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Assessment of genetic variability, correlation and path analysis for yield and its component traits in chickpea (*Cicer arietinum* L.)

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Abstract
Plant breeding requires the existence, magnitude, and recording of genetic heterogeneity in a gene pool. Understanding genetic factors is important for assessing and managing them during crop improvement, along with variability. According to this theory, the number of secondary branches per plant, the number of pods and seeds per plant, the number of seeds per plant and the number of seeds produced per plant all showed higher PCV than GCV. A higher PCV than GCV was seen in the number of seeds per pod, seed yield, biological yield, and number of pods per plant. For the majority of the characteristics, the genotypes displayed abundant diversity with enormous heritability (> 60.20%). A significant genotypic level correlation with days to maturity was seen in the seed yield per plant (0.0435 *). Biological yield (0.89166), followed by harvest index (0.23921), plant height (0.0483), number of secondary branches (0.3347), days to 50% flowering (0.1758), 100 seed weight (0.1715), days to maturity (0.1064), number of primary branches (0.0858), and number of seeds per pod (0.0796), revealed a significant direct effect on seed yield per plant during path analysis. 110 genotypes of chickpea were examined for genetic variation using phenotypic characteristics.

Keywords: Chickpea; heritability; correlation coefficient; path coefficient

Introduction
One of the earliest grain legumes that humans cultivated was the chickpea (*Cicer arietinum* L., 2n=2x=16, Fabaceae) (Pokorny *et al*., 2015) [20]. It has its origin in Western Asia and has since expanded to India and other countries. In addition to being a relatively affordable source of high-quality dietary proteins (such as albumins and globulins), chickpea seeds also contain minerals (such as calcium, magnesium, potassium, and phosphorus), vitamins (such as thiamine, riboflavin, and niacin), unsaturated fatty acids (such as linoleic and oleic acids), unsaturated dietary fibres, and carbohydrates (Jimenez-Lopez *et al*., 2020) [11]. India is a major producer of chickpeas, accounting for around 70% of global output. The leading states for chickpea production in the country are Madhya Pradesh, Uttar Pradesh, Maharashtra, Rajasthan, Gujarat, Andhra Pradesh, Karnataka, and Bihar.
Since a broad range of genetic diversity across parents is necessary for hybridization programmes, the morphological characterisation of germplasm is utilised to understand the genetic variance. Any effective hybridization programme must meet certain requirements in order to produce the desired segregants, including the nature and extent of genetic diversity and heritability in a population as genetic and non-genetic variables. Any crop improvement programme needs genetic diversity for traits with important economic quantitative and qualitative characteristics. Being a self-pollinated plant, chickpea, with lack of sufficient variety and vulnerability of current cultivars to different abiotic and biotic challenges are the main obstacles to increasing production (Parameshwarappa *et al*., 2011 and Gaur *et al*., 2012) [17, 10]. With numerous economically significant parameters, such as flowering time, grain weight, grain yield, etc., genetic variability studies in chickpea have been conducted. As a complex characteristic, the expression of yield is controlled by related traits that are associated with it. The correlation coefficient may be used to identify this relationship, but path analysis can explain both the direct and indirect relationships between the traits (Tejasree *et al*., 2021) [26]. In light of the aforementioned perspectives, the present experiment was designed to identify the morphological and genetic diversity in chickpea germplasm, followed by a path analysis for crop production.

Material and Methods

The 110 germplasm samples and four checks that comprised the study material were sown at the G.B. Pant University of Agriculture and Technology, Pantnagar, during the rabi seasons of 2021. In the crop season 2021–2022, the experimental material was assessed using an augmented block design with 11 blocks. Plants were spaced 10–15 cm apart, and rows were kept apart at 30 cm. To grow a healthy crop, the usual set of practices for chickpea cultivation were used. The observations were made on plant height, height of first pod bearing node, number of primary branches, number of secondary branches, number of pods per plant, number of seeds per pod, 100 seed weight, biological yield, seed yield, and harvest index from random samples of three visually healthy plants chosen at random from each row, each row representing a genotype of chickpea. The characteristics like days to 50% blooming and days to maturity were, however, taken into consideration on a plot basis. The genotypic and phenotypic coefficients of variation were estimated using biometrical techniques (Burton 1952) [6], whereas heritability in general and predicted genetic progress (Allard 1960) [2]. According to Dewey and Liu (1959) [8], correlation and path coefficient analyses were calculated.

Result and Discussion

Analysis of variance

Knowing that chickpeas are an inbreeding and self-pollinating species, genetic variety is necessary to enhance quantitative attributes (Anbessa *et al*. 2006) [3]. The ANOVA for the studied characteristics showed that differences between genotypes were very significant (P <0.01) in the overall F tests. This shown that genotypes have a lot of diversity that may be used to enhance chickpeas (Talekar *et al*. 2017) [25].

Genetic parameters

The number of seeds per pod, followed by seed yield, biological yield, and number of pods per plant, was predicted to have the highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variance (GCV). This greater score indicates the potential for direct selection. Additionally, Singh *et al*. (2014) [23] showed higher GCVs for seed yield per plant (>35%) and 100 seed weight (>25%). More significant GCV and PCV differences were found in the seed yield per plant, 100 seed weight, secondary branches, and number of pods per plant by Aswathi *et al* (2019) [4]. Greater estimates for yield-related economically significant traits and GCV values that were closer to their corresponding PCV values suggested that the environment had little effect on the expression of the trait and that there was also a lot of variability. According to the findings, phenotypic-based selection for the aforementioned features may be fruitful for the enhancement of chickpeas. Low PCV and GCV values, however, suggest that simple selection is ineffective for enhancing any of these characteristics for days to 50% flowering or days to maturity. Singh *et al*. (2014) [23] observed a similar outcome and found that PCV and GCV estimates for days to 50% flowering and days to maturity were low. Even so, breeders have access to a wide range of cutting-edge genomic techniques for use in their breeding programmes for chickpeas. However, knowledge of genetic gain and heritability is necessary for selection processes. It is clear that parent's qualities are passed on to their offspring via heritability (Falconer, 1960) [9]. Heritability and GA

knowledge aid in predicting gain in selection (Boghara *et al*. 2016) [5]. Except for days to 50% flowering (52.71), all the characteristics in the present experiment were highly heritable according to the Robinson *et al*. (1949) [21] scale since their H2 values were more than 60%. Numerous researchers have found significant heredity for the number of seeds per plant, days to maturity, weight in hundred seeds, number of pods per plant, height of the plant, and seed production per plant (Thudi *et al*. 2014; Thakur *et al*. 2018; Parida *et al*. 2018) [28], [27], [18]. The environment seems to have less impact on the expression of characteristics, according to higher heritability estimates. As the character is anticipated to be regulated by additive gene action that is repairable, greater levels of heritability permit bigger benefits of selection. Genetic advance as a percentage of mean explains the expected gain when a simple section for a character is practised. It is preferable to have greater genetic advance followed by higher heritability since these variables are often the ones that may be chosen to indirectly enhance the dependent variable. Genetic advance as % mean (GAM) ranged from 5.06% for days to 50% flowering to 149.66% for number of seeds per pod. For the majority of the traits with the exception of days to 50% flowering and days to maturity, both GAM and heritability were high. Waseem *et al*. (2014) [29] and Sharanappa *et al*. (2014) [22] reported strong heritability and high GAM for seed yield/plant and pods/plant in earlier literature (Talekar *et al*. 2017) [25]. Different sets of germplasm might be the cause of such conflicting results. Due to the existence of additive gene action, the qualities with high heritability and high GAM may be enhanced by phonological selection with minimal effort (Parameshwarappa *et al*. 2009) [16]. Days to maturity, a characteristic with high heritability and low GAM, showed the dominance of non-additive gene effects and might be improved by population-level approaches. Anbessa *et al*. (2006) [3] and Singh *et al*., (2014) [23] found a similar conclusion for days to physiological maturity. Number of pods per plant, number of seeds per pod, biological yield, and seed yield all showed significant heritability along with high genetic progress as a percentage of mean. The findings of Srivastava *et al*. (2017) [24] and Aswathi *et al*. (2019) [4] are comparable to those of the current results.

Estimation of correlation coefficients

Yield is a complex attribute that is governed by a number of simply inherited traits. The correlation coefficients show how strongly two variables are related, which aids in understanding the nature and degree of the relationship between yield and its component traits. In the current study, the correlation coefficient between the twelve characteristics was calculated with the goal of learning more about the type, magnitude, and direction of the connection as well as the selection pressure process in order to provide useful and practical outcomes. Days to maturity and seed yield per plant showed a positive and significant correlation. Meena *et al*., (2021) [21] and Agrawal *et al*., (2016) revealed similar findings in their prior research. In contrast, a substantial negative association was found for the quantity of seeds per pod. These characteristics have become significant determinants of chickpea seed output. According to research, choosing one yield-attributing characteristic might raise the other, thus limiting the plant type for high yield.

Path Coefficient analysis

The expression of yield is regulated by a number of variables both directly and indirectly via other related characteristics as a result of the complex and polygenic nature of the trait. Therefore, selecting a genotype only based on correlational data may be ineffective without dichotomizing the cause-and-effect relationship (Boghara *et al.* 2016) [5]. The relative contribution of each causal factor to the grain yield per plant is shown via path coefficient analysis. A technique known as the path coefficient is used to divide the observed correlation coefficient into the direct and indirect impacts of yield components on seed yield in order to show the proportionate contribution of causative factors to the grain yield per plant. The objective of this research is to calculate the direct and indirect effects of various plant traits on seed yield per plant. The biological yield, harvest index, plant height, number of secondary branches, days to 50%

blooming, 100 seed weight, days to maturity, number of primary branches, and number of seeds per pod had the most positive direct effects on seed yield per plant. Yucel and Anlarsal (2010) [31] also reported a significant positive association of seed yield per plant with plant height and the number of secondary branches. The strongest positive direct influence of biological yield and plant height on seed yield was observed by Ciftci *et al.* (2004) [7]. The findings are in agreement with those of Jivani *et al.* (2013) [12], who concluded that harvest index had a positive and significant direct influence on seed yield/plant. Additionally, Paul *et al.*, (2022) [19] and Kobraee *et al.* (2010) [13] revealed that seeds/plants are a significant direct contribution to seed yield. Similar to the current study, Muhammad *et al.* (2009) [15] and Yadav *et al.* (2009) demonstrated good and high direct effects of 100 seed weight on seed yield.

Table 1: Analysis of variance (ANOVA) for yield and yield contributing traits of chickpea genotypes

Source	Df	Days to 50% flowering	Days to maturity	Plant height (cm)	Height of first pod beearing node	Number of primary branches	Number of secondary branches	Number of pods per plant	Number of seeds per pod	100 seed weight	Biological yield	Seed yield	Harvest index
Block	10	10.22 ns	2.07 ns	6.89 *	0.21 ns	0.15 ns	0.01 ns	0.12 ns	0.03 ns	3.45 ns	0.99 ns	0.43 ns	2.23 ns
Entries	113	8.2 ns	101.42 **	131.52 **	46.02 **	0.45 **	6.25 **	63.84 **	1.6 **	47.84 **	86.79 **	14.76 **	114.5 **
Check	3	33.76 *	38.45 **	325.35 **	356.47 **	1.66 **	15.26 **	52.93 **	1.02 **	263.29 **	940.6 **	104.73 **	621.91 **
Genotypes	109	5.74 ns	104.05 **	114.59 **	37.25 **	0.37 **	3.85 **	64.69 **	1.61 **	32.04 **	56.53 **	12.39 **	81.41 **
Check vs. genotype	1	199.3 **	4.16 ns	1395.19 **	70.8 **	5.16 **	241.23 **	4.59 **	1.92 **	1124.03 **	823.81 **	2.54 *	2198.01 **
Error	30	8.71	3.72	2.66	0.2	0.001	0.01	0.1	0.003	2.61	1.6	0.48	2.54
LSD at 5%													
between checks	1	2.57	1.68	1.42	3.87	3.33	0.80	2.77	5.18	2.47	2.83	0.74	5.92
between genotypes	1	8.52	5.57	4.72	12.84	11.03	2.65	9.19	17.19	8.19	9.38	2.46	19.66
between entries of same block	1	9.53	6.23	5.27	14.36	12.34	2.97	10.28	19.22	9.16	10.49	2.75	21.98
between check vs genotypes	1	7.14	4.67	3.95	10.76	9.24	2.22	7.70	14.40	6.86	7.86	2.06	16.47

ns P > 0.05; * P <= 0.05; ** P <= 0.01

Table 2: Estimation of genetic parameters for twelve quantitative characters in chickpea genotypes.

Trait	Mean	GCV	PCV	hBS	GA	GAM
Days to 50% flowering	86.7	1.15	2.76	52.71	4.13	5.06
Days to maturity	116.88	8.57	8.73	96.42	20.29	17.36
Plant height (cm)	50.71	20.86	21.11	97.67	21.57	42.53
Height of first pod bearing node	23.63	25.76	25.82	99.47	12.52	52.99
Number of primary branches	2.61	23.27	23.31	99.63	1.25	47.91
Number of secondary branches	7.79	25.17	25.2	99.78	4.04	51.88
Number of pods per plant	17.8	45.15	45.18	99.84	16.57	93.07
Number of seeds per pod	1.75	72.63	72.71	99.78	2.61	149.66
100 seed weight	26.42	20.54	21.43	91.85	10.73	40.6
Biological yield	14.73	50.33	51.05	97.18	15.07	102.35
Seed yield	5.94	58.15	59.3	96.16	6.98	117.64
Harvest index	39.58	22.44	22.8	96.88	18.03	45.57

GCV = Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, hBS= Heritability broad sense, GA= Genetic Advance, GAM= Genetic advance as percent mean value.

Table 3: Correlation among yield and its contributing traits in chickpea genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Height of first pod bearing node	Number of primary branches	Number of secondary branches	Number of pods per plant	Number of seeds per pod	100 seed weight	Biological yield	Seed yield	Harvest index
Days to 50% flowering	1.0000	-0.0397*	-0.0002**	-0.0389*	0.0598 *	0.1097 ns	0.0977 ns	-0.0655 ns	0.2055 ns	0.1055 ns	0.1547 ns	0.1657 ns
Days to maturity		1.0000	0.0751 ns	0.0146 **	-0.0429 *	0.0713 ns	0.087 ns	-0.0141 **	-0.0024 **	0.0873 ns	0.0435 *	-0.1889 ns
Plant height (cm)			1.0000	0.7037 ns	0.0177 **	0.416 *	0.087 ns	-0.0183 **	0.4219 *	0.7517 ns	0.7343 ns	0.142 ns
Height of first pod bearing node				1.0000	-0.0027 **	0.1593 ns	0.0026 **	0.0101 **	0.2393 ns	0.3854 ns	0.385 ns	0.1214 ns
No. of primary branches					1.0000	0.263 ns	0.188 ns	-0.0458 *	0.1378 ns	0.2137 ns	0.2072 ns	0.019 **
No. of secondary branches						1.0000	0.4437 ns	-0.0141 **	0.4406 ns	0.5572 ns	0.5764 ns	0.164 ns
No. of pods per plant							1.0000	0.071 ns	0.5008 ns	0.5588 ns	0.5368 ns	0.1588 ns
Number of seeds per pod								1.0000	-0.0423 *	-0.0148 **	-0.0239 *	-0.0471 *
100 seed weight									1.0000	0.4878 ns	0.4913 ns	0.1272 ns
Biological yield										1.0000	0.9588 ns	0.1556 ns
Seed yield											1.0000	0.382 ns
Harvest index												1.0000

ns P > 0.05; * P <= 0.05; ** P <= 0.01

Table 4: Path coefficient analysis showing direct and indirect effect of various characters on seed yield per plant

Characters	Days to 50% flowering	Days to maturity	Plant height	Height of first pod bearing node	No. of primary branches	No. of secondary branches	No. of pods per plant	No. of seeds per pod	Hundred seed weight	Biological yield	Harvest index
Days to 50% flowering	0.01758	-0.00042	-0.00001	0.00118	0.00051	0.00367	-0.0046	-0.0005	0.00352	0.0941	0.03964
Days to maturity	-0.0007	0.01064	0.00363	-0.00044	-0.00037	0.00239	-0.0041	-0.0001	-0.00004	0.07781	-0.0452
Plant height	0.0000	0.0008	0.0483	-0.02142	0.00015	0.01392	-0.0188	-0.0002	0.00724	0.67028	0.03396
Height of first pod bearing node	-0.00068	0.00015	0.03399	-0.03044	-0.00002	0.00533	-0.0001	0.00008	0.0041	0.34361	0.02904
No. of primary branches	0.00105	-0.00046	0.00085	0.00008	0.00858	0.0088	-0.0088	-0.0004	0.00236	0.19055	0.00454
No. of secondary branches	0.00193	0.00076	0.02009	-0.00485	0.00226	0.03347	-0.0208	-0.0001	0.00756	0.49682	0.03924
No. of pods per plant	0.00172	0.00093	0.01934	-0.00008	0.00161	0.01485	-0.0469	0.00057	0.00859	0.49823	0.03799
No. of seeds per pod	-0.00115	-0.00015	-0.00088	-0.00031	-0.00039	-0.0005	-0.0033	0.00796	-0.00073	-0.0132	-0.0113
Hundred seed weight	0.00361	-0.00003	0.02038	-0.00728	0.00118	0.01475	-0.0235	-0.0003	0.01715	0.43492	0.03042
Biological yield	0.00185	0.00093	0.03631	-0.01173	0.00183	0.01865	-0.0262	-0.0001	0.00836	0.89166	0.03722
Harvest index	0.00291	-0.00201	0.00686	-0.0037	0.00016	0.00549	-0.0075	-0.0004	0.00218	0.13874	0.23921

Residual = 0.02267

Conclusion

According to the results of the present study, the characters like number of seeds per pod, seed yield, biological yield, and number of pods per plant, showed high genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), and high heritability is coupled with genetic gain as a percent of mean. Days to maturity indicated a significant and positive correlation with seed yield. According to path analysis, biological yield and harvest index offered highest contribution to seed yield; as a result, these characters need to be given prime importance. The genotype identified here is evaluated further for performance consistency, and these genotypes may be used in future multilocational studies to assess their stability and adaptability to various environmental conditions.

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