



## Cause and Effect Relationship in Chickpea (*Cicer arietinum* L.) Genotypes under Temperate Conditions

Mohd Aslam Dar<sup>1\*</sup>, Noor-ul-Saleem Khuroo<sup>2</sup>, Reyaz-ul-Rouf Mir<sup>1</sup>,  
Zahoor Ahmad Dar<sup>2</sup>, Parvaze Ahmad Sofi<sup>1</sup>, Sher A. Dar<sup>1</sup>, Bilal Ahmad Lone<sup>3</sup>,  
Farooq A. Sheikh<sup>1</sup> and Umer Rashid Bhat<sup>1</sup>

<sup>1</sup>Division of Genetics and Plant Breeding, Sher- e -Kashmir University of Agricultural Sciences and  
Technology of Kashmir, Jammu and Kashmir, India.

<sup>2</sup>Dryland Agriculture Research Station, Sher- e -Kashmir University of Agricultural Sciences and  
Technology of Kashmir, Jammu and Kashmir, India.

<sup>3</sup>Agro-Meteorology, Sher- e -Kashmir University of Agricultural Sciences and Technology of Kashmir,  
Jammu and Kashmir, India.

### Authors' contributions

This work was carried out in collaboration among all authors. Author MAD designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors NUSK and ZAD managed the analyses of the study. Author BAL managed the literature searches. All authors read and approved the final manuscript.

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### ABSTRACT

Thirty-five genotypes and 3 varieties of chickpea were undertaken to determine the variability, interrelationship among yield and its components and their primary and secondary impact on seed quantity. The research work performed at FoA, Wadura Sopore, SKUAST-Kashmir in the rabi 2017-18. The treatment differences were statistically highly significant for all the traits along with higher magnitude of genotypic and phenotypic coefficient of variation indicating presence of good amount of variability. The character, plant height showed maximum difference preceding by pod number plant<sup>-1</sup>, days taken to maturity, 50% flowering, seed yield plant<sup>-1</sup>, 100 seed weight, number

\*Corresponding author: E-mail: [aslamagriculture123@gmail.com](mailto:aslamagriculture123@gmail.com);

of secondary and primary branches plant<sup>-1</sup> and seeds pod<sup>-1</sup>. Genotypic and phenotypic coefficient of variation have been seen maximum in case of seed yield plant<sup>-1</sup> preceding by plant height, pod number plant<sup>-1</sup>, secondary branch number, seeds pod<sup>-1</sup> and 100-seed weight. Pod number plant<sup>-1</sup>, plant height, days to maturity (99%) exhibited maximum heritability (b.s.) then secondary branches plant<sup>-1</sup>, days to 50% flowering (98%), 100-seed weight, seed yield plant<sup>-1</sup> (96%). Seed yield plant<sup>-1</sup> showed maximum genetic advance as mean% (54.17) then plant height (50.93) and pods per plant<sup>-1</sup> (50.02). The seed yield plant<sup>-1</sup> exhibited significant and positive correlation with pods plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, seeds pod<sup>-1</sup> and 100-seed weight. By comprehending path coefficient maximum primary effect shown by pods plant<sup>-1</sup> on seed yield plant<sup>-1</sup> then seeds pod<sup>-1</sup>, 100-seed weight, primary branches plant<sup>-1</sup>.

**Keywords:** Chickpea; genetic variability; correlation; path analysis; pods plant-1; seed yield plant-1.

## 1. INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a self-pollinated crop of family *Leguminaceae*. Chickpea (*Cicer arietinum* L.) commonly known as Gram, Chana, Bengal gram and Garbanzo bean is the most important pulse crop of arid and semiarid regions. The somatic chromosome number in chickpea is  $2n = 16$ . Domestication leads the formation of two major cultivar types designated as 'desi' (=microsperma) and 'kabuli' (=macrosperma). Desi chickpeas are small and angular with rough brown to yellow testas, while Kabuli types are relatively large, plump and with smooth cream colored testas. Kabuli types are considered relatively more advanced because of their larger seed size and reduced pigmentation achieved through conscious selection [1]. Desi chickpea cultivated mostly in Indian subcontinents, Ethiopia, Mexico and Iran. Desi chickpea is good for people with blood sugar problems because having markedly higher fiber content and low glycemic index. Kabuli, mainly grown in southern Europe, Northern Africa, Afghanistan, Pakistan, Turkey and India. Chickpea (*Cicer arietinum* L.) is the third most important food legume, grown in over 45 countries around the world. 75% of total world production is being shared by India. Chickpea possesses quality protein and is being considered healthy food in the developed countries. Chickpea grain contains 18-24% protein, 2.0-7.0% fats, 64% total carbohydrates (47% starch, 6% soluble sugar) and 6% crude fiber. Being a legume crop it takes care of soil fertility by fixing 41-65 kg atmospheric nitrogen per hectare through *Rhizobium* spp. Out of total production in India about 75% is being consumed as 'Dal'. India ranked first in area (9.93 million hectares) and production (9.88 million tonnes) of chickpea in the world followed by Pakistan, Iran and Australia. In India productivity was 995 kg/ha (annual report of

DPD, 2016-17). In India, Pakistan, Bangladesh and UK Chickpeas are considered one of the most popular vegetarian food. Green leaves/twigs of a chickpea are used in preparing a nutritious vegetable in the countries of South Asia. Chickpea (*Cicer arietinum* L.) is considered as the premier pulse crop of Indian subcontinent. Chickpea (*Cicer arietinum* L.) grown under both rainfed and irrigated conditions. Low productivity in the country is generally because maximum area is under rainfed farming.

Improvement of yield and quality of crop is the primary objective of plant breeder. For crop improvement selection of superior plants plays a vital role. The efficiency of selection depends on the identification of genetic variability from the phenotypic expression of the character. Variability means differences among the individuals of a single species or different species. The variability may be due to environment or genotypes or interaction of both. Assessment of genetic variability in the original population is the first step in any breeding programme.

The concept of correlation was first proposed by [2] which was later elaborated by [2]. It is a very useful technique for a plant breeder to quickly assess high yielding genotypes in the selection programme. Correlation depicts the extent of association between a particular character and seed yield but do not provide a complete picture of components affect the seed yield. Path coefficient analysis developed by [3] is a standardized partial regression analysis which further permits the partition of correlation coefficient into components of primary and secondary effects. It provides the true nature of cause and effect relationship of some of the yield contributing characters with yield. By using path coefficient analysis, the primary and secondary

effects of one variable on another can be estimated. Thus, knowing the variability, correlation and path coefficient we can select the genotypes with desired traits, which leads the yield improvement.

## 2. MATERIALS AND METHODS

The present investigation was conducted under wet condition at Regional Research Station, Faculty of Agriculture, Wadura Sopore that lies between 34° 21'N latitude and 74° 23' E longitude at an altitude of 1590 m above the mean sea level during rabi season of 2017-18. The climate is temperate, average annual precipitation is 812 mm and average temperature 14°C. The soil was silty clay loam in texture, with medium in available nitrogen, phosphorus and potassium and neutral pH. The fertilizer dose is 25: 50: 30 NPK kg/ha and applied at the time of sowing, after sowing light irrigation was given, in order to facilitate easy and better germination. In order to ensure satisfactory crop growth, operations like thinning, weeding, hoeing and

plant protection measures were carried out regularly.

The experimental material used for the study consisted of 38 genotypes which were obtained from the ICARDA-BIGMP. Thirty-five genotypes and 3 varieties of chickpea Shalimar Chickpea-1 (SC-1), Y8 and Y10 as checks as shown in Table 1, were evaluated in a Randomized Block Design (RBD) with three replications during Rabi 2017-2018. Each genotype was sown in three rows of 2 m length with spacing 30 cm between rows and 10 cm within rows. Standard agronomic practices were adopted. Observations were recorded on days to flowering and maturity (50%), plant height (cm), number of primary and secondary branches, pods plant<sup>-1</sup>, 100-seed weight (g), seeds pod<sup>-1</sup> and yield plant<sup>-1</sup> (g). The data were subjected to the analysis of variance [4] and further, biometrical procedures were followed to estimate genotypic and phenotypic coefficient of variation [5], heritability in broad sense [6], genetic advance [7] and correlation and path coefficient analysis [8].

**Table 1. List of 35 genotypes and three varieties of chickpea**

Sr. no.	Genotype	Sr. no.	Genotype	Sr. no.	Genotype
1	IR-1	14	IR-14	27	IR-27
2	IR-2	15	IR-15	28	IR-28
3	IR-3	16	IR-16	29	IR-29
4	IR-4	17	IR-17	30	IR-30
5	IR-5	18	IR-18	31	IR-31
6	IR-6	19	IR-19	32	IR-32
7	IR-7	20	IR-20	33	IR-33
8	IR-8	21	IR-21	34	IR-34
9	IR-9	22	IR-22	35	IR-35
10	IR-10	23	IR-23	36	SC-1
11	IR-11	24	IR-24	37	Y8
12	IR-12	25	IR-25	38	Y10
13	IR-13	26	IR-26		

## 3. RESULTS AND DISCUSSION

### 3.1 Variability Studies

Table 2 shows that all traits revealed wide range of variability except seeds pod<sup>-1</sup> (1.03-1.63), primary branches plant<sup>-1</sup>(2.70-4.06). Plant height (31.56-95.90) showed broader variability and pods plant<sup>-1</sup> (21.70-64.60), days to maturity (171-195), days to 50% flowering (135-155), 100 seed weight (17.09-27.15) exhibited considerable amount of variability. Minimum variability shown by seeds pod<sup>-1</sup> (1.03-1.63), primary branches plant<sup>-1</sup> (2.70-4.06). Similar results were obtained by [9,10]. [11,12] reported highest range of variability for pods plant<sup>-1</sup>. Presence of genetic variability refers evolutionary survival of a species. Yield improvement in any crop is being attained by plant breeding but desired variability on which selection is to be made must be present in the genetic material. Therefore, before starting any crop improvement programme, a plant breeder must survey and assess the variability for yield component characters which can be estimated through variance, coefficient of variability (GCV, PCV), heritability and genetic advance.

Genetic variability forms basis for any heritable improvement in the crop plants. The estimates of GCV and PCV showed little difference among characters the latter being slightly greater than the former, thus indicating that the variability present in these characters was not only due to genetic factors but also due to environmental factors. The estimates of genotypic (GCV) and phenotypic coefficients of variation (PCV) in the present study were maximum for seed yield plant<sup>-1</sup> then plant height, pods plant<sup>-1</sup> exhibited broader variation within the genotypes in the said characters. [13] highlighted maximum GCV and PCV in seed yield plant<sup>-1</sup>. [14] noticed highest GCV for 100 seed weight then seed yield plant<sup>-1</sup>, pods plant<sup>-1</sup> and seeds pod<sup>-1</sup> under rainfed condition. GCV and PCV estimates lowest for days to maturity. This is also reported by [15,16]. [9] reported highest values of GCV and PCV for 100 seed weight and lowest for days to maturity.

The estimates of GCV, PCV, heritability (b.s.) and genetic advance as per cent of mean for the different characters studied are presented in Table 2. Plant height (246.77) registered maximum genotypic variance then pods plant<sup>-1</sup> (88.31), days to maturity (38.88) and days to 50% flowering (30.39). The phenotypic variance, ranged between 0.03 and 246.94. Plant height recorded highest phenotypic variance (246.94) followed by pods plant<sup>-1</sup> (88.51) and duration of maturity (39.17). Seed yield plant<sup>-1</sup> (26.77) showed maximum genotypic coefficient of variation (GCV) then plant height (24.73), pods plant<sup>-1</sup> (24.31), secondary branches plant<sup>-1</sup>

(21.41) and 100 seed weight (10.63). The maximum phenotypic coefficient of variation was recorded for seed yield per plant (27.26) followed by plant height (24.74), number of pods per plant (24.33), number of secondary branches per plant (21.60) and 100 seed weight (10.85). In general, genotypic coefficient of variation was smaller than phenotypic coefficient of variation. Genotypic coefficient of variation alone does not indicate the proportion of total heritable variation. However, the heritability estimates are better indicators of heritable portion of the variation. The broad sense heritability comprises the contribution of additive gene effects, allelic interactions due to dominance and non-allelic due to epistasis. In the present study, pods plant<sup>-1</sup>, days to maturity, plant height (99%) then days to 50% flowering, secondary branches (98%) and all other characters showed high estimates of heritability (b.s.). Similar findings were reported by [17]. In the present study, seed yield plant<sup>-1</sup>, plant height, pods plant<sup>-1</sup>, secondary branches, 100 seed weight noticed maximum heritability (b.s.) along with genetic advance as mean% with the result the said characters based on additive gene action. It is supported by similar finding of [17,9,18]. Thus considering the estimates of genetic parameters like genotypic coefficient of variation, heritability and genetic advance mean%, selection should be performed in traits, seed yield plant<sup>-1</sup>, pods plant<sup>-1</sup>, plant height, secondary branches plant<sup>-1</sup> and 100 seed weight in order to modify yield in chickpea. Highest heritability noticed in days to maturity, plant height, pods plant<sup>-1</sup> (99%) then days to 50% flowering, secondary branches (98%), 100-seed

**Table 2. Variability parameters for nine different characters in chickpea**

S. no.	Parameters	Range	PV	GV	E.V	PCV	GCV	h <sup>2</sup> (b. s)	G.A
1	DF	135-155	30.71	30.39	0.325	3.80	3.78	0.98	7.75
2	DM	171-195	39.17	38.88	0.292	3.43	3.42	0.99	7.02
3	NPB	2.70-4.06	0.31	0.12	0.194	16.50	10.20	0.38	12.99
4	NSB	6.06-14.70	3.64	3.58	0.064	21.60	21.41	0.98	43.72
5	PH	31.56-95.90	246.94	246.77	0.165	24.74	24.73	0.99	50.93
6	NPP	21.70-64.60	88.51	88.31	0.192	24.33	24.31	0.99	50.02
7	NSP	1.03-1.63	0.03	0.02	0.006	14.65	14.65	0.83	25.10
8	100-SW	17.09-27.15	6.13	5.88	0.248	10.85	10.63	0.96	21.45
9	SYP	5.83-18.69	8.90	8.58	0.315	27.26	26.77	0.96	54.17

PV= Phenotypic variance, GV= Genotypic variance, EV= Env. Variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, h<sup>2</sup> (b.s)= Heritability(broad sense), G.A.= Genetic advance mean%, DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NPB = Primary branches, NSB = Secondary branches, NPP = Pods plant<sup>-1</sup>, NSP = Seeds pod<sup>-1</sup>, SW = Seed weight, SYP = Seed yield plant<sup>-1</sup>

weight, seed yield plant<sup>-1</sup> (96%). The evaluated traits showed good heritability. GA mean% ranged from 7.02 to 54.17 high in seed yield plant<sup>-1</sup>.

### 3.2 Correlation Coefficient Analysis

Correlated traits refers the fundamentals i.e., genetic nature of correlation due to linkage and pleiotropic action of genes, modifying one trait at the same time changes other traits and connection with natural selection [19]. Strong association between secondary branches plant<sup>-1</sup> and pods plant<sup>-1</sup> was noticed through the highly significant positive values of correlation coefficients. This indicates the simultaneous improvement of these characters through selection. Days to 50% flowering highly correlated with days to maturity and plant height implies maturity period get detected with the help of days taken to 50% flowering. A negative correlation of these characters observed with seed yield per plant would help in developing early maturity varieties.

The genotypic and phenotypic correlations for nine characters studied are presented in Table 3. In general, genotypic correlation coefficients were higher than their corresponding phenotypic correlations. Similar results were also reported by [20]. It is revealed from Table 3 that, significant positive correlation was reported within seed yield plant<sup>-1</sup>, pods plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, seeds pod<sup>-1</sup>. Results to certain extent are in accordance with the findings of

[21,22,23]. Non-significant positive correlation was reported within seed yield plant<sup>-1</sup>, 100-seed weight, plant height.

### 3.3 Path Coefficient Analysis

It provides basis for selection of superior genotypes from the diverse breeding population. Seed yield is the result of interaction of component traits. Apart from correlation studies, path coefficient analysis plays an utmost role in obtaining information about how the component characters effect the seed yield through each other. To know the direct and indirect contribution from each of the characters towards seed yield plant<sup>-1</sup>, path coefficient analysis was worked out. The genotypic correlation coefficients being more important were only partitioned into primary and secondary effects which are presented in Table 4.

In the present investigation, pods plant<sup>-1</sup> possesses high impact (1.02) on seed yield plant<sup>-1</sup> then seeds pod<sup>-1</sup>, 100 seed weight, primary branches plant<sup>-1</sup>. This implies pro- association of the said traits with seed yield plant<sup>-1</sup>. Same results were observed by [21,18]. Secondary branches plant<sup>-1</sup> shows anti-association with seed yield. Similar results were reported by [24,25]. The findings of the present investigations it could be enforced that the most desirable plant type in chickpea should possess high primary branches plant<sup>-1</sup>, pods plant<sup>-1</sup>, seeds pod<sup>-1</sup> and higher 100 seed weight, i.e. bold seeds.

**Table 3. Estimation of genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficients in chickpea**

S. no.	DF	DM	NPB	NSB	PH	NPP	NSP	100-SW	SYP
	1	2	3	4	5	6	7	8	9
1	1.00	0.885*	-0.216	-0.130	0.800*	-0.138	-0.200	-0.269	-0.303
2	0.883*	1.00	-0.251	-0.209	0.376*	-0.187	-0.214	-0.235	-0.334
3	-0.112	-0.145	1.00	0.641*	0.014	-0.145	0.537*	-0.185	-0.114
4	-0.128	-0.206	0.634*	1.00	0.088	0.989*	0.034	-0.101	0.839*
5	0.079	0.017	0.006	0.088	1.00	0.028	-0.074	0.265	0.074
6	-0.137	-0.187	-0.091	0.985*	0.028	1.00	0.054	-0.584*	0.855*
7	-0.180	-0.193	0.037	0.017	-0.070	0.044	1.00	-0.384*	0.364*
8	-0.261	-0.227	0.037	-0.102	0.260	-0.118	-0.360*	1.00	0.128
9	-0.295	-0.325	-0.027	0.812*	0.072	0.837*	0.392*	0.129	1.00

\*, indicate significant at 5 % level of probability or level of significance  
 DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NPB = Primary branches,  
 NSB = Secondary branches, NPP = pods plant<sup>-1</sup>, NSP = seeds pod<sup>-1</sup>, SW = Seed weight,  
 SYP = Seed yield plant<sup>-1</sup>

**Table 4. Direct (diagonal) and indirect effect of eight causal variables on seed yield in chickpea**

S. no.	Parameters	DF	DM	NPB	NSB	PH	NPP	NSP	100-SW	SYP
1.	DF	0.0255	0.0226	-0.0055	-0.0033	0.0020	-0.0035	-0.0051	-0.0069	-0.3031
2.	DM	0.0315	0.0356	-0.0090	-0.0075	0.0006	-0.0067	-0.0076	-0.0084	-0.3345
3.	NPB	-0.0109	-0.0126	0.0501	-0.0071	0.0007	-0.0073	-0.0027	0.0009	-0.1141
4.	NSB	0.0161	0.0258	0.0174	-0.1229	-0.0109	-0.1217	-0.0043	0.0125	0.8394
5.	PH	-0.0024	-0.0005	-0.0004	-0.0026	-0.0294	-0.0008	0.0022	-0.0078	0.0743
6.	NPP	-0.1412	-0.1919	-0.1482	1.0113	0.0288	1.0216	0.0553	-0.1210	0.8553
7.	NSP	-0.1002	-0.1073	-0.0269	0.0174	-0.0375	0.0271	0.5002	-0.1921	0.3648
8.	100-SW	-0.1215	-0.1062	0.0084	-0.0459	0.1199	-0.0534	-0.1732	0.4509	0.1282

DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), NPB = primary branches, NSB = secondary branches, NPP = pods plant<sup>-1</sup>, NSP = seeds pod<sup>-1</sup>, SW = Seed weight, SYP = Seed yield plant<sup>-1</sup>

#### 4. CONCLUSION

The range of variability, genotypic and phenotypic coefficient of variation, heritability percentage and genetic advance mean% have been found. Plant height trait showed high range of variability then pods plant<sup>-1</sup>, days to maturity. Seeds pod<sup>-1</sup> possesses less variability. Genotypic and phenotypic coefficient of variation observed high in case of trait seed yield plant<sup>-1</sup> then plant height, pods plant<sup>-1</sup>. High heritability implies high genetic advance as mean% in case of seed yield plant<sup>-1</sup>, plant height, pods plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, 100 seed weight, which refers the said characters are being controlled by additive gene action with the result these traits can be modified by simple selection. Correlation studies at both genotypic and phenotypic levels have been done in order to resolve the direction and magnitude of association within characters. The significant positive correlation was reported within seed yield plant<sup>-1</sup>, pods plant<sup>-1</sup>, secondary branches plant<sup>-1</sup>, seeds pod<sup>-1</sup>, plant height, 100 seed weight. This refers that simultaneous improvement of these characters through selection, whereas days to 50% flowering indicated significant negative correlation with seed yields plant<sup>-1</sup> at genotypic and phenotypic level showed early genotype also produce higher grain yield. Path coefficient analysis implies pods plant<sup>-1</sup> possesses high impact (1.02) on seed yield plant<sup>-1</sup> then seeds pod<sup>-1</sup> (0.50), 100 seed weight (0.45), primary branches plant<sup>-1</sup> (0.05), with the result one should recognize the given traits at the time of selection in order to modify the desired trait, grain yield in chickpea. Said characters possesses significant pro-association with seed yield plant<sup>-1</sup>. Secondary branches impacts on seed yield via pods plant<sup>-1</sup> and 100 seed weight, which implies indirect selection through such traits would be effective in yield improvement.

#### COMPETING INTERESTS

Authors have declared that no competing interests exist.

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