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ASSESSMENT OF CORRELATION AND SELECTION INDICES IN CHICKPEA (*CICER ARIETINUM* L.)

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SUMMARY

This study used 20 chickpea genotypes (*Cicer arietinum* L.) introduced by the International Center for Agricultural Research in the Dry Areas (ICARDA) and one French variety. The genotypes' sowing had a randomized complete block design with three replicates at the University of Dohuk, Iraq, during the harvest season of 2018–2019. Stability analysis revealed significant averages for all traits, except days to 50% flowering, secondary branches per plant, and grain pods. According to the analysis of variance, the chickpea genotypes showed significant ($p \leq 0.01$) differences for all morphological and yield-related traits, except plant height, secondary branches per plant, the height of the first pod above the ground, and the grains per pod. The chickpea genotype FLIP09-114C, followed by four other local genotypes, including FLIP09-222C, FLIP09-230C, and FLIP09-220C, displayed the best performance and exceeded the rest of the genotypes for yield-related traits. The results provided positive phenotypic and genetic correlations between traits like secondary branches, grains per pod, and grain yield, and positive environmental correlations with 100-grain weight, primary branches, and pod number per plant. Meanwhile, negative correlations were evident with pod number per plant, and it was significantly negative among the number of grains per pod, grain yield, and the number of secondary branches per each plant.

Keywords: Chickpea (*Cicer arietinum* L.), phenotypic and genetic correlations, selection indices, yield-related traits

Key findings: The results demonstrated the traits secondary branches per plant, grains per pod, and grain yield had significant positive phenotypic and genetic correlations; selection index I4, which included features related to pods per plant, appeared to be superior. This further confirmed genetic diversity observed in most chickpea genotypes and their variables, which may be effective to select promising genotypes with desirable traits to maximize crop productivity.

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INTRODUCTION

Chickpea (*Cicer arietinum L.*) is a member of the Fabaceae family and ranks third in importance in the world's food legumes, grown on 10 million hectares, which produced 7.8 million tons (Rubio *et al.*, 2004; Gowda *et al.*, 2005). Chickpea seeds contain protein (17%–24%), carbohydrates (41%–50.8%), as well as, an atmospheric nitrogen stabilization cycle through the root nodules bacteria rhizobium (Al-Mayouf and Al-Fakhry, 1982).

Estimating genetic and phenotypic associations between pairs of traits is useful in planning and evaluating promising genotypes for economic traits. Knowing the correlation between important variables makes it easier to lay the right foundation for a more efficient breeding program. Several studies by various researchers have progressed to estimate phenotypic and genetic association and selection indices. Hussein (2018) reported the grain yield showed significant negative phenotypic and genetic correlations with plant height and a relevant positive correlation with grains per plant and harvest index.

According to Philanim *et al.* (2019), in 380 genotypes of chickpea, a significant and positive genetic correlation existed between the pods per plant, grains per plant, and 100-grain weight with grain yield. Pods per plant and grains per plant also showed a meaningful positive correlation with each other. In another study, an assessment of 20 chickpea genotypes occurred, grown under irrigated conditions. Shafique *et al.* (2016) reported the trait grains per plant have a positive genetic correlation with grain yield. Likewise, pods per plant had a significant positive genetic correlation with grain yield.

The use of a selection index in different studies differentiated several new genotypes and selected the best ones by drawing on some qualities that fall within the selection index's components. Samad *et al.* (2014) studied eight genetic structures of the chickpea crop and found the main branches per plant gave maximum genetic values among traits of selection indicators. Debnath (2021) observed through a study on 21 genotypes of chickpeas that traits of biological yield, grains per plant, and 100-grain weight were the most crucial selection indices to improve grain yield. Nineteen genotypes of the chickpea crop showed the highest efficiency qualities of selection indices were grains, branches, and pods per plant (Parmar *et al.*, 2022).

In a past study, evaluating 36 genotypes of the chickpea disclosed the characteristics of pods per plant, seeds per pod, 100-grain weight, biological yield, and harvest index were among the most essential choice indicators as selection criteria to improve chickpea production (Aftab *et al.*, 2023). Therefore, the presented study aimed to estimate genetic and phenotypic correlations and evaluate the selection indices for several genotypes of chickpeas.

MATERIALS AND METHODS

An experiment on chickpea (*Cicer arietinum* L.) genotypes commenced during the growing season of 2018–2019 at the Duhok University, Iraq. Twenty genotypes and one local check cultivar were samples used in this study (Table 1). Genotype seeds came from the International Center for Agricultural Research in the Dry Areas (ICARDA). The data analysis used the statistical program SAS, in addition to Word and Excel programs. All sown genotype grains had a randomized complete block design (RCBD) with three replications, in three rows 4 m long and spacing of 50 cm and 20 cm between and within rows, respectively. The addition of fertilizer urea (46% N) had a mean rate of 30 kg/ha^{-1} in two steps—first, after germination, and second, at the beginning of the flowering stage, as recommended for chickpea productions.

Five plants, randomly selected in each genotype and replication, had their data recorded on traits, as follows: days to 50% flowering, plant height (cm), main branches per plant, secondary branches per plant, height of first pod above ground, pods per plant, grains per plant, biological yield (g), 100-grain weight (g), and grain yield per plant (g). All the recorded data underwent the analysis of

Table 1. Chickpea genotypes used in the study.

No.	Genotypes	Pedigree
1	FLIP07-180C	X03TH-29/(S99858XFLIP97-26) XS00432
2	FLIP07-193C	X02TH 61/S99520XL.Mt-1
3	FLIP09-63C	X05TH7/X04TH-126XFLIP01-18
4	FLIP09-88C	X05TH64/X04TH-202XFLIP00-17
5	FLIP09-97C	X05TH64/X04TH-202XFLIP00-18
6	FLIP09-113C	X05TH64/X04TH-202XFLIP00-19
7	FLIP09-114C	X05TH64/X04TH-202XFLIP00-20
8	FLIP09-122C	X05TH64/X04TH-202XFLIP00-21
9	FLIP09-220C	X05TH64/X04TH-202XFLIP00-22
10	FLIP09-221C	X05TH64/X04TH-202XFLIP00-23
11	FLIP09-222C	X05TH64/X04TH-202XFLIP00-24
12	FLIP09-223C	X05TH64/X04TH-202XFLIP00-25
13	FLIP09-224C	X05TH64/X04TH-202XFLIP00-26
14	FLIP09-225C	X05TH64/X04TH-202XFLIP00-27
15	FLIP09-226C	X05TH64/X04TH-202XFLIP00-28
16	FLIP09-227C	X05TH64/X04TH-202XFLIP00-29
17	FLIP09-228C	X05TH64/X04TH-202XFLIP00-30
18	FLIP09-230C	X05TH64/X04TH-202XFLIP00-31
19	FLIP09-231C	X05TH64/X04TH-202XFLIP00-32
20	FLIP09-232C	X05TH64/X04TH-202XFLIP00-33
21	Local	

variance to define genotypic, phenotypic, and environmental variances and coefficients of variation (Johnson *et al.*, 1955). The same also explained the coefficients of phenotypic (rP), hereditary (rG), and environmental (rE) correlations, with estimates among studied traits following the equations below (Walter, 1975):

$$rP = \frac{\sigma_{px\,py}}{\sqrt{\sigma^2 px \cdot \sigma^2 py}}, \quad rG = \frac{\sigma_{gx\,gy}}{\sqrt{\sigma^2 Gx \cdot \sigma^2 Gy}},$$

$$rE = \frac{\sigma_{Ex\,Ey}}{\sqrt{\sigma^2 Ex \cdot \sigma^2 Ey}}$$

The selection indices' calculation followed the method of Al-Rawi and Ahmad (1984), as given below:

$$I = b1x1+b2x2+\ldots\ldots+bnxn$$

Where, I = Selection index **,**X1, X2,..., Xn = the phenotypic values of the traits included in the selection index, and b1,b2,…,bn = the relative weights of the attributes included in the index**.**

Calculating the Bi depended on the index giving the sum of values of genotypes, with the index calculated for each entry and selection resulting among the components, according to their index to facilitate mathematical operations (Al-Rawi and Ahmed, 1984).

$$[P][b] = [G]$$

$$b = [P]^{-1}[G]$$

Where, b = the vector of the coefficient of partial regressions of trait values in the selection index, [P]-1 = the inverse of the covariance matrix of phenotypic values of traits in an index, and [G] = the vector of the variance of genetic values between grain yield and other traits included in the index. Thus, values of bi can be the estimate of multiplying the inverse of matrix 'p' with vector 'G', with the aforementioned equation applied to extract the selection index.

RESULTS AND DISCUSSION

Results expressed chickpea genotypes appeared with significant ($p \leq 0.01$) differences for all traits, except plant height, secondary branches per plant, height of first pod above ground, and grains per pod (Table 2). Analysis of variance results also confirmed further continuation of genetic analysis and utilization of significant traits in plant breeding programs (Shafique *et al.*, 2016; Raghu *et al.,* 2023). The genetic structures were noteworthy at a probability level of 1% for the traits of plant height, main branches per plant, pods per plant, height of first pod above ground, biological yield, 100-grain weight, and seed yield. Meanwhile, the days to 50% flowering, secondary branches per plant, and grains per pod are nonsignificant, and this indicates the existence of notable differences between these genetic structures. Likewise, it is an indicator for the continuation of future breeding experiments for these genetic structures, as these results align with Astereki *et al.* (2015).

Results further revealed the mean performance of genotypes for 10 traits, and it was evident that the chickpea genotype FLIP09-230C took the least early days to 50% flowering (64.33 days), while the genotype FLIP09-113C's delay was 95.33 days (Table 3). The highest mean of plant height recorded was in genotype FLIP09-114C (33.912 cm). For the number of main branches per plant, genotype FLIP09-114C was superior with the topmost mean of branches (17.223). On the number of secondary branches per plant, the local genotype showed the most number of branches (51.876). For the description of the number of pods per plant, the genotype FLIP09-114C excelled with the maximum mean (66.686 pods), which occurred at par with two other chickpea genotypes (FLIP09-222C and FLIP09-230C). Al-Qaisi and Al-Bayati (2023) reported the introduction of chickpea genotypes with the best performance for yield-related traits under different environmental conditions.

For the height of the first pod above the ground, the highest mean resulted in genotype FLIP09-114C (34.157 cm); however, it was the same as with other genotypes FLIP09-227C and FLIP09-228C (32.616 and 32.290 cm, respectively). By estimating traits of the number of grains per pod, two genotypes FLIP09-232C (28.813 cm) and the local genotype (30.467 cm) exceeded, which were also with similar performance for two other chickpea genotypes FLIP09-63C and FLIP09-224C (27.827 and 27.547 cm, respectively). On estimating biological yield, the chickpea local genotype showed the highest average (76.163 g), although found at par with genotype FLIP09-232C (69.889 g). For choosing the high-yielding genotypes, plant traits, i.e., moderate to high heritability, expected genetic advance, and favorable correlation of yield-related traits, with grain yield per plant are advised factors to consider. These results are greatly analogous to the findings of Debnath (2021) and Parmar *et al.* (2022).

For 100-grain weight, the local genotype exceeded and showed the highest mean (49.657 g). As for grain yield, the local genotype and FLIP09-114C had the topmost mean grain yield (60.899 and 60.781 g plant^{-1}), while the genotype FLIP09-114C provided a mean of 59.513 g plant^{-1}; however, the genotypes did not differ significantly for grain yield. The local genotype exceeds in five traits, namely, secondary branches per plant, grains per pod, biological yield, 100-grain weight, and grain yield (Table 3). The said promising genotype preceded the genotype FLIP09-114C, which excelled in four traits, viz., plant height, main branches per plant, pods per plant, and the height of the first pod above ground. Through these results, the researchers conclude a wide variation in performance of genotypes exists, allowing selection of promising genotypes, namely, FLIP09-114C and Local (Table 5). Raghu *et al*. (2023) evaluated chickpea (*C. arietinum* L.) genotypes for morphological and yield-related traits and their association, and they reported the same findings.

According to correlation coefficients, the genetic correlation coefficient appeared positive among the traits grains per pod, secondary branches per plant, pods per plant, 100-grain weight, secondary branches per plant, main branches per plant, and grain yield (Table 4). Genetic variability, correlation, and path coefficient analyses continued in chickpea (*C. arietinum* L.) genotypes for grain yield and its component traits and reported similar findings (Prasad *et al.*, 2021; Raghu *et al.*, 2023). Overall positive genetic correlation is

Table 2. Analysis of variance for the studied traits' genotypes.

S.O.V	d.f.	Days to 50% flowering (days)	Plant height (cm)	Main branches per plant	Secondary branches per plant	Pods per plant	Height of first pod aboveground (cm)	Seeds per pod	Biological yield (g)	100-seed weight (g)	seed yield (g plant^{-1})
Replications	2	0.242	19.616	10.716	21.133	103.483	31.09	57.106	26.881	77.528	47.109
Genotypes	20	48.142^{ns}	232.58**	8036.588**	77.039 ^{NS}	1561.948**	672.621**	29327.862**	5546.115**	5162.243*	1805.319**
Error	40	197.071	24.499	11.936	147.053	451.736	23.355	59.86	370.86	157.824	328.577

** and * are significant at 1% and 5% probability levels.

Table 3. Means performance of chickpea genotypes for studied traits.

Genotypes	Days to 50% flowering (days)	Plant height (cm)	Main branches per plant	Secondary branches per plant	Pods plant^{-1}	Height of first pod aboveground	Seeds pod^{-1}	Biological yield (g)	100-grain weight (g)	Grain yield (g/plant)
FLIP07-180C	77.33i	27.300abc	11.914ab	30.411e-h	51.053a-e	26.617a	17.827ab	42.437ij	26.301dc	30.968efg
FLIP07-193C	84.33e	26.546abc	9.900b	30.750e-h	37.980c-g	25.141a	12.520b	29.176k	20.075d	23.383g
FLIP09-63C	76.33j	26.428abc	14.303ab	28.387gh	45.878b-f	29.514a	27.827a	68.808abc	36.976a-d	57.469ab
FLIP09-88C	80.33g	22.573c	11.345ab	28.569fgh	29.203b-f	24.503a	20.633ab	49.573ghi	29.113dc	40.971cde
FLIP09-97C	76.33j	30.460abc	13.469ab	31.847e-h	46.590b-f	31.654a	24.489ab	58.375d-g	29.793dc	45.048bcd
FLIP09-113C	95.33a	25.778abc	13.018ab	32.432e-h	35.918d-g	28.148a	23.567ab	58.929d-g	37.604abc	47.749a-d
FLIP09-114C	65.33o	33.912a	17.223a	45.549ab	66.686a	34.157a	23.933ab	61.314b-f	39.489abc	60.781a
FLIP09-122C	90.33b	29.301abc	10.092b	26.963h	20.582g	29.795a	16.207ab	39.409j	22.510dc	27.308fg
FLIP09-220C	67.33n	30.284abc	15.468ab	38.757b-e	54.988a-d	31.886a	26.837ab	66.113bcd	36.559a-d	57.294ab
FLIP09-221C	70.33m	29.266abc	12.008ab	33.065d-h	30.331fg	31.164a	24.867ab	57.862d-g	28.353dc	38.339efd
FLIP09-222C	80.33g	28.762abc	15.466ab	41.455bcd	62.039ab	28.582a	22.180ab	55.401e-h	32.976a-d	50.790a-d
FLIP09-223C	86.33c	25.391abc	11.581ab	26.988h	32.599efg	27.866a	20.767ab	52.549fgh	33.889a-d	50.100a-d
FLIP09-224C	72.33l	25.902abc	13.659ab	37.436b-f	48.043a-f	27.837a	27.547ab	63.714b-e	29.222dc	42.681cde
FLIP09-225C	72.33l	26.099abc	11.484ab	25.110h	29.798fg	28.948a	24.387ab	58.259d-g	32.844a-d	48.492a-d
FLIP09-226C	81.33f	24.186bc	13.675ab	38.098b-e	57.571abc	23.731a	19.587ab	48.249hij	28.745dc	42.049cde
FLIP09-227C	78.33h	30.600abc	14.619ab	43.455bc	40.413c-f	32.616a	25.180ab	64.243b-e	38.629abc	59.513a
FLIP09-228C	85.33d	32.203ab	13.385ab	33.471d-h	47.632a-f	32.290a	18.033ab	46.147hij	32.301bcd	46.029bcd
FLIP09-230C	64.33p	29.510abc	15.835ab	36.397c-g	60.436ab	30.612a	23.162ab	59.667c-f	48.228ab	44.161bcd
FLIP09-231C	70.33m	29.395abc	12.403ab	28.448gh	35.898d-g	31.623a	25.650ab	61.662b-f	30.277dc	45.396bcd
FLIP09-232C	72.33l	27.421abc	13.242ab	28.716fgh	38.686c-g	30.841a	28.813a	69.889ab	36.537a-d	53.723abc
Local	75.33k	24.032bc	16.294ab	51.876a	47.676a-f	27.881a	30.467a	76.163a	49.657a	60.899a
Average	77.235	27.874	13.352	34.199	43.810	26.617a	23.070	56.569	33.337	46.340

Table 4. Genetic, environmental, and phenotypic correlation of some studied traits.

Traits	Correlation	Traits				
		Seed yield (g plant^{-1})	100-seed weight (g)	Main branches plant^{-1}	Secondary branches plant^{-1}	Pods plant^{-1}
Seeds pod^{-1}	Rg	0.336**	0.150	-0.013	0.328**	0.265**
	Re	-0.642**	0.516**	0.685**	-0.381**	0.023
	Rp	0.371**	0.675**	0.638**	0.418**	0.589**
Pods plant^{-1}	Rg	0.189*	0.167*	0.074	0.205*	
	Re	-0.345**	0.265**	0.350**	0.173*	
	Rp	0.410**	0.493**	0.322**	0.573**	
Secondary branches plant^{-1}	Rg	0.142	0.126	0.015		
	Re	-0.222*	0.140	0.258**		
	Rp	0.291**	0.349**	0.185*		
Main branches plant^{-1}	Rg	0.350**	0.078			
	Re	-0.749**	0.624**			
	Rp	0.332**	0.638**			
100-grain weight (g)	Rg	0.342**				
	Re	-0.910**				
	Rp	0.416**				

** and * are significant at 1% and 5% probability levels.

Table 5. Selection index values for the studied genotypes in chickpeas.

No.	Genotypes	Value selection index
1	FLIP07-180C	123.523
2	FLIP07-193C	102.867
3	FLIP09-63C	136.934
4	FLIP09-88C	105.942
5	FLIP09-97C	129.624
6	FLIP09-113C	124.976
7	FLIP09-114C	187.310
8	FLIP09-122C	80.602
9	FLIP09-220C	159.796
10	FLIP09-221C	106.976
11	FLIP09-222C	167.447
12	FLIP09-223C	115.445
13	FLIP09-224C	135.871
14	FLIP09-225C	106.831
15	FLIP09-226C	150.986
16	FLIP09-227C	152.751
17	FLIP09-228C	137.184
18	FLIP09-230C	159.994
19	FLIP09-231C	113.222
20	FLIP09-232C	124.611
21	Local	177.555

that genetic synergistic systems cooperate by influencing both attributes and selection, which affect each other in the same direction.

Environmental correlation was significantly positive among the chickpea variables, as follows: grains per pod with 100-grain weight and main branches per plant; pods per plant with 100-grain weight, main branches per plant, and secondary branches per plant; secondary branches per plant with main branches per plant, and main branches per plant with 100-grain weight. The environmental correlations were remarkably positive among the chickpea variables. These are grains per pod with 100-grain weight, main branches per plant with pods per plant and 100-grain weight, main branches per plant with secondary branches per plant, and main branches per plant with 100-grain weight. The presented results were in greater analogy with past findings (Shafique *et al*., 2016; Hussein, 2018). Meanwhile, phenotypic correlation was considerably positive among all traits, and the significant positive phenotypic correlation indicates that any increase in one of two or more traits leads to an increase in other traits.

These results occurred highly analogous to past findings in different chickpea genotypes studied for genetic variability and association among various traits (Debnath, 2021). Moreover, research outcomes align with the study on 17 diverse genotypes of chickpeas for genetic and phenotypic correlation coefficients in 12 quantitative traits (Bhavani *et al*., 2008). Results showed the number of main branches per plant, the number of secondary branches, 100-grain weight, the number of pods per plant, harvest index, and the number of days for flowering up to 50% were the most important traits. They contribute to increasing yield. Hence, an emphasis on these qualities needing more consideration when choosing to obtain the highest yield (Bhavani *et al.,* 2008; Shafique *et al.,* 2016; Hussain, 2018; Debnath, 2021; Aftab *et al.*, 2023).

Results further revealed that making the values of selection indices for the studied genotypes can be more reliable on the selection manual I4, with the highest relative efficiency on the rest of selection indices (Table 6). The chickpea genotype FLIP09-114C, followed by four other genotypes—local, FLIP09-222C, FLIP09-230C, and FLIP09-220C—showed the best performance and exceeded the rest of the genotypes for yield-related traits. Outcomes were consistent with past findings in various chickpea genotypes grown under diverse environmental conditions (Debnath, 2021; Parmar *et al.,* 2022**;** Raghu *et al.,* 2023).

Table 6. Expected genetic advance in seed yield and relative efficiency using several selection indices.

No.	Selection index and its components	Expected advance	Relative efficiency (%)
1	I_1=Seed yield (kg/h) 0.874 X_1	34.921	100
2	I_2=Weight of 100 seeds 0.670 X2(gm)0.670 X_2	21.193	60.687
3	I_3=Number of seeds per pods 0.511X_3	11.402	32.651
4	I_4=Number of pods per plant 0.814X_4	39.493	113.090
5	I_5=Number of secondary branches per plant 0.874	23.358	66.887
6	I_6= Number of main branches per plant 0.527	5.166	14.794
7	I_7=(-0.362)X_1+ 0.755X_2	22.550	64.573
8	I_8= 0.457X_1+ 0.789 X_3	31.643	90.612
9	I_9=0.063X_1+ 0.852X_4	25.007	71.610
10	I_{10}=0.170X_1+ 0.827X_5	25.257	72.325
11	I_{11}= 0.958X_1+0.787 X_6	38.711	72.325
12	I_{12} = 0.405X_2+0.577X_3	23.938	110.851
13	I_{13}= 0.107$X_{2+0.701X4}$	22.889	68.548
14	I_{14}=0.310X2+0.629X5	23.245	65.544
15	I_{15}=0.912X2+0.569X6	28.438	66.564
16	I_{16}=0.195X3+0.849X4	24.995	81.436
17	I_{17}=0.478X3+0.0.743X5	24.075	71.576
18	I_{18}=1.355X3+0.547X6	27.141	68.941
19	I_{19}=0.594X4+0.080X5	20.331	77.720
20	I_{20}=1.932X4+0.104X6	35.200	58.220
21	I_{21}=1.623X5+0.350X6	29.282	100.798
22	I_{22}=0.255X1+0.253X2+0.744X3	29.843	85.458
23	I_{23}=0.295X1+(- 0.017X4+0.800X5	28.072	80.385
24	I_{24}=0.063X1+0.159X5+0.8.25X6	18.336	52.506
25	I_{25}=0.116X2+0.421X3+0.507X4	24.535	70.257
26	I_{26}=0.031X2+0.307X5+0.625X6	17.367	49.732
27	I_{27}=0.036X3+0.473X5+0.735X6	19.930	57.070
28	I_{28}=0.108X4+0.576X5+0.077X6	19.046	54.539
29	I_{29}=0.011X1+0.257X2+0.248X3+0.741X4	28.154	80.622
30	I_{30}=(-0.004X1+0.012X2+0.257X3+0.249X4+0.742X5	25.370	72.648
31	I_{31}=0.23X1+(- 0.022)X2+0.007X3+0.221X4+0.227X5+0.741X6	20.143	57.680

CONCLUSIONS

The findings demonstrated a positive and substantial phenotypic and genetic association among the grains per pod, grain yield, and secondary branches per plant. Selection index I4, which comprised features related to pods per plant, emerged superior. It further authenticated the genetic diversity seen in most chickpea genotypes and their variables, which may benefit the selection of promising genotypes with desirable traits to maximize crop productivity.

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