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GENETIC VARIABILITY AND ASSOCIATION PATTERN OF YIELD AND IT'S ATTRIBUTING CHARACTERS AMONG DIALLEL POPULATION OF PIGEONPEA (*CAJANUS CAJAN* (L) MILLS.)

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A nature gifted crop Pigeonpea [*Cajanus cajan* (L.) Mill sp.] alternatively termed tur, arhar, etc. is manage status as leading pulse crop of India. Pigeonpea breeders are looking as important asset which genotypes are adapted broadly and favourable to input deficient as well as input intensive agriculture in demand to boost productivity and production of the crop. Research in the present context was carried out in Research-cum-Instructional Farm, Department of Genetics & Plant Breeding, IGKV, Raipur, (C.G.). Material under study subject comprised of 5 parents, 10 direct crosses and 10 reciprocals of pigeonpea using parent Rajeevlochan as check variety. The parents were crossed during *Kharif* 2020-2021 on 5x5 diallel fashion. Parent and F_1 's in all combinations were evaluated by utilizing Full Diallel Analysis, Method- I, Model- I, (Griffing's Approach) in Complete Randomized Block Design (RBD) by 3 replications through out *Kharif* 2021-2022. Observations were taken on 9 different quantitative characters.

ABSTRACT Result: The results revealed that character seed yield per plant genotypic and phenotypic coefficient of variation value indicated highest. High heritability was reported by seed yield per plant followed by 100 seed weight, primary branches/plant, number of pods per plant, plant height, shelling percentage and number of seeds per pod. Low heritability was reported by days to 50% flowering. Genetic advance estimated high on Seed yield per plant followed by number of pods per plant, primary branches per plant, 100 seed weight, shelling percentage and plant height. Heritability together with genetic advance both estimated high stated by seed yield per plant followed by primary branches per plant, 100 seed weight and shelling percentage. Heritability together with genetic advance estimated low stated by days to 50% flowering.

Association analysis results reported that characters 100 seed weight and number of pods per plant showed significant positive correlation at both genotypic and phenotypic orders and seed yield per plant stated positive direct effect. Whereas, negative significant correlation days to 50% flowering at phenotypic order and seed yield per plant aid negative direct effect.

Keywords: Association Analysis, Correlation Coefficient, Genetic Variability, Path Coefficient.

Introduction

Among various leguminous grains pigeonpea [*Cajanus cajan* (L.) Millsp] is another greatest imperative crop in India, a perennial pulse from the tribe - Phaseoleae, subtribe- cajaninae, family -

Fabaceae, genus- *Cajanus* and species-*cajan* with somatic chromosome number 2n =22. It names is mentioned by assorted of expressions *viz.*, Cango Pea, Arhar, Rahar, Tur, Red Gram and Angole. Under sub tribe *Cajaninae*, *C. cajan* is the only species that's under cultivation practice.

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Probably Peninsular India is the centre of origin, where the closest wild relative (Cajanus cajanifolia) occurs in tropical deciduous woodlands. From India it travelled to E. Africa and W. Africa. It is largely grown in the rain based sustainable agricultural systems of sub tropical and tropical Asian regions, Caribbean Islands and the Africa. It is worldwide grown in 7mha with productivity and production of 969 kg/ha and 5.4 mt. respectively. (FAO STAT 2019). The cultivation of pigeonpea in India during year 2023-24 an area of 4.04 million ha with production at 3.34 million ha and productivity level of 826 kg/ha. The area under Pigeon pea in Chhattisgarh during 2022-23 was 39.87 thousand ha while production was 27.55 thousand tonnes with an average productivity in 467 kg/ha. (Project coordinator AICRP on Kharif pulses annual report 2023-24).

It has been more challenging to breed in pigeonpea compared to its pulses group plant because of its rare particular flower traits. An often-cross pollinated crop with an insect aided natural out crossing range from 20-70%. (Saxena et al., 1990) which narrow down the use of effective selection and breeding strategies in self-pollinated species. Pure line breeding, population breeding, mutation breeding, and wide hybridization are the techniques employed to enhance the yield potential of pigeonpea, contributing to incremental improvements in its development. (Varshney et al., 2009). The achievement of yield enhancement fundamentally be contingent upon the magnitude and nature of genetic assortment existent in the present material. Understanding about order and amount of diversity present in a cluster owing to nongenetic and genetic bases is a crucial requirement aimed at efficient breeding plan.

Materials and Methods

The present investigation "Genetic variability and association pattern of yield and it's attributing characters among diallel population of pigeonpea (*Cajanus cajan* (L) Mills.)" was conducted throughout *Kharif* 2021-22 at trial region of Genetics and Plant Breeding Department, at Research-cum-Instructional Farm, IGKV, Raipur (C.G). The study material for the present investigation, 25 genotypes included used to develop a diallel set including the reciprocals. The five parents involved were (G.R.G.-152, C.G. Arhar-2, BDN-716, Rajeevlochan and Vipula). Thus, the study of 5X5 full diallel analysis (Griffing's approach, 1956) in F₁ generation included 10 F₁, 5 parents and 10 reciprocals.

Research place Chhattisgarh are located on $17^{\circ}14'$ N and $24^{\circ}45'$ N latitudes and $79^{\circ}16'$ E and $84^{\circ}15'$ E longitudes. capital of the Chhattisgarh state are Raipur and its lies on 21° 16' N latitude and 81° 36' E longitude with an altitude of 289.60 meters above the mean sea level and the latitude and longitude of experiment field projected at 19° 4'0' N and 82° 2'0' E, respectively.

Subject under studied traits were days to maturity, days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant (g), shelling percentage, and100 seed weight (g).

Results and Discussion

The ANOVA results (Table 1) reveal significant genetic variation for most traits at both the 5% and 1% significance levels. Traits like plant height, number of pods per plant, and seed yield per plant show highly significant differences, indicating that these traits are strongly influenced by genetic factors. This provides an excellent opportunity for breeders to select superior genotypes for these traits. The presence of genetic variability in important agronomic traits, especially those directly related to yield (number of pods, seeds per pod, seed yield), suggests that substantial progress can be made through selection and breeding efforts aimed at improving pigeonpea productivity. The outcomes unveiled that the dependent character of the investigation seed yield/plant varied from 78.11 g to 5.63 g with a mean value of 23.37 g. Mean value revealed that, genotype G.R.G.-152 had maximum seed yield/plant and minimum seed yield/plant was recorded in G.R.G.-152 X C.G. Arhar-2. Among the various characters studied, high value of PCV was estimated for the traits viz., seed yield/plant (72.97) followed by number of pods/plant (35.41), primary branches/plant (30.65) and 100 seed weight whereas moderate value of PCV was observed for traits, shelling % (18.63), plant height (14.67) and seeds/pod (11.21). Low value of PCV was detected for the traits, days to 50% flowering (1.05) and days to maturity (0.80). (Table 2)

Similarly, the genotypic coefficient of variation estimated high in magnitude for characters *viz.*, seed yield/plant (72.06), number of pods/plant (33.99) and primary branches/plant (29.63) whereas, low value of GCV was observed for, days to maturity (0.58) and days to 50% flowering (0.55). Comparable verdicts has been stated by Bathini *et al.* (2021) and Sahu (2021) for high value of PCV and GCV for seed yield/plant, primary branches/plant and number of pods/plant.

The results testified that high heritability together with high genetic advance was revealed in character *viz.*, seed yield/plant, pods/plant, primary branches/ plant, plant height, 100 seed weight and shelling %. Whereas, low heritability united with low genetic advance was showed by character days to 50% flowering. These finding are in accordance to results reported by Jimma *et al.* (2013) and Mula *et al.* (2019) for plant height; Saroj *et al.* (2013), Pandey *et al.* (2015), Mula *et al.* (2019) and Sharma *et al.* (2013), Pandey *et al.* (2015) and Mula *et al.* (2013), Pandey *et al.* (2015) and Mula *et al.* (2019) for 100 seed weight Sahu *et al.* (2022).

The correlation coefficient analysis results reported that (Table 3) plant height, primary branches/plant, no. of pods/plant and 100 seed weight indicated significant positive correlation with seed yield/plant at genotypic and phenotypic level both. Days to maturity exhibited negative correlation with seeds/pod (-0.29) and plant height (-0.36) at genotypic level only, whereas, days to 50% flowering exhibited significant negative correlation with seed yield/plant (-0.27) at phenotypic level only. These finding are in accordance to results reported by Sahu (2019) and Sahu *et al.* (2021).

Path coefficient analysis (Table 4) of different traits contributing towards seed yield/plant showed that 100 seed weight (0.53) had the highest positive direct effect relationship with seed yield/plant followed by no. of pods/plant (0.32), plant height (0.19) and days to maturity (0.17). It's stated that significance of these characters in decisive the seed yield.

Similar results were obtained as positive direct effect of no. of pods/plant on seed yield/plant earlier by Patel *et al.* (2011), Kujur and Sahu (2019) & Verma *et al.* (2018). Furthermore, comparable verdicts have been described by Sodavadiya *et al.* (2009) that character high direct effect on 100 seed weight has like seed yield/plant.

Conclusion

From this experiment, it was concluded that the ANOVA results indicate significant genetic variation across most of the studied traits at both the 5% and 1% significance levels. Traits such as plant height, number of pods per plant, and seed yield per plant exhibit highly significant differences, underscoring the strong influence of genetic factors. This variation presents a valuable opportunity for breeders to select and enhance superior genotypes for these key traits. The observed genetic variability, particularly in traits directly associated with yield, suggests that focused selection and breeding strategies have the potential to

substantially improve pigeonpea productivity. From the genetic parameter seed yield/plant exhibited the highest values for both genotypic coefficient of variation (GCV%) and phenotypic coefficient of variation (PCV%). Additionally, high GCV values were observed for primary branches/plant and number of pods/plant, while high PCV values were noted for primary branches/plant, number of pods/plant, and seed yield/plant. Characters such as seed yield/plant, number of pods/plant, primary branches/plant, plant height, 100 seed weight, and shelling % showed high heritability combined with high genetic advance. This indicates the predominance of additive gene action, suggesting that simple selection can effectively improve these traits. In contrast, days to 50% flowering exhibited low heritability and low genetic advance, implying the influence of non-additive gene action and that selection may be less effective for this trait.

The correlation analysis revealed a strong, significant positive association of seed yield/plant with primary branches/plant, number of pods/plant, and 100 seed weight at both the genotypic and phenotypic levels. Plant height also showed a positive correlation with seed yield/plant at the genotypic level. However, seed yield/plant was negatively correlated with days to 50% flowering at the phenotypic level, which could suggest that earlier flowering does not necessarily translate to higher yields.

Path coefficient analysis provided further insights into the direct and indirect effects of various traits on seed yield/plant. Traits such as 100 seed weight, number of pods/plant, plant height, and days to maturity exhibited a significant positive direct effect on seed yield/plant, indicating their strong potential for direct selection to enhance yield. Conversely, traits such as shelling %, number of seeds/pod, primary branches/plant, and days to 50% flowering had negative direct effects on seed yield/plant. Understanding these direct and indirect relationships, along with the correlation between traits, allows for more targeted selection in breeding programs. By prioritizing traits with high heritability, genetic advance, and positive direct effects on yield, breeders can improve overall productivity efficiently.

Traits with high heritability and genetic advance, such as seed yield per plant, 100-seed weight, and number of pods per plant, can be directly targeted in breeding programs for improving crop yield. Breeders can use these traits as selection criteria in early generations of breeding programs, ensuring that the genetic potential for higher yield is captured. Path analysis results show that 100-seed weight, number of pods per plant, and plant height have significant

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positive direct effects on seed yield, making them important for direct selection. On the other hand, traits like days to 50% flowering showed a negative direct effect on seed yield, suggesting that reducing flowering duration may lead to a decrease in yield under certain conditions.

Source of variation	Degree of freedom	Days to 50% flowering	Duration of maturity	Plant height (cm)	Primary branches /plant	No. of pods /plant	No. of seeds/pod	Shelling %	100 seed weight (g)	Seed yield/ plant (g)
Replication	2	36.5572	110.90	40.69	0.43	288.82	0.25	35.92	0.10	1.81
Treatment	24	2.61482*	4.60878**	1413.547**	7.930511**	2244.183**	0.313658**	253.8742**	7.766412**	858.4868**
Error	48	1.21633	1.072134	39.85108	0.17973	61.86013	0.023557	11.17196	0.15321	7.171929

Table 1: Analysis of variance for different traits in Pigeonpea.

*,**; Significant at 5 % and 1 % level of significance respectively.

Table 2: Estimation of genetic parameters for different traits in Pigeonpea.

S.	Characters	Mean	Range		PCV	GCV	Heritability	GA	GA (%)	C.V.
No.	Characters		Max.	Min.	(%)	(%)	Heritability	GA	mean	(%)
1	Days to 50% flowering	123.017	124.69	121.46	1.054	0.555	27.706	0.74	0.602	0.896
2	Days to maturity	185.836	188.23	182.74	0.807	0.584	52.371	1.619	0.871	0.557
3	Plant height (cm)	152.023	234.12	116.8	14.676	14.076	91.994	42.28	27.811	7.513
4	Primary branches/plant	5.423	10.55	3.45	30.65	29.636	93.495	3.202	59.032	7.816
5	No. of pods/plant	79.342	134.29	37.12	35.41	33.994	92.163	53.339	67.227	9.912
6	No. of seeds/pod	3.091	3.78	2.4	11.214	10.055	80.402	0.574	18.573	4.964
7	Shelling %	51.552	70.17	19.19	18.613	17.448	87.866	17.368	33.691	6.483
8	100 Seed weight (g)	8.159	11.29	4.68	20.106	19.525	94.307	3.187	39.061	4.80
9	Seed yield/plant (g)	23.374	78.11	5.63	72.975	72.069	97.535	34.271	146.622	11.457

Table 3: Genotypic (G) and Phenotypic (P) Correlation Coefficient of Seed yield and its components in Pigeonpea.

S. No.	Characters		Days to maturity	Plant height (cm)	Primary branches /plant	No. of pods/ plant	No. of seeds /pod	Shelling %	100 Seed weight (g)	Seed yield /plant (g)
1	Doug to 5007 flowering		0.482^{**}	-0.091	-0.445**	-0.603**	-0.449**	-0.104	-0.337***	-0.29
	Days to 50% flowering	Р	0.092	0.009	-0.245*	-0.230*	-0.268*	-0.045	-0.227*	-0.272*
2	Dave to maturity	G		-0.368**	0.414^{**}	-0.200	-0.296***	-0.155	-0.215	-0.028
2	Days to maturity	Р		-0.199	0.262^*	-0.123	-0.170	-0.102	-0.200	-0.037
3	Plant height (cm)	G			-0.069	0.022	-0.078	0.188	0.031	0.244^{*}
3		Р			-0.085	0.012	-0.130	0.170	0.009	0.223
4	Primary branches/plant	G				0.651**	0.062	-0.144	0.539**	0.339**
		Р				0.613**	0.040	-0.139	0.519**	0.321**
5	No. of pods/plant	G					0.418^{**}	-0.154	0.668^{**}	0.466**
5		Р					0.395**	-0.132	0.632**	0.430**
(No. of seeds/pod	G						-0.185	0.189	-0.089
6		Р						-0.119	0.210	-0.076
7	Shelling %	G							0.136	0.121
'		Р							0.149	0.131
8	100 G J	G								0.593**
δ	100 Seed weight (g)									0.573**

*, ** Significant at 5% and 1% level of significance respectively.

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Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches /plant	No. of pods/ plant	No. of seeds/pod	Shelling %	100 Seed weight (g)	r _{xy}
Days to 50% flowering	-0.23424	0.01614	0.0018	0.05579	-0.07409	0.08445	0.00002	-0.12148	-0.29
Days to maturity	-0.02158	0.17523	-0.038	-0.05982	-0.03972	0.05363	0.00005	-0.10699	-0.028
Plant height(cm)	-0.00221	-0.0348	0.19138	0.0193	0.00402	0.04091	-0.00008	0.00491	0.244*
Primary branches/plant	0.05729	0.04595	-0.01619	-0.22813	0.19767	-0.01244	0.00007	0.27718	0.339**
No. of pods/plant	0.05384	-0.02159	0.00239	-0.1399	0.32233	-0.12426	0.00006	0.33746	0.466**
No. of seeds/pod	0.06284	-0.02985	-0.02487	-0.00901	0.12724	-0.31478	0.00006	0.11214	-0.089
Shelling %	0.01051	-0.01779	0.03256	0.03174	-0.04266	0.03738	-0.00047	0.07952	0.121
100 SeedWeight (g)	0.05329	-0.03511	0.00176	-0.11842	0.2037	-0.0661	-0.00007	0.53399	0.573**

Table 4: Genotypic path coefficient analysis (Direct and indirect) for seed yield and its components in Pigeonpea.

*, ** Significant at 5% and 1% level of significance respectively.

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