RESEARCH ARTICLE

GENETIC VARIABILITY AND CORRELATION ANALYSIS FOR SEED AND SEEDLING VIGOUR TRAITS IN PIGEON PEA [*CAJANUS CAJAN* (L.) MILLSP.] GENOTYPES

Oyi Perme, H.P. Chaturvedi* and M.B. Sharma

Department of Genetics and Plant Breeding, School of Agricultural Sciences & Rural Development,
Nagaland University, Medziphema-797106 Nagaland
Email: hpchaturvedi68@gmail.com

Received-01.09.2022, Revised-11.09.2022, Accepted-28.09.2022

Abstract: The present investigation entitled 'Genetic variability for seed and seedling vigour traits in Pigeon pea [*Cajanus cajan* (L.) Millsp.] Genotypes' was conducted with twenty genotypes including two check varieties. The experiment was conducted during the month of May 2021, at the laboratory of Department of Genetics and Plant Breeding, NU: SASRD, Medziphema Campus, Nagaland. The main goal of the study was to assess the genetic information of twenty genotypes of Pigeon pea for seed and seedling vigour traits. The experiment was laid out in Completely Randomized Design (CRD) with three replications. Data were recorded on eleven characters. For all of the traits studied, the phenotypic coefficient of variation (PCV) was found to be larger than the genotypic coefficient of variation (GCV), indicating that their expression is influenced by environment to some extent. High heritability coupled with high genetic advance as percent of mean were observed for seedling vigour index II. The majority of the seedling traits had a positive and significant correlation with seedling vigour index I & II, implying the importance seedling traits in predicting seedling vigour. Germination percentage, root length at the 20th DAS, fresh shoot weight at the 20th DAS, fresh root weight at the 20th DAS, dry shoot weight at the 20th DAS, dry root weight at the 20th DAS, and seed vigour index I were all factors that contributed to seedling vigour and hence good plant stand. The study suggests that while screening of germplasm for seed and seedling characteristics germination percentage, shoot length at 20th DAS, root length at 20th DAS, dry shoot weight at 20th DAS, dry root weight at 20th DAS, seedling vigour index I and seedling vigour index II should be taken into consideration. The outcomes of this study led to the conclusion that the genotypes ICPH-2433, ICPL-88039, ICPL-11301, and PA-636 were found to be promising in terms of performance for seedling vigour traits.

Keywords: Correlation, Genetic variability, Genotypes, Pigeon pea, Traits

INTRODUCTION

Pigeon pea [*Cajanus cajan* (L.) Millsp.] is a popular tropical and sub tropical perennial, multi-purpose shrub and leguminous crop. It belongs to the family Leguminoseae and sub-family Papilionoideae, and is often cross pollinated (20%-70%). Pigeonpea evolved in India as a result of selection for favourable features like as non-shattering pods and larger seeds, and then spread to Africa and Australia. Mostly used as dal, a key part of the Indian diet. Pigeon pea is a resilient crop that thrives in water-stressed conditions. It is preferred as a component crop in inter or mixed cropping situations with sorghum, maize, millets, cotton, and peanuts in rainfed upland settings. Pigeon pea is a desirable crop for small-scale farmers in a number of emerging nations because it possesses numerous significant properties. It is a resilient multipurpose crop that provides several benefits such as protein, fuel, feed, improved soil fertility, and erosion prevention. With a high protein level ranging from 21% to 25%, it serves as a backbone for sustained food and nutritional security. It is crucial for the livelihood of small-holder farmers in the semi-arid tropics because of its wider adaptability, drought tolerance, and ability to use residual moisture with low inputs throughout the dry season (Jones *et al.* 2002).

Pulses are in high demand, with estimates 32 million tonnes necessary by 2030 and 50 million tonnes required by 2050 (Vision 2050: Indian Institute of Pulses Research). Many genomic breeding approaches are being used to improve pulse production and productivity. Pigeon pea, being a legume crop, helps to maintain soil productivity by fixing atmospheric nitrogen into the soil via symbiotic fixation and recycling nutrients in the soil. The production of pigeon pea in North Eastern Region of India is on a very low key in the agricultural system. The low production in this region could be due to a number of biotic and abiotic stresses, socio-economic and institutional factors. However, the region has enormous potential for the cultivation and production of pigeon pea because of its existing favourable weather conditions. In Nagaland, pigeon pea occupies an area of 3210 hectare with production of 2920 metric tonnes (Statistical Handbook of Nagaland, 2019).

Breeders should examine seed-related variables while developing new cultivars with outstanding agronomic features, because new cultivars with good germination capacity are widely desired. Seed and seedling vigour is an aspect of seed quality which affects field establishment and performance. Several variables have been observed to impact low pigeon pea yields, including poor quality seed with low seed and seedling vigour. Highly vigorous seeds are

*Corresponding Author

prerequisites for high field emergence rate and vigorous seedlings (Hampton and Coolbear, 1990). As a result, determining seed vigour prior to sowing is critical. Information is minimal on seed and seedling vigour in pigeon pea. Therefore, the current study has been carried out in order to determine the extent of genetic variability in seed and seedling vigour characteristics.

MATERIALS AND METHODS

The present investigation was carried out in the laboratory of Department of Genetics and Plant Breeding, School of Agricultural Research and Rural Development, Nagaland University, Medziphema Campus, Nagaland during the year of 2021. It has a sub tropical climate and is located at 23˚ 24’49” N latitude and 90˚33’04” S longitude at an altitude of 305 metres above sea level. The experiment was carried out following a Completely Randomized Design in three replications with twenty genotypes. Seeds of twenty genotypes namely PA-421 (check), UPAS-120 (check), PA-636, PA-638, PA-639, PA-643, PA-644, PA-645, PA-3, PA-414, PA-461, PA-477, ICPL-11301, ICPL-11300, AL-1871, ICPH-2433, ICPL-88039, ICPL-11242, ICPL-87, PA-441 of pigeon pea were collected from AICRP Pigeon pea, SASRD Medziphema, Nagaland and used in the present investigation. Data were observed on eleven characters *viz.* emergence of radicle, emergence of plumule, germination percentage, shoot length at 20th DAS, root length at 20th DAS, fresh shoot weight at 20th DAS, fresh root weight at 20th DAS, dry shoot weight at 20th DAS, dry root weight at 20th DAS, seedling vigour index I and seedling vigour index II. The analysis of variance was carried out according to Panse and Sukhatme (1957) by using the mean performance of the genotypes. The phenotypic, genotypic and environmental coefficient of variation was calculated according to Burton and De Vane (1953). Heritability was calculated according to Allard (1960). Genetic advance possible through selection was calculated according to Johnson *et al.* (1955). Phenotypic and genotypic correlation coefficients were worked out as suggested by Al-Jibouri *et al.* (1958).

RESULTS AND DISCUSSION

Significant differences were recorded among twenty genotypes in all studied characters indicating high degree of variability in the material. The phenotypic coefficient of variation (PCV) was found to be larger than the genotypic coefficient of variation (GCV) for all of the traits studied, showing that they all interacted with the environment to some degree (Table- 1). Similar results were earlier reported by Manjeet *et al.* (2019). High estimates of GCV and PCV was observed in accordance with Kumawat and Gothwal (2018) and Mula *et al.* (2014) for root length, fresh root weight and dry root weight, Singh and Singh (2012) for seedling vigour index II and seedling vigour index I indicating the presence of ample variation for these characters under study.

Assessment of genetic variability present in the genetic material is important to estimate the magnitude of improvement that can be achieved in breeding material for various characters. Coefficient of variation measures the amount of variability present in the characters but alone is not sufficient to determine the expected progress that could be made in quantitative traits (Falconer, 1981). It has been suggested that estimates of GCV and heritability together provide a better portrait of amount of genetic gain expected under phenotypic selection (Burton & Devane, 1953). Heritability is a useful quantitative parameter, which considers the role of heredity and environment determining the expression of trait (Allard, 1960). Heritability usually considered being low if it is less than 30%, moderate between (30-60%) and high if it is more than 60% (Johnson *et al*, 1955). The range of genetic advance as percent of mean is classified as low if it is less than 10%, moderate between (10-20%) and high if more than 20% (Johnson *et al*, 1955). In the present study, high estimates of heritability coupled with high estimates of genetic advance were observed for seed vigour index II. Moderate heritability with high genetic advance was found for root length at 20th DAS, dry root weight at 20th DAS and seedling vigour index I (Table- 1). Thus the above mentioned traits on selection is likely to accumulate more additive genes which will lead to further improvement of their performance and may also be used as a criteria for selection in pigeon pea breeding programme. Similar findings were also observed by Kumawat and Gothwal (2018) for root length and shoot length.

Table 1: Mean, Range, Coefficient of Variation, Heritability and Genetic Advance as % of mean

Characters	**Mean ± S.E**	**Range**	**Coefficient of variation**			**Heritability h^2 (broad sense)**	**Genetic advance as % of mean**
			Genotypic GCV	**Phenotypic PCV**	**Environmental ECV**		
Emergence of Radicle (days)	2.15 ± 0.20	2-2.67	5.15	16.93	11.78	9.27	3.12
Emergence of Plumule (days)	8.30 ± 0.59	7-10	4.22	12.94	8.72	10.63	2.82

Germination percentage	70.67 ± 8.63	53.33-93.33	11.23	23.95	12.72	22.01	10.85
Shoot length at 20th DAS	11.58 ± 0.97	8.25-14.88	13.42	19.80	6.38	45.95	18.71
Root length at 20th DAS	3.16 ± 0.51	1.96-5.43	29.77	40.91	11.14	52.94	44.46
Fresh shoot weight at 20th DAS	0.83 ± 0.10	0.58-1.23	15.31	26.79	11.48	32.67	17.95
Fresh root weight at 20th DAS	0.46 ± 0.06	0.24-0.68	21.29	33.76	12.47	39.76	2.72
Dry shoot weight at 20th DAS	139.33 ± 17.89	100-200	16.28	27.56	11.28	34.90	19.81
Dry root weight at 20th DAS	27.17 ± 4.65	13.33-46.67	27.79	40.66	12.87	46.73	39.11
Seedling Vigour Index I	1040.52± 146.29	769.6-1894.4	22.07	32.86	10.79	45.09	30.46
Seedling Vigour Index II	11.89 ± 1.78	7-23	31.92	41.16	9.24	60.15	42.72

Table 2. Estimates of genotypic correlation coefficient among seed and seedling vigour traits.

Characters	**Emergence of Radicle (days)**	**Emergence of Plumule(days)**	**Germination percentage**	**Shoot length at 20th DAS**	**Root length**	**Fresh shoot weight at 20th DAS**	**Fresh root weight at 20th DAS**	**Dry shoot weight at 20th DAS**	**Dry root weight at 20th DAS**	**Seedling Vigour Index I**
Emergence of Radicle(days)	-0.678**	0.095	-0.89**	-0.02	-0.488*	0.016	-0.487*	-0.398	-0.425	-0.286
Emergence of Plumule(days)		0.715**	0.173	-0.06	-0.392	-0.468*	-0.84**	-0.438	0.228	-0.242
Germination percentage			-0.161	0.29	0.962**	0.713**	0.112	0.903**	0.676**	0.102
Shoot length at 20th DAS				0.669**	0.519*	0.453*	0.122	0.255	0.609**	0.127
Root length					0.740**	0.665**	0.537*	0.845**	0.809**	0.524**
Fresh shoot weight at 20th DAS						0.889**	0.894**	0.829**	0.105	0.939**
Fresh root weight at 20th DAS							0.683**	0.819**	0.867**	0.768**
Dry shoot weight at 20th DAS								0.792**	0.897**	0.101
Dry root weight at 20th DAS									0.887**	0.853**
Seedling Vigour Index I										0.865**
Seedling Vigour Index II										1

*-significant at 5%, **-significant at 1%

Table 3. Estimates of phenotypic correlation coefficient among seed and seedling vigour traits.

Characters	**Emergence of Plumule(days)**	**Germination percentage**	**Shoot length at 20th DAS**	**Root length**	**Fresh shoot weight at 20th DAS**	**Fresh root weight at 20th DAS**	**Dry shoot weight at 20th DAS**	**Dry root weight at 20th DAS**	**Seedling Vigour Index I**	**Seedling Vigour Index II**
Emergence of Radicle(days)	0.13	-0.164	0.222	-0.018	0.136	0.063	0.148	0.019	-0.098	-0.019
Emergence of Plumule(days)		-0.254	0.889**	-0.139	0.033	-0.079	-0.009	-0.037	-0.166	-0.165
Germination percentage			-0.133	0.207	0.164	0.213	0.118	0.297	0.739**	0.702**
Shoot length at 20th DAS				0.411	0.574**	0.332	0.359	0.319	0.504*	0.249
Root length					0.449*	0.597**	0.38	0.656**	0.632**	0.466*
Fresh shoot weight at 20th DAS						0.737**	0.863**	0.715**	0.559*	0.739**
Fresh root weight at 20th DAS							0.619**	0.763**	0.509*	0.642**
Dry shoot weight at 20th DAS								0.620**	0.421	0.762**
Dry root weight at 20th DAS									0.578**	0.699**
Seedling Vigour Index I										0.819**
Seedling Vigour Index II										1

*-significant at 5%, **-significant at 1%

In a sound breeding programme the study of association between yield and its dependent characters are of particular interest and pre-requisite. Correlation coefficient analysis measures the mutual relationship between different characters and is used to determine the component character on which selection can be done for improvement in yield (Sumathi & Muralidharan, 2010). For the utilization of various quantitative characters in breeding programme, interrelationship between the characters is important (Lerner, 1958). Therefore, in the present study, correlations between 11 characters were studied at genotypic and phenotypic level (Table- 2 and 3). The positive and significant correlation of seedling vigour index I & II with the majority of the traits stated that all of the seedling traits were essential in determining seedling vigour. Germination per cent, root length at the 20th DAS, fresh shoot weight at the 20th DAS, fresh root weight at 20th DAS, dry shoot weight at the 20th DAS, dry root weight at the 20th DAS all contributed to seedling vigour and hence good plant stand. This is in agreement with the findings of Patil *et al.* (2014) and Nusrat and Subhash (2019) for germination percentage and root length. The present study suggests that while screening of germplasm for seed and seedling characteristics germination percentage, shoot length at 20th DAS, root length at 20th DAS, dry shoot weight at 20th DAS, dry root weight at 20th DAS, seedling vigour index I and seedling vigour index II should be taken into consideration. Genotypes namely ICPH-2433, ICPL-88039, ICPL-11301 and PA-636 were determined superior on performance basis for seedling vigour traits.

REFERENCES

Al-Jibourni, H. A., Miller, P. A. and Robinson, H. F. (1958). Genotyping and environmental variances, co-variances in upland cotton cross of interspecific origin. *Agronomy Journal*, **50:** 633-636.
Google Scholar

Allard, R. W. (1960). Principles of plant breeding. John Wiley & Sons, New York.
Google Scholar

Burton, G. W. and De Vane. (1953). Estimating heritability in tall Fescue (*Festuca arundinaceae*) from replicated clonal material. *Journal of Agronomy*, **45:** 478-485.
Google Scholar

Falconer, D. S. (1981). Introduction to Quantitative Genetics. 2nd Edition, Longman Group Ltd., London, 1-133.
Google Scholar

Hampton, J. G. and Coolbear, P. (1990). Potential versus actual seed performance-can vigour testing provide an answer? *Seed Science and Technology*, **18:** 215-228.
Google Scholar

Johnson, R. E., Robinson, H. W. and Comstock, H. F. (1955). Estimates of genetic and environmental variability in soyabean. *Agronomy journal*, **47**: 314-318.
Google Scholar

Jones, R., Likoswe, A. and Freeman, H. A. (2002). Improving the access of small farmers in Eastern and Southern Africa to global pigeon pea markets. *Agricultural Research and Extension Network*,

Network Paper No. 120, Overseas Development Inst.,Chatam, U.K.
Google Scholar

Kumawat, K. R. and Gothwal, D. K. (2018). Genetic variability for seedling characters in lentil under salinity stress. *Electronic Journal of Plant Breeding*, **9:** 1295-1302.
Google Scholar

Lerner, I. M. (1958). *The Genetic Theory of Selection*. John Wiley.
Google Scholar

Manjeet., Verma, P. K., Sangwan, V. P. S., Nain Mohit and Nisha. (2019). Assessment of genetic variability for seed germination per cent and seedling vigour traits in sesame (*Sesamum indicum* L.). *Journal of Pharmacognosy and Phytochemistry*, **8:** 328-331.
Google Scholar

Mula, M. G.,Thakare, D. P., Mehtre, S. P. and Rathore, A. (2014). Evaluation for early seedling vigour of hybrids and varieties of pigeonpea (*Cajanus cajan* L.). *Green Farming*, **6:** 1-4.
Google Scholar

Nusrat, J. and Subhash, C. K. (2019). Correlation and path analysis in rice (*Oryza sativa* L.) for seed and seed vigour traits. *Journal of Pharmacognosy and Phytochemistry*, **8:** 222-226.
Google Scholar

Panse, V. G. and Sukhatme, P. V. (1957). Statistical methods for agricultural workers. ICAR Publication New Delhi. India ,1995, 68-75.
Google Scholar

Patil, R., Diwan, J. R., Boranayaka, M. B. and Dikshit, S. (2014). Correlation and path coefficient analysis for seed and seedling characters for yield in rice (*Oryza sativa* L.). *Research Journal of Agricultural Sciences*, **5:** 1064-1066.
Google Scholar

Singh, D. and Singh, R. (2012). Path coefficient analysis for seedling vigour in radish (*Raphanus sativus* L.) genotypes. *Hort Flora Research Spectrum*, **1:** 339-343.
Google Scholar

Sumathi, P. and Muralidharan, V. (2010). Inheritance of branching and important biometrical traits in sesame (*Sesamum indicum* L.). *Indian Journal of Genetics and Plant Breeding*, **70:** 112.
Google Scholar