important for farmers to sustain their production and to ensure the sustainability of food and nutritional security in the target area. In view of this, the current research was conducted with the objectives

of to assess the magnitude of genetic diversity among kabuli type chickpea genotypes for yield and yield related traits.

2. Materials and Methods

2.1. Description of the Study Areas

The experiment was conducted under field condition at Arsi-Robe research station during the 2019/20 main cropping season. Arsi-Robe is located at latitude of 07°53'02"N, longitude of 39°37'40"E and an altitude of 2420 m.a.s.l. The average rainfall is 890 mm per annum having peaks in July and August. The mean maximum and minimum temperatures are 22.1°C and 6°C, respectively. The soil type is classified as heavy clay with pH value of 6.

2.2. Experimental Materials

A total of 49 Kabuli chickpea genotypes listed in Table 1 were used for the study. The seeds were obtained from Debre Zeit Agricultural Research Center (DZARC). The genotypes status was advanced breeding lines developed through hybridization and introduction material by ICARDA.

Table 1. List of experimental materials.

Genotype code	Genotype Name	Genotype code	Genotype Name
G-1	DZ-2012-CK-0310	G-26	DZ-2012-CK-0295
G-2	DZ-2012-CK-0303	G-27	Flip-03-101C
G-3	ICCMABCB-8	G-28	ICCV-07313
G-4	Flip-08-254C	G-29	ICCV-09315
G-5	Flip-07-6C	G-30	DZ-2012-CK-0271
G-6	Flip-09-155C	G-31	DZ-2012-CK-0267
G-7	DZ-2012-CK-0309	G-32	DZ-2012-CK-0242
G-8	Flip-84-92C	G-33	ICCV-09304
G-9	Flip-09-188C	G-34	Flip-09-184C
G-10	ICCMABCB-3	G-35	DZ-2012-CK-0062
G-11	Flip-11-34C	G-36	DZ-2012-CK-0281
G-12	DZ-2012-CK-0300	G-37	Flip-09-181C
G-13	Flip-93-93C	G-38	DZ-2012-CK-0286
G-14	DZ-2012-CK-0269	G-39	DZ-2012-CK-0066
G-15	ICCMABCB-5	G-40	DZ-2012-CK-0290
G-16	ICCMABCC-2	G-41	ICCV-10311
G-17	Flip-03-128C	G-42	DZ-2012-CK-0274
G-18	Flip-88-93C	G-43	Flip-09-377C
G-19	DZ-2012-CK-0276	G-44	DZ-2012-CK-0214
G-20	DZ-2012-CK-0287	G-45	Flip-06-14C
G-21	ICCU-09311	G-46	DZ-2012-CK-0266
G-22	ICC-8261	G-47	Flip-09-197C
G-23	Flip-05-63C	G-48	DZ-2012-CK-0305
G-24	Flip-06-135C	G-49	Flip-09-120C
G-25	DZ-2012-CK-0294		

2.3. Experimental Design and Trial Management

The experiment was carried out using 7 x 7 simple lattice designs with two replications. The plot size was 4 m long and 1.2 m wide, i.e. 4.8 m² areas with spacing of 0.3 m and 0.1 m between rows and plants, respectively as per research recommendation. Each plot had four rows and the spacing between incomplete blocks was 1 m and 0.6 m distance were kept between plots to separate two genotypes. The trial was planted at the end of September and planting was done on

randomly allocated plots within each replication by hand drilling. 100 kg ha⁻¹ of NPS fertilizer was applied and all other agronomic practices were done throughout the growing season as per research recommendation.

2.4. Data Collected

The data on the following characters were collected on plot basis; days to 50% flowering (DF), grain filling period (GFP), days to maturity (DM), stand count (SC), hundred seed weight (HSW), grain yield per hectare (GY).

Data collected from randomly taken five sample plants from two middle rows of each plot; plant height (PLHT), number of primary branches (NPB), number of secondary branches (NSB), number of pods per plant (PPP) and number of seeds per plant (NPPL).

3. Results and Discussion

3.1. Mean Performances of Genotypes

The result showed significant ($P < 0.05$) variation for days to 50% flowering, days to maturity, grain filling period, number of secondary branch, hundred seed weight, number of pods per plant and grain yield per hectare, number of seed per plant and plant height. These highly significant differences indicate the existence of wide genetic diversity among genotypes. Mean grain yield ranged from 563 Kg ha^{-1} to 2,690 Kg ha^{-1} with grand mean of 1,315 Kg ha^{-1} . Maximum mean grain yield was recorded from genotypes G-14 (2,690 kg/ha) followed by genotype G-29, G-12, G-2 and G-6 while lowest grain yield was recorded from genotype G-24 (563 kg/ha) (Table 2).

Days to 50% flowering ranged from 62 to 83 days after sowing with a mean of 68 days. The five genotypes (G-33, G-29, G-14, G-25 and G-26) showed early flowering (62 days after planting), while genotype G-45 showed delayed flowering. Early flowering genotypes have great importance for producing more yields within a year by reducing the days to maturity of the crops. The 49 chickpea genotypes had maturity ranging from 137 to 144 days after sowing. The range of days to maturity between genotypes is not large but eleven genotypes took 137 days after sowing to attain maturity while two genotypes matured late within 144 days

after sowing. The mean values of grain filling period for 49 genotypes ranged between 57- 82 days. 19 genotypes took 63 to 70 days for grain filling with non-significant differences, while 28 genotypes took 71 to 77 days of grain filling with non-significant difference (Table 2).

Number of secondary branches showed a wide range of variability ranged from 4 to 13 with a mean of 8. Maximum number of secondary branches were recorded in genotype G-32 followed by G-36 and G-30, while a minimum number was recorded in genotype G-21. Plant height showed a wide range of variability from 43 cm to 72 cm. The highest plant height was recorded from genotype G-11 and lowest value was recorded from genotype G-44 with a mean of 59 cm (Table 2).

Number of pods per plant ranged from 26 to 59 with a mean of 44. Number of pods per plant is a significant selection criterion for obtaining high yielder genotypes. The maximum numbers of pods per plant were recorded from genotype G-12 and G-36 followed by genotype G-32 and G-2, while minimum number of pods per plant recorded in genotype G-21. Significant variations ($P < 0.05\%$) were observed for number of seed per plant. Minimum and maximum numbers of seed per plant were recorded from genotype G-21 and G-2 respectively with a mean of 46 seeds. The nine genotypes have 28 to 33 numbers of seed per plant, while 34 genotypes have ranged from 36 to 59 seeds per plant. Other six genotypes have 63 to 69 numbers of seed per plant. Hundred seed weight ranged from 19.5 g to 39 g. Maximum hundred seed weight was recorded from genotype G-41 and G-42 with a value of 30 g, while minimum seed weight recorded from genotype G-11 (Table 2).

Table 2. Mean, range and LSD values of 49 kabuli chickpea genotypes.

Entry	FD	MD	GFP	SBR	PPP	SPPL	HGT (cm)	HSW (g)	GYH (kg ha^{-1})
G-1	63a-d	137a	73.5b-d	11.3b-e	57.0ab	65a	62.5ab	26.5a-c	1864.7c-f
G-2	65a-f	137ab	72.1b-d	10.3a-e	57.5ab	69a	63.7ab	25.5ab	2363.8f-i
G-3	65a-f	138a-c	72.7b-d	9.9a-e	53.0ab	57a	54.4ab	27.0a-d	1697.3b-h
G-4	76b-g	144e	68.6a-c	8.3a-e	38.5ab	33a	55.2ab	29.5b-e	912.3a-d
G-5	69a-f	139a-e	70.0a-d	6.5a-d	39.0ab	57a	64.2ab	35.5c-f	1160.5a-e
G-6	63a-d	140a-e	77.2cd	8.2a-e	46.0ab	33a	65.7ab	31.5b-f	2114.3e-i
G-7	63a-d	139a-e	75.4b-d	7.4a-e	49.5ab	48a	67.0ab	34.5b-f	1289.6a-g
G-8	70a-g	138a-c	68.6a-c	6.7a-e	28.5ab	42a	52.1ab	30.0b-f	872.7a-d
G-9	70a-g	140a-e	70.3a-d	10.1a-e	54.5ab	49a	64.7ab	31.5b-f	869.5a-d
G-10	65a-f	138a-d	73.5b-d	6.7a-d	49.0ab	47a	47.6ab	28.0a-d	1528.2a-h
G-11	72a-g	139a-e	67.6a-c	6.2a-d	49.0ab	50a	71.6b	19.5a	1366.7a-h
G-12	63a-d	138a-c	74.9b-d	8.3a-e	59.0b	63a	54.4ab	30.5b-f	2395.7g-i
G-13	67a-f	139a-e	72.2b-d	8.4a-e	49.5ab	49a	59.4ab	26.0ab	781.1a-d
G-14	62a-c	144e	81.8d	9.1a-e	57.0ab	65a	65.7ab	26.0ab	2690.0i
G-15	63a-d	137ab	73.5b-d	9.7a-e	45.0ab	47a	52.7ab	26.0ab	1810.8c-f
G-16	64a-e	137ab	72.5b-d	5.7a-d	43.0ab	45a	57.2ab	30.5b-f	1404.3a-h
G-17	69a-f	139a-e	69.7a-d	7.7a-e	33.0ab	31a	54.7ab	34.0b-f	999.3a-e
G-18	76b-g	144c-e	68.2a-c	8.6a-e	53.5ab	56a	64.0ab	26.5a-c	1185.3a-f
G-19	78fg	142b-e	64.5a-c	8.3a-e	31.5ab	33a	55.9ab	27.5a-d	619.0ab
G-20	65a-f	140a-e	74.5b-d	8.3a-e	31.0ab	31a	65.9ab	34.5b-f	979.5a-e
G-21	65a-f	138a-d	73.0b-d	3.7a	26.0a	28a	54.7ab	33.5b-f	1143.8a-e
G-22	64a-d	137ab	74.3b-d	6.4a-d	46.0ab	46a	54.5ab	28.0a-d	1538.5a-i
G-23	70a-g	140a-e	70.0a-d	5.6a-d	38.5ab	48a	63.2ab	33.5b-f	694.9a-c
G-24	71a-g	141a-e	70.8b-d	7.1a-e	36.0ab	40a	57.7ab	32.0b-f	563.0a
G-25	62a-c	138a-c	75.8b-d	8.6a-e	55.5ab	65a	66.7ab	29.5b-e	1884.0d-i

Entry	FD	MD	GFP	SBR	PPP	SPPL	HGT (cm)	HSW (g)	GYH (kg/ha ⁻¹)
G-26	62a-c	137a	74.6b-d	7.7a-e	38.0ab	36a	56.9ab	29.0b-d	1768.3c-f
G-27	69a-f	139a-e	70.6b-d	8.2a-e	41.5ab	41a	61.9ab	30.0b-f	1404.8a-h
G-28	69a-f	138a-d	69.0a-d	10.8b-e	56.5ab	67a	58.1ab	36.0d-f	1803.8c-f
G-29	62ab	138a-e	76.1b-d	8.7a-e	52.5ab	59a	67.7ab	29.0b-d	2499.7hi
G-30	69a-f	142a-e	72.1b-d	11.7c-e	54.0ab	48a	59.2ab	31.0b-f	716.2a-d
G-31	75c-g	141a-e	65.3a-c	6.3a-d	35.0ab	39a	64.7ab	33.0b-f	754.4a-d
G-32	71a-g	143b-e	71.6b-d	13.5d	59.0b	58a	55.9ab	29.0b-d	1013.3a-e
G-33	62a	137ab	75.2b-d	5.4a-d	47.5ab	44a	55.9ab	32.5b-f	1730.4a-i
G-34	75c-g	140a-e	64.6a-c	8.0a-e	32.0ab	31a	53.9ab	33.5b-f	761.3a-d
G-35	66a-f	138a-e	71.6b-d	5.0ab	30.0ab	43a	56.4ab	27.5a-d	1265.8a-g
G-36	63a-c	138a-d	74.8b-d	12.0de	58.0ab	52a	62.0ab	27.0a-d	953.4a-e
G-37	71a-g	138a-e	67.1a-c	8.2a-e	30.0ab	41a	63.8ab	30.5b-f	1344.7a-g
G-38	69a-f	139a-e	70.2a-d	9.8a-e	57.0ab	47a	60.7ab	26.0ab	1301.4a-g
G-39	73a-g	142a-e	69.2a-d	9.8a-e	45.0ab	36a	55.7ab	29.0b-d	892.9a-d
G-40	64a-d	139a-e	75.3b-d	11.3b-e	52.0ab	58a	61.7ab	28.5a-d	1566.9a-i
G-41	66a-f	138a-e	72.1b-d	5.4a-c	37.5ab	39a	53.5ab	38.5ef	1336.9a-h
G-42	71a-g	140a-e	69.1a-d	6.6a-d	35.0ab	37a	63.2ab	39.0f	1144.1a-e
G-43	64a-f	139a-e	74.5b-d	8.3a-e	38.0ab	37a	54.5ab	30.5b-f	952.5a-d
G-44	76d-g	140a-e	64.1a-c	8.5a-e	31.5ab	32a	43.2a	32.5b-f	796.5a-d
G-45	83g	140a-e	56.9a	7.1a-e	29.0ab	40a	60.5ab	32.5b-f	622.3ab
G-46	69a-f	141a-e	71.8b-d	7.0a-e	32.0ab	49a	52.3ab	32.5b-f	942.4a-d
G-47	73a-g	141a-e	68.1a-c	7.5a-e	44.5ab	31a	59.2ab	31.0b-f	1246.0a-g
G-48	63a-d	139a-e	75.4b-d	8.7a-e	52.5ab	46a	65.6ab	29.0b-d	1486.8a-h
G-49	77e-g	140a-e	63.1ab	8.3a-e	42.0ab	56a	64.5ab	30.5b-f	1405.0a-h
Mean	68	139	71	8	44	46	59	30	1315
Range	62-83	137-144	57-82	4-13	26-59	28-69	43-72	20-39	569-2690
SE	2.5	1.0	2.4	1.2	5.9	7.9	4.6	1.7	218.0
LSD	6.4	2.9	6.3	3.1	16.5	22.4	12.7	4.8	532.8

MD= days to maturity, FD= days to 50% flowering, GFP= grain filling period, SBR=secondary branches, PPP= number of pods per plant, SPPL= number of seeds per plant, HGT= plant height in cm, HSW= hundred seed weight in g, GYH (kg/ha⁻¹) = grain yield in kg/ha.

3.2. Genetic Divergence Analysis

3.2.1. Cluster Analysis

The distribution of 49 kabuli chickpea genotypes classified into six clusters. Cluster-IV consisted of maximum number of genotypes and has 14 genotypes that are 28.57% of the total genotypes evaluated. The genotypes in this cluster indicate had narrow genetic diversity among them. The higher number genotypes next to these cluster was cluster-V, cluster II and cluster-III which consist of eleven, ten and nine genotypes respectively. Cluster-I and cluster VI consists of a minimum number of genotypes have accounts five genotypes (10.2%). The 155 Ethiopian chickpea collection materials which are done on the study of genetic diversity and population structure,

they are grouped in to five distinct clusters [16].

Sharifi, Astereki and Pouresmael [8] classified 25 genotypes into four clusters. [9] classified 22 chickpea genotypes into five clusters and observed the presense of high genetic distance among genotypes. [10] studied the genetic diversity of 49 kabuli chickpea genotypes and grouped into eight clusters. The largest numbers of genotypes are in cluster I and II which consists of ten genotypes. Distances between these clusters showed significantly different for all the cluster except cluster I and IV. [11] classified 60 chickpea genotypes into five clusters and the maximum inter-cluster distance was found between cluster-III and IV followed by cluster-IV and V and cluster-II and IV; indicating that genotypes included in these clusters are genetically diverse.

Table 3. Clusters of 49 kabuli chickpea genotypes.

Cluster	No of genotype	Percent (%)	Genotype code
Cluster-I	4	8.16	G-4, G-6, G-12, G-22
Cluster-II	10	20.41	G-9, G-13, G-26, G-30, G-33, G-34, G-38, G-41, G-48, G-49
Cluster-III	9	18.37	G-5, G-11, G-16, G-17, G-24, G-25, G-28, G-39, G-40
Cluster-IV	14	28.57	G-3, G-8, G-10, G-14, G-20, G-29, G-31, G-32, G-36, G-37, G-42, G-44, G-45, G-47
Cluster-V	11	22.45	G-1, G-2, G-7, G-15, G-18, G-19, G-21, G-23, G-27, G-35, G-43
Cluster-VI	1	2.04	G-46

G= genotypes.

3.2.2. Distance Analysis

The intra and inter cluster distance showed the presence of significant genotypic difference among the clusters and within clusters except with in cluster VI as tested by chi-

square distribution. The intra cluster distances ranged from 0.00 to 514 (Table 4). The maximum intra cluster distance was found in cluster-I ($D^2 = 514$) followed by cluster-IV ($D^2 = 470$), cluster-V ($D^2 = 389$) and cluster-II and cluster-III ($D^2 = 347$). The higher intra cluster distance of cluster-I ($D^2 =$

514) indicates the genotypes included in this cluster were more divergent than other clusters. The highly significant ($P < 0.01$) and maximum inter cluster distances (Table 4) were recorded between cluster-III and cluster-IV ($D^2 = 2,127$) followed by cluster-IV and cluster-V ($D^2 = 2,073$), between cluster-II and cluster-IV ($D^2 = 1,974$) and between cluster-I and cluster-III ($D^2 = 1,831$) this indicates that the presence of maximum genetic distance among genotypes between those clusters. Thus crossing and selection of genotypes from these clusters can produce efficient genotypes or offspring that lead to the development of better performing varieties than the released varieties.

The minimum inter cluster distance was found between cluster-II and cluster-VI ($D^2 = 827$) followed by cluster-III

and cluster-VI, between cluster-V and cluster-VI ($D^2 = 1,420$) and between cluster-I and cluster-VI ($D^2 = 1,453$), this indicates that these clusters are relatively divergent from each other and the genotypes belonging to them can be used for hybridization program. [10] studied the genetic diversity of 49 kabuli chickpea genotypes and distances between these clusters showed significantly different for all cluster except cluster I and IV. Maximum inter-cluster distance between cluster-III and IV followed by cluster-IV and V and cluster-II and IV [11], indicating that genotypes included in these clusters are more genetically different. Crossing genotypes that are distant clusters for wide genetic distance (D^2) could maximize transgressive segregation [12].

Table 4. Intra (bold) and inter-cluster distances (D^2) values in 49 chickpea genotypes.

Clusters	Cluster-I	Cluster-II	Cluster-III	Cluster-IV	Cluster-V	Cluster-VI
Cluster-I	514					
Cluster-II	1678**	347				
Cluster-III	1831**	1205**	347			
Cluster-IV	1781**	1974**	2127**	470		
Cluster-V	1776**	1646**	1799**	2073**	389	
Cluster-VI	1453**	827**	943**	1749**	1420**	0

** = Significant at 1% of level of significance.

Table 5. Mean values of 9 traits of six clusters of 49 kabuli chickpea genotypes.

Traits	FD	MD	GFP	SBR	PPP	SPPL	HGT (cm)	HSW (g)	GYH (kg/ha ⁻¹)
Cluster-I	66	140	74	8	47	44	57	30	1,740
Cluster-II	68	139	71	8	46	45	59	31	1,216
Cluster-III	68	139	71	8	45	50	61	31	1,294
Cluster-IV	69	140	70	9	42	45	59	31	1,295
Cluster-V	67	139	71	8	43	47	60	29	1,326
Cluster-VI	69	141	72	7	32	49	52	33	942

MD= days to maturity, FD= days to 50% flowering, GFP= grain filling period, SBR=secondary branches, PPP= number of pods per plant, SPPL= number of seeds per plant, HGT= plant height HSW= hundred seed weight, GYH (kg/ha⁻¹) = grain yield.

3.3. Mean Values of the Clusters

Cluster-I consisted of four genotypes and the mean performances were characterized by the highest cluster mean values for grain filling period, number of pods per plant, root rot and grain yield per hectare. But it also characterized by the lowest cluster mean value for number of seed per plant, number of seed per pod and days to 50% flowering. Cluster II consisted of 10 genotypes and characterized by the second lowest cluster mean value in number of seed per plant, number of secondary branches and grain filling period. Cluster-III also consisted of 9 genotypes characterized by the highest cluster mean value for number of seed per plant and plant height.

The fourth cluster (IV) was characterized by the highest cluster mean value in number of secondary branches and days to 50% flowering. Cluster V consisted of 11 genotypes and characterized by the second highest cluster mean values for number of secondary branches, plant height and grain yield per hectare. Cluster VI consisted of only one genotypes characterized by the highest cluster mean value for days to

50% flowering, days to maturity, hundred seed weight, but it also characterized by the lowest mean cluster value for number of secondary branches, plant height and grain yield per hectare.

3.4. Principal Component Analysis

The principal component analysis showed that the first three principal components have Eigenvalues greater than 1 explained about 66.1% of the total variation among forty-nine kabuli chickpea genotypes evaluated for eleven quantitative traits. The three principal components had eigenvalues 3.8047, 2.1342 and 1.3332 respectively.

The first principal component accounts 34.58% of the total variation of genotypes. Days to 50% flowering, grain filling period, number of seed per plant, number of pods per plant and grain yield had high contributions for the variation in first principal components; those imply that they contribute significantly to the discrimination among the genotypes. The second principal component accounted about 19.40% of the total variation of the genotypes. Number of secondary branch, days to maturity, days to 50% flowering, root rot and

numbers of pods per plant had high contributions for the total variation. The third principal component analysis accounted

about 12.12% of total variation by number of seed per plant, root rot, hundred seed weight and grain filling period.

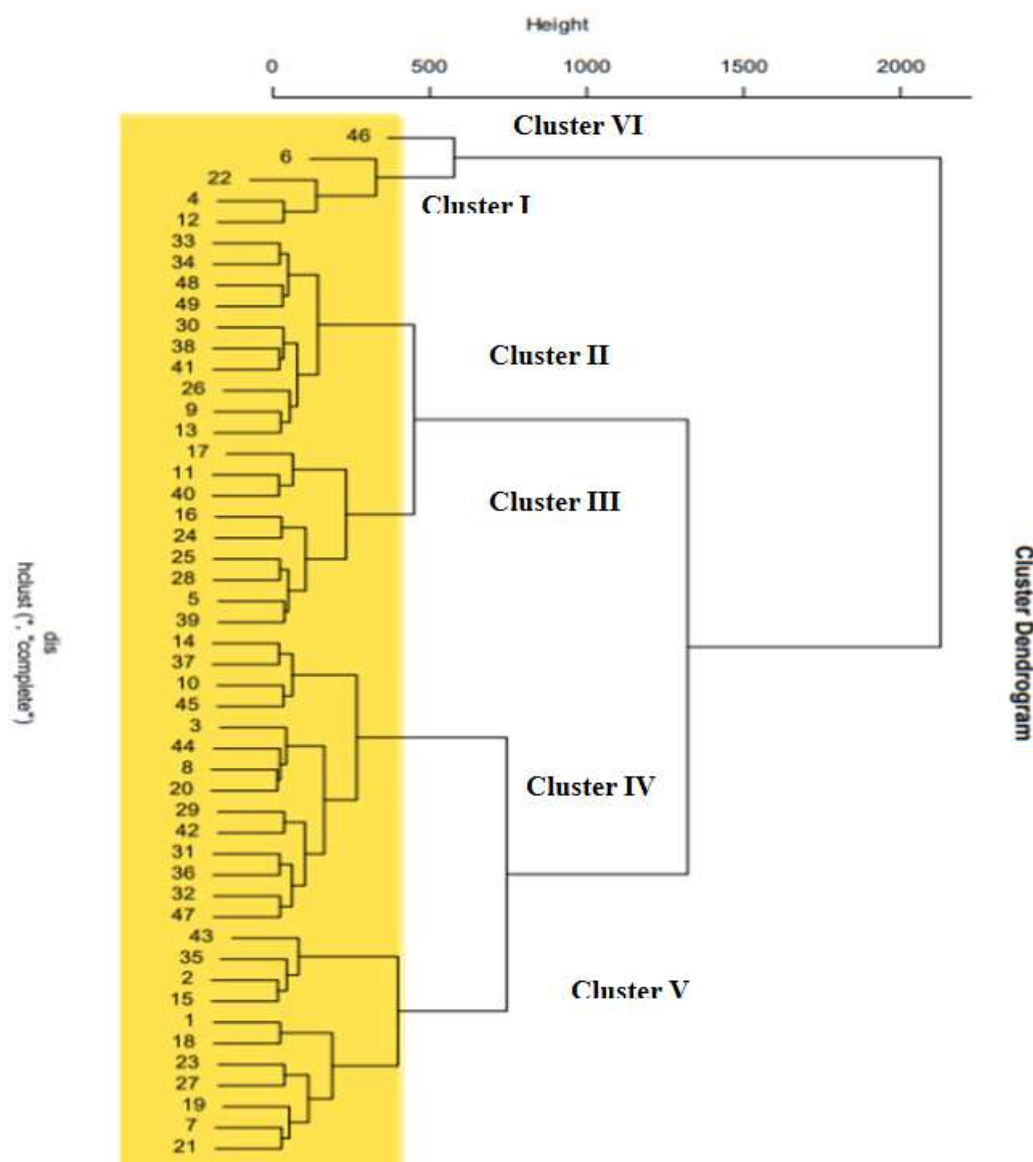


Figure 1. The dendrogram showing 49 chickpea genotypes clustering based on complete linkage.

Similar finding were reported by [8] in which 69.69% of variation were explained by the first three principal components. [10] evaluated 49 kabuli chickpea genotypes and reported that about 79.92% of the total variation were explained by the first four principal components. According to his study characters having higher contribution in the first principal components are days to 50% flowering, days to maturity, number of primary branch, number of secondary branch and number of seeds' per pod. Number of pods per plant, number of seeds per pod, number of branches per plant and 100 seed weight contributed greater variation to the total variance of the first two principal component axes [13].

Tesfamichael et al. studied 37 genotypes and reported 80.14% of the total variation explained by the first three principal components [14]. In his study about 56.96% of the variations were explained by the first principal components.

Days to 50% flowering, days to maturity, number of secondary branch, number of primary branch, number of pods per plant and hundred seed weight were contributed more for the variation. [8] studied 25 chickpea genotypes and reported that 69.69% of the total variation were explained by the first three principal components. The first two principal components explained about 93.7% of total variation and suggesting high genetic variability among the genotypes [15]. The first four principal components in the study of qualitative traits of desi and kbuli chickpea genotypes about 81.71% of the total variation in the genotypes were explained by these four components [17].

The first two principal components plot using variables revealed that days to 50% flowering, number of secondary branches, number of pods' per plant and grain yield loaded more contribution for the total variation (Figure 2).

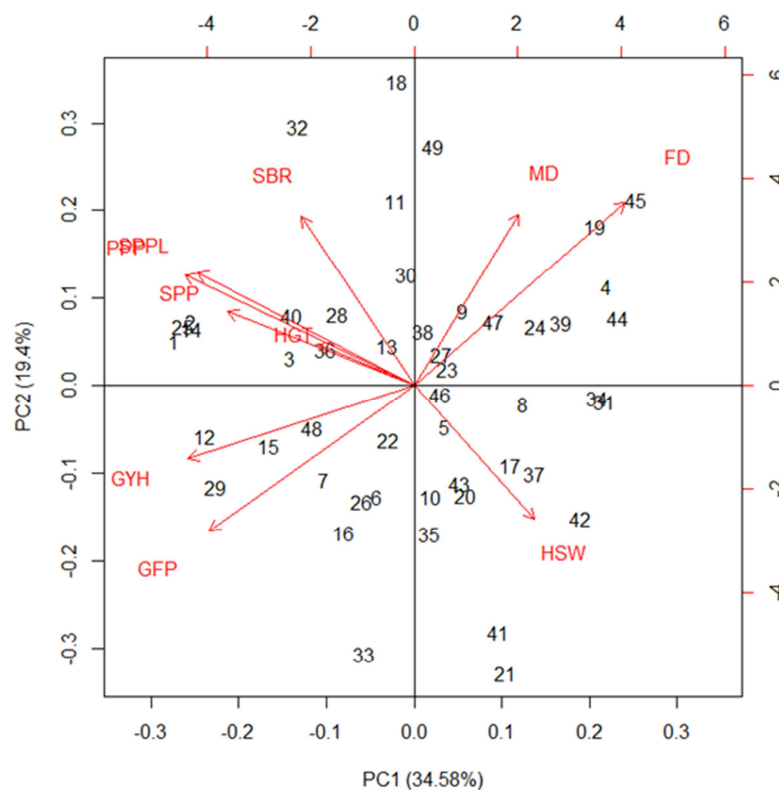


Figure 2. Plots of the first two principal components of 9 traits for 49 kabuli chickpea genotypes.

Table 6. First three principal components of 9 traits of kabuli chickpea genotypes.

Traits	Component-1	Component-2	Component-3
FD	0.424	0.335	0.296
MD	0.220	0.369	0.097
GFP	-0.408	-0.243	-0.307
SBR	-0.190	0.495	-0.251
PPP	-0.420	0.347	-0.001
SPPL	-0.359	0.225	0.339
HGT (cm)	-0.181	0.103	0.328
HSW (g)	0.204	-0.324	-0.235
GYH (kg/ha ⁻¹)	-0.433	-0.159	0.152
Eigenvalues	3.8047	2.1342	1.3332
Proportion (%)	0.3459	0.194	0.1212
Cumulative	0.3458	0.5398	0.661

MD = days to maturity, FD = days to 50% flowering, GFP= Grain filling period, SBR = Number of Secondary branches, PPP = Number of Pods per plant, SPPL = Number of seeds per plant, HGT = plant height in cm, HSW = Hundred seed weight in g, GYH (kg/ha⁻¹) = grain yield per hectare.

4. Conclusion

The kabuli chickpea genotypes grouped into six clusters. Intra and inter cluster distance showed the presence of highly significant genetic diversity among genotypes with the cluster. The maximum intra cluster distance was found in cluster-I ($D^2 = 514$) followed by cluster-IV ($D^2 = 470$) and cluster-V ($D^2 = 389$). The maximum inter cluster distance was recorded between cluster-III and cluster-IV ($D^2 = 2,127$) followed by cluster-IV and cluster-V ($D^2 = 2,073$). The principal component analysis showed about 66.1% of the

total variation was explained by the first three principal components. The first principal components accounted about 34.58% of the total variation and mainly contributed by days to 50% flowering, grain filling period, grain yield, number of pods per plant and seed per plant. The second principal component analysis accounted about 19.4% of the total variation, mainly contribution from number of secondary branch, days to maturity, days to 50% flowering and numbers of pods per plant.

The breeders can select the crossing materials from divergent or distant clusters. Distant inter clusters, cluster-IV and cluster-III, cluster-IV and cluster-V, and cluster-II and cluster-IV will be used as parent materials for crossing. In order to develop higher yielder varieties, available genetic resources should be exploited in the breeding program. In this study the amounts of genetic variability were determined among grain yield and yield related traits. However, it requires multi location and year trials to verify the consistency of existing genotypic variability.

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