



STUDY OF GENOTYPIC CORRELATION MATRIX IN PIGEON PEA (*CAJANUS CAJAN* (L.)) GENOTYPES

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ABSTRACT

Thirty-three genotypes of *kharif* Pigeon Pea were evaluated and correlation coefficient was estimated for the yield contributing traits. Correlation studies revealed that the hundred seed weight exhibits positive and highly significant association with yield per plant followed by number of pods per plant, number of seeds per pod, days to maturity and number of primary branches indicating the role of effects in yield per plant. Number of primary branches, number of secondary branches, number of pods per plant and number of seeds per pod showed positive and highly significant genotypic correlation with hundred seed weight. Plant height, number of primary branches and number of pods per plant showed highly significant with number of seeds per pod. Number of primary branches and days to maturity was highly significant with number of pods per plant. Number of primary branches was highly significant with number of secondary branches. Plant height was highly significant with number of primary branches. Days to maturity was highly significant with days to 50 % podding.

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INTRODUCTION

After chickpea, pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second-most important pulse crop in India and ranks fifth globally. It currently includes an area of around 4.6 million hectares and is the largest producer and consumer of pigeonpeas in the world, with an annual total production of 3.4 million tonnes and a mean productivity of 780 kg/hectare. In India, pigeonpea is grown on over 4.04 million hectares of land, and 2.65 million tonnes are produced annually. (2012) (Anonymous). Pigeonpea, often known as "dal," plays a significant role in Indian cuisine. It has a protein content of 20–21% (Sodavadiya et al., 2009).

The pigeon pea, *Cajanus cajan* (L.) Millsp., is open cross-pollinated crop (20–70%) and has $2n = 2x = 22$ diploid chromosomes. Pigeon pea seeds are planted at the ideal moisture and temperature range (29–36 °C). It belongs to the fabaceae family. It is a drought-

tolerant, multipurpose crop that is mostly grown for its edible seeds, which are rich in protein. In addition, it serves a variety of domestic and medical purposes. In addition to being utilized for human food, it is also fed to livestock, pigs, and fisheries as forage, meal, and feed. *Cajanus cajan* (L.) is a biological factory that fixes atmospheric nitrogen in soil and acts as a natural barrier against soil erosion (Varshney and Saxena, 2017).

The level of genetic variability, heritability, and genetic advancement in the base population determines how much the sorghum production may be improved. Additionally, knowledge of the nature of the relationship between yield and its constituent parts aids in the simultaneous selection of several characters linked to yield improvement. Correlation analysis has frequently been used to analyze the relationship between characteristics in order to

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identify the nature and significance of these relationships. The purpose of this study is to describe the relationships between various sorghum growth characteristics and yield components in order to identify those that might influence yield.

MATERIAL AND METHODS

The experiment was conducted at Experimental Field, School of Agriculture, GEHU, Uttarakhand-247662, India. It is situated at 30.134585° latitude and 77.884375° longitude. The experimental material comprised of 30 germplasms along with 3 check varieties. The material was sown in Randomized Block Design (RBD). Each genotype was sown in three rows, 5m long at 25 x 50 cm apart. Ten plants in each accession were selected for data recording of qualitative and quantitative traits. The data on 50% flowering (days) was recorded during the panicle emergence stage. Leaf length (cm) and leaf width (cm) were measured during the physiological maturity stage. The number of leaves, plant height (cm), panicle length (cm) was measured during the physiological maturity stage. Plant weights (g/10 plant) of stem were measured after harvesting. The 100-seed weight (g) was measured after threshing, number of seeds per panicle was counted after threshing and yield per plant was measure after threshing and counting of seeds per plant. The formulas proposed by Dewey and Lu (1959) were used to calculate the genotypic correlation coefficients.

RESULT AND DISCUSSION

Traits association studies showed that hundred seed weight (g) (0.882**) showed the highly positive correlated with yield per plant (g) followed by number of pods per plant (0.723**), number of seeds per plant (0.601**), number of primary branches (326**) and days to maturity (0.339**). Number of seeds per pod (0.580**) was highly positive correlated with hundred seed weight (g) followed by primary branches (0.400**), number of pods per plant (0.356**) and number of secondary branches (0.288**) while plant height (cm) (0.228*) was correlated. Plant height (cm) (0.405**), number of pods per plant (0.457**) and number of primary branches (0.378**) was highly positive highly correlated with number of seeds per pod. Days to maturity (-1.000**) and days to 50 % flowering (0.595**) was highly negative correlated with number of seeds per pod. Number of primary branches (0.447**) and days to maturity (0.387**) was highly positive correlated with number of pods per plant whereas days to 50 % flowering (-0.476**) was negative and highly correlated. Number of primary branches (0.299**) was positive and highly correlated with number of secondary branches whereas plant height (cm) (0.217*) was positive and correlated. Days to 50 % flowering (-0.291**) was highly negative correlated with number of secondary branches. Plant height (cm) (0.283**) was positive and highly correlated with number of primary branches whereas days to 50 % podding (0.199*) was positive and

Genotypic Correlations matrix

| | Days of 50% Flowering | Days to maturity | Days to 50% podding | Plant Height in cm | Number of Primary Branches | Number of secondary branches | Number of pods per plant | Number of seeds per pod | 100-seed weight (g) |
|------------------------------|-----------------------|------------------|---------------------|--------------------|----------------------------|------------------------------|--------------------------|-------------------------|---------------------|
| Days to 50% flowering | | | | | | | | | |
| Days to maturity | -0.064 | | | | | | | | |
| Days to 50 % podding | -0.467** | 0.681** | | | | | | | |
| Plant Height in cm | -0.204* | -0.650** | -0.269** | | | | | | |
| Number of Primary Branches | -0.168 | -0.474** | 0.199* | 0.283** | | | | | |
| Number of secondary branches | -0.291** | -0.161 | 0.009 | 0.217* | 0.299** | | | | |
| Number of pods per plant | -0.476** | 0.387** | 0.086 | 0.016 | 0.447** | 0.097 | | | |
| Number of seeds per pod | -0.595** | -1.000** | 0.108 | 0.405** | 0.378** | 0.155 | 0.457** | | |
| 100-seed weight (g) | -0.078 | -0.012 | -0.012 | 0.228* | 0.400** | 0.288** | 0.356** | 0.580** | |
| Yield per plant | -0.166 | 0.339** | 0.028 | 0.192 | 0.326** | 0.136 | 0.723** | 0.601** | 0.882** |

**Significant at 1% l.o.s.

*Significant at 5% l.o.s.

correlated. Days to maturity (-0.474**) was highly negative correlated with number of primary branches. Days to 50 % podding (-0.269**) and days to maturity (-0.650**) was highly negative and correlated with plant height (cm) while days to 50 % flowering (-0.204*) was negatively correlated. Days to 50 % flowering (-0.467**) was negative and highly correlated with days to 50 % podding while days to maturity (0.681**) was positive and highly correlated with days to 50 % podding. Present finding is in confirmation with Sodavadiya *et al.* (2009) and Thanki *et al.* (2010). Similar findings have also been reported by Sidhu *et al.* (1985), Saxena and Kataria (1993), Basavarajaiah *et al.* (2000) and Rathoreet *et al.* (2011).

CONCLUSION

The results indicated that the majority of the attributes assessed had positive relationships among themselves and could all be enhanced at once. Additionally, it was found that traits including plant weight, seed weight per hundred, number of seeds per pod, number of pods per plant, number of major branches, and seed weight exhibit a highly significant and favorable genotypic connection with yield per plant.

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REFERENCES

1. **Arunah, U., U. F. Chiezey, L. Aliyu, & A. Ahmed.** (2015). Correlation and Path Analysis between Sorghum Yield to Growth and Yield Characters. *Journal of Biology, Agriculture and Healthcare*, (5) 19.
2. **Basavarajaiah, D., Gowda, M. B., Lohithaswa, H. C., & Kulkarni, R. S.** (2000). Assessment of pigeonpea germplasm and isolation of elite genotypes for Karnataka. *Crop Research (Hisar)*, 20(3), 444-448.
3. **K., I., Vijayakumar G, & Khan A. K. F.** (2010). Correlation and path analysis in multicut fodder sorghum. *Electronic Journal of Plant Breeding*, 1 (4): 1006-1009.
4. **K., R., Varshney, & Saxena, R. K.** (2017). The Pigeonpea Genome. Gewerbestrasse, Cham, Switzerland: *Springer International Publishing*. doi:10.1007/978-3-319-63797-6.
5. **N., P. C., Rathod A. H., Vaghela P. O., Yadav S. R., Patade S. S., & Shinde A. S.** (2014). Study of correlation and path analysis in dual purpose sorghum [*Sorghum bicolor* (L.) Moench]. *International Journal of Agricultural Science*, 10 (2): 608-11.
6. **Narkhede, G. W., Mehtre, S., Jadhav, R., & Ghuge, V.** (2017). Correlation and Path Analysis for Grain Yield, its Components and Drought Tolerance in Sorghum [*Sorghum bicolor* (L.) Moench]. *Journal Agriculture Research Technology*, 42 (3) : 173-178.
7. **Patil, R., VV Kalpande, & SB Thawari.** (2022). Correlation studies in land races of kharif sorghum (*Sorghum bicolor* (L.) Moench). *The Pharma Innovation Journal*, 11(1): 562-564 .
8. **R.C., M., Wadikar P.B., Pole S.P., & Dhuppe M.V.** (2011). Variability, Correlation and Path Analysis Studies in Sorghum. *Research Journal of Agricultural Sciences*, 2(1):101-103.
9. **Sidhu, P. S., Verma, M. M., Cheema, H. S. and Sra, S. S.** (1985). Genetic relationships among yield components in pigeonpea. *Indian Journal Agricultural Science*. 55: 232-235.
10. **Singh, M., Upadhyaya, H. D., & Bisht, I. S.** (2013). Genetic and Genomic Resources of Grain Legume Improvement (Vol. first). 32 Jamestown Road, London NW1 7BY, UK: Elsevier publications. doi:https://doi.org/10.1016/B978-0-12-397935-3.00008-6.
11. **Sodavadiya, M. S., Pithia, J. J., Savaliya, A. G., Pansuriya and Korat, V. K.** 2009. Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp). *Legume Res.* 32 (3): 203-205.
12. **Thanki, H. P and Sawargaonkar, S. L.** 2010. Path coefficient analysis in Pigeonpea. *Electronic Journal, Plant Breeding*. 1(4): 936-939.
13. **V., K., Shukla M., Nathawat V. S. , & Jodha B. S.** (2015). Correlation and path coefficient analysis for agronomical traits in sorghum [*Sorghum bicolor* (L.) Moench] under shallow saline soil condition in arid region. *Electronic Journal of Plant Breeding*, 6 (4): 1143-1149.
14. **Verma, L. k., & Biradar, B.** (2021). Correlation and path analysis for grain yield and yield attributes in rabi sorghum [*Sorghum bicolor* (L.) Monech] . *The Pharma Innovation Journal*, 10(10): 1211-1214 .