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Research Article

Genetic Variability of Chickpea (*Cicer arietinum* L.) Genotypes under Irrigation of Middle Awash, Ethiopia

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ABSTRACT

Chickpea is grown from moderate to sub-tropical regions of the world and is the third most important pulse crops full-grown on about 13.5 million hectares of land in the World and Ethiopia stands first among chickpea producers in Africa and Seventh in the world and contributed about 4.5% to the world production. Chickpea is being valued for its high dietary protein content, its ability to fix atmospheric nitrogen and absence of specific major anti-nutritional factors. In Ethiopia, chickpea improvement program has focused mainly on selection of genotypes for rain fed areas. However, there is no adequate information on variability and heritability of grain yield for the new chickpea accessions under irrigated agriculture of the middle awash rift valley: The present investigation was conducted to estimate the extent of genetic variability among 65 chickpea genotypes including one local check which was evaluated during off-season 2017/18 under 6 x11 alpha lattice design having three replications. Genetic parameters including phenotypic and genotypic coefficients of variations, broad sense heritability and genetic advance as percent of mean were estimated, and cluster analysis was performed. Phenotypic coefficients (PVC) were found to be higher than genotypic coefficients of variation (GCV) for all traits. This high PCV reflect environmental influence. High heritability values along with high genetic advance as percent mean were observed for days of 50% flowering, number of pods per plant, number of secondary branches per plant, 100-seed weight and harvest index. This indicating that traits are controlled mainly by additive genes and that selection of such traits may be effective for improving seed yield. The 66 chickpea genotypes were grouped under four major clusters. These four major clusters consist more than one up to 32 accessions. It is multivariate techniques that can conveniently show the pattern of genetic relationships. Such that each group is homogeneous with respect to certain characteristics and each group should be different from other groups with respect to the same characteristics. Finally, this investigation should be repeated over years and locations to confirm future breeding program.

Key words: Cicer arietinum, Genetic Variability, Heritability, Genetic advance, clustering

INTRODUCTION

Chickpea is the third most important pulse crop and is full-grown on about 13.5 million hectares of land in the World (FAO, 2015). Ethiopia stands first among chickpea producers in Africa and seventh in the world. It accounts for 60% of Africa's total Chickpea production and contributes to about 4.5% to the total world production (FAOSTAT, 2014). Annual area coverage Chickpea production in Ethiopia is about 242,703.73 hectares and with the national average productivity of 20.58 Qt/ha (CSA, 2017).

Chickpea is being valued for its high dietary protein content, its ability to fix atmospheric nitrogen and the absence of specific major anti-nutritional factors. This makes it an important component of the cropping system and considered as nutritious and healthy food (Mohammed *et al*., 2011). The seeds of chickpea contain protein of 16.7% to 30.6% for desi type and 12.6% to 29.0% for kabuli type, commonly 2–3 times higher than that of cereal grains; carbohydrate of 51– 65% in desi type and 54 -71% in kabuli type (Wood and Grusak, 2007); lipid of 2.9% to 7.4% for desi and 3.4% to 8.8% for kabuli types, and high percentage of different minerals nutrients such as calcium, magnesium, potassium, phosphorus, iron, zinc and manganese (Ibrikci *et al*., 2003).

The cropping system of north east Ethiopia is predominantly mono crop type with cotton being the principal main season crops. After the harvest of cotton the

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fields are left fallow till the next main season. Of-season offers a greater opportunity for growing chickpea due to following reasons: (1) availability of cultivable land, (2) availability of irrigation water during spring season, (3) the ability of chickpea to withstand temperature. To explore the suitability of chickpea in this region it is necessary to estimate the genetic variability of different plant characters of economic importance and their heritability. Genetic variability is critical to the success of crop improvement. The existence of adequate genetic variability among the genotypes determines probability of improving crop under consideration to enhance food production. Success in breeding program mainly depends on availability of adequate information on the nature and magnitude of variation existing in breeding materials and interrelationships between quantitatively inherited plant traits is of great importance (Kotal *et al.*, 2010). For this, a measure of genetic variability in the available genotypes is important.

Crop improvement depends on the availability of genes for better agronomic traits, such as disease resistance, earliness and high yield. For these, evaluation of genetic variability of population is required since genetic variation within and among populations and between species determines the rate of response and adaptive evolution of crop species (Winter, 1997; Gupta and Varshney, 2000). Morphological markers are classical methods to distinguish variations based on the observation of the external morphological differences (Vienne *et al*., 2003).

Chickpea improvement program has focused mainly on selection of genotypes for rained fed area. However, there is no adequate information on variability and heritability of grain yield and its related components for the new chickpea accessions under irrigated agriculture of the middle awash rift valley, which can represent vast agricultural landmass. Hence, there is a need to investigate genetic variability, heritability and expected genetic advance among chickpea genotypes which could be exploited in crop improvement programs. Hence, this research was proposed with the objectives: To study the extent of genetic variability of chickpea genotypes under irrigation condition and to estimate genotypic and phenotypic coefficient of variation, heritability and expected genetic advance.

Crops' genetic variability not only helps varieties to adopt to diverse environments, to enhance the tolerance of unfavorable conditions and resistance to pest and diseases, but also to produce the diversity and to get better yield and quality of product to serve needs of the people (Lijalem *et al*., 2016). Genetic variability is prerequisites for crop improvement as it provides raw material to plant breeders to recombine the genes of different characters in same plants for development of desirable variety (Alemu *et al.*, 2017). Genotypic and Phonotypic variances make available the information of variability (Shengu, *et al., 2018*). Phenotypic variation, is the observable variation present in a character in a population, includes both genotypic and environmental components of variation and, as a result, its magnitude differs under different environmental conditions (Singh, 1993; Falconer and Mackay, 1996). Genetic variability expresses the presence of variation in their genetic constitution and it is out most important to provide the basis of effective selection (Kumar *et al*., 2013). For this reason, alertness of these principles of the resources in which breeders are reimbursing thoughtfulness is huge importance.

MATERIALS AND METHODS

Description of Experimental Site: The experiment was conducted at Werer Agricultural Research Center which is one of the Agricultural Research Centers of Ethiopian Institute of Agricultural Research during the cool season (November, 2017 to February, 2018 G.C). It is located in Afar National Regional State of the Federal Government of Ethiopia 280 km East of Addis Ababa with an altitude of 740 m.a.s.l. and at latitudes of 9° 60'N and 40° 09' E longitude. The dominant soil type of the study areas is Chromic Vertisol (clay to silt clay) with particle size distribution of Sand 3.83%, Silt 61.1% and clay 35.07 % with a bulk density of 1.17% (Wendemagegn and Abere, 2012). The pH of the soil is slightly alkaline and ranges from 7.5 to 8.5. The average annual rainfall 540 mm and the annual temperature range 190C -34^{0}C.

Treatments and Experimental Design: About 66 (65 accessions and one standard check) were obtained from Debre Zeit Agricultural research center. The Experiment was laid out in Alpha Lattice Design consisting of six incomplete blocks with three replications. Each block was planted with 11 entries. Each experimental plot was 4m x 0.60m (2rows per plot). Inter and intra row spacing of 30cm x 10 cm were used. Each plot was planted with two seeds per hill and thinned to one plant per hill 15 days after emergence. Agronomic practices such as irrigation, insecticides and weeding were applied to the crop during experiment.

Traits Evaluated: The data for the following traits were recorded from five randomly selected plants from each experimental plot, and average value was considered: Days to 50% flowering, Days to physiological maturity, Number of pods per plant, Number of Seeds per plant, Number of branches per plant: Number of primary branches, Number secondary branches**,** Hundred seed weight, Plant height, Biomass, Harvest index and Grain yield per plot.

Statistical Analysis

Analysis of Variances: All collected data were subjected to analysis of variance using appropriate computer using SAS software (SAS, 2004). Duncan's Multiple Range Test (DMRT) at probability of 0.05 was used to separate the means and ranges for significant parameters.

Estimation of Variance Components: The variability was estimated using range; SE, mean, genotypic and phenotypic variance and coefficient of variation and the resulting components of variances were used to compute the genotypic and phenotypic variation and genetic advance as:

The genotypic and phenotypic coefficients of variation were estimated using the formula as adopted from Burton (1953).

$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{Y}} * 100$, where σ^2 g = genotypic variance, $\bar{Y}$ = mean for the character Y, GCV = Genotypic coefficient of variation.

PVC = $\frac{\sqrt{\sigma^2 p}}{\bar{Y}} *$ 100, where σ^2p = phenotypic standard deviation, $\bar{Y}$ = grand mean for the character Y, PCV = phenotypic coefficient of variation.

The Phenotypic and genotypic variances were estimated using the formula adopted by Johnson *et al*. (1955).

Environmental variance (σ^2e) = EMS, Genotypic variances (σ^2 g) =$\frac{GMS-EMS}{r}$ and Phenotypic variance (σ^2P) = σ^2 g+ σ^2e Whereas, GMS = Genotypic mean square, EMS = Error mean square, r = number of replications

Heritability in broad sense was estimated for various characters as suggested by Hanson *et al*. (1956).

$H^2 = \frac{\sigma^2 g}{\sigma^2 P} * 100$ Where, σ^2 g = genotypic variance, σ^2p = phenotypic variance.

The high, medium and low heritability estimates was classified on the basis of values given by Robinson (1966).

High: more than 30%, Moderate: 10 to 30%, Low: less than 10 %

Expected Genetic advance (at 5% selection intensity) was calculated using the formula given by Allard (1960).

GA= σP* H^2 * K

Whereas, k = standard selection differential (at 5% selection intensity, the value of k = 2.063)

σP = phenotypic standard deviation of the character in the population

H^2 = heritability

Genetic Advance as percentage of means GAM was used: - High: more than 20%, Moderate: 10 to 20 % and Low: less than 10 %.

RESULTS AND DISCUSSION

Phenotypic and Genotypic Coefficient: Achievement of plant breeders in elite genotypes that produces higher yield and quality characters depends on existence and utilization of genetic variability to the fullest extent. Estimation of phenotypic coefficient of variation showed that environment does have significant effect on the studied traits. Phenotypic coefficient of variation was greater than genotypic coefficient of variation for all traits (Table 2). The results were similar with the findings of (Aybegün and Anlarsal, 2017) who reported that the phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation in all the traits. The lower phenotypic and genotypic coefficient of variation results were recorded for days to maturity (6.32%) and plant height (9.97%) (Table 2). The extent of the environmental that influence on any trait has been determined by the magnitude of the differences between the genotypic and phenotypic coefficients of variation (Shengu, *et al., 2018*). Large differences of PCV reflect high environmental influence, while small differences reveal high genetic influence.

Heritability in Broad Sense: The genotypic and phenotypic coefficients of variances make information available for the variability but only the transmissible portion of this variability was determined by the estimates of heritability.

Traits with higher heritability estimates were recoded for hundred seed weight (87.74%), number of secondary branches per plant (75.74% and days of flowering (69.98%), days to plant height (68.94%), seeds per pod, (50.00%), days to maturity (38.46%), pods per plant (38,39%), harvest index (35.83%) and yield per ha (Table 2). This result was similar with (Zali *et al*., 2011) who reported high heritability values for number of days to 50% maturity (98.43%), number of days to 50% flowering (98.19%), plant height (58.87%), number of secondary branches (45.81%), number of primary branches (42.03%) and number of seeds per plant (35.42%), except for biomass and primary branches per plant. If heritability of character is high; it is fairly easy for selection. Because there would be a close correspondence between the genotypic and phenotypic variations due to relatively small contribution of the environment to the phenotypic expression of the traits (Singh *et.al*., 1990). Heritability indicates the effectiveness of selection of genotypes based on phenotypic performance. The high heritability may have been exhibited due to less influence of environmental conditions rather higher roles of genotypic component. Moreover, higher values of broad sense heritability may imply possibility and ease of using phenotype-based selection particularly when it is accompanied by relatively higher genotypic coefficient of variation and Phenotypic coefficient of variation.

Genetic Advance as Percentage of Mean (GAM): Genetic advance as percentage of mean (GAM) at 5% selections is presented (Table 2). In this study, genetic advance as percent of means ranged from 5.02% days to 90% maturity to 60.56% for number of secondary branches per plant. High genetic advances were observed for days to 50% flowering (23.32%), number of pod per plant (30.22%), and number of seeds per pod (26.27%), number of secondary branches (60.56%), hundred seed weight (27.43%) and harvest index (22.38%). This result was similar with Zali *et al*. (2011) who reported high genetic advance (5% selection intensity) for number of secondary branches, and number of seeds per plant. Paneliya *et al*. (2017) also reported similar high expected genetic advance as percent of mean for number of branches per plant, biological yield per plant, 100-seed weight. This indicated that these traits are controlled more of by additive gene.

High heritability values with high genetic advance results were observed for days to 50% flowering, total number pods per plant, number of secondary branches, 100-seed weight and harvest index (Table 2). The result is supported by Paneliya *et al*. (2017) who reported high heritability accompanied with high expected genetic advance as percent of mean for number of branches per plant, 100-seed weight and seed yield per plant. Similar result was reported by (Muhammad *et al*., 2008; Saki *et al.*, 2009; Kumar *et al*., 2012) and (Neelu *et al*., 2013) high heritability along with high genetic advance was also noted for 100-seed weight. Johnson *et al*. (1955) also suggested that heritability estimates along with genetic advance were more useful in predicting the effect of selecting the best individual. High heritability values for different traits coupled with high genetic advance revealed that additive gene action was important for these characters in respective selection schemes. The simultaneous GCV and PCV values for each trait showed that number of days to maturity, seeds per pod, plant height were least affected by environment having high heritability but had low genetic advance. Similar finding were with Sewak *et al*. (2012) who reported that high heritability for seeds per pod but had low genetic advance.

Table 1: Lists of 66 chickpea genotypes used in the study.

SerN0.	Name Genotypes	Status	Source	Types	Ser N0.	Name Genotypes	Status	Source	Types
1	FLIP-09-371C	Not released	ICARDA	Kabuli	34	FLIP-08-38C	Not released	ICARDA	Kabuli
2	FLIP-08-42C	Not released	ICARDA	Kabuli	35	ICCV-11106	Not released	ICARDA	Kabuli
3	FLIP-09-376C	Not released	ICARDA	Kabuli	36	FLIP-88-85C	Not released	ICARDA	Kabuli
4	FLIP-09-50C	Not released	ICARDA	Kabuli	37	FLIP-07-4C	Not released	ICARDA	Kabuli
5	FLIP-93-93C	Not released	ICARDA	Kabuli	38	FLIP-09-114C	Not released	ICARDA	Kabuli
6	FLIP-09-161C	Not released	ICARDA	Kabuli	39	FLIP-08-53C	Not released	ICARDA	Kabuli
7	ICCV-11102	Not released	ICARDA	Desi	40	FLIP-05-157C	Not released	ICARDA	Kabuli
8	FLIP-03-128C	Not released	ICARDA	Kabuli	41	FLIP-09-189C	Not released	ICARDA	Kabuli
9	FLIP-09-277C	Not released	ICARDA	Kabuli	42	FLIP-09-348C	Not released	ICARDA	Kabuli
10	FLIP-03-155C	Not released	ICARDA	Kabuli	43	FLIP-05-19C	Not released	ICARDA	Kabuli
11	FLIP-09-134C	Not released	ICARDA	Kabuli	44	FLIP-09-185C	Not released	ICARDA	Kabuli
12	FLIP-09-188C	Not released	ICARDA	Kabuli	45	FLIP-09-157C	Not released	ICARDA	Kabuli
13	FLIP-03-101C	Not released	ICARDA	Kabuli	46	FLIP-09-354C	Not released	ICARDA	Kabuli
14	FLIP-07-26C	Not released	ICARDA	Kabuli	47	FLIP-09-360C	Not released	ICARDA	Kabuli
15	FLIP-09-184C	Not released	ICARDA	Kabuli	48	FLIP-09-379C	Not released	ICARDA	Kabuli
16	FLIP-09-179C	Not released	ICARDA	Kabuli	49	FLIP-08-41C	Not released	ICARDA	Kabuli
17	FLIP-09-187C	Not released	ICARDA	Kabuli	50	FLIP-09- 240C	Not released	ICARDA	Kabuli
18	FLIP-09-146C	Not released	ICARDA	Kabuli	51	FLIP-03-125	Not released	ICARDA	Kabuli
19	FLIP-09-359C	Not released	ICARDA	Kabuli	52	FLIP-09-6C	Not released	ICARDA	Kabuli
20	FLIP-09-171C	Not released	ICARDA	Kabuli	53	FLIP-09-343C	Not released	ICARDA	Kabuli
21	FLIP-09-174C	Not released	ICARDA	Kabuli	54	FLIP-09-233C	Not released	ICARDA	Kabuli
22	FLIP-09-126C	Not released	ICARDA	Kabuli	55	FLIP-09-380C	Not released	ICARDA	Kabuli
23	FLIP-09-438C	Not released	ICARDA	Kabuli	56	FLIP-09-140C	Not released	ICARDA	Kabuli
24	FLIP-09-244C	Not released	ICARDA	Kabuli	57	FLIP-09-393C	Not released	ICARDA	Kabuli
25	FLIP-09-347C	Not released	ICARDA	Kabuli	58	FLIP-09-357C	Not released	ICARDA	Kabuli
26	FLIP-03-40C	Not released	ICARDA	Kabuli	59	FLIP-09-120C	Not released	ICARDA	Kabuli
27	FLIP-09-339C	Not released	ICARDA	Kabuli	60	ICC-4958/EJERE-P6-19	Not released	ICC-4958XEJEREP6-19 CROSSING	Desi
28	FLIP-09-162C	Not released	ICARDA	Kabuli	61	ICCX-060045-F3-P203-BP	Not released	ICCX060045-F3-P203-BP TLL	Desi
29	FLIP-09-241C	Not released	ICARDA	Kabuli	62	ICCV-11115	Not released	ICCV-11115	Desi
30	FLIP-09-18IC	Not released	ICARDA	Kabuli	63	ICC-4958/EJERE-P2-20	Not released	ICC-4958XEJEREP2-20 CROSSING	Desi
SerN0.	Name Genotypes	Status	Source	Types	Ser N0.	Name Genotypes	Status	Source	Types
31	FLIP-09-261C	Not released	ICARDA	Kabuli	64	ICCX-060039-F3-P65-BP	Not released	ICCX-060039-F3-P65-BP TLL	Desi
32	FLIP-08-98C	Not released	ICARDA	Kabuli	65	ICCV-09108	Not released	ICCV-09108 ICRSAT	Desi
33	FLIP-09-309	Not released	ICARDA	Kabuli	66	Habru variety (Check)	released	DZARC	Kabuli

Table 2: Estimations of variability parameters for some quantitative characters of chickpea genotypes under irrigation.

Traits	Range	Mean	Error	CV	σ2g	σ2e	σ2p	GCV	PCV	H^2	GA	GAM
DFF	33-63.3	53.5	0.29	8.9	52.31	22.45	74.75	13.51	16.15	69.98	12.48	23.32
DM	83.7-110	101.4	25.31	5	15.82	25.31	41.13	3.92	6.32	38.46	5.09	5.02
PPP	39-125.2	62.8	353.78	30	220.47	353.78	574.25	23.64	38.15	38.39	18.98	30.22
SPFP	1-1.39	1.13	0.02	11.41	0.01	0.02	0.02	8.32	14.12	50	0.15	13.02
PHT	46.6-73	59.8	11.04	5.6	24.5	11.04	35.54	8.28	9.97	68.94	8.48	14.18
SPP	34.5-171.1	59.1	680.31	44.1	226.71	680.31	907.02	25.47	50.94	25	15.53	26.27
PB	5.1-11.4	7.6	2.49	20.9	0.47	2.49	2.96	9.07	22.8	15.88	0.56	7.46
SB	5.6-26.5	12.4	5.63	19.1	17.58	5.62	23.21	33.72	38.74	75.74	7.53	60.56
BM	3.2-10.7	6.9	0.23	29.1	0.87	4	4.87	13.55	32.13	17.86	0.81	11.86
HSW	34.7-47.4	33.6	3.18	5.3	22.68	3.18	25.85	14.19	15.16	87.74	9.2	27.43
HI	21.3-54.5	35.9	0.29	24.3	42.31	75.77	118.08	18.12	30.28	35.83	8.03	22.38
YLD	1.2-3.3	2.3	0.01	3.7	0.11	0.29	0.4	14.5	27.77	27.5	0.36	15.74

Keys: σ^2g = Genotypic variance, σ^2e = Error variance, σ^2p = Phenotypic variance, GCV = Genotypic coefficient of variance, PCV = phenotypic coefficient variance, H^2 = heritability in broad sense, GA = genetic advance, GAM = genetic advance mean present, DF = degree of freedom, DFF = days of flowering, DM = days of maturity, PPP = number of pod per plant, SPFP = number of seed per pod, PHT = plant height, SPP = number of seed per plant, PB = primary branch, SB = Secondary Branch, BM = biomass(ton per ha), HSW = hundred seed weight, and YLD (ton per ha) = yield ton per hectare, HI = harvest index.

Cluster Analysis: The distance matrix from 12 agronomic traits was used to construct dendrograms based on the Unweight pair-group method with Arithmetic means (UPGMA). The cluster analysis result is presented in the form of dendrogram in (Figure 1). The 66 chickpea genotypes were grouped under four major clusters. Three genotypes were solitary that each cluster consists of one accession. The four major clusters consist more than one up to 32 accessions. Those Clusters I, III and IV were containing large number of genotypes 11, 15, and 32, respectively. While cluster II contains two accessions. Although Clusters III and IV have two sub-clusters with each other's as shown in the Figure1.

The clustering grouped accessions in specific dendrogram without overlapping indicating clustering was efficient. Number of accessions and accessions included in each cluster where presented (Table 3). Clustering is multivariate techniques that can conveniently show the pattern of genetic relationships or proximity among accessions (Afifi and Clark, 1990) such that each group is homogeneous with respect to certain characteristics and each group should be different from other groups with respect to the same characteristics (Anderson, 1989).

Conclusion: The results clearly showed that the presence of considerable variations among genotypes for the traits measured. This indicated possibility of making further study on these genotypes exploit the existing variability in chickpea improvement program. The ranges of the mean values for the most of traits were large showing the existence of variation among the tested genotypes. Phenotypic coefficients (PVC) were found to be higher than genotypic coefficients of variation (GCV) for all the traits. The two values deferred somewhat indicating less influence of the environmental factors. High heritability values were obtained for yield per ha, hundred seed weight,

Table 3: Clusters, accession code and number of accessions in the clusters.

Clusters	Number of Accessions	Accession code
	Solitary	ICC-4958/EJERE-P2-20
	Solitary	FLIP-09-380C
I	11	FLIP-03-128C
		FLIP-09-188C
		FLIP-09-438C
		FLIP-07-4C
		FLIP-09-114C
		FLIP-08-41C
		FLIP-09-6C
		ICCX-060045-F3-P203-BP
		ICCV-11115
		ICCX-060039-F3-P65-BP
		ICCV-09108
	Solitary	Habru (Check)
II	2	FLIP-09-179C
		FLIP-09-348C
III	15	FLIP-93-93C
		FLIP-09-134C
		FLIP-03-101C
Clusters	Number of Accessions	Accession code
		FLIP-09-162C
		FLIP-09-18IC
		FLIP-07-4C
		FLIP-08-53C
		FLIP-09-360C
		FLIP 03 125C
		FLIP-09-343C
		FLIP-08-42C
		FLIP-07-4C
		FLIP-09-187C
		FLIP-08-38C
IV	32	FLIP-09-50C
		FLIP-09-161C
		FLIP-03-155C
		FLIP-07-26C
		FLIP-09-184C
		FLIP-09-146C
		FLIP-09-359C
		FLIP-09-174C
		FLIP-09-126C
		FLIP-09-244C
		FLIP-09-261C
		ICCV-11106
		FLIP-88-85C
		FLIP-09-189C
		FLIP-09-348C
		FLIP-09-157C
		FLIP-09-379C
		FLIP-09-357C
		ICC-4958/EJERE-P6-19
		FLIP-09-371C
		FLIP-09-376C
		FLIP-03-40C
		FLIP-09-339C
		FLIP-09-241C
		FLIP-08-98C.
		FLIP-09-309
		FLIP-09-348C
		FLIP-05-19C
		FLIP-09-185C
		FLIP-09-354C
		FLIP-09-140C
		FLIP-09-393C

Grouping of 66 chickpea genotypes under irrigation from 12 phenotypic traits at Werer condition.

number of secondary branches per plant and days of flowering, days to plant height, seeds per pod, days to maturity, pods per plant and harvest index. This High heritability signify the effectiveness of these traits through selection for the crop improvement, as less environmental effects and that will be utilized in future breeding program. High heritability values with high genetic advance results

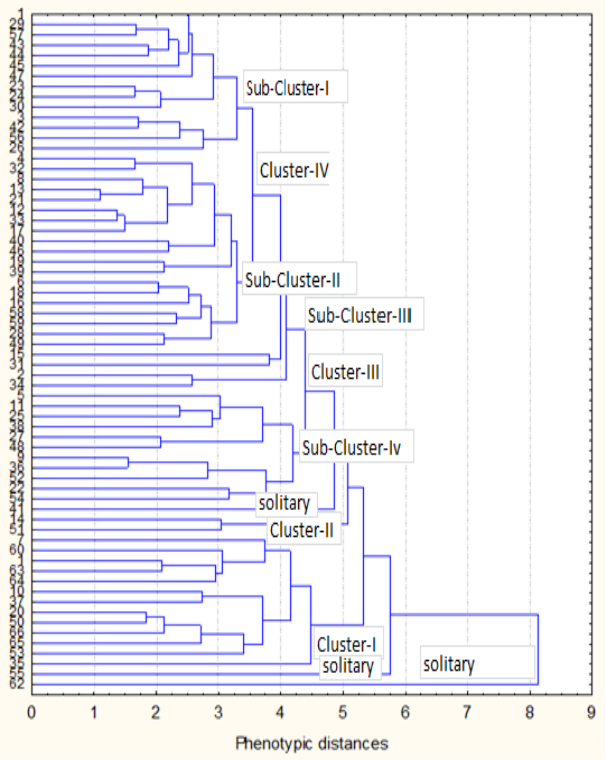

Fig. 1: Dendirogram with Average Linkage and Euclidean Distance of genotypes with 12 agronomic characters at Werer : **Keys:**1 = FLIP-09-371C, 2 = FLIP-08-42C, 3 = FLIP-09-376C, V4 = FLIP-09-50C, 5 = FLIP-93-93C, 6 = FLIP-09-161C, 7 = ICCV-11102, 8 = FLIP-03-128C, 9 = FLIP-09-277C, 10 = FLIP-03-155C, 11= FLIP-09-134C, 12 = FLIP-09-188C, 13 = FLIP-03-101C, 14 = FLIP-07-26C, 15 = FLIP-09-184C, 16 = FLIP-09-179C, 17 = FLIP-09-187C, 18 = FLIP-09-146C, 19 = FLIP-09-359C, 20 = FLIP-09-171C, 21 = FLIP-09-174C, 22 = FLIP-09-126C, 23 = FLIP-09-438C, 24 = FLIP-09-244C, 25 = FLIP-09-347C, 26 = FLIP-03-40C, 27 = FLIP-09-339C, 28 = FLIP-09-162C, 29 = FLIP-09-241C, 30 = FLIP-09-18IC, 31 = FLIP-09-261C, 32 = FLIP-08-98C, 33 = FUB-09-309, 34 = FLIP-08-38C, 35=ICCV-11106, 36 = FLIP-88-85C, 37 = FUB-07-4C, 38 = FLIP-09-114C, 39 = FLIP-08-53C, 40 = FLIP-05-157C, 41= FLIP-09-189C, 42 = FLIP-09-348C, 43 = FLIP-05-19C, 44 = FLIP-09-185C, 45 = FLIP-09-157C, 46 = FLIP-09-354C, 47 = FLIP-09-360C, 48 = FLIP-09-379C, 49 = FLIP-08-41C, 50 = FLIP-09- 240C, 51 = FLIP-03-125, 52 = FLIP-09-6C, 53 = FLIP-09-343C, 54 = FLIP-09-233C, 55 = FLIP-09-380C, 56 = FLIP-09-140C, 57 = FLIP-09-393C, 58 = FLIP-09-357C, 59 = FLIP-09-120C, 60 = ICC-4958/EJERE-P6-19, 61 = ICCX-060045-F3-P203-BP, 62 = ICCV-11115, 63 = ICC-4958/EJERE-P2-20, 64 = ICCX-060039-F3-P65-BP, 65 = ICCV-09108, 66 = Habru (Check).

were observed for days to 50% flowering, total number pods per plant, number of secondary branches, 100-seed weight and harvest index. High heritability along with genetic advance indicates more useful in predicting the effect of selecting the best individual. The 66 chickpea genotypes were grouped under four major clusters. These four major clusters consist more than one up to 32 accessions. The study has to be repeated over years and location to confirm the future breeding programs.

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