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Genetic Variability, Correlation and Path coefficient Studies in Chickpea (*Cicer arietinum* L.) Genotypes in South Eastern Rajasthan

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ABSTRACT: The experiment entitled "Genetic variability, correlation and path coefficient studies in chickpea (*Cicer arietinum* L.) Genotypes" was conducted at Agricultural Research Station, Ummedganj, Kota, Agriculture University, Kota, (Rajasthan). The experiment was carried out in randomized block design involving forty chickpea genotypes with three replications during *rabi* 2019-20. Good amount of variation was recorded for number of pods per plant, biological yield per plant, plant height, days to 50 per cent flowering, harvest index, seed yield per plant and days to maturity. The maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were found for protein content followed by seed yield per plant, number of pods per plant and number of branches per plant. High heritability associated with high genetic advance as per cent of mean for protein content, seed yield per plant, number of pods per plant, plant height and 100 -seed weight were denotative that more weightage should be given to these all the characters while selection assist for improvement in crop yield. Correlation study manifested that seed yield per plant expressed highly significant positive correlation along with biological yield per plant, number of seeds per pod, no. of pods per plant, harvest index and number of branches per plant. Path coefficient analysis manifested the highest positive direct and indirect effect of biological yield per plant and harvest index on seed yield per plant, thereby contributing positively to seed yield per plant both directly as well as indirectly. Number of pods per plant had high heritability, genetic advance as per cent of mean and indicates significant positive correlation with seed yield. Biological yield and harvest index also had significant positive correlation and highest positive direct and indirect effect on seed yield. Therefore, these characters should be used in breeding programme for further crop advancement.

Keywords: Chickpea, Genetic Variability, Path coefficient, South Eastern Rajasthan.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is important annual food legume crop belongs to genus *Cicer* tribe *Cicereae* family Leguminosae (Fabaceae) and sub family Papilionaceae (Bentham and Hooker, 1972). India is one of the leading pulses producing country of the world. It is growing mainly on lands under rainfed condition in *rabi* season (Shiyani *et al.*, 2001).

In India, chickpea is cultivated in 10.76 million hectares area with a production of 11.16 million tons and productivity of 1037 kg/ha. (Project Coordinators Report, AICRP on Chickpea, IIPR, Kanpur, 2017-18). Rajasthan ranked third in area and production with 14% and 15% share of the chickpea area along with production in India (Anonymous, 2017-18). Chickpea is cultivated in 15.72 lakh hectares area in Rajasthan with a production of 16.70 lakh tons and productivity of 1062 kg/ha (2017-18). Therefore, urgent need of the hour is to increase pulses and chickpea production and productivity in order to reduce imports, monetary savings and to achieve self-sufficiency.

Availability of sufficient genetic variability found in the experimental material is very important in a successful crop improvement programme. Hence, it is necessary for a plant breeder to scale the variability with the aid of parameters like GCV, PCV, heritability and genetic advance. These parameters provide the information with respect to the availability of genetic variability for different traits in experimental genotypes. Hence, the investigation of genetic variability for seed yield and its contributing characters amid contrasting varieties give a strong support for selection of favored genotype for magnification of yield and other agronomic traits.

Different elements of seed yield fairly often exhibit varied degree of associations with seed yield furthermore as among themselves. In order to collect optimum combination of seed yield contributing traits in the single genotype, it's essential to grasp the connection among themselves. Further, the seed yield is affected by its numerous parts directly or indirectly *via* different characters that make a posh scenario before a breeder for creating fascinating choice. Therefore, path coefficient analysis may offer a lot of realistic image of the interrelation, because it partitions the correlation coefficient into direct and indirect effects of variables. Thus, characters association and path analysis offer the data for the isolation of superior accession from the population.

A major limit line within the improvement of chickpea is that the restricted genetic variability available for most different agronomic traits. Genetic variability in any crop species is a prerequisite for making effective selections. Correlation and path coefficient analysis are also important tools to gain information about the interrelationship of various characters, which are also of immense help in a selection programme to be adopted by a plant breeder for rapid genetic enhancement. The current investigation was undertaken to review extent genetic variability, correlation and path coefficient for yield and yield contributory characters in chickpea genotypes.

MATERIALS AND METHODS

Forty chickpea genotypes were sown in randomized block design along with three replications during *rabi* 2019-20 at Agricultural Research Station, Ummedganj, Kota, Rajasthan. All genotype were accommodated in four row plot of 4.0 m length with plant to plant spacing of 30×10 cm. The genotypes were randomly allotted to each plot in each replication. All the recommended agronomic package of cultivation practices were followed timely for successful rising of crop. Observations were recorded on five randomly selected plants per replication for eleven traits *viz.*, plant height, number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100-seed weight, protein content and seed yield per plant except days to 50% flowering and maturity which were recorded on plot basis. The mean values were used for calculate variance by Panse and Sukhatme (1985). The coefficient of variation was analyses by Burton, (1952). Heritability (bs) and genetic advance were calculated by following Hanson *et al.*, (1956). Correlation coefficients at phenotypic and genotypic level were estimated by as per the methods suggested by Al-Jibouri *et al.*, (1958). Path coefficients were calculated according to Dewey and Lu (1959). Protein content was estimated according to (Lowry *et al.*, 1951).

Analysis of variance: The analysis of variance including source of variations, their degree of freedom (D.F.) and expectations of mean squares are given below:

Source of variation	D. F.	M. S.	Expectations of M. S.
Replication	(r-1)	MSr	$\sigma^2 e + g\, \sigma^2 r$
Genotypes	(g-1)	MSg	$\sigma^2 e + r\, \sigma^2 g$
Error	(r-1) (g-1)	MSe	$\sigma^2 e$
Total	(r g – 1)		

Where,

r = Number of replications

g = Number of genotypes

MSr = Mean sum of square due to replications

MSg = Mean sum of square due to genotypes

MSe = Mean sum of square due to error

$\sigma^2 g$ = Genotypic variance

$\sigma^2 r$ = Replication variance

$\sigma^2 e$ = Error variance

Correlation coefficients analysis: The correlation coefficients were calculated to determine the degree of association of the characters with yield and its attributes. Genotypic and phenotypic correlation coefficients were worked out by a method described by Singh and Chaudhary, (1979).

(a) The genotypic correlation

$$r_{xy}\,(g) = \frac{\text{Cov. xy (g)}}{\sqrt{\text{Vx(g).Vy(g)}}}$$

(b) The phenotypic correlation

$$r_{xy}\,(p) = \frac{\text{Cov. xy (p)}}{\sqrt{\text{Vx(p).Vy(p)}}}$$

Where,

r_{xy} (g) = Genotypic correlation between x and y traits

r_{xy} (p) = Phenotypic correlation between x and y traits

Cov. xy (g) = Genotypic covariance for x and y traits

Cov. xy (p) = Phenotypic covariance for x and y traits

V_x (g) = Genotypic variance for x trait

V_y (g) = Genotypic variance for y trait

V_x (p) = Phenotypic variance for x trait

V_y (p) = Phenotypic variance for y trait

Test of significance: The significance of correlation coefficient was tested using the following formula:

$$t = \frac{r\sqrt{n-2}}{\sqrt{1-r2}}$$

Path coefficient analysis: The direct and indirect effects were estimated using path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959). The following equations were solved for estimating the various direct and indirect effects.

$r_{1y} = P_{1y} + r_{12}P_{2y} + \ldots\ldots\ldots\ldots + r_{1p}P_{py}$

$r_{2y} = r_{21}P_{1y} + P_{2y} + \ldots\ldots\ldots\ldots + r_{2p}P_{py}$

$R_{py} = r_{p1}P_{1y} + r_{p2}P_{2y} + \ldots\ldots\ldots\ldots + P_{py}$

Where,

P_{1y}, P_{2y}……………P_{py} are direct effects of character 1,2, ………..p on y and

r_{1y}, r_{2y}…………r_{py} denotes correlation coefficient between independent characters

1,2……..p and dependent character 'Y'.

Residual effect was calculated using the following formula:

$$P_{Ry} = \frac{1 = P^2Ry + \Sigma P_{iy}R_{iy}}{\sqrt{}\, 1 - (P_{1y}r_{1y}) - (P_{2y}r_{2y}) \ldots (P_{iy}r_{iy})}$$

Where,

P_{Ry} is the residual effect

RESULTS AND DISCUSSION

The analysis of variance manifested that mean square due to the genotypes were highly significant for every characters take in present experiment justifying the choice of the experimental material. The overall analysis of ANOVA indicated wide genetic variability available in the experimental material studied that can be further exploited for chickpea improvement program. Ample range of variations were recorded for number of pods per plant, biological yield per plant, plant height, days to 50 per cent flowering, harvest index, seed yield per plant and days to maturity. The protein content, 100-seed weight and number of branches per plant indicated moderate range of magnitude. That variability available for quantitative characters in the current study could effectively utilized for chickpea Improvement. Similarly, considerably high amount of variability was reported earlier by many workers for different characters (Jadhav *et al.*, 2012; Dev *et al.*, 2017).

Table 1: Mean, range, phenotypic and genotypic coefficients of variation, heritability (broad sense), genetic advance and genetic advance expressed as percentage of mean for eleven characters in chickpea.

Sr. No.	Characters	Range		Mean	Phenotypic coefficient of variation (%)	Genotypic coefficient of variation (%)	Heritability (broad sense) (%)	Genetic advance	Genetic advance as % of mean
		Min.	Max.						
1.	Days to 50% flowering	62.67	77.67	72.69	6.40	6.17	92.87	8.90	12.24
2.	Days to maturity	113.00	125.00	119.17	2.79	2.59	86.79	5.94	4.98
3.	Plant height (cm)	43.27	64.80	57.10	10.47	9.97	90.56	11.16	19.54
4.	No. of branches plant^{-1}	7.67	13.07	10.40	16.49	13.46	66.63	2.35	22.63
5.	No. of pods plant^{-1}	36.80	77.60	54.78	18.33	18.07	97.12	20.09	36.68
6.	No. of seeds pod^{-1}	1.00	1.53	1.26	14.33	10.98	41.25	0.15	12.18
7.	100-seed weight (g)	16.60	25.48	21.23	11.20	10.40	86.35	4.23	19.92
8.	Biological yield plant^{-1} (g)	19.47	42.13	31.59	9.77	8.37	73.51	6.53	14.79
9.	Harvest index (%)	36.55	50.78	44.19	10.12	8.55	71.30	3.21	14.87
10.	Protein content (%)	18.07	25.60	21.60	25.43	24.41	92.11	6.76	48.26
11.	Seed yield plant^{-1} (g)	8.43	21.40	14.02	20.97	20.42	94.81	12.94	40.97

The PCV was higher than that of GCV in most of the experiments, pointing impression of environmental factors in the expression of the trait as also recorded by Jivani *et al.*, (2013); Alemayo *et al.*, (2021). The calculation of GCV and PCV are mostly required for the knowledge about the act of environmental effects on different characters. The maximum GCV and PCV were recorded for protein content followed by seed yield per plant, number of pods per plant and number of branches per plant. High magnitude of GCV revealed that, the presence of high variation for the traits under experiment to allow further crop improvement by selection of the particular traits. Same data were also recorded by Balasaheb *et al.*, (2018). The plant height, 100-seed weight, harvest index, biological yield per plant and number of seeds per pod had moderate GCV and PCV. While low estimates of GCV and PCV was observed for days to 50% flowering and days to maturity. Such results were also reported by Jadhav *et al.*, (2012); Yadav *et al.*, (2015).

The relative magnitude of difference between Phenotypic coefficient of variation and genotypic coefficient of variation was low for days to maturity, days to 50% flowering, plant height, number of pods per plant, seed yield per plant, 100- seed weight and protein content, revealed that these all characters were less influenced by the environmental factors. Similar results were also reported by Yadav *et al.*, (2015). Jivani *et al.*, (2013); Shanmugam and Kalaimagal (2019) also observed lesser environmental influence for days to maturity and days to 50 per cent flowering.

Findings of GCV and PCV recommended that selection can be useful on the premise of phenotype along with equable consideration of genotypic values.

Characters are showing high heritability along with high genetic advance often indicates that heritability is high due to the additive gene effect and advocates the exploitation of high heritability estimates along with high volume of genetic advance for genetic improvement in any character through selection. Based upon the present investigation, it's suggested that the protein content, seed yield per plant, number of pods per plant, plant height and 100-seed weight showing high heritability along with high genetic advance as per cent of mean should be utilized for direct selection for future genetic enhancement of chickpea. Similar findings were recorded by Aarif *et al.*, (2014); Yadav *et al.*, (2015); Gautam *et al.*, (2021).

The yield is a complex character and the multiplicative end product of many quantitative traits (Whitehouse *et al.*, 1958). The various components of crop yield usually exhibit considerable degree of association into themselves and with seed yield. Therefore, knowledge about the relationship of various plant traits with crop yield and among themselves is very important as it facilitates the quicker evaluation of high yielding genotypes in crop improvement programme. The capability for crop yield improvement through tempering of yield contributes has needed a proper understanding of the magnitude of correlations amid different yield characters. The phenotypic selection may sometime mislead the breeder as phenotypic expression is the result of interplay between genotypes and environmental factors. The estimate of any phenotypic correlation coefficient is not providing sufficient information to fully evaluate the correlation amid couple of characters. Only Genotypic correlation is providing true information about correlation with eliminates the environmental effects.

In the investigation, the estimates of phenotypic correlation coefficient in general were higher than the genotypic correlation coefficient. The phenotypic correlation of days to 50 per cent flowering with days to maturity, plant height, number of seeds per pod and harvest index; days to maturity with plant height, number of seeds per pod and harvest index; plant height with 100-seed weight and biological yield; number of branches per plant with number of seeds per pod, biological yield per plant and seed yield per plant; number of pods per plant with seed yield per plant, number of seeds per pod and harvest index; harvest index with protein content; biological yield per plant with seed yield and harvest index was higher than the genotypic correlation. Similar findings were also earlier recorded by Jivani *et al.*, (2013); Bhanu *et al.*, (2017); Shanmugam and Kalaimagal (2019). Seed yield per plant was found to be positive and highly significantly correlated with biological yield per plant, number of pods per plant, harvest index, number of seeds per pod and number of branches per plant at both the genotypic and phenotypic level indicating that these traits contributed directly towards seed yield and were important yield contributing characters in chickpea and any positive increase in such traits will accelerate the boost in seed yield per plant. Similar results were also earlier reported by Anita *et al.*, (2015); Shanmugam and Kalaimagal (2019); Manikanteswara *et al.*, (2019). The 100-seed weight, days to maturity and plant height showed non-significant but positive correlation with seed yield per plant at both levels, which is in conformity with the earlier reports by Singh *et al.*, (2017). While the seed yield per plant had negative and non-significant correlation with protein content and days to 50% flowering also reported by Anita *et al.*, (2015). Number of branches per plant, number of pods per plant, number of seeds per pod, biological yield per plant and harvest index are the important yield determiners because they had significant correlation with seed yield per plant and among themselves also showing importance of these yield contributing characters. These traits could appropriately be used as selection criteria.

Table 2: Estimates of Phenotypic and Genotypic correlation coefficient for different characters of chickpea (*Cicer arietinum* L.).

Characters		**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches plant^{-1}**	**No. of pods plant^{-1}**	**No. of seeds pod^{-1}**	**100 -seed weight**	**Biological yield plant^{-1}**	**Harvest index (%)**	**Protein content (%)**	**Seed yield plant^{-1}**
Days to 50% flowering	**GP**	**1.000** **1.000**	0.569** 0.655**	0.205* 0.226*	-0.351** -0.423**	-0.071 -0.065	0.053 0.205*	-0.055 -0.076	-0.048 -0.051	0.056 0.062	-0.191* -0.262**	-0.006 -0.008
Days to maturity	**GP**		**1.000** **1.000**	0.239** 0.282**	-0.244** -0.373**	0.066 0.065	0.014 0.107	0.020 0.005	-0.007 -0.006	0.215* 0.293**	-0.070 -0.117	0.093 0.117
Plant height (cm)	**GP**			**1.000** **1.000**	-0.080 -0.116	-0.111 -0.121	-0.069 -0.099	0.136 0.185*	0.030 0.039	-0.049 -0.088	-0.113 -0.102	0.012 0.011
No. of branches plant^{-1}	**GP**				**1.000** **1.000**	0.396** 0.366**	0.230* 0.572**	-0.046 -0.091	0.384** 0.491**	0.056 0.146	0.169 0.308**	0.334** 0.456**
No. of pods plant^{-1}	**GP**					**1.000** **1.000**	0.234* 0.486**	0.038 0.030	0.751** 0.772**	0.504** 0.579**	-0.117 -0.147	0.819** 0.851**
No. of seeds pod^{-1}	**GP**						**1.000** **1.000**	-0.194* -0.631**	0.421** 0.962**	0.135 0.305**	0.046 0.354**	0.399** 0.903**
100-seed weight	**GP**							**1.000** **1.000**	0.176 0.191*	-0.011 -0.006	-0.032 -0.015	0.159 0.178
Biological yield plant^{-1}	**GP**								**1.000** **1.000**	0.239** 0.269**	-0.011 -0.031	0.926** 0.941**
Harvest index (%)	**GP**									**1.000** **1.000**	-0.036 -0.003	0.580** 0.571**
Protein content (%)	**GP**										**1.000** **1.000**	-0.031 -0.032
Seed yield plant^{-1}	**GP**											**1.000** **1.000**

*, ** significant at 5% and 1% levels, respectively

Path coefficient analysis is most useful statistical techniques in appraise the inter-dependence of traits and the extent of effects of independent traits either directly or indirectly on seed yield (Mushtaq *et al.*, 2012). The information of direct and indirect effect of yield contributing traits on the ultimate last product i.e. yield in any crop is of elite needfulness in selecting high yielding genotypes.

In the present investigation, highest positive direct effect on seed yield per plant was recorded by biological yield per plant and harvest index. Both of these characters turned out to be the major components of seed yield as they also had high significant positive correlation with seed yield. So, these characters should be selected for yield improvement in chickpea. Similar results were reported earlier by Jivani *et al.*, (2013); Shanmugam and Kalaimagal (2019). The characters like 100-seed weight, days to maturity, days to 50% flowering exerted low positive direct effect towards seed yield per plant owing to their non-significant positive correlation with seed yield. These results are in agreement with the findings of Bhanu *et al.*, (2017).

The number of pods per plant, number of branches per plant, number of seeds per pod also had low positive direct effect on seed yield in spite of having significant positive correlation with seed yield. Although, the number of pods per plant and number of branches per plant had low positive direct effect on seed yield per plant but they had high positive indirect effect *via* biological yield per plant and harvest index thus indicating that these high positive indirect effects were responsible for their significant positive correlation with seed yield per plant. Similar results were also reported by Dev *et al.*, (2017). Number of seeds per pod had significant positive correlation with seed yield at both phenotypic and genotypic level but the high magnitude of difference between phenotypic and genotypic correlation estimates indicated the role higher of environmental component, thereby disturbing the correspondence between genotypic and phenotypic estimates and resulting in its low positive direct effect on seed yield.

Path analysis indicated that the traits biological yield per plant and harvest index showed highest direct and indirect effects on seed yield per plant. Similar results were obtained by Shanmugam and Kalaimagal (2019). Both these traits also exhibited significant positive association with seed yield per plant. Therefore, the importance should be given to the selection based on these traits to realize a significant yield increase in chickpea.

Table 3: Genotypic and Phenotypic path coefficient analysis showing direct and indirect effects of different characters on seed yield in chickpea (*Cicer arietinum* L.).

Characters		**Days to 50% flowering**	**Days to maturity**	**Plant height (cm)**	**No. of branches plant^{-1}**	**No. of pods plant^{-1}**	**No. of seeds pod^{-1}**	**100 - seed weight**	**Biological yield plant^{-1}**	**Harvest index (%)**	**Protein content (%)**	**Correlation with seed yield plant^{-1}**
Days to 50% flowering	**GP**	**0.001** **0.006**	0.01576 0.00729	-0.00056 -0.00026	-0.00212 0.00043	-0.00015 -0.00024	0.00093 0.00004	-0.00178 -0.00096	-0.04267 -0.04016	0.02066 0.02102	0.00143 0.00091	-0.006 -0.008
Days to maturity	**GP**	0.00053 0.00355	**0.024** **0.013**	-0.0007 -0.0003	-0.00188 0.0003	0.00015 0.00021	0.00049 0.00001	0.00011 0.00035	-0.00479 -0.00573	0.0981 0.08103	0.00064 0.00034	0.093 0.117
Plant height (cm)	**GP**	0.00018 0.00128	0.00679 0.00306	**-0.002** **-0.001**	-0.00058 0.0001	-0.00028 -0.00037	-0.00045 -0.00005	0.00433 0.00235	0.0325 0.02505	-0.02959 -0.01851	0.00056 0.00054	0.012 0.011
No. of branches plant^{-1}	**GP**	-0.00034 -0.00219	-0.00898 -0.00313	0.00029 0.0001	**0.005** **-0.001**	0.00084 0.00098	0.00261 0.00018	-0.00211 -0.0008	0.41158 0.31923	0.04894 0.02121	-0.00169 -0.00081	0.334** 0.456**
No. of pods plant^{-1}	**GP**	-0.00005 -0.00045	0.00157 0.00081	0.0003 0.00014	0.00184 -0.00037	**0.002** **0.003**	0.00222 0.00018	0.00069 0.00065	0.64735 0.62403	0.19384 0.18971	0.0008 0.00056	0.819** 0.851**
No. of seeds pod^{-1}	**GP**	0.00017 0.00033	0.00257 0.00017	0.00025 0.00009	0.00287 -0.00028	0.00111 0.00078	**0.005** **0.001**	-0.01472 -0.00334	0.80631 0.34946	0.10202 0.05099	-0.00194 -0.00022	0.399** 0.903**
100-seed weight	**GP**	-0.00006 -0.00035	0.00011 0.00026	-0.00046 -0.00017	-0.00045 0.00006	0.00007 0.00012	-0.00288 -0.00015	**0.023** **0.017**	0.16021 0.14602	-0.00211 -0.00408	0.00008 0.00015	0.159 0.178
Biological yield plant^{-1}	**GP**	-0.00004 -0.0003	-0.00014 -0.00009	-0.0001 -0.00004	0.00247 -0.00048	0.00176 0.00249	0.00438 0.00033	0.00446 0.00304	**0.838** **0.831**	0.09006 0.09001	0.00017 0.00005	0.926** 0.941**
Harvest index (%)	**GP**	0.00005 0.00035	0.00704 0.00275	0.00022 0.00006	0.00073 -0.00007	0.00132 0.00167	0.00139 0.0001	-0.00015 -0.00019	0.22543 0.1985	**0.335** **0.377**	0.00002 0.00017	0.580** 0.571**
Protein content (%)	**GP**	-0.00021 -0.00119	-0.00281 -0.0009	0.00025 0.00014	0.00155 -0.00021	-0.00034 -0.00039	0.00161 0.00004	-0.00035 -0.00055	-0.02568 -0.00946	-0.00105 -0.01365	**-0.005** **-0.005**	-0.031 -0.032

*,** Significant at 5 and 1 % levels, respectively **Residual = 0.00395 (Genotypic) Residual = 0.00544 (Phenotypic)**

The residual effect was very low (0.003) which indicated appropriate choice of characters in the study that accounted for maximum variation available in the genotypes. The other remaining characters like inter-nodal distance, number of effective pods, pod length, primary and secondary branches, number of nodules and nodule weight etc. can also be included in study to draw more authentic conclusions.

Based on the present investigation, the number of pods per plant had high heritability, genetic advance as percent of mean and significant positive correlation with seed yield. Biological yield and harvest index also had significant positive correlation and highest positive direct and indirect effect on seed yield therefore, these traits should be used in selection programme for further crop improvement.

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