**Original Research Article**

# Assessment of Genetic Variability, Character Association and Path Analysis in F$_2$ Segregating Population for Quantitative Traits in Chickpea

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### A B S T R A C T

An investigation was carried out to assess the genetic variability of seven quantitative characters in F$_2$ population, to study the association and path coefficient analysis of yield and its attributing traits. High phenotypic coefficient of variation and genotypic coefficient of variation estimates were recorded for number of pods per plant, seed yield per plant, number of pods per branch, number of branches per plant and 100-seed weight in the F$_2$ segregating population of the cross L 550 × PG 06102 which indicates greater scope for selection to improve upon these characters. High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for number of pods per plant, seed yield per plant, number of pods per branch, plant height, 100-seed weight and number of branches per plant indicating that these traits are under the control of additive gene action. Correlation studies for seed yield and its attributing traits revealed significant positive correlation of plant height, number of branches per plant, pods per plant, pods per branch and 100-seed weight with seed yield per plant inferring that these traits strongly influenced seed yield per plant. Path coefficient analysis revealed that number of pods per plant exhibited direct effect on seed yield per plant followed by number of pods per branch, number of branches per plant, 100-seed weight and plant height indicating the importance of these characters in selection programme for increasing the seed yield.

## Introduction

Chickpea (*Cicer arietinum* L.) is one of the oldest and widely cultivated pulse crops in the world. Southwest Asia and the Mediterranean are the two primary centers of origin and Ethiopia, the secondary centre of diversity (Vavilov, 1926; 1951). Wild annual *Cicer* originated mainly in the Mediterranean regions having a wide eco-geographic range, differing in habitat, topographic and climatic conditions (Abbo *et al.,* 2003; Berger *et al.,*

2003). Chickpea is a self-pollinated (0-1% cross pollination; Singh, 1987) annual diploid grain legume of the family Fabaceae, sub family Faboideae having 2n=2x=16 chromosomes with a genome size of 738 Mb (Varshney *et al.,* 2013). Chickpea is also known as garbanzo bean, Indian pea, ceci bean and bengal gram. Globally, chickpea is grown in an area of 11.08 million hectares with the production of 9.77millon tonnes and

an average productivity of 881.9 kgha$^{-1}$. It is the second most important pulse crop worldwide in terms of area under cultivation after dry bean but ranks third in production following dry bean and peas. India is the largest producer of chickpea in the world sharing 65.25 and 65.49 per cent (FAOSTAT, 2010) of the total area (11.97 million ha) and production (10.89 million tonnes) with productivity of 911 kg/ha. Among the two types of chickpea cultivated, desi occupies 85 per cent area and 15 per cent of the area is occupied by kabuli type. Six states *viz*., Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Karnataka and Andhra Pradesh together contribute 90 per cent of the area and 91 per cent of the production in the country (Singh, 2010). Karnataka is one of the major chickpea producing states in the country and it is grown over an area of 0.97 m ha with a production of 0.57 million tonnes having an average productivity of 670 kg/ha (Viswanatha *et al.,* 2011). The most important objective in any crop improvement programme is to increase the seed yield. Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability in the population where selection has to be made.

Further, the quantitative traits are governed by large number of genes and are more influenced by the environment. Phenotypic variability expressed by a genotype or group of genotypes in any species can be partitioned into genotypic and phenotypic components. The phenotypic component observed is not transmitted entirely to next generation. The genotypic components being the heritable part of the total variability, its magnitude for yield and its components characters influences the selection strategies to be adopted by the breeders.

Grain yield in any crop depends on many component characters which influence the yield either jointly or singly which may be either direct or indirectly through other related characters. Selection for yield on the basis of *per se* performance alone may not be effective compared to selection based on the component character associated with it, which is biometrically determined by correlation coefficient and path analysis. An understanding of the nature and extent of association of these components with grain yield and amongst themselves is an essential prerequisite for formulating sound breeding programme. This concept was given by Fisher (1918) and Wright (1921). The information on correlation is of great importance when simultaneous selection is to be carried out for more than one character to achieve the required improvement in seed yield.

The Association of characters can be expressed as phenotypic correlation and genotypic correlation. Phenotypic correlation is the observable correlation between two variables and includes both genotypic and environmental effects. Genotypic correlation on the other hand, is the inherent association between two variables may be either due to pleiotropic action of genes or linkage, more likely both or developmentally induced relationships.

Yield and its component traits sharing linear correlations may present a confusing picture due to the possible interrelationship between the components themselves. Path analysis is an effective tool for partitioning the direct effect of each trait on yield and its indirect effect through other traits. In this context, an investigation was carried out to assess the genetic variability of seven quantitative characters in $F_2$ population, to study the association and path coefficient analysis of yield and its attributing traits during *rabi* 2012-13 at Zonal Agricultural Research Station, University of Agricultural Sciences, GKVK, Bengaluru.

## Materials and Methods

The material for the study included the $F_2$ population developed from the cross L-550 × PG-06102 which comprised of 129 plants. A total of 129 plants of chickpea were sown during *rabi* 2012 in a 3 × 3 m plot with spacing of 30 cm between rows and 10 cm between plants. The crop was raised as per the recommended package of practices. The field was kept weed free by hand weeding and protective irrigation was given whenever the crop suffered moisture stress and during critical stages of crop growth. Observations were recorded on all the 129 individuals for days to 50 per cent flowering, plant height (cm), number of branches per plant, number of pods per plant, number of pods per branch, 100-seed weight (g) and seed yield per plant (g). The mean of five plants was used for the computation of all the traits except days to 50 per cent flowering.

The variability parameters *viz*., mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) as per the formula suggested by Burton and De Vane (1953), heritability in broad sense (Lush, 1946) and genetic advance as per cent of mean (Johnson *et al.,* 1955), genotypic and phenotypic coefficients of correlation (Al-Jibouri *et al.,*1958) and path coefficients (Dewey and Lu, 1959) was computed using computerized statistical packages like Window STAT and GENRES.

## Results and Discussion

The improvement of a character in a population is a function of variability existing in the population. Hence, formulation of objectives in breeding programme should be essentially accompanied with the assessment of existing variability. The variability quantified by range includes influence of environment and genotype × environmental

components of variation. Since, all these variations are not heritable it is appropriate to partition the phenotypic variation into heritable (genetic) and non-heritable (environmental) components, and thus, true breeding value of the genotype is precisely estimated by separating genetic variance from environmental variance. In this direction the components of variance such as PCV and GCV, heritability and predicted genetic advance as per cent mean were computed for all the seven characters in $F_2$ population of the cross L 550 × PG 06102.

The $F_2$ population of the cross L 550 × PG 06102 exhibited wide variation for all the traits studied (Table 1). Days to flowering ranged from 41 to 65 days with a mean of 51.59 days; plant height ranged from 14.00 to 42.00 cm with a mean of 26.74 cm; number of branches per plant ranged from 2 to 21 with a mean of 5.67; number of pods per plant ranged from 4.00 to 159.00 with a mean of 32.53. Number of pods per branch ranged from 0.75 to 36.17 with a mean of 7.18; 100-seed weight ranged from 10.00 to 27.51 g with a mean of 19.06 g; and seed yield per plant ranged from 1.20 to 43.06 with a mean of 10.26 g.

PCV and GCV estimates were high for number of pods per plant (73.88 % and 72.60 %) followed by number of branches per plant (63.55 % and 58.51 %), number of pods per branch (61.78 % and 59.94 %), seed yield per plant (45.11 % and 41.90 %) and 100-seed weight (20.92 % and 20.62 %). Whereas, moderate PCV and GCV values were recorded for days to 50 per cent flowering (10.44 % and 10.39 %) and plant height (19.95 % and 19.76 %). Genotypic coefficient of variation (GCV) would be more useful for the assessment of variability than the phenotypic coefficient of variation (PCV) since, it is the heritable portion of the total variability (Allard, 1970). Higher the

proportion of GCV, greater would be the expected genetic gain. Many practical decisions in breeding programs are based on the magnitude of heritable variation. In comparing PCV and GCV estimates it was evident that the influence of environment on the expression of most of the characters was low indicating the greater role of genetic factors causing variability in these characters. These observations indicated ample scope for improvement of the above traits based on phenotypic values.

Heritability in broad sense was high for days to 50 per cent flowering (99.08 %), plant height (98.13 %), 100-seed weight (97.07 %), number of pods per plant (96.57 %) and number of pods per branch (92.87 %), seed yield per plant (86.28 %) and number of branches per plant (84.79 %). The heritability in broad sense was high for all the traits studied. Genetic advance as per cent of mean was high for number of pods per plant (146.96 %) followed by number of pods per branch (118.20 %), number of branches per plant (111.00 %), seed yield per plant (80.17 %), 100-seed weight (41.84 %), plant height (40.33 %), and days to 50 per cent flowering (21.30 %). Heritability estimates alone cannot provide sufficient information on the amount of genetic progress that would result from selecting the best individuals since their scope is limited by their interaction with environment. Johnson *et al.,* (1955) reported that heritability estimates along with genetic gain would be more useful than the former alone, in predicting the effectiveness of selecting the best individuals from segregating population. Therefore, it is essential to consider the predicted genetic advance along with heritability estimates as a tool in the selection programme for better efficiency in the selection.

High heritability coupled with high genetic advance as per cent of mean (GAM) was observed for number of pods per plant, seed yield per plant, number of pods per branch, plant height, 100- seed weight and number of branches per plant indicating that these traits are under the control of additive gene action and directional phenotypic selection for these traits in genetically diverse genotypes or in the segregating populations could be effective for desired genetic improvement. Moderate heritability and genetic advance as per cent of mean was observed for days to 50 per cent flowering indicating considerable influence of environment apart from non-additive gene action. Therefore, pedigree selection or population improvement programs bring about desired improvement.

In any crop improvement programme, it becomes necessary to have simultaneous selection of more than one character, especially in the case of complex character like yield, which is influenced by many other contributing traits. Correlation of characters serves as a measure and forms the basis of selection as it gives strength and direction of relationship between the characters studied. Selection for yield will be effective, only when it is considered along with its yield components rather than relying on yield alone. When a breeder applies selection pressure for a trait, it also brings about a simultaneous change in all associated characters with it.

The phenotypic correlations estimated among seven characters to determine their nature of relationship in $F_2$ population of the cross L 550 $\times$ PG 06102 are presented in Table 2. Seed yield per plant exhibited significant positive association with number of pods per plant (0.945), number of pods per branch (0.752), plant height (0.599), number of branches per plant (0.560) and 100-seed weight (0.241), whereas the association was positive non-significant with days to 50 per cent flowering.

**Table.1** Estimates of genetic variability parameters for seed yield and its attributing characters in $F_2$ generation of the cross L-550 × PG-06102 in chickpea

| Sl. No. | Characters | Mean | Range | Vp | Vg | PCV (%) | GCV (%) | $h^2_{BS}$ | GAM (%) |
|---------|-----------|------|-------|----|----|---------|---------|-----------|---------|
| 1 | Days to 50 % flowering | 51.59 | 41.00 -65.00 | 28.99 | 28.73 | 10.44 | 10.39 | 99.08 | 21.30 |
| 2 | Plant height (cm) | 26.74 | 14.00 – 42.00 | 28.47 | 27.94 | 19.95 | 19.76 | 98.13 | 40.33 |
| 3 | Number of branches plant$^{-1}$ | 5.67 | 2.00 – 21.00 | 13.00 | 11.02 | 63.55 | 58.51 | 84.79 | 111.00 |
| 4 | Number of pods plant$^{-1}$ | 24.88 | 4.00 – 159.00 | 337.75 | 326.15 | 73.88 | 72.60 | 96.57 | 146.96 |
| 5 | Number of pods branch$^{-1}$ | 7.01 | 0.75 – 36.17 | 9.58 | 8.90 | 61.78 | 59.94 | 92.87 | 118.20 |
| 6 | 100 seed weight (g) | 19.06 | 10.00 – 27.51 | 15.91 | 15.44 | 20.92 | 20.62 | 97.07 | 41.84 |
| 7 | Seed yield plant$^{-1}$ (g) | 7.58 | 1.20 – 43.06 | 11.68 | 10.08 | 45.11 | 41.90 | 86.28 | 80.17 |

**Table.2** Estimates of phenotypic correlation coefficient of seed yield and its attributing character in $F_2$ generation of the cross L-550 × PG-06102 in chickpea

| Characters | Days to 50 % flowering | Plant height (cm) | Number of branches plant$^{-1}$ | Number of pods plant$^{-1}$ | Number of pods branch$^{-1}$ | 100 seed weight (g) | Seed yield plant$^{-1}$ (g) |
|-----------|------|------|------|------|------|------|------|
| Days to 50 % flowering | 1.000 | 0.023 | 0.422** | 0.147 | -0.096 | -0.132 | 0.120 |
| Plant height (cm) | | 1.000 | 0.516** | 0.592** | 0.456** | 0.184* | 0.599** |
| Number of branches plant$^{-1}$ | | | 1.000 | 0.570** | 0.112 | 0.108 | 0.560** |
| Number of pods plant$^{-1}$ | | | | 1.000 | 0.767** | 0.183* | 0.945** |
| Number of pods branch$^{-1}$ | | | | | 1.000 | 0.161 | 0.752** |
| 100 seed weight (g) | | | | | | 1.000 | 0.241** |
| Seed yield plant$^{-1}$ (g) | | | | | | | 1.000 |

*and **- significant at p=0.05 and 0.01

**Table.3** Path coefficient analysis of component characters towards seed yield per plant in $F_2$ population of cross L-550 × PG-06102 in Chickpea

| Characters | Days to 50 % flowering | Plant height (cm) | Number of branches plant[-1] | Number of pods plant[-1] | Number of pods branch[-1] | 100 seed weight (g) | Phenotypic correlation with seed yield |
|---|---|---|---|---|---|---|---|
| Days to 50 % flowering | **-0.0106** | 0.0006 | 0.0388 | 0.1125 | -0.0125 | -0.0083 | 0.120 |
| Plant height (cm) | -0.0002 | **0.0268** | 0.0475 | 0.4537 | 0.0594 | 0.0116 | 0.599** |
| Number of branches plant[-1] | -0.0045 | 0.0138 | **0.0921** | 0.4369 | 0.0146 | 0.0068 | 0.560** |
| Number of pods plant[-1] | -0.0016 | 0.0159 | 0.0525 | **0.7663** | 0.1001 | 0.0116 | 0.945** |
| Number of pods branch[-1] | 0.0010 | 0.0122 | 0.0103 | 0.5880 | **0.1304** | 0.0102 | 0.752** |
| 100 seed weight (g) | 0.0014 | 0.0049 | 0.0099 | 0.1406 | 0.0210 | **0.0632** | 0.241** |

*and **- significant at p=0.05 and 0.01
Residual effect: 0.31

Days to 50 per cent flowering exhibited significant positive association with number of branches per plant (0.422). Plant height recorded significant positive correlation with number of pods per plant (0.592), branches per plant (0.516), pods per branch (0.456) and 100-seed weight (0.184). Significant positive correlation was observed between number of branches per plant and pods per plant (0.570).

Number of pods per plant recorded significant positive association with pods per branch (0.767) and 100-seed weight (0.183) in $F_2$ population. The earlier studies also reported the association of seed yield with plant height (Kobraee *et al.,* 2010), number of branches per plant (Yadav *et al.,* 2010), number of pods per plant (Gohil and Patel, 2010; Biabani *et al.,* 2011) and 100-seed weight (Akhtar *et al.,* 2011; Talebi and Karami, 2011) in chickpea. The important yield attributing traits *viz*., number of branches per plant, pods per plant and 100- seed weight also had significant positive correlation among themselves. Hence, selection for any one of these traits will result in the improvement of seed yield.

The path coefficient analysis, a statistical device developed by Wright (1921) takes into account the cause and effect relation between the variables which is unique in partitioning the association into direct and indirect effects through other independent variables.

The path coefficient analysis also measures the relative importance of causal factors involved. This is simply a standardized partial regression analysis where in total correlation value is subdivided into causal scheme. Li (1956) emphasized the importance of path diagram which facilitates the understanding of the nature of cause and effect system. Path coefficient analysis reveals a relative contribution of different characters towards seed yield. The direct effect of a chosen trait on seed yield and its indirect effect through other characters were computed and are presented in Table 3.

Among the six characters, seed yield was primarily influenced by number of pods per plant, which had maximum direct effect on seed yield per plant. Hence, it would be rewarding to lay emphasis on number of pods per plant while developing selection strategies in chickpea (0.7663). Number of pods per branch (0.1304), number of branches per plant, 100-seed weight and plant height were next to number of pods per plant to exhibit positive direct effect on seed yield. In contrary to the above, days to 50 per cent flowering showed negative direct effect on seed yield.

High indirect positive effect on seed yield was exhibited by number of pods per branch through number of pods per plant (0.5880) followed by plant height via pods per plant (0.4537) and number of branches per plant through number of pods per plant (0.4369). However, 100-seed weight via number of pods per branch (0.1406), days to 50 per cent flowering through number of pods per plant (0.1125) and number of pods per plant via number of pods per branch (0.1001) exhibited low indirect positive influence on seed yield. The results of the present study suggested the importance to be given for number of pods per plant, branches per plant, 100-seed weight and plant height in indirect selection to recover segregants with increased seed yield in chickpea owing to their greater direct and indirect effects on yield.

## References

Abbo, S., Berger, J. and Turner, N. C., 2003, Evolution of cultivated chickpea: four bottlenecks limit diversity and constrain adaptation. *Functl. Plant Biol*., 30: 1081–1087.

Akhtar, L. H., Pervez, M.A. and Muhammad Nasim, 2011, Genetic divergence and inter-relationship studies in chickpea (*Cicer arietinum* L.). *Pakistan J. Agric. Sci.*, 48(1): 35-39.

Al-Jibouri, H.A., Miller,P.A. and Robinson, H.F., 1958, Genotypic and environmental variances in upland cotton of inter-specific origin. *Agron.* J., 50: 633-637.

Allard, R. W. and Bradshaw, A. D., 1964, Implication of genotype and environmental interaction in applied plant breeding. *Crop Sci.*, 4: 503-508.

Berger, J., Abbo, S. and Turner, N. C., 2003, Eco-geography of annual *Cicer* species: the poor state of the world collection. *Crop Sci.,* 43: 1076–1090.

Biabani, A., Mollashahi, M., Esmaeili, M., Bahlake, A. G. and Khani, A. H. G., 2011, Correlation and relationships between seed yield and other characteristics in chickpea (*Cicer arietinum* L.) cultivars under deterioration. *American Eurasian J. Agric. Environ. Sci.*, 10(4): 692-695.

Burton, G. W. De Vane, G. M., 1953, Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Agron. J.,* 45: 478-481.

Dewey, D. R. and Lu, K. H., 1959, Correlation and path coefficient analysis of components of crested wheat grass seeds production. *Agron. J.*, 51: 515-520.

FAOSTAT, 2010, (Food and Agricultural Organization Statistical) Database. Rome: available at http://www.faostat.fao.org/, 2010.

Fisher, R. A., 1918, The correlation among relatives on the supposition of Mendelian inheritance. *Trans. Royal Soc. Edinburgh*, 52: 399-433.

Gohil, D. P. and Patel, J. D., 2010, Character association and path analysis in chickpea (*Cicer arietinum* L.) under

conserved soil moisture. *Legume Res*., 33(4): 283-286.

Johnson, R. W., Robinson, H. F. and Comstock, R. E., 1955, Estimates of genetic and environment variability in soybean. *Agron. J.,* 47: 314-318.

Kobraee, S., Shamsi, K., Rasekhi, B. and Kobraee, S., 2010, Investigation of correlation analysis and relationships between grain yield and other quantitative traits in chickpea (*Cicer arietinum* L.). *African J. Biotech*., 9(16): 2342-2348.

Li, C. C., 1956, The concept of path coefficient and its impact on population genetics. *Biometrica*, 12: 190-210.

Lush, J. L., 1949, Heritability of quantitative characters m farm animals. It: *Proceedings of Congress Genetics Heridias (Suppl.),* pp. 356-375.

Singh, I. S., 1987, Recent advances in research on botrytis gray mold of chickpea: summary proceedings of the Third Working Group Meeting to Discuss Collaborative Research on Botrytis Gray Mold of Chickpea, ICRISAT. 31-32 pp.

Singh, N. P., 2010, Chickpea *Project Coordinator report*, Indian Institute of Pulses Research, Kanpur, 45pp.

Talebi, R. and Karami, E., 2011, Morphological and physiological traits associated with seed yield in different chickpea (*Cicer arietinum* L.) genotypes under irrigated and water-deficit environments. *South Asian J. Exptl. Biol*., 1(6): 260-267.

Varshney, R. K., Chi Song, Saxena, R. K., Sarwar Azam, Sheng Yu, Sharpe, A. G., Steven Cannon, Jongmin Baek, Rosen, B. D., Bunyamin Taran, Teresa Millan, Xudong Zhang, Ramsay, L. D., Aiko Iwata, Ying Wang, William Nelson, Farmer, A. D., Gaur, P. M., Carol Soderlund, Varma, R. P., Chunyan Xu, Bharti, A. K., Weiming He, Peter

Winter, Shancen Zhao, Hane, J. K., Garcia, N. C., Condie, J. A., Upadhyaya, H. D., Ming-Cheng Luo, Mahendar Thudi, Gowda, C. L. L., Singh, N. P., Judith Lichtenzveig, Gali, K. K., Josefa Rubio, Nadarajan, N., Jaroslav Dolezel, Bansal, K. C., Xun Xu, David Edwards, Gengyun Zhang, Guenter Kahl, Juan Gil, Singh, K. B., Datta, S. K., Jackson, S. A., Jun Wang, Cook., D. R., 2013, Draft genome sequence of chickpea (*Cicer arietinum*) provides a resource for trait improvement. *Nature Biotech*., 31: 240-246.

Vavilov, N. I., 1926, Studies on the origin of cultivated plants. Lenningrad. pp 129–133.

Vavilov, N. I., 1951, The origin, variation immunity and breeding of cultivated plants. *Chronica Botanica*, 6:26-38.

Viswanatha, K. P., Saifulla, M., Chandrashekara, K., Mudalagiriyappa, Nagaraju, K. and Nehru, S. D., 2011, *Chickpea research in Karnataka present status and future prospects,* AICRP on chickpea, pp. 42.

Wright, S., 1921, Correlation and causation. J. Agric. Res., 20: 557-587.

Yadav, A. K., Mishra, S. B., Singh, S. S. and Madhuri Arya., 2010, Character association and genetic divergence study in chickpea (*Cicer arietinum* L.). *Environ. Ecology*, 28(2B): 1276-1280.