

Elucidation of genetic variability for seed yield and its component traits, along with association studies in pigeon pea (*Cajanuscajan L.*)

Abstract: The experimental material consisted of fifty-five pigeon pea genotypes sown in Randomized Block Design (RBD) with three replications during the *kharif*, 2020-2021 crop seasons at the N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The components of genetic variance, correlation, and path coefficient were estimated for seed yield and its component by using fifty-five pigeon pea genotypes. The highest PCV (> 20%) was recorded for character, viz. number of secondary branches per plant (62.34%), number of primary branches per plant (37.65%), number of pods per plant (33.00%), and seed yield per plant (31.84%), and lowest estimates (< 10%) of PCV were found for days to 50% flowering (9.45%) and days to maturity (5.74%). The high estimates of GCV (> 20%) were recorded for traits viz., number of secondary branches (42.16%), number of pods per plant (32.65%), and seed yield/plant (30.54%), and lowest estimates of GCV were (<10%) for days to 50% flowering (9.43%) and days to maturity (5.71%) number of seeds per pod (5.28%) and 100-seed weight (9.51%). The number of pods per plant, (0.858) had high positive direct effects on the seed yield per plant along with a positive and significant correlation ($r_p=0.77$). Based on the present investigation, it is evident that delving into genetic variability, correlations, and path analyses provides a more effective approach for selection of superior cultivars for yield and related traits.

Keywords: Genetic variability, correlation, path, heritability, genetic advance.

Introduction: “Pigeon pea [*Cajanuscajan* (L.) Millspaugh], commonly known as Arhar, tur and red gram. Pigeon pea is an often-cross-pollinated crop with $2n=2x=22$ (diploid chromosome number) and a genome size of 833.07 Mb” (Varshney *et al.*, 2012). “Pigeon pea ranked sixth globally after pea, broad bean, lentil, chickpea, and common bean and was cultivated over an area of 5.4 million hectares, producing 4.49 million tons annually” (Fatokimi and Tanimonure, 2021). “It is the second-most significant pulse crop in India after chickpea, occupying 4.72 million hectares and producing 4.31 million tons annually with an average yield of 914 Kg/ha. It generates 15% of the nation's total pulse output. Pigeon pea was grown on 3,000 hectares in Uttarakhand in 2020–21, producing 3.56 thousand tons overall with an average yield of 1185 Kg/ha” (Directorate of Economics and Statistics, 2021).

“The effectiveness of the breeding programme would largely rely on the level of genetic variability available for important economic traits. The genetic variability components like GCV, PCV along with heritability and genetic advance, correlation, and path coefficient are some of the useful parameters that breeders employ at distinct phases of the crop improvement programme. Heritability estimates are important, as they help determine

the influence of the environment on the expression of genotypes and the reliability of characters. Since the heritability estimate alone does not mean the amount of improvement anticipated from selection, the heritability estimate, along with the genetic advance, is required to predict the particular impact of the selection of the most appropriate individuals” (Johnson *et al.*, 1955). Since the expression of morphological characters is likely to be affected by environmental influences, therefore, the knowledge of existing genetic variability and heritability of economically important traits is of utmost significance before executing any crop improvement program. Similarly, it is essential to find out the genetic association between yield and its component characters, which will facilitate the selection of desirable genotypes.

In addition to assessing the nature and magnitude of the correlation coefficient, path coefficient analysis, and genetic association between grain yield and its traits, it is crucial to identify traits contributing to yield through variability, correlation, and path coefficient analyses. Understanding genetic variability and trait associations plays a significant role in selecting elite genotypes and exploiting heterosis breeding programs. While studies on genetic variability and correlation provide valuable insights, they alone may not precisely determine the relative importance of the direct and indirect influences of each component trait on grain yield. In such cases, path coefficient analysis becomes an essential technique for delineating the direct and indirect effects of independent variables on the dependent variable. Consequently, genetic variability, correlation, and path coefficient analyses serve as important tools for breeders aiming to enhance pigeonpea production and productivity. This study was conducted to evaluate genetic variability, heritability, and path coefficient analysis of yield and its component characters, providing essential information for pigeonpea improvement programs focused on enhancing grain yield.

Methodology

The experimental material consisted of fifty-five pigeonpea genotypes sown in Randomized Block Design (RBD) with three replications during the *khari* 2020-2021 crop seasons at N. E. B. Crop Research Centre of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand. The observations were recorded for nine different morphological characters, *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight (g), and seed yield per plant (g). The row- to- row distance of 60 cm and plant- to- plant distance of 20 cm was maintained. The recommended packages of agronomic practices relevant to the crop were followed throughout the crop period. The observations recorded for all the traits were subjected to an analysis of variance. The genotypic and phenotypic coefficients of variability were calculated using the formula of Burton and De Vane (1953), heritability and genetic advance by using formula of Burton and De Vane (1953), and the genetic advance as percent of mean was evaluated using the formula provided by Johnson *et al.* (1955). The correlation coefficients at phenotypic and genotypic levels were estimated from the analysis of variance and covariance as given by Searle (1961).

The direct and indirect effects of various characters on seed yield were estimated with the help of path coefficient analysis, as suggested by Wright (1921) and Dewey and Lu (1959).

Result and Discussion:

Study of ANOVA and genetic variability parameters

“The analysis of variance (ANOVA) for the years 2020-2021 revealed that the mean sum of squares for all the traits under study was highly significant, indicating a considerable amount of genetic variability in the experimental material in **Table 1**. The presence of sufficient genetic variability is an indication that selection would be effective in improving the traits. The significance of ANOVA for these traits” was earlier also reported by Pandey *et al.* (2016), Gaur *et al.* (2018), and Pal *et al.* (2018).

The results of variance analysis, presented in **Table 1**, indicate that the mean sum of squares (MSS) due to genotypes was highly significant for all studied characters except the number of seeds/pods. These results indicated the preponderance of genetic variability in the studied experimental material and hence proved the suitability of the experimental materials chosen for the present investigation. Significant differences for different characters among genotypes were also reported earlier by Srivarsha *et al.*, (2017), Meena *et al.* (2017), Pal *et al.* (2018), and Gaur *et al.* (2020).

Table 1 Analysis of variance for nine different characters in fifty-five pigeonpea genotypes.

| S.No. | Characters | Mean sum of squares | | |
|-------|-------------------------------------|---------------------|-------------|---------|
| | | Replication | Treatment | Error |
| | Degree of freedom | 2 | 54 | 108 |
| 1. | Days to 50% Flowering | 3.460** | 181.923** | 0.355 |
| 2. | Days to Maturity | 7.460** | 193.057** | 0.559 |
| 3. | Plant Height (cm) | 542.986 | 3152.242** | 357.560 |
| 4. | Number of Primary Branches / plant | 5.115 | 31.572** | 18.695 |
| 5. | Number of Secondary Branches/ plant | 137.618 | 177.356** | 50.241 |
| 6. | Number of Pods/ Plant | 60.187 | 25071.659** | 176.058 |
| 7. | Number of Seeds/ Pod | 0.224 | 0.646 | 0.520 |
| 8. | 100 - Seed Weight (g) | 0.004 | 1.850** | 0.133 |
| 9. | Seed yield/ Plant (g) | 33.049 | 1251.673** | 35.283 |

* Significance at 5 % and ** significance at 1 % level of probability

The GCV of various characters A critical analysis of **Table 1** indicated that the Genotypic Coefficient of Variation (GCV) ranged from 5.28 (number of seeds per pod) to

42.16 (number of secondary branches), followed by the number of pods per plant (32.65 %), and seed yield per plant (30.54%). PCV (Phenotypic Coefficients of Variation) estimates were higher than the corresponding GCV estimates for all nine characters, indicating the sufficient influence of the environment on these characters. A higher estimate of PCV than the corresponding GCV estimates for different characters in pigeonpea were also reported earlier by **Rangareet et al. (2013)**, **Sharma et al. (2012)**, **Lakhoteet al. (2015)**, **Pandeyet al. (2015)**, **Pal et al. (2018)**, and **Gaur et al. (2020)**. In the present study, high estimates of both the PCV and GCV were recorded for traits like number of secondary branches, number of pods per plant, and seed yield per plant, which indicated that the sufficient genetic variability existed in the experimental genotypes for these traits and that selection may be effective in bringing desirable improvements in these traits. These findings are in conformity with the earlier findings for these traits in pigeonpea by **Sharma et al. (2012)**, **Lakhoteet al. (2015)**, **Pal et al. (2018)**, and **Gaur et al. (2020)**.

“Although GCV is indicative of the presence of a high degree of genetic variation, the amount of the heritable portion can only be determined with the help of heritability estimates and genetic gain” (**Saroj, S. K. 2013**).

“The ratio of genotypic variance, to phenotypic variance, or total variance is known as heritability in a broad sense. It is generally expressed in percentages. The heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to their offspring” (**Falconer, 1981**). “The estimates of heritability help the plant breeder in the selection of superior genotypes from diverse genetic populations”. (Falconer, 1981)

The high estimate of heritability (> 60%) was reported for days to 50% flowering (99.42%), days to maturity (99.14%), number of pods per plant (97.92%), seed yield per plant (91.99%), 100- seed weight (81.14%), and plant height (72.26%), and whereas, the heritability estimates were recorded to be low for the traits *viz.*, number of primary branches per plant (18.67%), and number of seeds per pod (7.46%). In the present study though, the high estimates of heritability in broad sense were obtained for the traits like days to 50 % flowering (99.42%), days to maturity (99.14 %), number of pods per plant (97.92%), seed yield per plant (91.99%) 100- seed weight (81.14 %) and plant height (72.26 %) indicating that these traits are least influenced by the environment. Similar results for the estimates of heritability were also reported earlier in pigeonpea by **Pal et al. (2018)**, **Bisht et al. (2018)** and **Gaur et al. (2020)**. High heritability indicates the scope of genetic improvement of these characters through selection. Similar type of heritability was recorded by **Patel and Patel (1998)** and **Lingee et al. (2010)**.

According to **Johnson et al. (1955)**, “heritability estimates coupled with genetic advance as percent of mean together provide a better judgment than heritability alone in predicating the resultant effect of selection Table 2. High estimates of genetic advance as percent of mean (>20%) were recorded for the number of pods per plant (66.57%), seed yield per plant (60.34%), number of secondary branches per plant (58.75%) and plant height (21.80%), whereas low estimates of genetic advance as percent of mean (< 10%) were

obtained for the number of seeds per pod (2.97%)”. These results suggested that traits like number of pods per plant, seed yield per plant, number of secondary branches per plant, and plant height are governed by additive genes, and the selection will be rewarding for improvement of these traits. **Sharma et al. (2012), Lakhoteet al. (2015), Pal et al. (2018), and Gaur et al. (2020)** also reported “comparable results for different traits for the estimates of genetic advance. The traits like plant height, number of secondary branches, number of pods per plant, and seed yield per plant exhibited high heritability coupled with high genetic advance, indicating that for these characters, the high estimates of heritability were due to additive gene effects and the selection may be effective”. The characters like days to flowering, days to maturity, and 100-seed weight exhibited high heritability, coupled with moderate / low estimates of genetic advance, indicating that for these characters the high heritability is being exhibited due to favorable influence of environment rather than genotype, and selection for these characters may not be rewarding. For the rest of the traits, viz., number of primary branches and number of seeds per pod, the low estimates of heritability coupled with moderate or low estimates of genetic advance were obtained, indicating that characters are highly influenced by the environment and selection would be totally ineffective. The results of heritability and genetic advance for different traits in the present study were in accordance with the earlier findings of **Shunyu et al. (2013), Vanisree et al. (2014), Bhadru, (2011), Chethana et al. (2015), and Hemavathy et al. (2019)**.

Table 2 Estimates of different genetic parameters for different characters in pigeonpea genotypes.

| | Characters | PCV | GCV | Heritability | Genetic advance | GA as (%) of mean |
|----|---------------------------|-------|-------|--------------|-----------------|-------------------|
| 1. | Days to 50% Flowering | 9.45 | 9.43 | 99.42 | 15.97 | 19.37 |
| 2. | Days to Maturity | 5.74 | 5.71 | 99.14 | 16.42 | 11.72 |
| 3. | Plant Height | 14.65 | 12.45 | 72.26 | 53.44 | 21.80 |
| 4. | No. of Primary Branches | 37.65 | 16.27 | 18.67 | 1.84 | 14.48 |
| 5. | No. of Secondary Branches | 62.34 | 42.16 | 45.75 | 9.07 | 58.75 |
| 6. | No. of Pods/ Plant | 33.00 | 32.65 | 97.92 | 185.69 | 66.57 |
| 7. | No. of Seeds/ Pod | 19.33 | 5.28 | 7.46 | 0.11 | 2.97 |
| 8. | 100 Seed Weight | 10.56 | 9.51 | 81.14 | 1.40 | 17.66 |
| 9. | Seed yield/ Plant | 31.84 | 30.54 | 91.99 | 39.78 | 60.34 |

4.3.1. Character association studies

Correlation analysis is conducted in plant breeding experiments to estimate the association among two or more series of variables. The genotypic correlation coefficient (r_g) estimates the magnitude of genotypic association among various characters, while the phenotypic correlation (r_p) measures both genotypic as well as environmental influences. As seed yield is a complex character, correlation analysis is conducted to estimate the mutual relationship between various plant characters based on which seed yield improvement can be made. It is a well-known fact that yield depends upon a number of component characters that are less complex and simply inherited. Usually, these component characters are simply interlinked. Thus, selection pressure may be more easily exerted on those characters that are independent and are interrelated among themselves.

Table 3 indicates that, in general, both phenotypic and genotypic correlation coefficients possess similar signs. The magnitude of genotypic correlation coefficients was found to be higher as compared to the magnitude of corresponding phenotypic correlation coefficients. The higher magnitude of genotypic correlation coefficients than the corresponding phenotypic correlation coefficients clearly indicates that there is a strong genetic association between these two traits, however the genotypic values were lessened by the significant interaction of environment. A similar trend of genotypic and phenotypic correlation coefficients in sign and magnitude was also reported earlier in pigeonpea by **Bisht et al. 2018** and **Gaur et al. (2020)**. In general, seed yield per plant exhibited a positive and significant phenotypic association with all other studied characters. A positive and significant association between these characters and seed yield per plant was also reported by several workers (**Bisht et al. 2018** and **Gaur et al. 2020**). The character days to 50% flowering showed significant and positive correlation with days to maturity ($r_p=0.75$ and $r_g=0.76$), plant height ($r_p=0.37$ and $r_g=0.44$), number of pods per plant ($r_p=0.66$ and $r_g=0.66$), number of seeds per pod ($r_p=0.28$ and $r_g=1.00$) and hundred seed weight ($r_p=0.43$ and $r_g=0.49$) at both genotypic and phenotypic levels. Plant height showed a significant and positive correlation with the number of pods per plant, number of seeds per pod, and the hundred seed weight at both the genotypic and phenotypic levels. The number of pods in the plant exhibited a significant and positive association with the number of seeds per pod and the hundred seed weight. Similar kinds of results between these traits in pigeonpea were also reported earlier by **Rangareet al. (2013)**, **Sharma et al. (2012)**, **Pal et al. (2018)**, and **Gaur et al. (2020)**.

Table 3: Phenotypic (r_p) and genotypic (r_g) correlation coefficients among various characters in Pigeonpea.

| Characters | | DF | DM | PH | NPB | NSB | NPP | NSP | HSW | SYP |
|------------|----|------|---------|-------|-------|--------|--------|--------|--------|--------|
| DF | rp | 1.00 | 0.75 ** | 0.37* | -0.03 | -0.12 | 0.66** | 0.28** | 0.43** | 0.46** |
| | rg | 1.00 | 0.76** | 0.44* | 0.01 | -0.19 | 0.66** | 1.00** | 0.49** | 0.49** |
| DM | rp | | 1.00 | 0.17* | -0.02 | -0.14 | 0.38** | 0.24** | 0.32** | 0.36** |
| | rg | | 1.00 | 0.21 | -0.04 | -0.20 | 0.38 * | 0.91** | 0.35* | 0.38* |
| PH | rp | | | 1.00 | 0.17* | -0.09 | 0.47** | 0.18* | 0.29** | 0.30* |
| | rg | | | 1.00 | 0.01 | -0.06 | 0.55** | 0.80** | 0.38* | 0.56** |
| NPB | rp | | | | 1.00 | 0.45** | 0.21** | 0.05 | 0.16* | 0.26** |
| | rg | | | | 1.00 | 1.00** | 0.51** | 1.00** | 0.39** | 0.25 |
| NSB | rp | | | | | 1.00 | 0.16* | 0.18* | 0.06 | 0.16* |
| | rg | | | | | 1.00 | 0.25 | 0.52** | 0.10 | 0.32 |
| NPP | rp | | | | | | 1.00 | 0.31** | 0.49** | 0.77** |
| | rg | | | | | | 1.00 | 1.00** | 0.56** | 0.81** |
| NSP | rp | | | | | | | 1.00 | 0.26** | 0.28** |
| | rg | | | | | | | 1.00 | 0.72** | 0.99** |
| HSW | rp | | | | | | | | 1.00 | 0.44** |
| | rg | | | | | | | | 1.00 | 0.51** |
| SYP | rp | | | | | | | | | 1.00 |
| | rg | | | | | | | | | 1.00 |

* Refers to significance at 5 % and ** refers to significance at 1 %

Where, DF= days to 50 % flowering; DM= days to maturity; PH= plant height; NPB= number of primary branches; NSB= number of secondary branch; NPP= number of pods per plant; NSP= number of seeds per pod; HSW= 100-seed weight; SYP= seed yield per plant.

4.3.2.Path Coefficient Studies

Path coefficient analysis is used to partition the observed correlation coefficient into a series of direct and indirect effects of yield components on yield. The term path coefficient was first used by **Wright (1921)**, and its use was elaborated by **Dewey and Lu (1959)**. Path coefficient analysis quantifies the direct effect of an independent variable and its indirect effect through other variables on dependent variable. In the present study, path coefficient analysis was carried out by taking seed yield per plant as a dependent and all other traits as independent variables. The results of path coefficient analysis are presented in Table 4.

A critical preview of Table 3 revealed that the number of pods per plant (0.858) had high positive direct effects on the seed yield per plant, along with a positive and significant correlation ($r_p=0.77$). Since the magnitude of the phenotypic correlation coefficient between the number of pods per plant is almost equal to the direct effect of this trait on seed yield, it revealed the true relationship between these two traits and direct selection for improvement in the number of pods per plant will certainly result in the enhanced seed yield. Similar results for the high direct effect of pods per plant on seed yield per plant were also reported earlier by **Gaur et al. (2020)**. Days to maturity also showed a high positive direct effect on seed yield (0.236), along with a positive and significant association ($r_p=0.36$). Rest of the traits exhibited exceptionally low direct effect on seed yield and were also non-significantly associated with seed yield. The low magnitude of the direct effect of different traits was also reported earlier by **Rangareet et al. (2013)**, **Sharma et al. (2012)**, **Lakhoteet et al. (2015)**, **Pandeyet et al. (2015)**, and **Pal et al. (2018)**.

Table 4: Path coefficient analysis showing the direct and indirect effects of various characters on seed yield at the phenotypic level.

| Characters | Correlation with SYP | Direct effect | Indirect effect via | | | | | | | |
|------------|----------------------|---------------|---------------------|--------|--------|--------|--------|-------|-------|-------|
| | | | DF | DM | PH | NPB | NSB | NPP | NSP | HSW |
| DF | 0.46** | -0.291 | - | 0.178 | -0.029 | -0.001 | 0.006 | 0.567 | 0.010 | .028 |
| DM | 0.36** | 0.236 | -0.220 | - | -0.014 | -0.002 | 0.006 | 0.329 | 0.008 | 0.021 |
| PH | 0.30* | -0.079 | -0.109 | 0.042 | - | 0.004 | -0.079 | 0.404 | 0.006 | 0.019 |
| NPB | 0.26** | 0.111 | 0.001 | -0.005 | -0.013 | - | -0.022 | 0.186 | 0.002 | 0.010 |
| NSB | 0.16* | -0.049 | 0.036 | -0.033 | 0.007 | 0.050 | - | 0.142 | 0.006 | 0.003 |
| NPP | 0.77** | 0.858 | -0.192 | 0.090 | -0.037 | 0.024 | -0.008 | - | 0.011 | 0.032 |
| NSP | 0.28** | 0.036 | -0.082 | 0.058 | -0.014 | 0.006 | -0.008 | 0.272 | - | 0.017 |
| HSW | 0.44** | 0.065 | -0.127 | 0.076 | -0.023 | 0.017 | -0.002 | 0.426 | 0.009 | - |

Table 5: List of 20 selected superior cultivars of pigeonpea on the basis of yield and yield related traits.

| Genotypes | DF | DM | NPB | NSB | PH | NPP | NSP | HSW | SYP |
|-------------|----|-----|------|------|-------|-------|-----|------|-------|
| PA 426 | 80 | 135 | 23 | 32 | 260 | 393.3 | 4.7 | 8.25 | 101.6 |
| PUSA 2015-1 | 95 | 149 | 8.7 | 8.3 | 280 | 395 | 4 | 8.84 | 97.3 |
| PA 421 | 82 | 137 | 19 | 37 | 222.5 | 390 | 3.7 | 7.66 | 96 |
| PA 455 | 92 | 146 | 12 | 18.3 | 270 | 406.7 | 4.7 | 8.07 | 95 |
| AL 2046 | 92 | 146 | 11.7 | 3.3 | 295 | 391.7 | 3 | 8.37 | 95 |
| AL 1932 | 92 | 147 | 11.3 | 6.3 | 285 | 330.3 | 4 | 8.05 | 93.3 |
| PA 443 | 81 | 135 | 12.3 | 11.7 | 257.5 | 385 | 4 | 9.17 | 91.7 |
| PA 444 | 92 | 147 | 14.3 | 14 | 177.5 | 384.3 | 4 | 8.23 | 91.7 |
| AL 1758 | 92 | 144 | 9.3 | 3.7 | 270 | 400.7 | 4.3 | 7.83 | 91.7 |
| PA 477 | 84 | 135 | 10.3 | 14 | 270 | 379.3 | 4 | 7.89 | 87.3 |
| PA 493 | 95 | 150 | 11.7 | 4 | 270 | 369.3 | 3.7 | 8.84 | 85 |
| PA 449 | 92 | 146 | 17.3 | 40.3 | 237.5 | 313.3 | 4.3 | 8.72 | 84.7 |
| GAUT 98023 | 82 | 147 | 13.1 | 15 | 247.1 | 258.3 | 4 | 7.76 | 81.9 |
| PA 441 | 90 | 148 | 9.3 | 13 | 245 | 303.3 | 4.7 | 8.49 | 81.7 |
| PA 429 | 81 | 134 | 15 | 21.7 | 295 | 385 | 4 | 8.14 | 81.2 |
| PUSA 992 | 80 | 125 | 15.3 | 16 | 250.3 | 293.3 | 4 | 8.15 | 81 |
| PA 374 | 81 | 135 | 23 | 33.7 | 275 | 376.7 | 4.3 | 8.96 | 80.2 |
| PA 440 | 81 | 135 | 15.7 | 13 | 252.5 | 346.7 | 4 | 8.68 | 80 |
| ICPL 93081 | 80 | 147 | 14 | 19 | 252 | 266.7 | 4 | 8.31 | 78.73 |
| PUSA 2002-1 | 75 | 147 | 12 | 11 | 179 | 260 | 3 | 7.44 | 78.53 |
| PA 426 | 80 | 135 | 23 | 32 | 260 | 393.3 | 4.7 | 8.25 | 101.6 |

Conclusion:Based on the present investigation, it is evident that assessing genetic variability, correlations, and path analyses proves more beneficial in identifying superior cultivars for yield and related traits. Notably, cultivars such as PA 426, PUSA 2015-1, PA 421, PA 455, and AL 2046 exhibited consistently high yields among the 50 cultivars based on individual performance. These particular cultivars are recommended for inclusion in breeding programmes aimed for developing high-yielding varieties.

References:

- Burton GW, Devane EH 1953.** Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal material. *Agronomy Journal*. 1953. 45:478-481.
- Bhadru, D. 2011.** Genetic studies in pigeonpea [*Cajanus cajan* (L.) Millsp.]. *Electron. J. Plant Breed.*, 2(1):132-134.
- Bisht, C., 2018.** Estimation of combining ability, heterosis and molecular diversity for *Fusarium* wilt in some elite lines of pigeonpea [*Cajanus cajan* (L.) Millsp.]. M.Sc.

thesis, G.B. Pant University of Agriculture and Technology, Pantnagar- 263145, Uttarakhand.

Chethana, C.K., Dharmaraj, P.S., Muniswamy, S., Gangadhara, K., and Nagaraju, C.H. 2015a. Studies on genetic variability in stable male sterile, maintainer and restorer lines of pigeonpea [*Cajanuscajan* (L.) Millsp.]. *Trends Bio Sci.*, 8(1): 9-12.

Dewey, D.R. and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.*, 51(9):515-518.

Directorate of Economics and Statistics 2021. Department of Agriculture and Farmers welfare. Ministry of Agriculture and Farmers welfare. Government of India. Data retrieved on March 1st, 2023, from <https://eands.dacnet.nic.in>.

Falconer D. S. (1981). Introduction to quantitative genetics (2nd ed.). London: Longman.

Fatokimi, E. O. and Tanimonure, V. A. 2021. Analysis of the current situation and future outlooks for pigeon pea (*CajanusCajan* L.) production in Oyo State, Nigeria: a Markov Chain model approach. *J. Agric. Food Inf.* 6, 100218.

Gaur, A.K., Verma, S.K. and Panwar, R.K. 2020. Estimation of genetic variability and character association for development of selection criteria in pigeonpea [*Cajanuscajan* (L.) Millsp.]. *Int. J. Chem. Stud.*, 8(2): 391-394.

Hemavathy, A.T., Bapu, J.R.K. and Priyadharshini, M. 2019. Genetic variability and character association in pigeonpea [*Cajanuscajan* (L.) Millsp.] core collection. *Indian.J. Agr. Sci.*, 53(3): 362-365.

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

Lakhote, S. J., Patil, H. E., Mali, R. A. and Ingle, P. 2015. Genetic analysis for yield and yield contributing traits in vegetable type genotypes in pigeonpea [*Cajanuscajan*(L.) Millsp.]. *Int. J. Trop. Agric.*, 33 (2):161-167.

Linge, S. S., Kalpande, H. V., Sawargaonlar, S. L., Hudge, B. V. and Thanki, H. P. 2010. Study of genetic variability and correlation in interspecific derivatives of pigeonpea (*Cajanuscajan*(L.) Millsp.). *Electronic j. plant breed.* 1 (4): 929-935.

Meena, S.S., Verma, S.K., Choudhary, R., Nehra, M., Panwar, R.K. and Singh, J.P. 2017. Interpretation of genotype x environment interaction and grain yield stability in some advance lines of pigeonpea [*Cajanuscajan*(L.) Millsp.] grown at different altitudes. *Chem. Sci. Rev. Lett.* 6(22): 1113-19.

- Pal, D., Verma, S.K., Panwar, R.K., Arora A. and Gaur, A. K. 2018.**Correlation and Path Analysis Studies in Advance Lines of Pigeonpea [*Cajanuscajan*(L.) Millsp.]under Different Environments. *Int. J. Curr. Microbiol.Appl. Sci.*, **7 (4)**: 378-389.
- Pandey, P., Pandey, V.R., Tiwari and Yadav, S.K. 2015.**Studies on direct selection parameters for seed yield and its component traits in pigeonpea [*Cajanuscajan*(L.) Millsp.].*African J. Agric. Res.*, 10(6): 485-490.
- Pandey P, Kumar R, Pandey VR. 2016.**Genetic association studies for yield and yield related traits in pigeonpea [*Cajanuscajan* (L.) Millsp.].*Legume Research*. 2016; 39(2):189-193.
- Rangare, N.R., Reddy, G.E. and Kumar, S.R. 2013.** Study of heritability, genetic advance and variability for yield contributing characters in pigeonpea (*Cajanuscajan* L. Millspaugh). *Trends biosci.*,6(5): 660-662.
- Searle S.R. 1961.**Phenotypic, genotypic and environmental correlations.*Biometrics*.1961; 17:474-480.
- Saroj, S. K., Singh, M. N., Ravindra, K.,Tejveer, S. and Singh, M. K. (2013).** Genetic variability, correlation and path analysis for yield attributes in pigeonpea. *The bioscan*, 8(3), 941-944.
- Sharma, R., Gangwar, R.K. and Yadav, V. 2012.**A study on genetic variability and correlation in pigeonpea [*Cajanuscajan* (L) Millsp.]. *Int. J. Sci. Res.*, 3(9): 826-828.
- Shunyu, V., Chaturvedi, H. P., Changkija, S. and Singh, J. 2013.** Genetic Diversity in Pigeonpea [*CajanusCajan* (L) Millsp.]Genotypes of Nagaland. *Int. J. Agric. Innov. Res.*, 2: 89-90.
- Srivarsha, J., J.E. Jahagirdar, C.V. Sameer Kumar, A.J. Hingane, D.K. Patil, V.K.Gite, H.B. Shruthi and Bhosle, T.M. 2017.** Study of CGMS based Short Duration Hybrids of Pigeonpea [*Cajanuscajan* (L.) Millsp.]in Terms of Heterosis. *Int. J. Curr. Microbiol. App. Sci.*, 6(11): 682-692.
- Patel, K. N. and Patel, D. R. 1998.**Studies on genetic variability in pigeonpea.*International chickpea and pigeonpea Newsletter*.5: 28- 30.
- Vanisree, S. and Sreedhar, M. 2014.**Genetic analysis of yield and yield components and determination of selection criteria in pigeonpeagermplasm.*J. Food Leg.*, 27(1): 68-70.
- Varshney, R. K., Chen, W., Li, Y., Bharti, A. K., Saxena, R. K., Schlueter, J. A., and Jackson, S. A. 2012.** Draft genome sequence of pigeonpea (*Cajanuscajan*), an orphan legume crop of resource-poor farmers. *Nat. Biotechnol*, 30(1), 83.
- Wright, S. 1921.**Correlation and causation. *J. Agric. Res.* 20: 557-585.