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Correlation and path coefficient analysis for yield and its attributing traits in pigeonpea [*Cajanus cajan* (L.) Mill sp.] under multiple environments

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Abstract

An test comprising 20 unique genotypes of pigeonpea become performed at some point of kharif 2022–23 in 3 distinct environments. Every genotype changed into planted in a 6-row, 4×3.6 -metre plot in each environment the use of a randomised whole block layout with replications. Observations have been recorded on 8 exclusive characters, *viz.*, days to 50% flowering, days to maturity, plant top (cm), variety of branches in line with plant, variety of pods per plant, quantity of seeds in keeping with pod, a hundred seed weight (g) and seed yield in step with plant (g) in every replication, 5 randomly decided on flora from every genotype. Over all of the environments, days to 50% flowering, plant peak, and quantity of seeds in line with pod showed genotypically bad institutions with the seed yield in step with plant (g). The variety of pods in step with plant no longer most effective had an instantaneous impact however additionally showed a advantageous and big association with the seed yield in line with plant in all three environments.

Keywords: Pigeonpea, genotypic, phenotypic, significant

Introduction

Amongst legumes, pigeonpea [*Cajanus cajan* (L.) Millsp.] occupies an vital location in rainfed agriculture. In India, pigeonpea (2n=22) holds maximum large fame as it's far a multipurpose maximum adaptable meals legume, with large uses as meals, feed, fodder, and fuel. It has the strength to noticeably reduce the chance posed with the aid of weather exchange, soil deterioration, and growing production prices to the trouble of world pulse production. (Saxena *et al.*, 2016) ^[6]. Pigeonpea is a perennial plant with a short lifespan, hardy, extensively grown, and drought-tolerant crop (Chaudhary *et al.*, 2011) ^[2]. It plays a vital position in keeping the soil fertility with the aid of solving the atmospheric nitrogen and through falling down the dry leaves of pigeon pea at the soil floor.

Break up seed, popularly referred to as "Dal," which lacks the seed coat, has round 24% more protein than mature seeds (18. Eight %) and green pigeonpeas (21%) combined. The green seed has the biggest crude fibre (8.2%) and fats (2. Three %) values whilst in comparison to mature seeds and split-seeds. Moreover, pigeon pea has trace quantities of minerals like calcium, magnesium, copper, iron, and zinc. Due to the fact lysine and threonine, vital amino acids, are found in good quantities, it's far a brilliant source of protein. It's far an critical a part of traditional people medicine in international locations like China, India, and others, similarly to having dietary benefits. In India, pigeonpea leaves are used to cure wounds, sores, and stomach tumours (Sivaraj *et al.*, 2022)^[9].

Pigeonpea is grown on about 28.78 million hectares in India, with a complete manufacturing of 25.46 million tonnes and a productiveness of 919 kg in line with hectare, compared to approximately sixty five. 9 thousand hectares in Chhattisgarh, with a complete production of 39.9 million tones and a productivity of 605 kg in line with hectare. (Anonymous, 2021)^[1].

The affiliation between yield and its various components facilitates the development of a ramification software. Estimates of the degree of relationship between grain yield and its diverse components, in addition to most of the components, might be supplied by way of correlation research. Whilst the inherent character of the affiliation of element traits is further described with the aid of direction coefficient analysis by means of determining the direct or oblique contribution of these tendencies to yield (Kandarkar *et al.*, 2020)^[5], the consequences of an analysis of seventy pigeonpea genotypes at the side of 5 tests indicated that the wide variety of pods in line with plant, the load of a hundred seeds, and the wide variety of seeds in

step with pod were all quite and positively correlated with the seed yield. The course coefficient evaluation's findings confirmed that the quantity of pods in keeping with plant's direct impact on seed yield turned into tremendously fantastic. Devi *et al.* (2020) ^[3] 11 early pigeonpea types have been studied together with one check range, and it was located that, in course analysis, seed yield consistent with plant confirmed a great and superb correlation with secondary branches consistent with plant at both the phenotypic and genotypic stages. The number of pods consistent with plant had the most powerful and most nice effect on seed yield per plant, observed by the quantity of secondary branches consistent with plant and days to adulthood.

Yield is a complicated trait that is motivated by means of genotype, the environment, and GxE interactions. In any crop breeding programme, breeders' first priority is to growth the production of crops. Considering this reality the current research turned into achieved to examine. The association of different yield attributing developments and their relative level of correlation with a yield that helps breeders pick out superior, high-yield genotypes.

Materials and Methods

For gift observe 20 pigeonpea genotypes had been consisting of two exams (BDN-716 & Chhattisgarh Arhar-1) used as the experimental fabric. The AICRP pigeonpea phase of branch of Genetics and Plant Breeding university of Agriculture, Raipur provided the look at's cloth. Two replications have been layied out in a randomized entire block design at each web site. The present investigation was accomplished at three environments *viz.*, research Cum guidance Farm university of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Sant Kabir college of Agriculture and research Station, Kabirdham and Shaheed Gundadhur college of Agriculture and research station, Jagdalpur.

Every genotype became sown in a single plot that had 6 rows of four x 3.6 metres every, spaced 60 cm inter row and 20 cm intra row. To growth the uniform crop stand, counseled agronomic practises and plant protection measures had been implemented. Five aggressive plants from each genotype and replication, randomly selected, have been determined at every place on eight special morphological characters viz; days to 50% flowering, days to maturity, plant height (cm), quantity of branches in line with plant, range, variety of pod consistent with plant, variety of seed consistent with pod, 100 seed weight (g) and seed yield in keeping with plant (g).

The evaluation of variance and covariance as defined by way of Searle (1961)^[8] was used to assess the correlation coefficients on the phenotypic and genotypic stages. Direct and indirect outcomes of numerous characters on seed yield were predicted with the assist of course coefficient evaluation as suggested through Wright (1921)^[10] and Dewey and Lu (1959)^[4].

Results and Discussion

Correlations and path analysis

The phenotypic and genotypic coefficients of correlation had been determined amongst yield components in all viable character mixture and are offered in (table 1) most of the characters phenotypic turned into better in magnitude than the genotypic correlation suggesting excessive environmental interplay. Days to 50% flowering exhibited undoubtedly phenotypic and genotypic degree of substantial correlation with days to adulthood (0.317, 0.825). Days to maturity exhibited positively genotypic degree of widespread correlation with plant peak (zero.461) and range of seeds in step with pod (0.340) and negatively large correlation with one hundred seed weight (-zero.403), number of branches (0.542) and wide variety of pods in step with plant (zero.620) at genotypic stage. Plant peak exhibited positively considerable correlation with range of seeds per pod (0.475)and negatively good sized correlation with seed yield according to plant (-zero.313) and quantity of pods per plant (-zero.560) at genotypic level. Wide variety of branches exhibited undoubtedly considerable at phenotypic and genotypic correlation with wide variety of pods in line with plant (zero.372, 0.349) and 100 seed weight (zero.534) at genotypic and stage. Number of pods consistent with plant exhibited undoubtedly at phenotypic and genotypic massive correlated with seed yield in keeping with plant (0.504, 0.593) and number of seeds per pod (0.535) at genotypic degree. The outcomes are in harmony with findings of Kandarkar et al., (2020)^[5]. Number of seeds in step with pod at genotypic level negatively huge correlated with seed yield in line with plant (-0.393) at genotypic degree. The effects are in concord with findings of Devi et al., (2020)^[3]. One hundred seed weight exhibited effective but non considerable correlated with seed yield in keeping with plant (zero.073) at phenotypic stage and poor however non giant correlated (-0.293) at genotypic stage. Route coefficient analysis portioned the found genotypic correlation coefficient among yield and its components into direct and indirect outcomes. The genotypic route coefficient (direct and indirect results through other characters) has been follows supplied in (desk 2). Most advantageous direct consequences become proven by using range of pods consistent with plant (zero.872) followed with the aid of number of days to 50% flowering (zero. One hundred twenty five), days to adulthood (zero.060), plant top (zero.018). While bad direct impact were acquired thru wide variety of seeds consistent with pod (-0.089), one hundred seed weight (-zero. One hundred eighty), wide variety of branches (zero.407). Days to 50% flowering confirmed poor indirect impact on seed yield consistent with plant with great correlation via 100 seed weight (-zero.049), number of branches (-0.052), quantity of pods per plant (-0.103). Days to adulthood confirmed bad indirect impact on seed yield in keeping with plant with non huge correlation thru a hundred seed weight (-zero.024), variety of branches (-0.032) and quantity of pods in step with pod (-0.037). Plant top showed negatively oblique impact on seed yield in line with plant with tremendous correlation thru variety of branches (-0.002) observed by wide variety 100 seed weight (-zero.004) and number of pods per plant (-0.010). Quantity of branches confirmed negatively indirect impact on seed yield consistent with plant with non extensive correlation thru range of pods according to plant (-0.142) followed via 100 seed weight (zero.218). Number of pods in keeping with plant showed undoubtedly indirect impact on seed yield consistent with plant with sizable correlation thru number of branches (0.305) and one hundred seed weight (0.171). Variety of seeds in step with pod showed negatively indirect effect on seed yield in keeping with plant with substantial correlation via days to adulthood (-zero.030) accompanied via plant top (-zero.042) and days to 50% flowering (-zero. Half). 100 seed weight showed poor oblique effect on seed yield in line with plant with non substantial correlation thru range of pods in step with plant (-zero. Half) observed variety of branches (zero.096). Those locating are in conformity to the findings of previous employees Devi et al. (2020)^[3].

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Table 1: Pooled genotypic and phenotypic correlation analysis for seed yield and its attributing traits over three environments in pigeonpea

Traits		Days to maturity	Plant height (cm)	Number of Branches	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)			
Days to 50%	Р	0.317*	-0.144	-0.0095	-0.209	0.037	-0.084	-0.166			
flowering	G	0.825**	0.625**	-0.461*	-0.822**	0.507**	-0.393*	-0.318*			
Days to maturity	Р		-0.052	-0.082	-0.066	-0.023	0.061	-0.113			
	G		0.461*	-0.542**	-0.620**	0.340*	-0.403*	-0.106			
Plant height (cm)	Р			0.110	0.104	0.149	-0.172	0.170			
	G			-0.130	-0.560**	0.475*	-0.230	-0.313*			
Number of	Р				0.372*	-0.121	0.071	0.189			
Branches	G				0.349*	-0.118	0.534**	-0.281			
Number of pods	Р					0.094	0.060	0.504**			
per plant	G					0.535**	0.196	0.593**			
Number of seeds	Р						-0.149	0.028			
per pod	G						-0.126	-0.393*			
100 seed weight	Р							0.073			
(g)	G							-0.293			
*, ** significant at 5% and 1% level respectively											

Table 2: Pooled path coefficient analysis matrix of direct and indirect effects on its contributing traits in pigeonpea over three environments

Traits	Days to 50% flowering	Days to Maturity	Plant height (cm)	Number of Branches	Number of pods per plant	Number of seeds per pod	100 seed weight (g)	Seed yield per plant (g)	
Days to 50% flowering	0.125	0.103	0.078	-0.058	-0.103	0.063	-0.049	-0.318*	
Days to Maturity	0.049	0.060	0.028	-0.032	-0.037	0.020	-0.024	-0.106	
Plant height (cm)	0.011	0.008	0.018	-0.002	-0.010	0.009	-0.004	-0.313*	
Number of Branches	0.188	0.221	0.053	-0.407	-0.142	0.048	-0.218	-0.281	
Number of pods per plant	-0.717	-0.540	-0.489	0.305	0.872	-0.467	0.171	0.593**	
Number of seeds per pod	-0.045	-0.030	-0.042	0.011	0.048	-0.089	0.011	-0.393*	
100 seed weight (g)	0.071	0.073	0.041	-0.096	-0.035	0.023	-0.180	-0.293	
Residual effect = 0.577									
* ** significant at 5% and 1% level respectively									

Conclusion

Over all of the environments, days to 50% flowering, plant top and range of seeds in step with pod display genotypically negatively sizeable with the seed yield in line with plant (g) quantity of pods per plant no longer handiest had direct effect however also showed effective and significant affiliation with seed yield in keeping with plant in all of the 3 environments therefore direct choice or development thru this developments could be profitable for the increment of seed yield according to plant in pigeonpea.

References

- 1. Anonymous. Project coordinator's report 2021-22. AICRP on pigeonpea; c2021. p. 27-31.
- Chaudhari AK, Sultana R, Pratap A, Nandarajan N, Jha UC. Breeding for abiotic stress in pigeonpea. Journal of Food Legumes. 2011;24(30):165-174.
- Devi OP, Sharma MB, Seyie K, Ozukum C. Correlation and path analysis studies in pigeonpea genotypes under foothill condition of Nagaland. International Journal of Bio-resource and Stress Management. 2020;11(3):311-314.
- 4. Dewey DR, Lu KH. A correlation and path coefficient analysis of components of crested wheat grass seed production. Agronomy Journal. 1959;51(9):515-518.
- 5. Kandarkar KG, Kute NS, Tajane SA, Ingle AU. Correlation and path analysis for yield and its contributing traits in pigeonpea. Journal of Pharmacognosy and Phytochemistry. 2020;9:1629-1632.
- 6. Saxena KB, Sawargaonkar SL. Genetic enhancement of seed proteins in pigeonpea methodologies,

accomplishment and opportunities. International Journal of Science Research. 2016;4:3-7.

- 7. Saxena KB, Singh L, Gupta MD. Variation for natural out-crossing in pigeonpea. Euphytica. 1990; 46: 143-148.
- 8. Searle, S.R. Phenotypic, genotypic and environmental correlations. Biometrics. 1961;17:474-480.
- 9. Sivaraj P, Kumar Anil, Koti SR. Training concepts in noice clustering classifier. A case study for pigeonpea crop mapping. Remote Sensing Applications Society and Environment. 2022;26:100736.
- 10. Wright S. Correlation and causation. Journal Agriculture Research. 1921;20:257-287.