

Genotypic and Phenotypic Variability for Yield and its Components in Normal and Late Sown Chickpea (*Cicer arietinum* L.)

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ABSTRACT

Chickpea (*Cicer arietinum* L.) is one of the important legumes widely grown for dietary proteins in semi-arid Mediterranean climatic conditions. The main goal of any breeding programs in the world is to produce high yield and better quality genotypes for farmers and commercial growers to be released as cultivars. Present research has been conducted to select more desirable characteristics that may contribute to the improvement of drought tolerant chickpea. Thirty-two chickpea genotypes along with two control varieties were evaluated in winter and late sowing conditions in 2015 and 2016, in randomized complete block design with three replications. Phenotypic coefficients of variation were found to be higher than genotypic coefficients of variation for all the traits. The highest heritability along with high genetic advance was found for hundred seed weight followed by podding day, plant height, flowering day and first pod height in normal and stress conditions. These traits can be improved by giving special attention during selection.

Key words: Cicer arietinum, Genotypic variability, Heritability, Seed yield.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is an important, semiarid food legume crop. While in the developed world it represents a valuable crop for export, in the developing world it provides a protein-rich supplement to cereal-based diets. The principal uses of chickpea are as good source of protein (20 to 30%) as compared with cereals (8 to 10%), about 40% carbohydrates and 3 to 6% oil (Jukanti *et al.*, 2012). It is also a good source of calcium, magnesium, potassium, phosphorous, iron, zinc and manganese (Ibrikci *et al.*, 2003). In Turkey, the area under chickpea is 52 thousand hectares with the productivity of 1220 kg ha⁻¹ and production of 630 thousand tones (TUIK, 2018).

The total yield production is quite low in most chickpea growing countries and a wide gap exists between the potential (5 ton ha⁻¹) and actual (0.96 ton ha⁻¹) yields (FAOSTAT, 2013). This is due to biotic (wilt, root rot, blight diseases and weeds infestation) and abiotic (drought, high and low temperature) stresses. Drought is one of the most important abiotic stresses, which limits crop production. Chickpea is generally grown without irrigation, planted in marginal regions, and due to lack of rainfall during flowering, podding and seed filling time, terminal drought stress is the major environmental stress, which reducing chickpea production (Yucel, 2018).

Estimates of yield losses due to drought range from 15 to 60% depending on geographical region, duration of the crop season and dry spell (Sabaghpour *et al.*, 2006).

In the last decade, the main breeding strategy used to cope with terminal drought in chickpea was selecting for drought escape by reducing crop duration and securing seed yield before soil water was depleted. Knowledge of the University of Sirnak, Faculty of Agriculture, Field Crops Department, Sirnak-Turkey.

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relative magnitude of various genetic parameters for seed yield and yield components is essential for an efficient breeding program. Genetic variation among traits is important for breeding and selecting desirable types. Direct selection only for higher yield could be misleading because many factors interact to determine crop yield. Separate yield components are less influenced by the environment than yield itself; hence, selection for such yield components can be useful to acquire genotypes with better yield abilities. Consequently, several researchers emphasized the usefulness of estimates of genetic components inpredicting the response of quantitative characters to selection of different traits to gain yield (Mohammed et al., 2019; Alemu et al., 2017). Heritability estimates are used to determine the amount of variation present in the population. Heritability combined with genetic advance will bring out the genetic gain expected from selection.

Therefore, the present study was carried out to estimate genetic variability, heritability and genetic advance for yield

and yield components in chickpea genotypes under normal and drought stress conditions.

MATERIALS AND METHODS

Experimental site

The present research was carried out at the Eastern Mediterranean Agricultural Research Institute, Adana, TURKEY. The site of experiment is located at 35° 18'E longitude, 37° 01' N latitude and 23 m above the sea level. Air temperature, relative humidity and distribution of rainfall from December to July during the years of 2014-2016 are shown in Table 1. The soil is silty-clay; total content of salts was 0.026%, organic matter content 2.0%, pH level 7.72 and P level 87.0 kg and rich in term of lime.

Experimental materials and design

The experimental material consisted of 32 genotypes along with FLIP 87-59 C (Kanouni et al., 2012) as drought tolerant as well as ILC 8617 (Cancı and Toker, 2009) as drought susceptible. Thirty-four chickpea (Cicer arietinum L.) genotypes with their names, types and registration institution or origins were given in Table 2. The experiment was set up during the winter and late sowing conditions in 2015 and 2016, in randomized complete block design (RCBD) with three replications. Each plot was accommodated in two rows of 4 meters' length, spaced 45 cm between row to row with approximate plant to plant distance of 10 cm. Sowing was performed in December 01, 2014 and December 21, 2015 for winter; March 4, 2015 and February 28, 2016 for late sowing. Drought stress condition was created by delaying sowing time. So, winter sowing was evaluated as normal condition, while late sowing was evaluated as drought stress condition. Fertilizer was applied at a rate of 30 kg nitrogen and 60 kg phosphorus per ha before sowing.

Traits evaluated

Observation was recorded for all traits under normal and drought stress conditions. The data for emergence day, vegetative period, flowering day, podding day, vegetation time and maturity day were recorded in each replication and each genotype was represented by single value. For other morphometric traits *viz.*, plant height and first pod height from five randomly selected plants were taken from each genotype in each replication to record the data. After harvest, hundred seed weight was calculated by weighting of counted 100 seeds in four replications. Seed yields were calculated after harvesting collectively the 3.6 m² area and the data were transformed to kg har¹

Statistical analysis

The data were analyzed for simple statistics, i.e. mean, min., max., standard deviation using the computer software program of SPSS. (Anonymous, 1983).

The mean values of the recorded data were subjected to analysis of variance. The mean squares were used to estimate genotypic and phenotypic variance. The variability present in genotypes were calculated as suggested by Burton (1952) as follows:

$$\sigma_{GY}^2 = (GY MS-EMS)/r$$
 (1)

$$\sigma G^2 = (GMS-EMS)/yr$$
 (2)

$$\sigma_P^2 = \sigma_G^2 + \sigma_{GY}^2 / y + \sigma_E^2 / r y \tag{3}$$

$$\sigma e^2 = EMS$$
 (4)

Where.

GY MS= Genotype*Year mean square, GMS = genotype mean square, EMS= error mean square, y= number of year; r = number of replication.

According to Singh and Chaudhary (1999), the phenotypic (PCV) and genotypic coefficients of variances (GCV) are expressed by the following formula:

GCV (%) =
$$(\sqrt{g^2} / X) \times 100$$
 (5)

PCV (%) =
$$(\sqrt{\sigma_P^2}/X) \times 100$$
 (6)

Where,

GCV% = Genotypic Coefficient of variation; PCV% = Phenotypic Coefficient of variation; X = Mean value of the trait.

GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) as indicated by Burton and De Vane (1953) and Sivasubramanian and Madhavamenon (1973). The broad sense heritability (h²b) of the traits was calculated (Hanson *et al.*, 1956). Heritability in broad sense was calculated for each trait by using the following formula (Allard, 1960):

$$h^2b$$
 (%) =($\sigma g^2/\sigma P^2$) ×100 (7)

The heritability estimates were categorized as low (0-30%), moderate (31-60%) and high (60% and above) as suggested by Robinson *et al.* (1949).

The expected Genetic Advance for each trait was calculated as

GA= K*
$$\sqrt{\sigma_P^{2*}} h^2 b$$
 (8)

Where, K = 1.40 at 20% selection intensity for trait as suggested by Hanson *et al.* (1956).

RESULTS AND DISCUSSION

The analysis of variance for investigated traitsindicated highly significant differences (P≤0.01) among the chickpea genotypes in both normal and stress conditions (Table 3). This significant variation suggests the existence of inherent genetic variability among the genotypes. Genetic variation in any given crop population is essential to successfully select and manage yield improvement programs. Similar results have also reported by Meena and Kumar (2015); Kadir *et al.* (2017); Yucel, (2018).

The phenotypic variance (PV) of the traits in this research was divided into genotypic, genotype by environment interaction and error variances in both growing conditions (Table 4). The highest genotypic (GV) and phenotypic (PV) variance were obtained from seed yield and hundred seed weight. The genotypic variance $(\sigma^2 \ g)$ was lower than the phenotypic variance $(\sigma^2 \ p)$ as compared to the variances due to error $(\sigma^2 \ e)$ in all of the traits. This

Table 1: Selected meteorological datas of the experimental Site (2014-2016).

Month	Years	Air	Temperature (°C	C)	Rela	ative Humidity (%)	Total
		Max	Mean	Min	Max	Mean	Min	Precipitation (mm)
December	2014	22	13.0	2	100	71.6	17	50.05
	2015	22	11	-1	93	48.4	4	2.03
January	2015	21	8.9	-3	100	66.3	13	56.39
	2016	19	8	-4	100	57.5	4	42.17
February	2015	22	10.9	-1	100	70.1	07	90.68
	2016	28	14	1	100	62.4	9	43.18
March	2015	28	13.9	3	96	64.6	13	115.81
	2016	27	16	3	94	57.1	9	36.83
April	2015	28	13.9	3	96	64.6	13	115.81
	2016	34	20	8	100	56.1	4	8.89
May	2015	38	21.7	11	100	64.3	08	81.02
-	2016	33	26	20	94	67.2	8	26.7
June	2015	33	24.2	15	100	69.1	11	9.5
	2016	39	32	25	100	69.0	12	1.5
July	2015	36	28.0	18	100	69.3	19	8.8
•	2016	37	31	26	100	70.9	18	0.0

Table 2: List of chickpea genotypes used for evaluation in normal and stress conditions.

Genotype Name	Type	Registration Institution or Origin
Hasanbey	Kabuli	Eastern Mediterranean Agri. Res. Inst.
Seckin	Kabuli	Eastern Mediterranean Agri. Res. Inst.
Inci	Kabuli	Eastern Mediterranean Agri. Res. Inst.
Azkan	Kabuli	Transitional Zonal Agri. Res. Inst.
Cakır	Kabuli	Transitional Zonal Agri. Res. Inst.
Cagatay	Kabuli	Black Sea Agri. Res. Inst.
Arda	Kabuli	GAP International Agri. Res. And Training Center
İzmir-92	Kabuli	Aegean Agri. Res. Inst.
Dikbas	Kabuli	Field Crops Central Agri. Res. Inst
Aksu	Kabuli	East Mediterranean Transitional ZoneAgri. Res. Inst
FLIP 05-150 C	Kabuli	ICARDA
FLIP 05-170 C	Kabuli	ICARDA
FLIP 03-126 C	Kabuli	ICARDA
FLIP 03-28 C	Kabuli	ICARDA
FLIP 03-108 C	Kabuli	ICARDA
FLIP 03-42 C	Kabuli	ICARDA
FLIP 03-21 C	Kabuli	ICARDA
FLIP 01-24 C	Kabuli	ICARDA
FLIP 01-54 C	Kabuli	ICARDA
FLIP 01-39 C	Kabuli	ICARDA
F4 09 (X 05 TH 80-16105-31-2)	Kabuli	ICARDA
F4 09 (X 05 TH 69-16124-8)	Kabuli	ICARDA
F4 09 (X 05 TH 21 16189-12-4)	Kabuli	ICARDA
EN 808	Kabuli	National Breeding Material
EN 766	Kabuli	National Breeding Material
EN 952	Kabuli	National Breeding Material
ENA 144-10	Kabuli	National Breeding Material
ENA 8-2	Kabuli	National Breeding Material
EN 1685	Kabuli	National Breeding Material
EN 1750	Kabuli	National Breeding Material
ICC 1205	Desi	ICRISAT
ICC 4567	Desi	ICRISAT
FLIP 87-59 C (Drought Tolerant) Control	Kabuli	ICARDA
ILC 8617 (Drought Sensitive) Control	Kabuli	ICARDA

Table 3: Means Squares for Morphological Traits in Chickpea Genotypes.

Traits	Conditions	Genotype	Genotyp β Year	Error
Emergence Day	Normal	15,70**	13,72**	7,89
	Stress	12,17**	8,83*	5,43
Vegetative Period	Normal	22,1**	29,98**	11,91
	Stress	41,1**	27,21**	10,18
Flowering Day	Normal	48,15**	27,54**	3,02
	Stress	55,76**	20,36**	4,11
Podding Day	Normal	28,75**	6,60**	4,33
	Stress	62,60**	27,24**	6,56
Vegetation Time	Normal	42,09**	51,39**	13,03
	Stress	60,94**	52,67**	18,79
Maturity Day	Normal	39,70**	39,58**	6,13
	Stress	51,70**	46,75**	12,69
Plant Height	Normal	157,84**	77,38**	36,18
	Stress	135,25**	50,91	23,57
First Pod Height	Normal	77,10**	47,84**	15,97
	Stress	48,45**	14,03	11,61
Seed Yield	Normal	18260,11**	22528,27**	1361,7
	Stress	3259,07**	2826,44**	286,324
Hundred Seed Weight	Normal	260,32**	16,64**	4,53
	Stress	170,13**	8,42	6,84

^{*:} p≤0,05; **p≤0,01

showed that the observed phenotypic differences were not alone due to inherent genetic differences among the genotypes but also the substantial portion was due to environmental factor and the interplay between environment and genotype. These findings were agreement with Ene et al. (2016).

The highest PCV was obtained from seed yield followed by hundred seed weight in both normal and stress conditions. High PCV indicates the existence of a greater scope of selection for the trait being considered, which depents on the amount of variability present. Thus, a greater potential is expected in selecting for the seed yield and hundred seed weight among the investigated chickpea genotypes. The highest GCV was obtained from hundred seed weight in both normal and stress conditions. High GCV indicates the presence of exploitable genetic variability for hundred seed weight which can facilitate selection. However, there was no GCV for seed yield in normal condition because of the negative genotypic variance. These results were in agreement with Yucel et al. (2006). Although, estimates for PCV were higher than those for GCV, they were close, implying that genotype contributed more than environment in the expression of these characters and selection based on phenotypic values is therefore feasible. These results were in agreement with Ewoll and Akromah (2017).

These values alone are not helpful in determining the heritable portion of variation. The proportion of genetic variability which is transmitted from parents to all spring is reflected by heritability. Heritability in broad sense is considered to be of importance to breeding programs,

because only additive genetic variability is carried on to the next generation. Thus traits with high narrow sense heritability values can be selected more quickly with less intensive evaluation than those with low narrow-sense heritability values and are therefore use-ful in making selection progress estimates in early selection generations (Al-Tabbal and Al-Fraihat, 2012). Heritability estimates are classified as low (5-10%), medium (10-30%) and high (30-60%) (Dabholkar, 1992). Reliant on this suggestion, low value of broad sense heritability was noted for maturity day and moderate heritability was observed traits such as emergence day and seed yield. The highest heritability was found for hundred seed weight followed by podding day, plant height, flowering day and first pod height in normal and stress conditions. These results indicate that there is considerable genetic variation present in these traits to warrant selection for better accessions. These traits can therefore be given special attention for selections aimed at chickpea improvement. High heritability along with high genetic advance are important factors for predicting resultant effects of selecting best individuals. Johnson et al. (1955) suggested that without genetic advance heritability estimation will not render practical values, and they emphasized concurrent use of genetic advance along with heritability. High heritability and high GA for hundred seed weight, podding day, plant height, flowering day and first pod height in both normal and stress growing conditions indicates that genes governing these characters may have an additive effect. The phenotypic expression of these characters may be governed by the genes acting additively and thereby indicating the importance of these characters

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Table 4: Mean performance and estimates of genetic parameter for different traits of chickpea in normal and stress conditions (N=204).

Table 4. Mean pendinance and estimates of general par	alce ala Sil	ाबस्ट ज पुरा	3		direction trains of or		lonpod III	וומו מומ סוו	35.00 000	07-11	· F			
Traits	Conditions	Mean ±	SE	Min.	Мах.	St. Dev.	$\sigma^2 g$	σ^2 gy	σ^2 e	$\sigma^2 p$	GCV (%)	PCV (%)	h²b (%)	GA
Emergence Day	Normal	32,82	99'0	22	48	9,42	0,33	1,94	7,89	2,62	1,75	4,93	12,60	28,55
	Stress	15,59	0,21	12	23	3,04	0,56	1,14	5,43	2,03	4,79	9,14	27,44	54,73
Vegetative Period	Normal	91,38	1,61	61	124	22,94	-1,32	6,02	11,91	3,68		2,10	-35,96	-96,52
	Stress	54,22	0,30	44	65	4,33	2,31	2,68	10,19	6,85	2,81	4,83	33,77	123,74
Flowering Day	Normal	123,13	1,0	98	146	14,29	3,44	8,17	3,02	8,02	1,51	2,30	42,81	169,78
	Stress	69,32	0,34	26	79	4,63	2,90	5,42	4,11	9,29	3,50	4,40	63,49	270,95
Podding Day	Normal	134,03	1,0	110	153	14,41	3,69	0,76	4,33	4,79	1,43	1,63	90,77	236,17
	Stress	79,07	0,3	89	88	4,56	5,89	6,89	99'9	10,43	3,07	4,09	56,49	255,44
Vegetation Time	Normal	145,22	1,93	109	175	27,64	-1,55	12,79	13,03	69'6		1,82	-22,09	-81,91
	Stress	148,04	3,77	84	212	53,89	1,38	11,29	18,79	14,05	0,79	2,15	13,57	60,54
Maturity Day	Normal	176,99	1,32	155	202	18,86	0,02	11,15	6,13	6,62	0,08	1,45	0,30	1,10
	Stress	162,61	3,70	105	224	52,58	0,83	11,35	12,69	8,62	0,56	1,81	6,59	39,42
Plant Height	Normal	59,61	99'0	35	84,0	9,46	13,41	13,73	36,18	26,31	6,14	8,60	50,98	366,04
	Stress	47,21	0,50	30	71	2,06	14,06	9,11	23,57	22,54	7,94	10,06	62,36	414,51
First Pod Height	Normal	32,65	0,47	17	52,5	92'9	5,03	10,62	15,99	13,00	6,87	11,04	38,66	195,15
	Stress	26,82	0,39	12,5	43	5,55	5,74	08'0	11,61	8,07	8,93	10,60	71,05	282,66
Seed Yield	Normal	231,87	8,23	26,7	516,0	117,61	-711,36	7055,52	1361,7	3043,35	•	23,79	-23,37	-1805,26
	Stress	73.33	2.51	11,3	187,5	35,96	72,11	846,70	286,32	543,18	11,58	31,78	13,27	433,14
Hundred Seed Weight	Normal	41,21	0,53	12	9,55	2,5	40,61	4,04	4,53	43,39	15,46	15,98	93,61	863,22
	Stress	34,34	0,43	10,4	47,0	6,17	26,92	0,53	6,84	28,36	15,12	15,51	92,05	708,60

σ₆²:Genotypic variance.

σρ²: Phenotypic variance.

σ_{Gv²}: Genotype Year variance.

 σ_{E^2} . Environmental variance. PCV: Phenotypic coefficient of variation.

h²b: Heritability in broad sens.

GCV: Genotypic coefficient of variation.

for selection. A simple selection model will be good enough to do what is necessary and no additional gain is achieved by using sophisticated models. These results indicated that the expected gain from selection would be high if these traits were used as selection criteria in chickpea breeding. The above report is akin with the findings of Meen *et al.* (2014); Degal *et al.* (2016); Ton and Anlarsal (2017).

High values of heritability, PCV and GCV obtained for hundred seed weight in normal and stress growing conditions showed that this trait was under control of additive genes and effective selection could be possible for improvement. However, negative heritability coupled with high PCV and high GCV for seed yield may indicate non-additive gene effects governing this trait with limited scope of improvement for this trait which is complex and is mostly influenced by environment. These results are in agreement with Ewoll and Akromah, (2017); Mohammed et al. (2019); Alemu et al. (2017).

CONCLUSION

The range of mean values for most of the traits were large showing the existence of variation among the tested genotypes. Phenotypic coefficients of variation (PCV) were found to be higher than genotypic coefficients of variation (GCV) for all the traits. The two values differed slightly indicating less influence of the environmental factors. The highest heritability was found for hundred seed weight followed by podding day, plant height, flowering day and first pod height in normal and stress conditions. High heritability along with high genetic advance for hundred seed weight, podding day, plant height, flowering day and first pod height in both normal and stress growing conditions indicates that genes governing these characters may have an additive effect. These traits can be improved by giving special attention during selection. Genetic evaluation in these genotypes indicated that there is considerable genetic variation in the studied genotypes to warrant selection for both seasons.

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