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# Dissection of Genetic Variability, Correlation and Path Analysis of Seed Yield and Yield Contributing Traits in Chickpea (*Cicer arietinum* L.) and their Implication in Selection

***Manoranjan Biswal[1]*, R.S. Solanki[2], Shailendra Sagar Prajapat[1], R. Shiv Rama Krishnan[3] and Anita Babbar[4]***
*[1]Ph. D. Scholar, Department of Plant Breeding and Genetics,*
*Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, (Madhya Pradesh), India.*
*[2]Teaching Assistance, Department of Plant Breeding and Genetics,*
*Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, (Madhya Pradesh), India.*
*[3]Assistant Professor, Department of Plant Physiology,*
*Jawaharlal Nehru Krishi Vishwa, Vidyalaya, Jabalpur, (Madhya Pradesh), India.*
*[4]Principal Scientist, AICRP on Chickpea, Department of Plant Breeding and Genetics,*
*Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, (Madhya Pradesh), India.*

*(Corresponding author: Manoranjan Biswal*)*
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**ABSTRACT: The present experiment was conducted at Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur during *Rabi* 2019-20 and 2020-2021. The experimental materials consisted 30 advanced breeding lines of desi chickpea laid out in Randomized Complete Block Design with three replications. The analysis of variance showed genotypes were highly significant for all the traits suggesting presence of considerable amount of variation for all the traits among the genotypes suggesting genotypes evaluated in this present study has broad genetic base. The phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the traits. The highest genotypic and phenotypic coefficient of variation was noted for the trait; biological yield per plant. High heritability along with high genetic advance as % of mean were detected for seed yield per plant, biological yield per plant, number of effective pods per plant, total number of pods per plant, number of seeds per pod. The seed yield per plant showed positive and significant correlation with biological yield, days to 50% flowering, days to pod initiation and days to flower initiation. This experiment revealed that days to flower initiation had the highest positive direct effect on seed yield per plant followed by biological yield per plant. For increasing seed yield due importance should be put on number of primary and secondary branches, more number of total and effective pods per plant. In addition, an ideotype should be designed from evident of phenotypic and genotypic coefficient of variation, heritability and genetic advance and association studies. Hence, effective selection strategy can be practiced on these traits to intensify the yield level.**

**Keywords:** Chickpea, Correlation, Path analysis, Heritability, Genetic advance, Seed yield

## INTRODUCTION

Chickpea (*Cicer arietinum* L.) an important *Rabi* pulse crop of India has active contribution in pulse economy. This crop occupies an essential role in our daily diet as a very good source of protein and well adopted in cropping systems. Nevertheless, it is failing the competition with wheat in irrigated areas and with mustard in rainfed region by virtue of dearth of high yielding varieties. For enhancing its yield potential, different methods of genetic improvement have been enforced. As, seed yield being polygenetically controlled complex trait and altered by many environmental factors, hence it manifests low heritability and direct selection based on yield alone often ambiguous Xiong (1992). Hence, the present study was attempted to explicate the genetic variation, association studies between yield and yield contributing traits chickpea over two different seasonal conditions.

## MATERIALS AND METHODS

The present study was carried out at Seed Breeding Farm, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur during *Rabi* 2019-20 and 2020-2021. The experimental materials consisted 30 advanced breeding lines of desi chickpea laid out in Randomized Complete Block Design with three replications including pooled analysis of two years data. All recommended package of practices was followed during the cropping period to raise a good crop.

Observations were recorded for fourteen quantitative characters *viz*., days to flower initiation, days to 50% flowering, days to pod initiation, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, total number of pods per plant, number of effective pods per plant, number of seeds per pod, 100 seed weight (g), biological yield per plant (g), harvest index (%) and seed yield per plant (g). The data was subjected to the standard statistical analysis for genetic parameters, correlation coefficient and path analysis.Correlation coefficients were estimated for all the character combinations at genotypic and phenotypic levels by the procedure suggested by Miller et al. (1958). Genotypic path coefficients were calculated separately for yield and yield components by the technique proposed by Wright (1921) and Dewey and Lu (1959). The dependent variable for association studies were seed yield per plant. Heritability for the present study was calculated in broad sense by adopting the formula suggested by Hanson *et al.* (1956). Expected genetic advance was calculated by the method suggested by Johnson *et al.* (1955). Genotypic and phenotypic coefficient of variance was evaluated according to Burton and Devane (1953) based on estimate of genotypic and phenotypic variance.

## RESULTS AND DISCUSSION

*A. Analysis of variance*

The analysis of variance showed genotypes were highly significant for all the traits suggesting presence of considerable amount of variation for all the traits among the genotypes suggesting genotypes evaluated in this present study has broad genetic base (Table 1). As, genetic variability, the indispensable demand for any crop improvement programme, hence, utilization of these variability may accelerate to develop promising genotype in the future is the ultimate aim of plant breeder. It provides broad genetic base to genotypes to survive under wide range of changing environmental conditions. The existing of high genetic variability for seed yield per plant and its contributing traits furnish greater opportunity for utilization in further chickpea breeding programme. Results revealed that phenotypic coefficient of variation was higher than genotypic coefficient of variation that agreement with findings of Borate *et al.,* (2010) suggesting considerable role of environment over these traits.

**Table 1: Analysis of variance for yield and yield contributing traits in chickpea.**

| Sr. No. | Observations | Mean sum of square | | | | | |
|---|---|---|---|---|---|---|---|
| | | Replicate | Environments | Interactions | Total | Treatments | Error |
| | **d.f.** | 2 | 1 | 2 | 5 | 29 | 145 |
| 1. | **DTFI** | 1.267 | 13.339 | 0.622 | 3.423 | 26.859** | 5.681 |
| 2. | **DT50%F** | 2.606** | 16.806 | 0.039 | 4.419 | 30.835** | 4.214 |
| 3. | **DTPI** | 1.617 | 5.689 | 0.006 | 1.787 | 33.869** | 9.428 |
| 4. | **DTM** | 60.972** | 61.25 | 46.55 | 55.259 | 144.845** | 69.854 |
| 5. | **PH** | 1.076* | 11.909 | 5.408 | 4.976 | 103.358** | 34.169 |
| 6. | **PB** | 1.217* | 0.089 | 0.506 | 0.707 | 0.409** | 0.578 |
| 7. | **SB** | 4.650** | 1.8 | 0.117 | 2.267 | 1.867** | 0.823 |
| 8. | **TNPPP** | 0.606 | 1.8 | 0.35 | 0.742 | 858.859** | 167.678 |
| 9. | **NEPP** | 12.717** | 48.05 | 0.35 | 14.837 | 520.855** | 81.421 |
| 10. | **NSPP** | 0.093 | 0.157 | 0.038 | 0.084 | 0.057** | 0.172 |
| 11. | **100 SW** | 1.848* | 3.99 | 0.123 | 1.587 | 41.983** | 6.753 |
| 12. | **BY** | 0.916 | 1735.385 | 2.886 | 348.598 | 589.313** | 87.399 |
| 13. | **HI (%)** | 0.568 | 169.362 | 1.237 | 34.595 | 105.579** | 14.683 |
| 14. | **SYPP** | 2.080* | 2.113 | 0.803 | 1.576 | 68.267** | 11.366 |

*Significant at 5% level of significant, ** Significant at 1% level of significant

Where, **DFI:** Days to flower initiation, **DF50%F:** Days to 50% flowering, **DPI:** Days to pod initiation, **DTM:** Days to maturity, **PH:** Plant height, **PB:** Number of primary branches per plant, **SB:** Number of secondary branches per plant, **TNPPP:** Total number of pods per plant, **NEPP:** Number of effective pods per plant, **NSPP:** Number of seeds per pod, **100 SW :** 100 seed weight, **BY:** Biological yield per plant, **HI:** Harvest index, and **SYPP:** Seed yield per plant.

*B. Genetic parameters of variability*

**Phenotypic and genotypic coefficient of variances.** A relative comparisons of magnitude of GCV (%) and PCV (%) for different traits revealed that the maximum amount of variability were found in biological yield per plant. Similarly, maximum amount of variability were also present in seed yield per plant, number of effective pods per plant and total number of pods per plant. This indicates substantial phenotypic variation in respect of these traits. The PCV % was higher than the GCV% for all the traits. The highest genotypic and phenotypic coefficient of variation were recorded for the trait biological yield per plant (20.2% and 21.4%) followed by number of effective pods per plant (17.9 % and 18.4 %), total number of pods per plant (14.8 % and 16.5 %), seed yield per plant (13.1 % and 14.3 %), 100 seeds weight (10.3 % and 10.5%), harvest index (7.5 % and 8.2 %), number of seeds per pod (7.1% and 10.2 %), plant height (6.6 % and 8.1 %), number of secondary branches per plant (5.3 % and 7.2 %), number of primary branches per plant (4.5 % and 7.0%), days to flower initiation (3.7 % and 4.1 %), days to pod initiation (3.5 % and 4.5 %), days to 50% flowering (3.5 % and 3.9 %) and days to maturity (3.3 % and 4.6 %). (Table 2 & Fig. 1). A trait having high GCV reveals high potential for effective selection for further breeding programme. Information about extent of parental traits contribution towards progeny is the major success indicator; helps in formulation of breeding strategies because higher heritability of a trait facilitate the selection procedure.

**Table 2: Genetic parameters of variation for yield and yield contributing traits in chickpea.**

| Characters | Coefficient of Variation | | | $h^2_{(bs)}$ (%) | GA as % of mean at 5% |
|---|---|---|---|---|---|
| | GCV (%) | PCV (%) | ECV (%) | | |
| **DTFI** | 3.7 | 4.1 | 4.6 | 78.8 | 6.7 |
| **DT50%F** | 3.5 | 3.9 | 3.6 | 86.3 | 6.9 |
| **DTPI** | 3.5 | 4.5 | 3 | 72.2 | 5.2 |
| **DTM** | 3.3 | 4.6 | 7.9 | 51.8 | 4.9 |
| **PH** | 6.6 | 8.1 | 11.4 | 66.9 | 11.2 |
| **PB** | 4.5 | 7 | 20.4 | 55.1 | 5.9 |
| **SB** | 5.3 | 7.2 | 11.6 | 63.9 | 8.2 |
| **TNPPP** | 14.8 | 16.5 | 17.9 | 80.5 | 27.4 |
| **NEPP** | 17.9 | 18.4 | 16.9 | 84.4 | 32.1 |
| **NSPP** | 7.1 | 10.2 | 30.5 | 86.6 | 28.4 |
| **100 SW** | 10.3 | 10.5 | 9.6 | 91.9 | 18.1 |
| **BY** | 20.2 | 21.4 | 19.8 | 85.2 | 37.6 |
| **HI (%)** | 7.5 | 8.2 | 7.6 | 86.1 | 14.6 |
| **SYPP** | 13.1 | 14.3 | 14.3 | 83.4 | 24.6 |

Where, **PCV**- Phenotypic Coefficient of Variance, **GCV**- Genotypic Coefficient of Variance**,** **$H^2_{bs}$** - Heritability in Broad Sense and **GA** - Genetic Advance as per cent mean

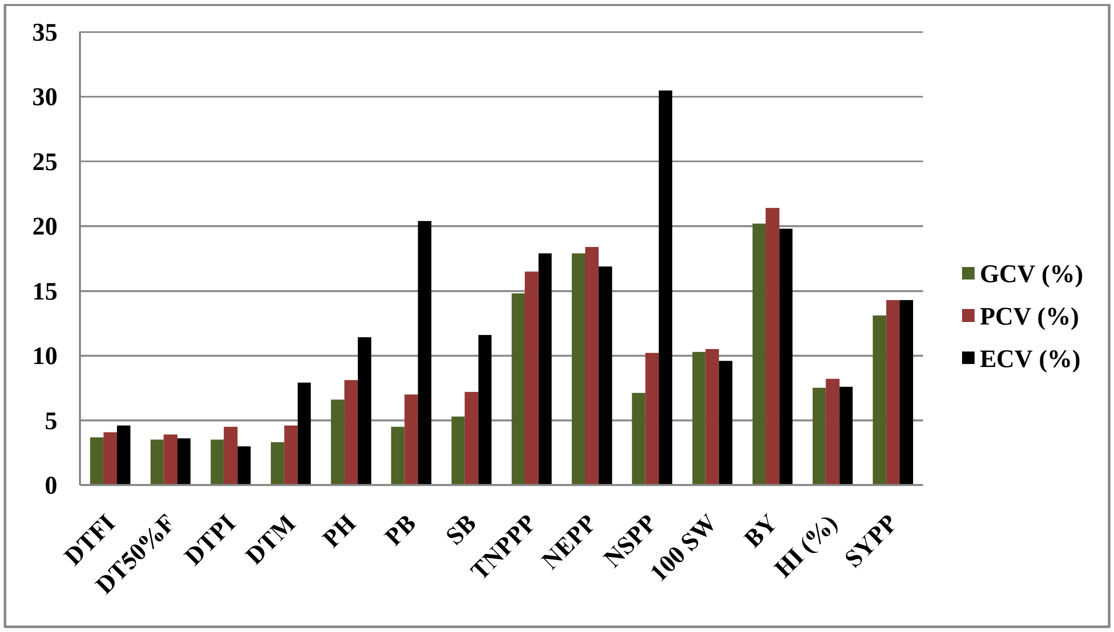

**Fig. 1.** GCV (%), PCV (%) and ECV (%) of yield and yield contributing traits in chickpea.

These results were in agreement with the finding of Akhtar *et al.,* (2011), Aarif *et al.,* (2014), Yadav *et al.,* (2015), Shivwanshi and Babbar (2016), Babbar *et al.,* (2012), Joshi *et al*., (2018) and Manikanteswara (2019).

**Heritability and Genetic advance.** Heritability depicts the proportion of phenotypic variance that is due to genotype. It is a good index of the transmission of characters from parents to their offspring and provides effectiveness of selection for improving traits. The magnitude of heritability ranged from 51.8% for days to maturity to 91.9% for 100 seed weight (Table 2 & Fig. 2). The estimates of high heritability (broad sense) was observed for 100-seed weight (91.9 %) followed by number of seeds per pod (86.6%), days to 50% flowering (86.3%), harvest index (86.1%), biological yield per plant (85.2%), number of effective pods per plant (84.4%), seed yield per plant (83.4%), total number of pods per plant (80.5 %), days to flower initiation (78.8%) and days to pod initiation (72.2%), plant height (66.9%) and number of secondary branches per plant (63.9%). On the other hand, number of primary branches per plant (55.1 %) and days to maturity (51.8%) exhibited medium heritability. Similar findings were noted by Gautam *et al*., (2021), Rozina *et al*., (2011), Chaudhary *et al*., (2012), Muhammad *et al.* (2013), Kuldeep *et al.,* (2014), Honappa *et al.,* (2018) and Tiwari *et al*., (2016).

High genetic advance as percentage of mean was noted for biological yield per plant (37.6%) followed by number of effective pods per plant (32.1%), number of seeds per pod (28.4%), total number of pods per plant (27.4%) and seed yield per plant (24.6%) (Table 2). These findings are in proximity with Singh and Singh (2013), Padmavathi *et al.,* (2013), Tesfamichael *et al.,* (2015).

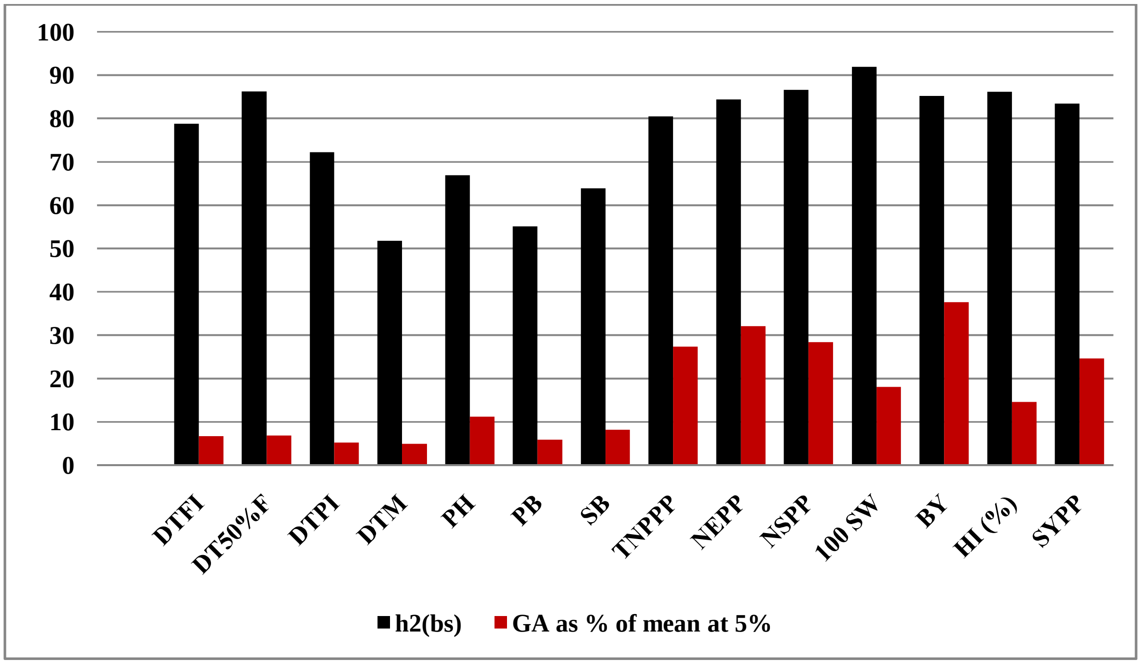

**Fig. 2.** Heritability (%) and G. A. (as % of mean at 5%) of yield and yield contributing traits in chickpea.

High heritability along with high genetic advance as % of mean were observed for seed yield per plant, biological yield per plant, number of effective pods per plant, total number of pods per plant, number of seeds per pod. Traits with high heritability and genetic advance could be described by additive gene action and have high response to selection and due importance should be specified to these traits in further chickpea breeding programme. These results were in close agreement with Padmavathi *et al.*, (2013), Kuldeep *et al*., (2014) and Desai *et al*., (2015). High heritability coupled with moderate genetic advance as percentage of mean were observed in traits *viz.*, harvest index, plant height, 100 seeds weight. Similar finding were been reported by Mishra and Babbar (2014) and Dhuria and Babbar (2015). High heritability estimates accompanied with low genetic advance as percentage of mean was estimated in days to pod initiation, days to 50% flowering, days to flower initiation, Number of secondary branches per plant. These results were in close agreement with Pundir *et al*., (1991), Das *et al.*, (1992) and Yadav *et al*., (2015). High or moderate heritability is coupled with high or moderate genetic advance reveals inheritance of respective traits deals with additive gene action, whereas, high or moderate heritability coupled with low genetic advance illustrated the predominance of non-additive gene action.

**Association analysis among quantitative traits.** Economic value/seed yield in crop plants is determined by many component traits, which are contributing towards directly as well as indirectly. Trait association analysis, hence considered to be imperative in assessment of relation of component traits over yield which in turns helps in selection of superior genotypes. In general, genotypic correlation coefficients were higher than phenotypic correlation coefficient in direction and magnitude revealed that there is a strong association between each pair of traits. Higher magnitude of positive genotypic correlation coefficient suggested strong linkage at genetic level. In the positive correlation; relationship of each traits move in an increasing direction while, in negative correlation, the values of one trait increase and the other decreases. A positive correlation between the desired traits is required by breeder for effective selection (Table 3). The correlation coefficient analysis revealed that seed yield per plant showed positive and significant correlation with biological yield (0.7608), days to 50% flowering (0.3952), days to pod initiation (0.3843) and days to flower initiation (3703). Seed yield pre plant showed significant and negative association with phenological traits *viz.*, Number of seeds per pod (-0.2592), plant height (-0.1655) and 100 seed weight (-0.1118) (Table 2). Days to flower initiation is highly significant and positively correlated with days to 50% flowering (0.9197), days to pod initiation (0.6719), total number of pod per plant (0.3441), number of effective pod per plant (0.2186), biological yield per plant (0.4997) and seed yield per plant (0.3703). Days to 50% flowering exhibited highly significant positive correlation with days to pod initiation (0.6027), total number of pod per plant (0.4231), number of effective pod per plant (0.3386), biological yield per plant (0.4601). Number of primary branches exhibited highly significant and positive correlation with number of secondary branches per plant (0.5484), number of seed per pod (0.2236) and harvest index (0.1332). However, highly significant and negative correlation was found with 100 seed weight (-0.1627). Number of effective pods per plant was highly significant and positively correlated with number of seed per pod (0.3518) and harvest index (0.3976).

Highly significant and negatively correlations was found with number of secondary branches per plant (-0.4196). Total number of pods per plant was highly significant and positive correlation with number of effective pods per plant (0.9201), number of seed per plant (0.2769), harvest index (0.4470). These findings supported by Santosh *et al.*, (2011), Nobile *et al.*, (2013), Kabuo *et al*., (2015) and Serrano *et al*., (2017). The trait association analysis revealed that for increasing seed yield emphasis should be given on number of primary and secondary branches per plant, more number of total and effective pods per plant, while took more days for maturity but less days taken for phonological traits like flower initiation, 50% flowering and pod initiation. Hence, these traits might be very useful for considering for designing high yielding promising ideotype in chickpea.

Path analysis depicts direct and indirect effects of various independent traits on the dependent traits. It represents even if the association of these independent traits with seed yield is as result of their direct effect on yield or outcomes of their indirect effect through other component traits. The present experiment was suggested that the highest positive direct effect (2.0542) on seed yield per plant was found by days to flower initiation followed by biological yield per plant (0.5693). However, days to 50% flowering had the maximum negative direct effect (-2.3679) on seed yield per plant (Table 4 & Fig. 3). Similar findings were observed by Dar *et al.*, (2012), Kumar *et al.*, (2012), Padmavathi *et al.*, (2013) and Waseem *et al*., (2014). Days to flower initiation revealed positive indirect effect through days to 50% flowering (1.9306), days to pod initiation (1.3780), number of primary branches per plant (0.5523), total number pod per plant (0.8569), number effective pod per plant (0.4972), biological yield (1.1186) and seed yield per plant (0.3806). Days to 50% flowering positive and indirect effects via days to maturity (0.8276), plant height (0.3424), number of secondary branches per plant (0.5306), number of seed per pod (0.1936), 100 seed weight (0.2648), and seed yield per plant (0.4122), whereas, it exhibited negative indirect effect through days to flower initiation (-2.2255), days to pod initiation (-1.4025), number of primary branches per plant (-0.5098), total number pod per plant (-1.2239), number effective pod per plant (-0.9250), biological yield (-1.1682). Number of primary braches per plant revealed positive indirect effect through plant height (0.0025), number of secondary braches per plant (0.0626) and harvest index (0.0432) with relatively low in magnitude. Number of effective pod per plant exhibited positive indirect effects were manifested through days to flowering initiation (0.0918), days to 50 % flowering (0.1481), total number of pod plant (0.3533). Total number of pod per plant exhibited positive indirect effect through day to maturity (0.0354), number of secondary branches per plant (0.0537), number of seed per pod (0.0256), 100 seed weight (0.0035) and seed yield per plant (0.0732). Very low value of residual effects (0.5432) was noticed in the experiment indicated majority of traits considering in this study.

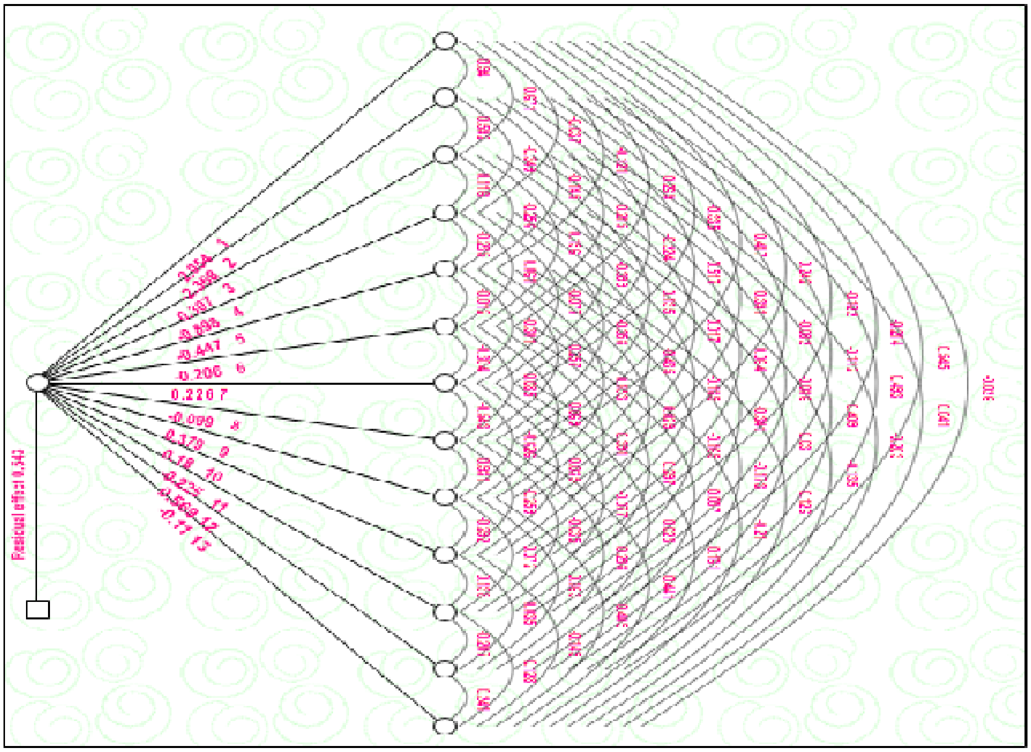

**Fig. 3.** Genotypic path diagram of yield and yield contributing traits in chickpea.

**Table 3: Phenotypic correlation coefficient analysis for yield and yield contributing traits in chickpea.**

| CH | DTFI | DT50%F | DTPI | DTM | PH | PB | SB | TNPPP | NEPP | NSPP | 100 SW | BY | HI (%) | SYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DTFI** | | 0.9197** | 0.6719** | -0.0035 | -0.0367 | -0.1231 | -0.2078 | 0.3441** | 0.2186** | 0.0451 | -0.1616 | 0.4997** | -0.0324 | 0.3703** |
| **DT50%F** | | | 0.6027** | -0.2164* | -0.054 | -0.1259 | -0.152 | 0.4231** | 0.3386** | 0.0546 | -0.0712 | 0.4601** | 0.0208 | 0.3951** |
| **DTPI** | | | | 0.1009 | -0.1208 | -0.1757 | -0.2903** | 0.1081 | 0.0452 | -0.1659 | -0.0582 | 0.3419** | -0.1739 | 0.3843** |
| **DTM** | | | | | -0.1693 | 0.0137 | 0.0017 | -0.1466 | -0.2067* | 0.193 | -0.2260* | 0.0349 | -0.074 | -0.0133 |
| **PH** | | | | | | 0.0332 | -0.1895 | 0.1515 | 0.1001 | -0.0477 | -0.0539 | -0.072 | 0.1469 | -0.1655 |
| **PB** | | | | | | | 0.5484** | -0.0758 | -0.069 | 0.2236* | -0.1627 | 0.0194 | 0.1332 | 0.0982 |
| **SB** | | | | | | | | -0.3577** | -0.4196** | -0.024 | -0.0271 | 0.0093 | 0.0964 | 0.0147 |
| **TNPPP** | | | | | | | | | 0.9201** | 0.2769** | -0.0417 | 0.2104* | 0.4470** | 0.073 |
| **NEPP** | | | | | | | | | | 0.3518** | 0.0366 | 0.1004 | 0.3976** | 0.0141 |
| **NSPP** | | | | | | | | | | | -0.2128* | -0.083 | 0.2001 | -0.2592* |
| **100 SW** | | | | | | | | | | | | -0.1482 | 0.1169 | -0.1118 |
| **BY** | | | | | | | | | | | | | 0.1865 | 0.7608** |
| **HI (%)** | | | | | | | | | | | | | | 0.0083 |
| **SYPP** | | | | | | | | | | | | | | |

*Significant at 5%    **highly significant at 1%

**Table 4: Genotypic path coefficient analysis for yield and yield contributing traits in chickpea.**

| CH | DTFI | DT50%F | DTPI | DTM | PH | PB | SB | TNPPP | NEPP | NSPP | 100 SW | BY | HI (%) | SYPP |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **DTFI** | **2.0542** | 1.9306 | 1.378 | -0.075 | -0.2487 | 0.5523 | -0.6879 | 0.8569 | 0.4972 | -0.2513 | -0.4402 | 1.1186 | -0.0525 | 0.3806 |
| **DT50%F** | -2.2255 | **-2.3679** | -1.4025 | 0.8276 | 0.3424 | -0.5098 | 0.5306 | -1.2239 | -0.925 | 0.1936 | 0.2648 | -1.1682 | -0.0977 | 0.4122 |
| **DTPI** | 0.2063 | 0.1821 | **0.3075** | 0.0356 | -0.0788 | 0.0602 | -0.1227 | 0.0414 | 0.0053 | 0.0197 | -0.0264 | 0.1256 | -0.0623 | 0.4421 |
| **DTM** | 0.0328 | 0.3139 | -0.104 | **-0.898** | 0.2107 | -0.0547 | 0.0696 | 0.3218 | 0.3909 | 0.1695 | 0.3065 | -0.0265 | 0.1216 | -0.0903 |
| **PH** | 0.0541 | 0.0646 | 0.1145 | 0.1048 | **-0.4467** | 0.0053 | 0.1345 | -0.1147 | -0.0685 | -0.013 | 0.0756 | 0.0771 | -0.0563 | -0.3226 |
| **PB** | -0.0553 | -0.0443 | -0.0403 | -0.0125 | 0.0025 | **-0.2058** | 0.0626 | -0.0174 | -0.0142 | -0.0805 | -0.0611 | -0.0076 | 0.0432 | -0.1553 |
| **SB** | -0.0755 | -0.0505 | -0.09 | -0.0175 | -0.0679 | -0.0686 | **0.2256** | -0.1224 | -0.1412 | 0.008 | -0.0174 | 0.0053 | 0.0363 | 0.0478 |
| **TNPPP** | -0.0412 | -0.0511 | -0.0133 | 0.0354 | -0.0254 | -0.0084 | 0.0537 | **-0.0988** | -0.0921 | 0.0256 | 0.0035 | -0.0285 | -0.0436 | 0.0732 |
| **NEPP** | 0.0918 | 0.1481 | 0.0065 | -0.1651 | 0.0582 | 0.0262 | -0.2374 | 0.3533 | **0.3793** | -0.1108 | 0.0271 | 0.0619 | 0.155 | 0.0111 |
| **NSPP** | -0.022 | -0.0147 | 0.0115 | -0.034 | 0.0052 | 0.0704 | 0.0063 | -0.0465 | -0.0526 | **0.1799** | 0.0249 | 0.0064 | -0.0268 | 0.1459 |
| **100 SW** | 0.0482 | 0.0251 | 0.0193 | 0.0767 | 0.038 | -0.0667 | 0.0173 | 0.0079 | -0.0161 | -0.0311 | **-0.2247** | 0.0465 | -0.0289 | -0.1992 |
| **BY** | 0.31 | 0.2809 | 0.2326 | 0.0168 | -0.0982 | 0.0212 | 0.0133 | 0.1641 | 0.093 | 0.0201 | -0.1177 | **0.5693** | 0.137 | 0.7534 |
| **HI (%)** | 0.0028 | -0.0045 | 0.0222 | 0.0149 | -0.0138 | 0.0231 | -0.0177 | -0.0484 | -0.0449 | 0.0163 | -0.0141 | -0.0264 | **-0.1098** | 0.0154 |

R square = 0.7049 residual effect = 0.5432

## CONCLUSIONS

The analysis of variance showed genotypes were highly significant for all the traits suggesting presence of considerable amount of variation for all the traits among the genotypes suggesting genotypes evaluated in this present study has broad genetic base. Hence, utilization of these variability may accelerate to develop promising genotype in the future is the ultimate aim of plant breeder. High GCV (%) and PCV (%) exhibited by total number of pods per plant, number of effective pods per plant and biological yield per plant which indicates appreciable amount of phenotypic variation was noticed in these traits, hence, selection of these traits may be productive for further chickpea breeding programme. High heritability coupled with high genetic advance as % of mean were noted for biological yield per plant, number of effective pods per plant, number of seeds per pod, total number of pods per plant and seed yield per plant suggested primarily the existence of additive gene action and provides the possibility of enhancing these traits through simple selection. Seed yield per plant were highly significant and positively correlated with days to flower initiation, days to 50% flowering, days to pod initiation, biological yield per plant, hence, designing the plant ideotype by selecting these traits for seed yield. Genotypic path coefficient exhibited that the highest positive direct effect on seed yield per plant was found by days to flower initiation followed by biological yield per plant, number of effective pod per plant and days to pod initiation. Hence, effective selection strategy can be practiced on these traits to intensify the yield level.

## FUTURE SCOPE

This present analysis provides the better path for advancing the chickpea breeding programme conducted at Department of Plant Breeding and Genetics, Jawaharlal Nehru Krishi Vishwa Vidyalaya, Jabalpur, Madhya Pradesh during *Rabi* 2019-20 and 2020-2021. In addition, an ideotype should be designed from evident of phenotypic and genotypic coefficient of variation, heritability and genetic advance and association studies. Promising genotypes should be assessed over years and locations to estimate their stability and obtaining date regarding yield and yield attributing traits in different agro-climatic zones for sustained chickpea production. Hence, implementing these genotypes in hybridization programme may give rise to conceivable pre-breeding in chickpea.

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