



Determination of Genetic Association of Yield and Quality Traits in *Cicer arietinum* L. (chickpea)

Binita Xalxo^{1*}, Gabriel M. Lal¹, Sneha Debnath¹ and Avneesh M. Tripathi¹

¹*Department of Genetics and Plant Breeding, Sam Higginbottom University of Agriculture Technology and Sciences, Prayagraj, 211007, Uttar Pradesh, India.*

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was carried out at the field Experimentation Centre, Department of genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P. The experiment on 22 genotypes was laid out in Randomised Block Design with three replications. Observations were recorded on five randomly selected plants to each treatment and replication for 13 quantitative characters viz., days to 50 per cent flowering, days to 50 per cent pod setting, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, 100-seed weight, harvest index, biological yield, seed yield per plant and one qualitative character protein content to estimate the variability, heritability, genetic advance, correlation and path coefficient analysis among yield. Maximum GCV and PCV were recorded for number of pods per plant and 100-seed weight. High genetic advance as percentage of mean recorded for number of pods per plant. High heritability was recorded for 100-seed weight. High genetic advance was recorded for 100-seed weight. Seed yield per plant had showed high positive significant correlation with biological yield per plant, harvest index, number of pods per plant and number of seeds per plant at phenotypic and genotypic levels.

*Corresponding author: E-mail: binita.reshma30@gmail.com;

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1. INTRODUCTION

Chickpea (*Cicer arietinum* L.), is one of the widely grown pulse crop which is consumed by majority of the world's population to supplement protein in our diet. In the Indian sub-continent, where cereal based cropping system occupies maximum acreage, the pulses are now being introduced into the farming system due to its qualitative traits like high protein content, carbohydrates, minerals, nitrogen fixing ability and indispensability as alternative crop for crop diversification. Among these, chickpea is most commonly grown pulse crop which belongs to sub-family Faboideae of family Leguminosae. It is commonly known as gram or Bengal gram in India and is said to have originated in western Asia. Chickpea was cultivated in about 106 Lakh ha during the year 2017-18 and the country harvested a record production of 111 Lakh tones with a productivity level of 1056 kg/ha. Among the pulses growing states M.P has contributed a significant 34 percent of the total chickpea area and 41 percent of total chickpea production in the country, thereby ranking first both in area and production. However, Uttar Pradesh has contributed 5.78 (6.11 Lakh ha) percent of the total chickpea area and 6.13 (6.84 Lakh tones) percent of the total chickpea production in the country [1]. However, this annual legume is mainly grown in arid or semiarid environments.

Legume grains are known to contain 38 to 59% carbohydrate, 4.8 to 5.9% oil, 3% ash, 3% fiber, 0.2% calcium, and 0.3% phosphorus [2]. The protein requirement of about 25g per day for normal individual's health can be met by supply of 120g dal in one's daily diet.

In chickpea association of one or more characters influenced by a large number of genes is elaborated statistically by correlation coefficients. In this regard, varietal improvement and adoption of improved production technology can help in improving the productivity of chickpea. Therefore, the present experiment was conducted to assess genetic variation, trait association and significant contribution of each trait towards yield and quality of the chickpea.

2. MATERIALS AND METHODS

The present investigation was carried out at the field Experimentation Centre, Department of

genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Allahabad, U.P during rabi – 2019 with Twenty Two chickpea genotypes KWR 108, IPC 14-69, Flip 09-109C, IPC 08-69, Flip 09-182C, PDG 8416, ILC – 5411, IPC 71, Flip 07 - 201C, IPCK - 96 – 3, ICCV – 96030, ICC - 12 – 238, Bpm, ICC 12 – 236, ICC 20 – 80, ICCV 15614, ICC 595463, IPC 11 – 09, ICC. 46(K), IPC - 08 – 83, IPC - 06 – 11, Uday (Check) was laid out in Randomised Block Design suggested by Panse and Sukhatme with three replications.

All types of facilities necessary for cultivation of successful crop including field preparation, input and irrigation facilities were provided.

Readings from five plants were averaged, replication wise and the mean data was used for statistical analysis for the characters thirteen quantitative characters viz., days to 50 per cent flowering, days to 50 per cent pod setting, days to maturity, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, number of seeds per plant, 100-seed weight [3] harvest index, biological yield, seed yield per plant and one qualitative character protein content, estimated by using Lowry's method (Lowry *et al.*, 1951) to estimate the variability, heritability, genetic advance and correlation among yield.

Biometric analysis including analysis of variance was carried out for each character separately as per the method outlined by Panse and Sukhatme (1985). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated as per the formula suggested by Burton (1952) while heritability in broad sense by Lush (1940) and genetic advance as per cent of mean by Johnson *et al.* [4] and correlation coefficient analysis (Al Jibouri *et al.*, 1958) were done with the assistance of software **Windostat 9.3 ver.**

3. RESULTS AND DISCUSSION

The analysis of variance for all the characters revealed differences among the genotypes studied, indicating sufficient amount of variability present among 22 genotypes under study.

The variation among the chickpea genotypes in this study would provide great opportunities for

the genetic improvement of the crop through direct selection of genotypes or through hybridization using as parents possessing the desirable traits.

Estimates of genotypic and phenotypic coefficient of variation, heritability percentage in broad sense, genetic advance and expected genetic advance expressed as percent of mean are presented in Table 2.

Genotypic coefficient of variation (GCV) ranged from 4.21 % for Days to 50 % Pod setting to 43.37 % for number of pods per plant. High GCV was recorded for number of pods per plant. Similar findings were reported by Arora and Jeena (2001), who found high genotypic variation for seed yield per plant. It was depicted that in general, estimates of the phenotypic coefficient of variation was found higher than their corresponding genotypic coefficient of variation, indicating that the influence of environment on the expression of these characters. Phenotypic coefficient of variation (PCV) ranged from 6.91 % for Days to 50 % pod setting to 45.21 % for number of pods per plant. High PCV was recorded for number of pods per plant [3]

The estimates of heritability (%) in the broad sense for 14 characters studied, which ranged from 100-seed weight (99.50) and low for days to 50% flowering (32.30). High heritability (broad sense) (>60%) was recorded for character 100-seed weight, protein content, biological yield, seed yield per plant, days to maturity, number of seeds per plant, number of pods per plant, plant height and harvest index. Similar finding were described by Arshad et al. (2002). Moderate heritability (broad sense) (30-60%) was recorded for characters *i.e.*, days to 50% flowering, days to 50% pod setting, number of primary branches, number of secondary branches, number of seeds per pod. Low heritability (broad sense) (<30%) was not recorded for any of the characters.

High genetic advance was recorded for 100-seed weight (19.54). The worth of genetic advance indicates additive gene action whereas low value indicates non-additive gene action. Genetic advance as % mean varied from 85.71 to 4.93 for number of pods per plant and days to 50 % flowering [3]

Low GCV with moderate to high heritability along with medium to low genetic advance as

per cent mean was observed for the characters days to maturity, plant height, harvest index, seed yield per plant, number of seeds per pod. It indicates that the character is highly influenced by environmental effects and selection would be ineffective. This indicated these characters are under control of additive gene effect (Panse, 1957). Therefore, for further improvement in these traits, mass selection or progeny selection would be worthwhile. Whereas the character like 100-seed weight showed medium GCV along with high heritability coupled with high genetic advance as present of mean pointing towards the fact that is appreciable genetic potential and further improvement possible by practicing simple selection technique.

3.1 Correlation Analysis

The results of present study, which revealed comparative higher degree of genotypic correlation coefficients than their phenotypic counterparts in most of the characters, indicated that there was a higher degree of association between two characters of genotypic association, their phenotypic association was lessened due to the influence of environment.

Positive and significant correlation were observed for number of pods per plant (0.522**, 0.533**), number of seeds per plant (0.454**, 0.465**), biological yield (0.887**, 0.879**) and harvest index (0.570**, 0.562**) with seed yield per plant at genotypic level and phenotypic level. Similar results were obtained by Toker and Cagirgan (2004) and Obaidullah et al. [5] While with rest of the characters has non-significant association with seed yield. Days to 50 per cent pod setting showed significant and positive correlation with days to maturity, days to maturity showed significant and positive correlation with plant height, plant height showed significant and positive correlation with primary branches per plant and harvest index [3] number of primary branches showed significant and positive correlation with number of secondary branches, number of pods per plant showed significant and positive correlation with number of seeds per plant and biological yield per plant, number of seeds per pod showed significant and positive correlation with 100-seed weight, number of seeds per plant showed significant and

positive correlation with biological yield per plant, harvest index, protein content and seed yield per plant. Biological yield per plant showed significant and positive correlation with protein content. And all the other characters showed either negative or non-significant correlation.

Therefore, the number of pods per plant is likely to be used as selection parameter for yield improvement in chickpea as by Toker and Cagirgan (2004) and [6,7].

4. DISCUSSION

If different yield related traits are well documented, selection based on yield components is advantageous (Pundir *et al.*, 1988, Singh *et al.*, 1990, Verma *et al.*, 2008). The present investigation will help us in selection of parameters well suited for yield improvement in chickpea [8-15].

Our results are in agreement with those reported by Arora *et al.*, 2003 having significant and positive correlation with number of pods per

plant, number of seeds per plant, biological yield and harvest index with seed yield per plant revealing these parameters of utmost importance. Subsequently, the number of pods per plant is most likely to be utilized as choice parameter for surrender change in chickpea as by Toker and Cagirgan (2004) and Ali *et al.*, 2010, 2011. Protein content showed low levels of PCV and GCV signifying limited scope for further genetic improvement through selection. These findings were in conformity with findings of Jayalakshmi and Trivikrama Reddy (2018) for protein content. And those of genetic advance and heritability pertained additive gene effect, hence the characters showing additive gene effect is not suitable for selection. Accordingly, the study indicated that the parameters considered in the present study can be effectively used for selection in chickpea. Seed yield is determined by these characteristics, which can be used as most dependable traits for further improving chickpea crop productivity. And those of genetic advance and heritability pertained additive gene effect, hence the characters showing additive gene effect is not suitable for selection [16-24].

Table 1. Analysis of variance for 14 biometrical traits of 22 chickpea genotype

S.No.	Character	Mean Sum of Squares		
		Replication (d.f = 2)	Treatment(d.f = 21)	Error (d.f=42)
1	Days to 50% flowering	38.652	52.211**	21.477
2	Days to 50% Pod setting	11.561	72.428**	18.783
3	Days to Maturity	2.924	208.906**	3.099
4	Plant height	2.511	205.386**	9.711
5	No. of primary branches	0.255	0.643**	0.157
6	No. of secondary branches	0.15	1.657**	0.244
7	No. of pods per plant	0.937	66.777**	1.874
8	No. of seeds per pod	0.024	0.52**	0.099
9	No. of seeds per plant	0.116	222.513**	3.893
10	100 Seed weight	5.337**	271.849**	0.486
11	Biological yield	0.642	22.36**	0.252
12	Harvest Index	55.841**	292.673**	8.985
13	Seed yield per plant	0.139	12.378**	0.185
14	Protein Content	0.338*	9.908**	0.071

Table 2. Estimates of genetic components for yield and quality traits of chickpea

S.No	Character	Vg	Vp	GCV	PCV	Heritability (Broad Sense)(%)	GA	GA as %mean
1	Days to 50% flowering	10.24	31.72	4.21	7.41	32.30	3.75	4.93
2	Days to 50% Pod setting	17.88	36.65	4.82	6.91	48.80	6.08	6.94
3	Days to Maturity	68.60	71.70	7.34	7.51	95.70	16.69	14.80
4	Plant height	65.25	74.93	15.48	16.60	87.00	15.52	29.76
5	No. of primary branches	0.162	0.391	12.42	17.42	50.90	0.59	18.24
6	No. of secondary branches	0.471	0.715	12.28	15.13	65.80	1.15	20.52
7	No. of pods per plant	21.63	23.50	43.37	45.21	92.00	9.19	85.71
8	No. of seeds per pod	0.14	0.239	28.61	37.38	58.60	0.59	45.11
9	No. of seeds per plant	72.87	76.76	35.56	36.50	94.90	17.13	71.37
10	100 Seed weight	90.45	90.94	39.66	39.77	99.50	19.54	81.49
11	Biological yield	7.36	7.62	26.41	26.86	96.70	5.50	53.50
12	Harvest Index	94.56	103.54	16.16	16.91	91.30	19.14	31.81
13	Seed yield per plant	4.06	4.24	32.43	33.16	95.60	19.14	31.81
14	Protein content	3.27	3.35	8.09	8.17	97.90	3.69	16.48

Vg = Genotypic variance, *Vp* = Phenotypic variance, *GCV* = Genotypic coefficient of variance, *PCV* = Phenotypic coefficient of variance, *h² (BS)%* = Heritability (broad sense), *GA* = Genetic advance, *GA as % of mean* = Genetic advance as percent of mean

Table 3. Genotypic and phenotypic correlation for yield and quality traits of chickpea

	DF 50%	DP 50%	DM	PH	NPB	NSB	NP/Plant	NS/Pod	NS/Plant	100 SW	BY/Plant	HI	Protein Content	SY/Plant
DF 50%														
G	1.000	0.378**	0.071	0.296*	0.552**	0.559**	-0.051	-0.043	0.060	0.124	0.084	-0.039	0.072	0.049
P	1.000	1.000	0.1266	0.0476	0.3025	0.1355	-0.0364	0.0427	0.0443	0.0677	0.0555	-0.0268	0.0398	0.0323
DP 50%														
G		1.000	0.587**	-0.119	0.276*	0.043	0.296*	-0.059	0.262*	-0.422**	0.356	-0.388**	0.419**	0.110
P		1.000	0.4156**	-0.0977	0.0714	0.073	0.2244	-0.0001	0.1724	-0.2774	0.2233	-0.2117	0.2735	0.0839
DM														
G			1.000	0.376**	0.188	0.004	0.313*	-0.095	0.037	-0.185	0.225	-0.017	0.152	0.132
P			1.000	0.3461**	0.1728	0.0009	0.3140*	-0.0825	0.0359	-0.1797	0.2253	-0.0185	0.1404	0.1319
PH														
G				1.000	0.336**	-0.120	0.009	-0.010	-0.177	0.203	0.029	0.394**	-0.299*	0.168
P				1.000	0.2859*	-0.0961	0.0256	-0.0447	-0.163	0.1877	0.0441	0.3391**	-0.2768*	0.1614
NPB														
G					1.000	0.662**	-0.374**	-0.119	-0.113	0.128	-0.126	-0.149	0.011	-0.157
P					1.000	0.4073**	-0.2630*	-0.0926	-0.1071	0.0833	-0.0899	-0.1109	0.0198	-0.1227
NSB														
G						1.000	-0.174	-0.385**	0.079	0.035	-0.113	-0.286*	-0.017	-0.212
P						1.000	-0.1367	-0.2563*	0.0229	0.0279	-0.1154	-0.2268	-0.0126	-0.201
NP/Plant														
G							1.000	0.096	0.779**	-0.014	0.595**	0.136	0.236	0.522**
P							1.000	0.1081	0.7635**	-0.0096	0.5999**	0.1321	0.2137	0.533**
NS/Pod														
G								1.000	0.160	0.323**	0.050	0.208	-0.482**	0.174
P								1.000	0.1409	0.2460*	0.064	0.1566	-0.3609**	0.1573
NS/Plant														
G									1.000	-0.052	0.375**	0.324**	0.326**	0.454**
P									1.000	-0.0464	0.3816**	0.3155**	0.3108*	0.465**
100 SW														
G										1.000	0.044	0.074	-0.465**	0.089
P										1.000	0.0429	0.0783	-0.4620**	0.0909

BY/Plant				
G	1.000	0.135	0.253*	0.887**
P	1.000	0.1134	0.2429 *	0.879**
HI				
G		1.000	-0.095	0.570**
P		1.000	-0.0948	0.562**
Protein Content				
G			1.000	0.171
P			1.000	0.1578
SY/Plant				
G				1.000
P				1.000

** Significant at 1% level and * significant at 5% level

5. CONCLUSION

The assesment of genetic parameters like genotypic and phenotypic coefficient of variation, heritability and genetic advance as per cent of mean indicated that selection must be done in the characters like number of pods per plant, number of seeds per plant, biological yield and harvest index for improving the yield and nutritional traits to generate genetic variability followed by selection in further generations to identify superior segregants for these characters.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Anonymous. DES, Ministry of Agri. & FW (DAC & FW), Govt. of India; 2017-18-IIIrd *Adv. Est*; 2018.
2. Hulse JH. Nature, composition and utilization of grain legumes. In: Uses of tropical Legumes: Proceedings of a Consultants' Meeting. 27-30 March 1989, ICRISAT Center ICRISAT, *Patancheru, A.P.* 502324 India. 1991;11-27.
3. Teklu DH, Kebede SA, Gebremichael DE. Assessment of genetic variability, genetic advance, correlation and path analysis for morphological traits in sesame genotypes. *Asian Journal of Agricultural Research*. 2014;8(4):181-94.
4. Johnson PL, Pandey RL, Gour PM, Sharma RN, Nair SK, Kashyap OP. Study of genetic diversity and variability in desi chickpea (*Cicer arietinum* L.) for rainfed rice (*Oryza sativa*) chickpea cropping system of Chhattisgarh. *Current Advances in Agricultural Sciences*; 2009; 1(2):80-82.
5. Obaidullah S, Munawar K, Iqbal A, Hamayun K, Regression and correlation analysis in various cultivars of chickpea. *Indian Journal of Plant Science*. 2006;5(1):680-685.
6. Ali Q, Ahsan M, Farooq J, Saleem M Genetic variability and trait association in chickpea (*Cicer arietinum* L.). *Elec. Journal of Plant Breeding*. 2010;1(3):328-333.
7. Ali Q, Ahsan M, Khaliq Ihsan, Elahi M, Shahbaz M, Ahmed W, Naees M. Estimation of genetic association of yield and quality traits in chickpea (*Cicer arietinum* L.) . *International Research Journal of Plant Science*. 2011;2(6):166-169
8. Assefa A, Hagos T, Desalegn, Tesfay B. Genetic variability, correlation and path analysis for quantitative traits of seed yield, and yield components in chickpea (*Cicer arietinum* L.) at Maichew. Northern Ethiopia, *African Journal of Plant Sciences*. 2018;12(30):58-64.
9. Aswathi PV, Ganesamurthy K, Jayamani P. Genetic variability for morphological and biometrical traits in chickpea (*Cicer arietinum* L.). *Electronic Journal of Plant Breeding*. 2019;10(2):699-705.
10. Budh B, Singh S, Kumar P. Study on correlation and path analysis in blackgram (*Vigna mungo*. L. Hepper). *Legumes Research*. 2014;18(2):25-28.
11. Caliskan S, Erdogan C, Arslan M, Caliskan ME. Comparison of organic and traditional production systems in chickpea (*Cicer arietinum* L.). *Turkish Journal Field Crops*. 2013;18:34-29.
12. Dehaiindu Bala, Kalia, R, Kumar, B. Genetic variability, correlation of kabuli type chickpea (*Cicer arietinum* L.) under normal and late sown environments. *Legumes Research*, 2016; 39(4):510-516.
13. Kumar A, Nath S, Kumar A, Yadav AK. Study of variability, heritability and genetic advance for some quantitative traits in chickpea (*Cicer arietinum*L.). *Journal of Pharmacognosy and Phytochemistry*. 2018;7(2):487-489.

14. Mohan S, Thiyagarajan. Genetic variability, correlation and path coefficient analysis in chickpea (*Cicer arietinum* L.) for yield and its component traits. *International Journal of Current Microbiology and Applied Sciences*. 2019;8(5):1801-1808.
15. Mohammed A, Tesso B, Ojiewo C, Ahmed S. Assessment of genetic variability and heritability of agronomic traits in Ethiopian chickpea (*Cicer arietinum* L.) landraces. *Black Sea Journal of Agriculture*. 2019;2(1):10-15.
16. Neugschwandtner RW, Wichmann S, Gimplinger DM, Wagentristl H, Kaul H-P. Chickpea performance compared to pea, barley and oat in central Europe: growth analysis and yield. *Turkish Journal of Field Crops* 2013;18(2):179-184
17. Raju T, Sadhukhan R, Sathish V. Genetic variability studies in chickpea (*Cicer arietinum* L.) for yield and yield related traits. *Bull. Env. Pharmacol. Life Sci*. 2017;6(2):177-183
18. Smýkal P, Coyne CJ, Ambrose MJ, Maxted N, Schaefer H, Blair MW, Jens Berger, Stephanie L. Greene, Matthew N. Nelson, Naghmeh Besharat, Tomáš Vymyslický, Cengiz Toket, Rachit K. Saxena, Manish Roorkiwal, Manish K. Pandey, Jinguo Hu, Ying H. Li, Li X. Wang, Yong Guo, Li J. Qiu, Robert J. Redden & Rajeev K. Varshney. Legume crops phylogeny and genetic diversity for science and breeding. *Critical Reviews in Plant Sciences* 2015;34 (1-3): 43-104.
19. Srivastava S, Roopa Lavanya G, Lal GM. Genetic variability and character association for seed yield in chickpea (*Cicer arietinum* L.). *Journal of Pharmacognosy and Phytochemistry*. 2017;6(4):748-750.
20. Toket C, Cagiran MI. The use of phenotypic correlations and factor analysis in determining characters for grain yield selection in chickpea (*Cicer arietinum* L.). *Hereditas*. 2004;140(3):226-228.
21. Toket C, Uzun B, Ceylan FO, Ikten C. Chickpea. In: Alien Gene Transfer in Crop Plants, A. Pratap and J. Kumar Eds., Volume 2, Springer, Dordrecht. 2014;121-151.
22. Tonk FA, Ilker E, Tosun M. A study to incorporate high protein content from tetraploid wheat (*T. turgidum* dicoccoides) to hexaploid wheat (*T. aestivum* vulgare). *Turkish Journal of Field Crops*. 2010;15:69-72.
23. Yücel D. Response of chickpea genotypes to drought stress under normal and late sown conditions. *Legume Research*. 2018;41(6):885-890.
24. Zia-Ul-Haq M, Ahmad M, Iqbal S, Ahmad S, Hakooma A. Characterization and compositional study of oil from seeds of desi chickpea (*Cicer arietinum* L.) cultivars grown in Pakistan. *Journal of American Oil Chemical Society*. 2007;84:1143-11.

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