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Genetic variability, correlation and path coefficient analysis for yield and its components traits in chickpea (*Cicer arietinum* L.)

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Abstract
Chickpea is a crucial annual crop widely cultivated in semi-arid tropics. It is one of the most important pulse crops in India. Variability may be a greater need for initiating a breeding program for yield and yield contributing traits. A total of 30 lines, along with a check, were evaluated in Randomized Block Design (RBD) during *Rabi* 2020-21. Highest seed yield per plant was recorded by PHULE 4-5. All the traits showed significant variation among the lines. Number of seeds per plant, seed yield per plant, number of pods per plant showed high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV), whereas seed index, number of pods per plant, number of seeds per pod, showed moderate GCV and PCV. Traits exhibiting high heritability coupled with genetic advance as percent of mean suggest that the traits are governed by additive gene action, equal contribution of additive and non-additive gene action respectively. Genotypic correlation coefficient analysis revealed that seed yield per plant showed highly significant and positive association with harvest index (0.930**). Phenotypic correlation coefficient analysis revealed that seed yield per plant showed significant and positive association with number of pods per plant (0.493**), biological yield (0.457**), seed index (0.425**) and harvest index (0.362**). The path analysis results showed that positive and direct on grain yield was exhibited by harvest index, days to maturity, number of secondary branches per plant, number of pods per plant, biological yield per plant, seed index, days to 50% pod setting and seed index.

Keywords: chickpea, genetic variability, gcv, pcv, correlation analysis and path analysis

Introduction
Chickpea (*Cicer arietinum* L.) is an annual, self-pollinated, diploid (2n=16) grain legume crop grown in India. In India, mean annual production is over 11.07 mt from area of 9.69 m.ha with productivity of 1142 kg/ha., whereas in Uttar Pradesh, annual production is 0.85 mt from area of 0.62 m.ha with productivity of 1371 kg/ha. The states Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh and Karnataka account for major share in area and production and have largely benefitted from chickpea revolution in the country. (Ministry of Agriculture and Farmer's Welfare, Annual Report-2019-2020). Population explosion during the latter part of 20th century and early 21st century has created short fall in food grain availability and related mal-nutritional problems amongst the economically weaker sections. Globally there has not been any change in area under cultivation during the past four decades. Information on the nature and degree of genetic variability present in morphological, phenological, quality and traits associated to stresses of chickpea is an essential prerequisite of plant breeding.
Variance plays an important role in crop breeding. The magnitude of variants present in crop species is importance as it provides the basic for selection. The total variation present in a population arises due to genotyping and environmental effects full stop presence of genetic variance in the breeding materials is essential for a successful plant breeding program.
The estimates of genotyping coefficient of variance (GCV) reflect the total amount of genetic variability present in the germplasm. However the proportion of the genotyping variability which is transmitted from parents to the progeny is reflected by heritability. Broad sense heritability determines the efficiency with which genotypic variability in a breeding program.
Correlation coefficient studies helps in determination of interrelationship between various plant characters. The path coefficient is a standardized partial regression coefficient and as such it measures the direct influence of variable upon another and partitioning correlation coefficient into components of direct and indirect effects.
To improve the production potential of this crop breeding programme should be aimed at development of high yielding varieties by combining genes from diverse sources. These breeding strategies may be made more effective by gathering adequate information on genetic architecture, heterosis, inbreeding depression, correlation and path coefficient analysis for yield and its components. This helps the plant breeder in designing an ideotype and in isolation of superior genotypes from early segregating populations leading to success in crop improvement for various ecological conditions. Therefore, the present investigation was carried out to assess the genetic variability, association of different traits towards yield and selection of high yielding genotypes

with better architecture.

Materials and Methods

The experimental material comprised of thirty one germplasm of chickpea were sown on 9th October 2020 in rabi, 2020-21 at Field Experimentation Centre of the Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj (Uttar Pradesh). The experiment was laid in Randomized Block Design. Data for 13 quantitative traits were recorded viz; days to 50% flowering, days to 50% pod setting, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of seeds per plant, number of pods per plant, number of seeds per pod, biological yield per plant, harvest index, 100-seed weight and seed yield per plant. Recommended package of practices were followed to raise a healthy chickpea crop. Biometrical methods were followed to estimate genotypic and phenotypic coefficient of variation, heritability in broad sense, genetic advance and correlation and path coefficient analysis (Singh and Chaudhry, 1979).

Results and Discussion

For all of the examined traits, the analysis of variance indicated significant differences between genotypes, allowing for the selection of genotypes that perform better for the traits. For various agronomic and economic parameters, a large range of variability was observed. For all of the traits, the estimates of phenotypic coefficient of variation (PCV) were greater than the estimates of genotypic coefficient of variation (GCV), implying that the apparent heterogeneity is due not just to genotypes but also to the influence of environment. High genotypic coefficient of variation was found in number of seeds per plant followed by seed yield per plant and number of pods per plant. This indicates that certain variables are less susceptible to environmental variations, and hence, greater focus should be placed on these characters when breeding cultivars from the current material. High GCV for number of pods per plant and 100-seed weight were also earlier reported by Jeena *et al.* (2005) [3], Younis *et al.* (2008) [24], Alwani *et al.* (2010) [7], Kumar *et al.* (2019) [12] and Babbar *et al.* (2012) [8]. High phenotypic coefficient of variation was also found in number of seeds per plant followed by seed yield per plant and number of pods per plant. Environmental influences had a greater influence on the traits with a high phenotypic coefficient of variation. As a result, attention must be given during the selection process, as environmental fluctuations are highly unpredictable and may cause results to be affected.

Broad sense heritability was ranged from 25.4 % to 78.7 %. The heritability is high for all characters except for days to 50% flowering, days to maturity, biological yield per plant and harvest index suggested that environmental influences had the least impact on the features, as well as phenotypic expression, which shows the genotypic ability of cultivars to pass genes to their offspring. Similar results were also reported by Bicer and Sarkar (2008) and Younis *et al.* (2008) [24]. High genetic advance was noted for number of seeds per plant and number of pods per plant. High genetic advance as percent of mean was noticed for number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of seeds per pod, seed weight, biological yield, harvest index, and grain yield per plant. High estimates of heritability does not always mean high genetic advance. Johnson *et al.* (1955) [21] suggested that heritability estimates and the genetic advance as percent of mean together would provide a better judgement rather than heritability alone in predicting the resultant effect of selection. Evaluation of genetic advance helps in interpreting the type of gene action involved in the expression of various polygenic traits. High values and low values genetic advance are indicative of additive gene action and non-additive gene action respectively.

Table 1: Genetic parameters of yield and yield components in chickpea lines, during Rabi-2020

Characters	GCV (%)	PCV (%)	h^2 (%)	GA	GAM
Days to 50% flowering	2.701	5.365	25.4	3.476	3.591
Days to 50% pod setting	4.575	5.88	60.5	10.674	9.397
Days to maturity	1.758	3.493	25.3	2.993	2.337
Plant height (cm)	9.009	10.764	70.1	10.896	19.908
Number of Primary branches per plant	14.521	16.372	78.7	0.451	34.003
Number of secondary branches per plant	14.041	16.051	76.5	1.831	32.426
Number of pods per plant	17.64	21.116	69.8	26.634	38.903
Number of seeds per pod	15.327	17.75	74.6	0.394	34.941
Number of seeds per plant	21.162	25.374	69.6	40.43	46.596
Seed weight (g)	17.409	21.724	64.2	6.32	36.833
Biological yield per plant (g)	13.966	18.739	55.5	11.897	27.478
Harvest index (%)	16.499	21.314	59.9	10.649	33.716
Seed yield per plant (g)	18.735	23.386	64.2	6.847	39.625

GCV= Genotypic Coefficient of Variation, PCV= Phenotypic Coefficient of Variation, h^2= Heritability, GA= Genetic Advance, GAM= Genetic Advance at % Mean.

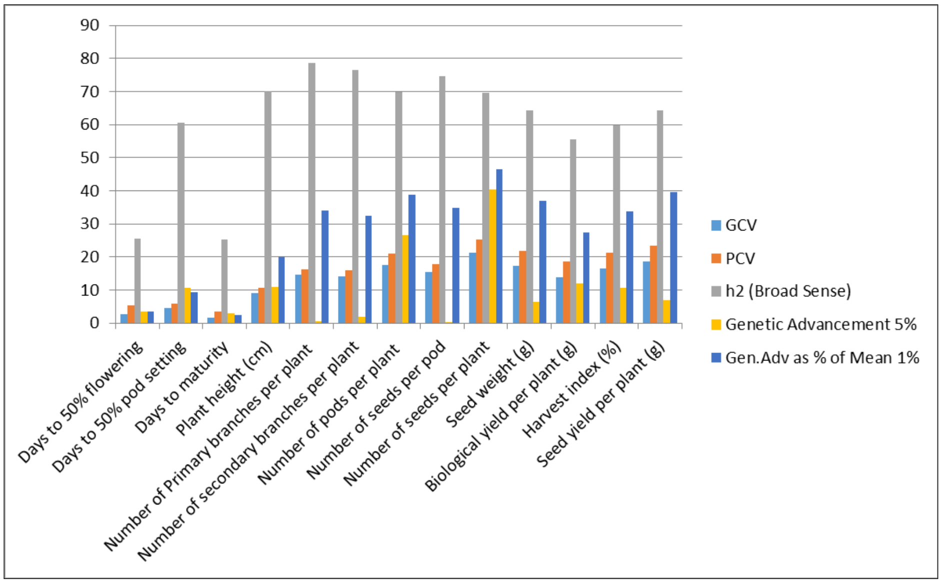

Fig 1: genetic summary of 31 genotype

Table 2: Genotypic (below diagonal) and Phenotypic (above diagonal) Correlation between seed yield and its components in chickpea

Traits	DF50	DP 50	DM	PH	NPB	NSB	NPP	NSPO	NSP	SI	BY	HI	SYPP
DF50	1.00	0.107	-0.014	-0.012	0.228*	-0.228*	-0.290*	0.067	-0.320*	0.135	-0.235*	-0.128	-0.154
DP 50	-0.112	1.00	0.465**	-0.089	-0.216*	0.171	0.392**	0.005	0.326*	-0.041	0.129	0.321*	0.289*
DM	-0.075	0.752**	1.00	0.072	-0.282*	0.097	0.203	-0.032	0.117	0.035	0.095	0.235*	0.312*
PH	0.183	-0.181	0.060	1.00	0.111	0.255*	0.107	-0.285*	-0.109	0.174	0.328*	-0.180	0.061
NPB	0.668**	-0.269**	-0.548**	0.147	1.00	-0.241*	-0.489**	-0.071	-0.553**	0.298*	-0.011	-0.361**	-0.202
NSB	-0.029	0.301**	0.349**	0.236*	-0.326**	1.00	0.407**	-0.021	0.263*	0.093	0.375**	0.124	0.397**
NPP	-0.598**	0.553**	0.543**	-0.011	-0.739**	0.510**	1.00	-0.116	0.766**	-0.203	0.409**	0.389**	0.493**
NSPO	0.188	0.039	-0.007	-0.341**	-0.090	0.014	-0.133	1.00	0.196	-0.228*	-0.346**	0.033	-0.134
NSP	-0.765**	0.359**	0.465**	-0.216*	-0.721**	0.335**	0.943**	0.200	1.00	-0.363**	0.193	0.462**	0.320*
SI	0.390**	-0.053	-0.004	0.228*	0.323**	0.174	-0.402**	-0.338**	-0.599**	1.00	0.224*	-0.012	0.425**
BY	-0.264*	0.275**	0.255*	0.429**	-0.108	0.383**	0.379**	-0.556**	0.119	0.382**	1.00	-0.167	0.457**
HI	-0.808**	0.527**	0.722**	-0.376**	-0.726**	0.563**	0.847**	0.138	0.889**	-0.301**	0.100	1.00	0.362**
SYPP	-0.274**	0.415**	0.769**	0.035	-0.392**	0.542**	0.490**	-0.210*	0.393**	0.449**	0.460**	0.930**	1.00

DF50: Days to 50% flowering, DPS: Days to 50% pod setting, DM: Days to maturity, PH-Plant height (cm), NPB-No. of primary branches, NSB: No. of secondary branches, NPP: No. of pods per plant, NSPO: No. of seeds per pod, NSP: No. of seeds per plant, SI: Seed index (g), BM: Biomass (g), HI: Harvest index (%), SYPP: Seed yield per plant (g).

Table 3: Direct (in bold) and indirect effects of 13 traits on seed yield in chickpea evaluated in Rabi 2020

Trait	DF50	DP 50	DM	PH	NPB	NSB	NPP	NSPO	NSP	SI	BY	HI
DF50	-0.371	0.041	0.028	-0.068	-0.248	0.011	0.222	-0.070	0.284	-0.145	0.098	0.300
DP 50	0.035	-0.312	-0.235	0.057	0.084	-0.094	-0.172	-0.012	-0.112	0.017	-0.086	-0.164
DM	-0.080	0.809	1.076	0.064	-0.589	0.376	0.585	-0.008	0.501	-0.004	0.274	0.776
PH	-0.034	0.033	-0.011	-0.184	-0.027	-0.044	0.002	0.063	0.040	-0.042	-0.079	0.069
NPB	0.323	-0.130	-0.265	0.071	0.484	-0.158	-0.358	-0.044	-0.349	0.156	-0.052	-0.352
NSB	-0.013	0.136	0.158	0.107	-0.147	0.451	0.230	0.006	0.151	0.078	0.173	0.254
NPP	0.507	-0.469	-0.461	0.010	0.627	-0.432	-0.848	0.113	-0.800	0.341	-0.321	-0.719
NSPO	-0.067	-0.014	0.003	0.121	0.032	-0.005	0.047	-0.355	-0.071	0.120	0.198	-0.049
NSP	-1.057	0.497	0.643	-0.298	-0.996	0.463	1.303	0.277	1.382	-0.828	0.164	1.228
SI	0.304	-0.041	-0.003	0.178	0.252	0.136	-0.314	-0.264	-0.468	0.780	0.298	-0.235
BY	0.050	-0.052	-0.048	-0.082	0.020	-0.073	-0.072	0.106	-0.023	-0.073	-0.190	-0.019
HI	0.128	-0.083	-0.114	0.060	0.115	-0.089	-0.134	-0.022	-0.141	0.048	-0.016	-0.158
SYPP	-0.274**	0.415**	0.769**	0.035	-0.392**	0.542**	0.490**	-0.210*	0.393**	0.449**	0.460**	0.930**
Partial R^2	0.101	-0.129	0.827	-0.006	-0.190	0.244	-0.416	0.075	0.544	0.351	-0.087	-0.147

DF50: Days to 50% flowering, DP50: Days to 50% pod setting, DM: Days to maturity, PH-Plant height (cm), NPB-No. of primary branches, NSB: No. of secondary branches, NPP: No. of pods per plant, NSPO: No. of seeds per pod, NSP: No. of seeds per plant, SI: Seed index (g), BM: Biomass (g), HI: Harvest index (%), SYPP: Seed yield per plant (g)

Table 4: Phenotypic direct (in bold) and indirect effects of 13 traits on seed yield in chickpea evaluated in Rabi 2020-21

Trait	DF50	DP 50	DM	PH	NPB	NSB	NPP	NSPO	NSP	SI	BY	HI	SYPP
DF50	0.002	0.000	0.000	0.000	0.001	-0.001	-0.001	0.000	-0.001	0.000	-0.001	0.000	-0.154
DP 50	-0.005	-0.044	-0.020	0.004	0.009	-0.008	-0.017	0.000	-0.014	0.002	-0.006	-0.014	0.289**
DM	-0.003	0.080	0.173	0.013	-0.049	0.017	0.035	-0.006	0.020	0.006	0.016	0.041	0.312**
PH	0.002	0.012	-0.009	-0.129	-0.014	-0.033	-0.014	0.037	0.014	-0.023	-0.042	0.023	0.061
NPB	0.006	-0.057	-0.192	-0.271	0.020	-0.083	-0.063	0.079	0.008	-0.051	-0.101	0.006	-0.202
NSB	-0.026	0.019	0.011	0.029	-0.027	0.113	0.046	-0.002	0.030	0.011	0.042	0.014	0.397**
NPP	-0.102	0.138	0.072	0.038	-0.172	0.144	0.353	-0.041	0.270	-0.072	0.144	0.137	0.493**
NSPO	0.004	0.000	-0.002	-0.017	-0.004	-0.001	-0.007	0.060	0.012	-0.014	-0.021	0.002	-0.134
NSP	-0.007	0.007	0.002	-0.002	-0.012	0.006	0.016	0.004	0.021	-0.008	0.004	0.010	0.320**
SI	0.063	-0.019	0.016	0.082	0.139	0.044	-0.095	-0.107	-0.170	0.469	0.105	-0.005	0.425**
BY	-0.058	0.032	0.023	0.081	-0.003	0.093	0.101	-0.085	0.048	0.055	0.247	-0.041	0.457**
HI	-0.025	0.063	0.046	-0.035	-0.071	0.024	0.076	0.007	0.091	-0.002	-0.033	0.196	0.362**
SYPP	-0.154	0.289**	0.312**	0.061	-0.202	0.397**	0.493**	-0.134	0.320**	0.425**	0.457**	0.362**	1.000
Partial R^2	0.000	-0.013	0.054	-0.008	0.000	0.045	0.174	-0.008	0.007	0.199	0.113	0.071	

DF50: Days to 50% flowering, DPS: Days to 50% pod setting, DM: Days to maturity, PH-Plant height (cm), NPB-No. of primary branches, NSB: No. of secondary branches, NPP: No. of pods per plant, NSPO: No. of seeds per pod, NSP: No. of seeds per plant, SI: Seed index (g), BM: Biomass (g), HI: Harvest index (%), SYPP: Seed yield per plant (g)

Genotypic correlation coefficient analysis revealed that seed yield per plant showed highly significant and positive association with harvest index (0.930**). Phenotypic correlation coefficient analysis revealed that seed yield per plant showed significant and positive association with number of pods per plant (0.493**), biological yield (0.457**), seed index (0.425**) and harvest index (0.362**). The study of interrelationships among various traits in the form of correlation is one of the most significant parts of a selection program for the breeder to make an efficient selection based on correlated and uncorrelated responses.

In the present investigation, results showed that the genotypic correlation coefficient in general were higher than the phenotypic correlation coefficient. The interrelationships were, therefore, strongly inherent and low phenotypic expression were due to environmental factors. The phenotypic expression of correlation coefficient, however appeared to be depressed in some cases due to environmental influence thus selection based on phenotype may be effective. Similar results were also reported by Pathak *et al.* (1986). Higher magnitude of genotypic correlation helps in selection for genetically controlled characters and give a better response for seed yield improvement than that would be expected on the basis of` phenotypic association alone (Robinson *et al.*, 1951) [13].

The yield related traits displaying positive and significant association with grain yield per plant suggested that grain yield can be improved through simultaneous selection for these traits. Selection is generally based on phenotypic expression of traits. Hence selection for the traits exhibiting positive significant genotypic and positive significant phenotypic correlation would be of major use in indirect and direct selection for grain yield respectively.

Phenotypic path coefficient analysis indicated that, the traits having direct effects on grain yield are understood to be strongly associated with it. The path analysis results showed that positive and direct on grain yield was exhibited by days to 50% pod setting, days to maturity, number of secondary branch per plant, number of pods per pod, number of seeds per pod, seeds index, biological yield, and harvest index. It means a slight increase in any one of the above traits may directly contribute towards seed yield. Similar results were reported by Talebi *et al.* and Babbar *et al.* Breeding strategies to improve yield in chickpea should aim in selection of above traits in further crop improvement programme.

Conclusion

It is concluded from the result of the present experiment that the characters number of seeds per plant, seed yield per plant, number of pods per plant, exhibited high genotypic coefficient variation (GCV), phenotypic coefficient of variation (PCV) and high heritability is coupled with genetic advance as percent of mean. The seed yield per plant exhibited a significant and positive correlation with harvest index paves the way of indirect selection of the traits for seed yield. Path analysis showed that the highest contribution to the seed yield was harvest index; hence harvest index should be given utmost importance. The genotype selected here is evaluated further for consistency in performance.

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