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Genetic Variability and Phenotypic Corelation between Yield and Yield Components in Nineteen Chick pea (*Cicer arietinum* L.) Genotypes, Sudan

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Abstract: Nineteen chickpea genotypes were evaluated to study genetic variability and phenotypic correlation between them for yield and yield components, at Shambat, the experimental farm, College of Agricultural studies, Sudan University of Science and Technology during two consecutive winter seasons of 2012/13 and 2013/14. A randomized complete block design with four replications was used in this study. Four characters were measured included Days to 50% flowering, number of pods/plant, 100 seed weight (gm) and seed yield/plant (Kg/ha). The estimates of phenotypic (PCV) and genotypic (GCV) Coefficients of variation, heritability (h^2), genetic advance (GA%) were determined. The phenotypic correlation between yield and yield components was calculated. The results showed that there were highly significant differences between chick pea genotypes for all studied characters in both seasons. The highest values of phenotypic and genotypic coefficients of variation were scored by number pods per plant in both seasons. The highest values of heritability were scored by days to 50 % flowering and the lower values for 100- seed weight for both seasons. The highest value of heritability and genetic advance were observed for number of pods/plant in the second season. Seed yield /plant was positively and significantly correlated with number of pods per plant and hundred seed weight. Days to 50% flowering was negatively and significantly correlated with yield components. The chick pea genotype Salwa (released variety) obtained the most highest means of number of pods/plant, seed yield/plant and 100 seed weight in both seasons. The variation between chick pea genotypes observed in this study and the correlation results could of a great value in any chick pea breeding program in the Sudan.

Keywords: Cicer arietinum, genetic variability, heritability, correlation.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is the third most important grain legume throughout the world, after dry bean (*Phaseolus vulgamris* L.) and dry pea (*Pisum sativum* L.). It belongs to the family Fabaceae (Leguminosae) and sub family Faboideae. The crop has a high adaptability to a wide range of environments, it can be successfully grown under rains, irrigation and under stored soil moisture. It is currently grown in many tropical and subtropical regions as winter crop as well as in the mediate winter and temperature regions [1]. The total cultivated area of this crop worldwide was estimated at about 12 million ha producing more than 11 million tons [2]. In Sudan, chickpea is an important legume crop cultivated in the Northern state, River Nile State, Hawata area in Eastern Sudan, Jabel Marra in Western Sudan (South Darfor State) and recently, the chick pea has been successfully cultivated in Jazera state [3]. The total cultivated area of chickpea in Sudan is about 10000 ha and an average yield was 1.92 t/ha [2].

Study of genetic variability, phenotypic correlation between different characters is essential for effective selection and improving of economic characters in any crop breeding program. The progress of selection is more important in any crop improvement and this progress depends on the existence of genetic variability for yield and yield contributing characters and their heritability [4]. Heritability in conjunction with genetic advance has a greater role in determining the effectiveness of selection of a character [5]. In Sudan few chick pea improved cultivars with different growth habits were released [3]. Therefore, the present study was conducted to assess genetic variability, heritability and genetic advance and to estimate phenotypic correlation between yield and yield components among nineteen chickpea genotypes in two consecutive winter seasons in order to select the appropriate genotype(s) that are suited to Sudan environment.

MATERIALS AND METHODS

Two field experiments were conducted for two consecutive winter seasons of 2012/13 and 2013/14, at Sudan University of Science Technology, farm of the College of Agricultural Studies, Shambat (15° 30´N; 32° 31´E). The genetic material used in the study consisted of nineteen genotypes of chick pea (*Cicer arietimum* L) (Table-1). These genotypes were obtained from Hudeiba Research Station, River Nile State, Agricultural Research Corporation (ARC), Sudan.

Table-1: List of nineteen genotypes of Chick pea (*Cicer arietinum* L.) **used in the study**

Code No.	Chic pea Genotypes	Source
1	LA-12-R1-(12)	Inbred line prepared by ARC, Sudan.
2	Shendi	Local variety at River Nile State, Sudan.
3	Atomor	Local variety at River Nile State, Sudan.
4	Ematemh	Local variety at River Nile State, Sudan.
5	Ayt-4	Inbred line prepared by ARC, Sudan.
6	LA-12.R1 (33)	Inbred line prepared by ARC, Sudan.
7	LA-12-R1 (29)	Inbred line prepared by ARC, Sudan.
8	Ayt-10	Inbred line prepared by ARC, Sudan.
9	Hawwath	Released variety by ARC, Sudan.
10	Salwa	Released variety by ARC, Sudan.
11	B. riqik	Released variety by ARC Sudan.
12	SL-2-12 RЦ-6	Inbred line prepared by ARC, Sudan.
13	SL-2-12 RЦ-5	Inbred line prepared by ARC, Sudan.
14	SL-2-12 RЦ-4	Inbred line prepared by ARC, Sudan.
15	SL-2-12 RЦ-10	Inbred line prepared by ARC, Sudan.
16	SL-2-12 RЦ-13	Inbred line prepared by ARC, Sudan.
17	Jebel marra	Local variety at Darfur State, Sudan.
18	Wad hamid	Local variety at River Nile State, Sudan.
19	LA-12-R1-(12)	Inbred line prepared by ARC, Sudan.

ARC= Agricultural Research Corporation, Sudan

The experiments were laid out in a randomized complete block design (RCBD) with four replications**,** the land was prepared by disc plough and then followed by harrowing, ridging up was north- south. The land was divided to 3× 4 m plots, each plot consisted of 4 ridges, 3m long. The space between ridges was 70cm and between holes was 20cm. Four seeds per hole were sown and then thinned to two plants per hole, two weeks after sowing. Weeding was practiced twice by hand hoeing during the period of the experiment, three and six weeks after sowing date, respectively. Five plants were selected randomly from each plot, and the following growth and yield traits were measured included: days to 50% flowering (DTF), number of pods/plant (NPP), seed yield/plant (SYP) (kg/ha). Hundred seed weight (HSW) (gm). The collected data were subjected to individual statistical analysis of variance for a randomized complete block design (RCBD) as described by [6]. To estimate the extent of variability, Genotypic (GCV %) and phenotypic (PCV) coefficients of variation were estimated based on formula reported by [7] as the following:

Genotypic coefficient of variation (GCV %) :

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sqrt{\sigma^2 g}}{\text{Grand mean}} \times 100$$

Phenotypic coefficient of variation (PCV %):

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sqrt{\sigma^2 ph}}{\text{Grand mean}} \times 100$$

The estimates of phenotypic (σ^2ph) and genotypic (σ^2g) variances were worked out according to the method suggested by [8]. using mean square values from the individual ANOVA tables in the two seasons as the following formula:

$$\sigma^2 g = (M2 - M1)/r$$

$$\sigma^2 ph = \sigma^2 g + \sigma^2 e$$

Where:
r = number of replications.
σ^2e = error or environmental variance.`
M1, M2 = error and genotype mean squares.

Broad sense heritability (h^2b)

It was estimated in each location separately, from the analysis of variance according to [8]. by the formula:

$$h^2 b = \sigma^2 g / \sigma^2 ph$$

$\sigma^2 g$ = genotypic variance
$\sigma^2 ph$ = phenotypic variance

Expected genetic advance as percentage of the mean (GA %):

It was estimated using the formula of [9]. as the following:

$$GA = K \frac{\sigma^2 g}{\sqrt{\sigma \ Ph}} \quad \text{and } GA\% = \frac{GA}{G} \times 100$$

Where

G= the grand mean
K = selection differential and it was 2.06 at selection intensity of 5%.

Phenotypic correlation

Phenotypic correlation between different characters was calculated using the formula suggested by [10]. As the following:

$$\text{Phenotypic correlation coefficient } (r\ ph) = \frac{\sigma^2 phxy}{\sqrt{(\sigma^2 ph\ x)\ (\sigma^2 ph\ y)}}$$

Where

$\sigma^2 ph\ x$ = genotypic variance for trait x,
$\sigma^2 ph\ y$ = genotypic variance for trait y ,
$\sigma phxy$ = phenotypic covariance between two traits x and y.

Table-2: Means of Chickpea (*Cicer aritetimum L.*) Genotypes for different characters evaluated at two seasons 2012/13 and 2013/14 at Shambat locations

Code No.	Chick pea Genotypes	DTF		NPP		SYP (Kg/Ha)		HSW (gm)	
		2012/13	2013/14	2012/13	2013/14	2012/13	2013/14	2012/13	2013/14
1	**LA-12-R1-(12)**	69.00	62.33	65.50	26.50	13.12	25.66	29.13	17.30
2	**Shendi**	57.00	45.00	98.00	31.16	18.56	21.8	18.28	40.88
3	**Atomor**	56.00	41.66	75.28	30.57	12.51	29.40	14.72	16.83
4	**Ematemh**	45.00	40.00	83.20	64.00	20.89	21.80	21.14	45.30
5	**Ayt-4**	73.00	49.66	56.85	31.18	14.97	22.53	26.39	35.33
6	**LA-12.R1 (33)**	71.00	51.00	43.75	20.54	13.07	31.06	26.06	24.30
7	**LA-12-R1 (29)**	75.00	62.66	48.85	36.41	11.18	21.46	25.35	16.70
8	**Ayt-10**	76.75	54.33	55.75	24.35	13.36	23.40	27.35	27.44
9	**Hawwath**	62.25	49.00	95.55	40.33	22.33	26.00	19.42	43.37
10	**Salwa**	59.75	50.66	99.55	42.33	22.67	29.13	31.35	27.08
11	**B. riqik**	58.50	46.00	91.45	42.97	18.97	30.13	18.82	31.16
12	**SL-2-12 RЦ-6**	67.50	49.66	60.65	41.82	15.41	28.46	28.02	36.60
13	**SL-2-12 RЦ-5**	79.25	50.66	20.00	24.13	3.85	21.73	32.35	21.17
14	**SL-2-12 RЦ-4**	67.25	62.66	57.10	38.03	12.52	22.86	23.78	23.63
15	**SL-2-12 RЦ-10**	74.75	58.30	26.15	30.00	6.24	29.40	25.11	23.2
16	**SL-2-12 RЦ-13**	76.25	51.00	24.70	27.13	5.33	29.26	20.95	21.75
17	**Jebel marra**	46.23	40.00	76.50	65.26	11.48	23.06	14.47	47.52
18	**Wad hamid**	47.00	53.33	51.10	63.16	9.50	20.60	16.92	20.91
19	**LA-12-R1-(12)**	69.23	45.00	46.30	21.75	9.04	29.60	25.04	43.67
Means		64.78	51.25	66.65	36.18	15.55	25.52	23.40	29.36
L.sd		1.81	4.81	5.28	17.1	1.38	6.73	2.26	12.1
C.V%		8.57	5.68	24.36	28.44	27.31	28.44	29.73	24.75

DTF=Days to 50% flowering, NPP= Number of pods/plant, SYP= Seed yield/plant (kg/ha). HSW=Hundred seed weight (gm).

Table-3: Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation, heritability (h^2)and genetic advance (GA%) for different characters of nineteen genotypes of chickpea (*Cicer arietimum)*

Characters	Seasons	PCV	GCV	h^2b	GA%
Days to 50% flowering	2012/13	18.27	16.14	78.01	2.81
	2013/14	15.08	13.96	85.2	13.7
Number of pods/plant	2012/13	32.18	21.04	42.73	2.02
	2013/14	45.12	35.03	60.3	26.9
Seed yield/plant (Kg/ha)	2012/13	31.02	14.70	22.48	6.28
	2013/14	19.29	10.85	59.5	13.98
100- seeds weight (gm)	2012/13	17.20	1.03	25.05	4.41
	2013/14	38.88	29.98	31.6	3.21

Table-4: Phenotypic correlation between different characters among nineteen genotypes of chickpea

Characters	Days to 50% flowering	Number of pods/plant	Seed yield/plant	100- seeds weight
Days to 50% flowering	-			
Number of pods/plant	-0.427 *	-		
Seed yield/plant (Kg/ha)	-0.77**	0.87**	-	
100- seeds weight (gm)	-0.74**	0.600**	0.892**	-

*, Significant at P< 0.01.,**, Significant at P< 0.05 and n.s= non significant

RESULTS AND DISCUSSION

Phenotypic variability

In both seasons, the analysis of variance revealed highly significant differences among the chick pea genotypes for all studied characters. This variability could be attributed to genetic factors, environmental effect and/or to their interaction. This considerable variability provides a good opportunity for improving traits of interest in chickpea breeding programs. Hence it provides a wide scope for improvement through selection, variability in chickpea genotypes for different characters was we reported by many investigators e.g [11-18]. The genotypes Elmatemh and Jebel marra (Local varieties) scored the most early days to 50% flowering and relatively high number of pods/plant, seed yield/plant and 100 seed weight in both seasons as shown in (Table-2), accordingly they can be characterized and selected as early flowering and high yield chick pea genotypes to be used by Sudanese chick farmers and/or in any chick pea breeding program aiming to produce chick pea hybrids characterized by high yield and early flowering and maturity. The chick pea genotype Salwa (released variety) as shown in (Table-2), obtained the most highest means of number of pods/plant, seed yield/plant (Kg/ha) and 100 seed weight (gm) in both seasons, in addition, this genotype also scored moderate days to 50% flowering compared with the another chick pea genotypes used in the study, therefore, it could be of a great benefit for Sudanese chick pea farmers and /or in any chick breeding program.

Phenotypic (PCV) and Genotypic (GCV) coefficients of variation, heritability (h^2) and genetic advance (GA):

The genotypic (GCV) coefficient of variation indicates the range of genetic variability for a trait in a population and help to compare genetic variability present in various traits [4]. The values of PCVs and GCVs in this study are presented in (Table 3). These values provide information on the extent of variability between the nineteen chick pea genotypes for the studied traits. The highest values of phenotypic and genotypic coefficients of variation were scored by number pods per plant in both seasons. The PCVs values were greater than GCVs values, indicating the influence of environmental effect. These results were in accordance with [14], [15]. On the other hand, higher values of heritability were scored for days to 50 % flowering and the lower values for 100- seed weight in both seasons (Table, 4). The highest value of heritability and genetic advance were observed for number of pods/plant in the second season indicate that, this character was good character for improving these genotypes. Similar findings were reported in chickpea by [19, 20, 16].

Phenotypic Correlation between different characters

In present results, the phenotypic correlation coefficients between different characters Showed that, negative and highly significant ($P \leq 0.01$) phenotypic correlation was detected between days to 50% flowering with number of pods/plant, seed yield/plant and 100 seed weight. These results indicate that early flowering tends to produce less yield [21]. reported that negative association between different traits might be due to the competition of two developing structures of plant limited sources like nutrients and water supply. On the other hand, positive and significant phenotypic correlation was observed between seed yield/plant with number of pods/plant and 100 seed weight. Therefore, determination of degree of association between these characters is an essential step for effective selection for chick pea yield improvement. Similar findings were reported in chickpea by [19, 20, 16], and in other crops by [22, 23].

CONCLUSIONS

Based on results of this study, it could be concluded that there was a wide range of genetic variability detected among the nineteen chickpea genotypes for all studied characters in both seasons. This variability is promising and can be exploited in the improvement of this crop through selection or hybridization. The positive and significant phenotypic correlation observed between seed yield/plant with number of pods/plant and 100 seed weight can also be useful for effective selection for chick pea yield improvement. The chick pea genotype Salwa (released variety) obtained the most highest means of number of pods/plant, seed yield/plant and 100 seed weight in both seasons, therefore it can be used by chick pea Sudanese farmers and/or as a parental line in any chick pea breeding program.

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