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## Correlation, path analysis and genetic variability, of yield, and yield Components in chickpea (*Cicer arietinum L.*)

**Manoj Kumar Singh, Anshuman Singh and Devi S Rhods**

### Abstract

This study was conducted to determine heritability, variability, and correlations between yield and yield components in 15 chickpea (*Cicer arietinum L.*) genotypes for 2 years. Direct and indirect effects of yield components on seed yield per plant were investigated. Genotypic variance was the highest for 1000 seed weight, followed by seed number per plant. Broad-sense heritabilities ranged from 5.47% (days to flowering) to 51.66% (seed number per plant). Heritability for seed number, 1000 seed weight, and number of full pods were greater than those for the other traits. Positive and significant ( $P < 0.05$ ) relationships were determined between seed yield per plant and plant height, first pod height, secondary branch, total pod, and number of full pods and seeds per plant. The path coefficient analysis based on seed yield per plant, as a dependent variable, revealed that all of the other traits, except days to flowering, first pod height, and total pod number, exhibited high positive direct effects. Number of seeds and full pods showed the highest direct influence with 47.49% and 44.73%, respectively. Therefore, this research suggests that seed and full pod numbers can be good selection criteria for improving seed yield per plant in chickpea.

**Keywords:** Chickpea, *Cicer arietinum*, genetic variability, correlation, path coefficient analysis, seed yield

### Introduction

Chickpea is the second most important pulse crop in the world after dry bean. As well as being an important source of human food and animal feed, it also helps to improve soil fertility, particularly in dry lands. The introduction of chickpea in a cereal-based rotation, which is used particularly in developing countries, can break the disease and pest cycle, and increase the productivity of the entire rotation (Jodha and Subba Rao, 1987) <sup>[10]</sup>. In the Mediterranean region, due to temperate climates with winter rainfall, chickpea is traditionally sown in the spring; therefore, the crop encounters heat and drought stress towards maturity, resulting in low and variable yields. However, with developing new cultivars that are resistant to cold and tolerant to ascochyta blight (caused by *Ascochyta rabiei* (Pass.) Lab.), as their winter sowing provides higher and more stable productivity and increased water-use efficiency, winter sowing of chickpea in the Mediterranean region has recently become more common. Genetic variation among traits is important for breeding and in selecting desirable types. On the other hand, an analysis of the correlation between seed yield and yield components is essential in determining selection criteria; however, path coefficient analysis helps to determine the direct effect of traits and their indirect effects on other traits. According to Arshad *et al.* (2002) <sup>[4]</sup>, low heritability percentage coupled with low and moderate genetic advancement has been observed for primary and secondary branches, respectively. Additionally, they indicated that these traits were greatly influenced by environment. As found by Noor *et al.* (2003) <sup>[12]</sup>, days to flowering, secondary branch number, and 100 seed weight exhibited high heritability. Both correlation and path analysis indicated that pod number per plant and 100 seed weight were potent contributors to grain yield through direct effects. Days to flowering, 100 seed weight, and seed yield per plant showed greater heritability, and a significant and positive correlation was observed between seed yield and pod number per plant. Pod number per plant had a positive direct effect on yield per plant (Uddin *et al.*, 1990) <sup>[17]</sup>.

The greatest genotypic variations were found in the number of pods per plant, pod weight, and 100 seed weight, as reported by Patil and Phandis (1997) <sup>[13]</sup>, and Adhikari and Pandey (1982) <sup>[1]</sup>. Conversely, as shown by Adhikari and Pandey (1982) <sup>[1]</sup>, and Samal and Jagadev (1989) <sup>[14]</sup>, great phenotypic variance was noted within the number of primary and secondary branches, first pod height, and days to flowering. Khorgade *et al.* (1985) <sup>[11]</sup> found that pod number had great

phenotypic variance. However, plant height was less affected by environment. Erman *et al.* (1997) <sup>[7]</sup> reported that pod number per plant, harvest index, and biological yield were the major contributors to seed yield as either direct or indirect effect via other characters. Eser *et al.* (1989) <sup>[8]</sup> reported that 100 seed weight, seed number, full pod number per plant, and the number of primary and secondary branches had major effects on yield and yield per plant. Furthermore, there were significant correlations between number of pods per plant and seed weight per plant. Guler *et al.* (2001) <sup>[9]</sup> reported that significant and positive relationships were found between seed yield per plant and seed number and pod number per plant. It was found that seed and biological yield per plant were the most important traits for determining the seed yield per hectare in chickpea (Akdag and Seherali, 1992) <sup>[2]</sup>. Singh *et al.* (1990) <sup>[15]</sup> reported that correlation and path coefficient analysis showed that biological yield and harvest index were the major direct contributors to seed yield. According to the results of correlation analysis, in spite of a negative correlation between plant height and harvest index, total pod number revealed a positive correlation with full pod and seed numbers (Anlarsal *et al.*, 1999) <sup>[3]</sup>. The purpose of this study was to estimate the total genotypic variability, correlations, and path analysis among some important traits for selection criteria for improving yield in winter-sown kabuli chickpea in the Bundelkhand region of India.

### Materials and Methods

Fifteen lines of kabuli chickpea obtained from AICRP, ICAR, New Delhi along with 1 cultivar (as a control, JG-11) originated in JNKV, Jabalpur were studied. The experiment was conducted during the winter seasons of 2015-16 and 2016-17, and utilised a randomized complete blocks design (RCBD) with 3 replications at arid conditions in the Research Area of the AICRP chickpea at the Rani Lakshmi Bai Central Agricultural University, Jhansi, India. Each line was sown in 4 rows, 4 m in length, with 35 cm inter-row spacing; there were 44 plants per square metre. Before sowing, 40 kg ha<sup>-1</sup> N and 60 kg ha<sup>-1</sup> P<sub>2</sub>O<sub>5</sub> fertilizers were applied. The soil of the research area was 20-40 cm deep and clayey. Depending upon soil depth, pH, calcium, and available phosphorus concentration and organic substance were 7.72-7.69, 7.30%-6.78%, 50.2-48.4 kg ha<sup>-1</sup>, and 1.81%-1.49%, respectively. The Bundelkhand region has a tropical climate. Observations of days to flowering (DTF: d), plant height (PH: cm), first pod height (FPH: cm), primary branch number (PBN: number/plant), secondary branch number (SBN: number/plant), total pods number (TPN: number/plant), full pods number (FPN: number/plant), seeds number (SN: number/plant), 1000 seed weight (1000 SW: g), seed yield (SY: g/plant), and harvest index (HI: %) were recorded.

The data were analysed according to the RCBD over years. In order to determine the relationships between examined traits and seed yield per plant, correlation coefficients were calculated with the MSTATC program. The path coefficient analysis was performed by examining SY per plant as a dependent variable for major contributors to SY per plant with TARISTS, a computer program, as suggested by Willims *et al.* (1990) <sup>[18]</sup>. In addition, total genotypic variance, phenotypic variance, and broad-sense heritability were calculated (Blum and Leherer, 1973; Corleto, 1976) <sup>[5,6]</sup>.

### Results and Discussion

Genetic parameters of yield and their components are given in Table 1. According to the mean values, DTF, PH, FPH, PBN, SBN, TPN, FPN, SN, 1000 SW, SY per plant, and HI were 118.9 d, 91.9 cm, 54.2 cm, 1.9, 4.3, 30.3, 25.1, 30.7, 337.5 g, 9.6 g, and 30.7%, respectively. According to Table 1, the greatest genotypic variance was for 1000 SW, followed by SN per plant. Phenotypic variance was greater than genotypic variance for whole traits, indicating the influence of environmental effect. However, the phenotypic variance of DTF, PH, and HI were greater than the genotypic variance of those same traits. Genotypic coefficients of variations were relatively greater in SN (12.83%), SBN (12.33%), and FPN (9.12%) than in other traits, while it was smaller in PBN (4.11%), HI (3.65%), FPH (3.26%), 1000 SW (2.50%), PH (2.0%), and DTF (0.35%). Similar findings were reported by Patil and Phandis (1977) <sup>[13]</sup>. Furthermore, Adhikari and Pandey (1982) <sup>[1]</sup> reported a high genotypic variation for 1000 SW. Phenotypic coefficients of variations were the highest in SBN (22.56%), SN (17.88%), FPN (15.82%), SY per plant (15.63%), and TPN (15.51%). Nevertheless, the smallest phenotypic coefficients of variation were for 1000 SW. Similar findings were reported by Adhikari and Pandey (1982) <sup>[1]</sup>, and Samal and Jagadev (1989) <sup>[14]</sup>. However, Khorgade *et al.* (1985) <sup>[11]</sup> stated that PH had a relatively low environmental effect. Broad-sense heritabilities ranged from 5.47% to 51.66%. The heritabilities were small for most of the characters due to larger phenotypic variances, indicating environmental influence (Singh *et al.* 2016) <sup>[16]</sup>. Heritabilities of SN per plant, 1000 SW, FPN, FPH, PBN, and SBN were greater than the heritabilities of SY per plant, DTF, PH, TPN, and HI. These results were in accordance with the findings of Uddin *et al.* (1990) <sup>[17]</sup>. Improvement of these traits that have greater heritability, through direct selection, could be limited to the lines used in the present study. The FPN and SN per plant indicated high heritability in connection with genotypic variation. In this manner, crop improvement, in terms of these traits, could be possible by simple selection because high heritability coupled with high genotypic variation revealed the presence of an additive gene effect (Noor *et al.*, 2003). On the other hand, low heritability coupled with low genotypic variation was observed for SY per plant, PH, TPN, and HI. The results indicated that these traits were greatly influenced by environment (Arshad *et al.*, 2002) <sup>[4]</sup>, and selection will be relatively more efficient in SN, 1000 SW, and FPN. Correlation coefficient analysis The SY per plant exhibited a significant positive correlation with PH, FPH, SBN, TPN, FPN, and SN (Table 2). These results suggested that any positive increase in such traits will accelerate the boost in SY per plant. These results were in accordance with those reported by Guler *et al.* (2000) <sup>[9]</sup> and Uddin *et al.* (1990) <sup>[17]</sup>. Significant and negative relationships were found between DTF and PH, FPN, and 1000 SW, whereas a positive relationship was found between SBN and HI. In this case, it could be suitable to select short bloom lines for increasing SY per plant. The high positive correlation between PH and FPH, FPN, and 1000 SW indicated that cultivars with higher PH contribute to SY. However, there was a negative correlation between PH and SBN and HI. Anlarsal *et al.* (1999) <sup>[3]</sup> indicated that an increase in PH leads to a decrease in HI and SBN. FPH was positively correlated with FPN and 1000 SW,

whereas it was negatively correlated with SBN and HI. A significant and positive correlation was observed only between PBN and SBN. There was a positive correlation between SBN and TPN, SN, and HI. Highly significant and positive correlations were found between TPN, and FPN, and SN. These results were in accordance with the study conducted by Anlarsal *et al.* (1999) [3]. Conversely, FPN had a positive correlation with SN. HI showed a positive correlation with SN and a negative correlation with 1000 SW. Therefore, this result

indicated that HI might serve to identify chickpea genotypes with higher SY per plant. The main purpose of breeders is to achieve an increase in chickpea yield. Yield and its components are multigenic traits, which are strongly influenced by the environment and other factors both known and yet to be identified. To this end, emphasis should be given to the development of chickpea lines with higher TPN, FPN, and SN to improve SY path coefficient analysis. In order to determine the relationships between SY per plant and the other examined traits, correlation coefficients were calculated. The path coefficients were partitioned into direct and indirect effects by using SY per plant as a dependent variable. Direct and indirect effects are given in Table 3. The path coefficient analysis based on SY per plant as a dependent variable revealed that all traits, except DTF, FPH, and TPN, exhibited positive direct effects. Compared to the simple correlation analysis, path analysis of SY per plant and its components demonstrated that SN and FPN exerted the highest direct influence, with 47.49% and 44.73%, respectively. Correlation and path coefficient analyses indicated that SN and FPN were the major contributors to SY per plant. Hence, they could be exploited more confidently for crop improvement. These results were in agreement with the study carried out by Uddin *et al.* (1990) [17]. Although 1000 SW and PBN had high positive direct effects on SY per plant, with 30.7% and 33.8%, respectively, the correlation between SY per plant and these traits was not significant. Conversely,

DTF had a negative and small direct effect on SY per plant, but a great indirect effect via FPN, SN, 1000 SW, and PH. These results suggested that the selection of shorter flowering lines contribute to increasing SY per plant with an indirect effect via these traits. Similar to DTF, the FPH also had a small negative direct effect.

However, this trait had a positive and high indirect effect, via FPN, SN, 1000 SW, and PH on SY per plant. These results were not in agreement with those of Noor *et al.* (2003) [12]. SBN had a small direct effect on SY per plant; however, the indirect effect of this trait, via FPN and SN on SY per plant, was great. Although the direct effect of TPN was negative and small, the indirect effect of this trait, via FPN and SN, was significant on SY per plant. These results were in accordance with those reported by Erman *et al.* (1997) [7]. On SY per plant, HI had an indirect effect via SN. Similar findings were reported by Sing *et al.* (1990) [15]. It was observed that a higher indirect contribution was exhibited on FPN and SN by most of the yield components; thus, these traits related to SY per plant should be given emphasis in selection. These results are in agreement with the findings of Erman *et al.* (1997) [7], Eser *et al.* (1989) [8], and Noor *et al.* (2003) [12]. This study suggests that a good selection for yield improvement should be based on both high FPN and SN in chickpea.

### Conclusions

In the studied traits, phenotypic variances of DTF, PH, and HI were greater than genotypic variances, and this indicated that these traits are more influenced by environmental effects. According to the results of the correlation analysis, SY per plant was significantly and positively correlated to PH, FPH, SBN, TPN, FPN, and SN per plant. Improving these traits may increase SY per plant. Path analysis of SY per plant indicated that SN and FPN exerted the greatest direct effect. These traits had major contributions to SY per plant, and hence can increase the success of breeding studies of chickpea in the Bundelkhand region of India.

**Table 1:** Genetic parameters of yield and yield components in chickpea

X	Mean ± SE	MS	GV	GYV	EV	PV	GCV (%)	PCV (%)	BSH (%)
DTF	118.9±1.32	12.6**	0.17	3.85	6.07	3.11	0.35	1.48	5.47
PH	91.9 ± 1.43	103.5**	3.38	17.54	30.66	17.26	2.00	4.52	19.58
FPH	54.2 ± 2.13	52.3 ns	3.13	1.23	37.21	9.95	3.26	5.81	31.45
PBN	1.9 ± 0.03	0.07 ns	0.006	0.01	0.07	0.023	4.11	7.89	26.09
SBN	4.3 ± 0.18	2.5 ns	0.28	0.54	2.49	0.94	12.33	22.56	29.78
TPN	30.3 ± 0.85	132.4 **	4.48	23.12	36.19	22.07	6.99	15.51	20.30
FPN	25.1 ± 0.79	94.4**	5.24	10.41	31.76	15.73	9.12	15.82	33.30
SN	30.7 ± 1.0	180.6**	15.55	8.00	63.32	30.10	12.83	17.88	51.66
1000 SW	337.5±3.96	1166.3*	70.90	80.9	498.17	194.38	2.50	4.13	36.48
SY	9.6 ± 0.33	13.5*	0.48	1.54	5.98	2.24	7.19	15.63	21.36
HI	30.7 ± 0.69	32.6 ns	1.25	4.67	26.07	7.93	3.65	9.19	15.76

NS = Not significant, \* = Significant at alpha level 5%, \*\* = Significant at alpha level 1%

Mean squares (MS) Genotypic variance (GV), Genotype x year interaction variance (GYV), Error variance (EV), Phenotypic variance (PV), Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), Broad-sense heritability(BSH) <sup>1</sup>: DTF: Days to flowering; PH: Plant height (cm); FPH: first pod height (cm); PBN: Primary branch number (number/plant); SBN: secondary branch number (number/plant); TPN: Total pods number (number/plant); FPN: full pods number (number/plant); SN: seeds number (number/plant); 1000 SW: 1000 seed weight (g); SY: seed yield (g/plant) and HI: Harvest index (%).

**Table 2:** Correlations among traits in chickpea. See Table 1 for abbreviations.

Traits	SY	DTF	PH	FPH	PBN	SBN	TPN	FPN	HI	SN	1000 SW
SY	1.000	-0.324**	0.213*	0.309**	0.012	0.306**	0.741**	0.886**	0.212	0.891**	0.201
DTF		1.000	-0.800**	-0.908**	0.120	0.386**	-0.123	-0.368**	0.530**	-0.191	-0.664**
PH			1.000	0.843**	-0.115	-0.352**	-0.054	0.207*	-0.544**	0.029	0.645**
FPH				1.000	-0.167	-0.302**	0.026	0.322**	0.542**	-0.171	0.710**
PBN					1.000	0.207*	0.010	-0.032	0.097	-0.012	-0.114
SBN						1.000 -	0.358**	0.266	0.325**	0.342**	0.204
TPN							1.000 -	0.896**	0.158	0.772**	0.100
FPN								1.000	0.118	0.866**	0.159
HI									1.000 -	0.285**	0.315**
SN										1.000	0.014
1000 SW											1.000

\*, \*\* significant at 5% and 1% level, respectively

**Table 3:** The direct, indirect, and % contribution of various traits to seed yield per plant in chickpea. See Table 1 for abbreviations

Trait	Direct Effect	Indirect Effects									
		DTF	PH	FPH	PB	SBN	TPN	FPN	SN	1000 SW	HI
DTF	-0.0230 (4.4%)		-0.0629 (12.0%)	0.0165 (3.2%)	0.0042 (0.8%)	0.0227 (4.3%)	0.0127 (2.4%)	-0.1786 (34.2%)	-0.0961 (18.4%)	-0.0631 (12.1%)	0.0429 (8.2%)
PH	0.0785 (21.6%)	0.0184 (5.1%)		-0.0154 (4.2%)	-0.0040 (1.1%)	-0.0207 (5.7%)	0.0056 (1.6%)	0.1005 (27.7%)	0.0146 (4.0%)	0.0614 (16.9%)	-0.0440 (12.1%)
FPH	-0.0182 (3.8%)	0.0208 (4.3%)	0.0662 (13.7%)		-0.0058 (1.2%)	-0.0178 (3.7%)	-0.0027 (0.6%)	0.1562 (32.2%)	0.0861 (17.8%)	0.0675 (13.9%)	-0.0438 (9.0%)
PBN	0.0350 (33.8%)	-0.0028 (2.7%)	-0.0091 (8.8%)	0.0030 (2.9%)		0.0122 (11.7%)	-0.0010 (1.0%)	-0.0157 (15.2%)	-0.0062 (6.0%)	-0.0108 (10.4%)	0.0078 (7.6%)
SBN	0.0588 (12.0%)	-0.0089 (1.8%)	-0.0277 (5.6%)	0.0055 (1.1%)	0.0072 (1.5%)		-0.0371 (7.6%)	0.1290 (26.2%)	0.1720 (35.0%)	-0.0194 (3.9%)	0.0263 (5.4%)
TPN	-0.1039 (10.6%)	0.0028 (0.3%)	-0.0042 (0.4%)	-0.0005 (0.1%)	0.0003 (0.1%)	0.0210 (2.2%)		0.4336 (44.4%)	0.3879 (39.7%)	-0.0095 (1.0%)	0.0128 (1.3%)
FPN	0.4857 (44.7%)	0.0084 (0.8%)	0.0162 (1.5%)	-0.0059 (0.5%)	-0.0011 (0.1%)	0.0159 (1.4%)	-0.0927 (8.5%)		0.4354 (40.1%)	0.0151 (1.4%)	0.0095 (0.9%)
SN	0.5026 (47.5%)	0.0044 (0.4%)	0.0023 (0.3%)	-0.0031 (0.3%)	-0.0004 (0.1%)	0.0201 (1.9%)	-0.0801 (7.6%)	0.4208 (39.8%)		0.0013 (0.1%)	0.0230 (2.2%)
1000SW	0.0951 (30.7%)	0.0152 (4.9%)	0.0507 (16.4%)	-0.0129 (4.2%)	-0.0040 (1.3%)	-0.0120 (3.9%)	0.0103 (3.3%)	0.0774 (25.0%)	0.0068 (2.2%)		-0.0255 (8.2%)
HI	0.0809 (19.5%)	-0.0122 (2.9%)	-0.0427 (10.3%)	0.0099 (2.4%)	0.0034 (0.8%)	0.0191 (4.6%)	-0.0165 (4.0%)	0.0571 (13.8%)	0.1432 (34.5%)	-0.0299 (7.2%)	

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