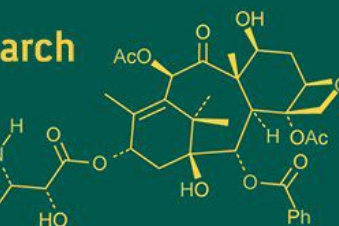
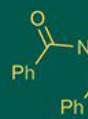
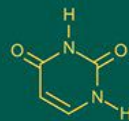
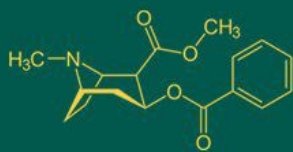


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Evaluation of genetic variability, correlation and path analysis for yield related traits in redgram [*Cajanus cajan* (L.) Mill sp.] suitable for the light soils of Prakasam tract

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Abstract

Background: Redgram is an inexpensive source of protein for vegetarians that is grown in dry and semi-arid tropical regions around the world. Genetic improvement is mostly determined by the amount of genetic variability available in the population. To create an efficient breeding program, a breeder must first understand the extent of genotypic and phenotypic variation in the germplasm.

Methods: Sixteen Redgram genotypes were tested for variability in yield and yield-related characteristics. The experiment was carried out at the Agricultural Research Station in Darsi during 2024 to 2025 in a randomized block design with two replications.

Result: Given their average performance, TRG 47, TRG 59, LRG 721, and TRG 59 were recognized as elite genotypes for increasing yield and nutritional quality. The features with the highest PCV and GCV estimates were the number of primary branches per plant (21.61, 20.12%), the number of secondary branches per plant (36.70, 35.33%), and the yield per plot (27.81, 24.71%). This suggests that there is a significant degree of variation in these features, making selection of these traits successful. High heritability paired with high genetic progress was observed for the variables viz., number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and yield per plot, showing the presence of additive gene action and can be improved by phenotypic selection. The traits initial plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and 100 seed weight all showed a significant positive relationship with yield, indicating that direct selection based on these traits would be beneficial for increasing yield in redgram.

Keywords: Correlation, path analysis, variability

Introduction

Redgram (*Cajanus cajan* L.), frequently referred to as pigeonpea, is one of the most notable legume crops grown in tropical and subtropical areas around the world. It plays an important role in the pulse economy because of its resilience to marginal soils, drought tolerance, and major contribution to food and nutritional security. Redgram is not only a staple pulse crop in many parts of India, but it also provides a significant income and livelihood for millions of small and marginal farmers. Redgram is grown in over 50 countries worldwide, with India, Myanmar, Kenya, Malawi, and Tanzania being the top producers. India alone is responsible for more over 25% of global Redgram production, making it the largest. Approximately 3.5 million tonnes per year, covering an area of around 4.2 million hectares, with an average yield of 830-850 kg/ha.

Redgram is important for the security of nutrition and food, especially in vegetarian diets, due to its high protein content (20-22%), essential amino acids, dietary fibre, minerals, and B-vitamins. In Andhra Pradesh, particularly in the Prakasam district, Redgram is extensively cultivated under rainfed conditions, spanning 60,000-70,000 hectares annually, owing to its adaptability to dryland environments, deep-rooted drought tolerance, and low input needs. Additionally, its ability to thrive with limited water and to enrich soil health enhances its role in promoting climate-resilient agriculture and sustaining farmer livelihoods in semi-arid regions. The individual state trend shows that Karnataka scored top in area and second in

production, followed by Maharashtra, second in area and first in production, and Uttar Pradesh, third in both area and production. Gujarat recorded the highest production (1163 kg/ha), followed by Jharkhand (1144 kg/ha) and Uttar Pradesh (1039 kg/ha), while Andhra Pradesh had the lowest productivity (521 kg/ha). In order to meet demand, it is essential to boost Redgram productivity in India, especially in Andhra Pradesh.

Correlation and path analysis aids in determining the characters which contribute to yield and are employed for achieving significant genetic gain. Any crop improvement initiative begins with the creation of variations among plant genetic resources. (Patel *et al.* 2021) ^[11]. The selection of parents for varietal development program is dependent on the crop's prevailing genetic diversity. As a result, a research endeavour was initiated with an objective of determining the genetic variability, heritability, genetic advance, principal components, and association among pigeonpea genotypes using quantitative traits. This would aid in selecting novel genotypes for beneficial characters, which may then be employed in pigeonpea breeding initiatives.

Materials and Methods

The current study was carried out from 2024 to 2025 on the experimental farms of the Agricultural Research Station in Darsi, Prakasam district. The experimental material included 16 red gram genotypes (LRG 616, LRG 618, LRG105©, LRG 621, LRG 623, LRG 703, LRG 704, LRG 709, LRG 721, LRG 713, LRG 711, LRG 708, LRG 52©, LRG 133-33, TRG 147, TRG 59©) evaluated under multi-locational testing and were sourced by Principal Scientist (Pulses), Department of Genetics and Plant Breeding, Regional Agricultural Research Station, Lam, Guntur.

The experiment was designed in a randomized block design (RBD), with two replications. Each genotype was raised in 4 rows of 5 m length, with a spacing of 180 cm x 20 cm. The genotypes were assessed for genetic variability by evaluating twelve quantitative traits: initial plant stand, final plant stand, days to first flowering, 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, hundred seed weight (g), and yield (kg/plot). All prescribed agronomic practices were followed to ensure a healthy crop. Five competitive plants from each genotype were selected at random for observation. All attributes were analysed for variation in accordance with Panse and Sukhathme's (1967) ^[9] criteria. The phenotypic and genotypic coefficients of variation were estimated using the procedures described by Burton and Devane (1952) ^[4]. Heritability and genetic progress were assessed using the methodologies developed by Lush (1940) ^[8] and Johnson *et al.* (1955) ^[6], respectively. Pearson (1897) proposed a strategy for estimating correlation coefficients, and Dewey and Lu (1959) ^[5] proposed a method for path analysis.

Results and Discussion

The presence of genetic variability for economically vital characteristics is a significant factor in developing local varieties in terms of specific character traits. The current study was undertaken to investigate variability, heredity, genetic advance, correlation, and path analysis. The data collected was statistically analyzed to determine the mean, variance, genetic characteristics, correlation, and path

coefficients among the various traits under examination. Tables 1 and 2 show the range, mean, genotypic, phenotypic, and environmental variance, phenotypic and genotypic coefficients of variation, heritability, and anticipated genetic progress as a percentage of mean for twelve traits, respectively.

Coefficients of variation

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) help us understand how the environment influences certain traits. The analysis of variance indicated highly significant variation among genotypes for all twelve quantitative traits in redgram, indicating the presence of significant genetic variability-a necessary requirement for genetic improvement.

The frequency range of PCV was marginally greater than GCV for all traits, indicating that environmental factors had little influence on their expression. The traits with the highest PCV and GCV estimates were the number of primary branches per plant (21.61, 20.12%), the number of secondary branches per plant (36.70, 35.33%), and the yield per plot (27.81, 24.71%). This suggests that there is a significant amount of genetic variation in these attributes, implying that selection will be effective. Whereas, the initial plant stand (3.69, 3.47%) and the final plant stand (6.40, 5.51%) displayed low magnitudes of PCV and GCV. Days to first flowering (8.17, 7.89%), days to 50% blooming (7.55, 7.26%), and 100 seed weight (7.33, 6.91%) all indicate modest genetic variation in the population. Even while qualities such as days to maturity and plant height are crucial in agriculture, the little genetic variety predicts that selection will be delayed and ineffective. In such circumstances, alternate approaches such as incorporating novel germplasm or hybridization may be more effective.

Heritability and genetic advance

Heritability estimations provided information on the transmission of characteristics from parents to progeny. Heritability was high for initial plant stand (88.83%), final plant stand (74.15%), days to first flowering (93.10%), days to half flowering (92.43%), days to maturity (89.79%), number of primary branches per plant (86.72%), number of secondary branches per plant (92.66%), number of pods per plant (99.06%), yield/plot (78.90%), and hundred seed weight (88.83%). This suggests low environmental impact and a high possibility for trait transfer to future generations. Plant height (51.29%) and number of seeds per pod (50.44%) had a moderate range of heritability, implying that selection for plant height and seeds per pod may be ineffective unless combined with high genetic advance or used in association with more heritable traits such as pods per plant or branches per plant.

The variables with the highest genetic advance as a percentage of the mean were the number of primary branches per plant (38.611%), number of secondary branches per plant (70.06%), number of pods per plant (71.01%), and yield per plot (45.21%). The variables of number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and yield per plot were found to have high heritability and genetic progress. Days to first flowering and days to 50% flowering, exhibited moderate to high heritability (93.10% and 92.43%), with genetic advance as percent of mean (GAM)

values of 15.68% and 14.38%, respectively, suggesting that early flowering can be effectively selected for the development of short-duration varieties, which is especially useful in rainfed areas. It demonstrates the supremacy of additive gene effects. Therefore, these features can be improved through direct selection.

Correlation and path analysis

The correlation coefficient reveals the type and amount of interaction between several characters. Yield is the most important consideration for breeders when selecting crops. Understanding the qualities related with yield allows breeders to simplify their breeding programs by directly selecting traits that are positively associated with yield. When the two attributes are positively connected, selecting one affects the selection of the other. When attributes are negatively correlated, it is extremely difficult to create a favourable combination.

In such cases, priorities should be established according to the breeding objectives to facilitate the selection process. Table 3 shows the genotypic (rg) and phenotypic (rp) correlation coefficients for eleven characteristics. In the current study, the genotypic correlation coefficients were generally higher than the phenotypic correlation coefficients. A highly substantial and positive connection with yield was observed for the qualities viz. Various traits, including initial plant stand, final plant stand, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and 100 seed

weight, showed a significant positive association with seed yield per plant in the desired direction at both genotypic and phenotypic levels. Hence, these characters should be given due consideration while selecting for increasing yield. While, days to first flowering, days to 50% flowering and days to maturity showed non-significant and positive association at both genotypic and phenotypic level, in redgram.

Correlation analysis solely illustrates the relationship between two variables, whereas path coefficient analysis identifies the direct and indirect impacts through additional attributes by segregating the correlation. In the current study, all 12 features were deemed causal variables for seed yield per plant. Table 4 shows the direct and indirect effects of several features on seed output per plant. The study found that the number of secondary branches per plant had the greatest positive direct effect on seed yield per plant, followed by plant height, days to first flowering, initial plant stand, and seed weight. The final plant stand, days to 50% flowering, days to maturity, primary branches per plant, and pods per plant all have a negative direct effect on seed yield. When generating the path diagram, it is critical to incorporate all of the major causal factors influencing seed yield per plant.

The path analysis suggested that to improve yield in redgram, selection should prioritize the number of secondary branches per plant, followed by plant height, days to first flowering, and initial plant stand, as these traits had the greatest positive direct influence on seed yield per plant.

Table 1: Analysis of variance for twelve quantitative traits in Redgram

Trait	MS Replication	MS Treatment	MS Error
Initial plant stand	0.281	16.031**	0.948
Final plant stand	15.125	36.325**	5.392
Days to 1 st flowering	144.5**	174.533**	6.233
Days to 50% flowering	338**	173.058**	6.800
Days to maturity	512**	136.367**	7.333
Plant Height (Cm)	53.561	307.719*	99.076
No. of Primary branches/plant	0.195	5.887**	0.419
No. of secondary branches/plant	0.053	108.269**	4.125
No. of pods/plant	11.52	5821.055**	27.354
No. of seeds/pod	0.151	0.411*	0.135
Yield (kg/plot)	0.081	1.082**	0.128
100 seed weight(g)	0.69*	1.934**	0.114

Table 2: Genotypic and phenotypic coefficient of variation, heritability, genetic advance and genetic advance as percent of mean for twelve traits in Redgram

Trait	Range		Mean	GCV (%)	PCV (%)	h ² b (%)	GA @5%	GAM (%)
	Max	Min						
Initial plant stand	80.0	71.0	78.969	3.478	3.690	88.834	5.332	6.752
Final plant stand	78.0	64.0	71.312	5.515	6.404	74.151	6.976	9.783
Days to 1 st flowering	130.0	93.0	116.250	7.891	8.178	93.103	18.234	15.685
Days to 50% flowering	141.0	110.5	125.562	7.261	7.552	92.438	18.058	14.382
Days to maturity	183.5	151.0	174.375	4.606	4.861	89.794	15.679	8.992
Plant Height (Cm)	172.8	129.8	154.469	6.612	9.233	51.290	15.068	9.755
No. of Primary branches/plant	12.4	5.5	8.216	20.127	21.613	86.722	3.172	38.611
No. of secondary branches/plant	38.0	7.3	20.422	35.335	36.708	92.660	14.309	70.068
No. of pods/plant	242.70	59.20	155.406	34.633	34.796	99.065	110.354	71.010
No. of seeds/pod	4.600	3.10	3.856	9.622	13.547	50.443	0.543	14.077
Yield (kg/plot)	3.628	1.24	2.796	24.710	27.817	78.908	1.264	45.217
100 seed weight(g)	16.05	12.10	13.797	6.913	7.334	88.836	1.852	13.422

*GCV- Genotypic coefficient of variation, PCV- Phenotypic coefficient of variation

h²b- Broad sense heritability, GA- Genetic advance, GAM- genetic advance as percent of mean

Table 3: Genotypic and phenotypic correlations of seed yield per plant with other characters in 16 genotypes of Redgram

Characters		Initial plant stand	Final plant stand	Days to 1 st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	100 seed weight (g)	Yield/ plot (Kg)
Initial plant stand	rg	1	0.544**	-0.1484	-0.0908	-0.0448	0.433*	0.440*	0.512**	0.651**	0.768**	-0.446*	0.814**
	rp	1	0.542**	-0.134	-0.0756	-0.0643	0.2411	0.382*	0.505**	0.627**	0.448*	-0.390*	0.692**
Final plant stand	rg		1	-0.277	-0.1321	-0.2224	0.798**	0.765**	0.777**	0.797**	0.460**	-0.391*	0.818**
	rp		1	-0.2927	-0.1332	-0.2443	0.543**	0.580**	0.686**	0.693**	0.2368	-0.2842	0.650**
Days to 1 st flowering	rg			1	0.893**	0.806**	0.2081	0.0694	-0.1597	0.0191	-0.0502	0.1509	0.0315
	rp			1	0.886**	0.794**	0.0674	0.0578	-0.1529	0.0167	-0.0884	0.1179	0.0152
Days to 50% flowering	rg				1	0.739**	0.404*	0.1318	-0.052	0.1212	-0.0272	0.0388	0.107
	rp				1	0.734**	0.2052	0.1016	-0.0354	0.1124	-0.096	0.0114	0.0868
Days to maturity	rg					1	-0.0794	-0.0469	-0.1042	0.0195	0.0081	-0.0133	0.0153
	rp					1	-0.1081	-0.0168	-0.092	0.0144	-0.0021	-0.0597	0.0046
Plant height (cm)	rg						1	0.464**	0.398*	0.562**	0.0854	-0.2083	0.508**
	rp						1	0.3454	0.3185	0.372*	0.3171	-0.1018	0.409*
Primary branches per plant	rg							1	0.921**	0.869**	0.0654	-0.484**	0.812**
	rp							1	0.833**	0.815**	0.1639	-0.404*	0.673**
Secondary branches per plant	rg								1	0.957**	0.2972	0.514**	0.952**
	rp								1	0.918**	0.1833	0.448*	0.814**
No. of Pods per plant	rg									1	0.447*	-0.503**	0.645**
	rp									1	0.3186	-0.477**	0.907**
No. of Seeds per pod	rg										1	-0.2692	0.655**
	rp										1	-0.1508	0.404*
100 seed weight (g)	rg											1	0.620**
	rp											1	0.483**
Yield/ plot (Kg)	rg												1
	rp												1

* rg- Genotypic correlation, rp-Phenotypic correlation

Table No 4: Direct and indirect effects of yield component characters on seed yield in 16 genotypes of redgram

Characters		Initial plant stand	Final plant stand	Days to 1 st flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches per plant	Secondary branches per plant	Pods per plant	Seeds per pod	100 seed weight (g)	Yield/ plot (Kg)
Initial plant stand	rg	0.2307	0.1255	-0.0342	-0.0209	-0.0103	0.1	0.1015	0.1182	0.1501	0.1771	-0.1029	0.814**
	rp	0.1559	0.0845	-0.0209	-0.0118	-0.01	0.0376	0.0595	0.0787	0.0977	0.0698	-0.0607	0.692**
Final plant stand	rg	-0.1381	-0.2539	0.0703	0.0335	0.0565	-0.2028	-0.1944	-0.1973	-0.2023	-0.1167	0.0994	0.818**
	rp	-0.0133	-0.0246	0.0072	0.0033	0.006	-0.0134	-0.0143	-0.0169	-0.0171	-0.0058	0.007	0.650**
Days to 1 st flowering	rg	-0.0425	-0.0794	0.2867	0.2561	0.231	0.0597	0.0199	-0.0458	0.0055	-0.0144	0.0433	-0.0315
	rp	-0.0083	-0.0181	0.0617	0.0547	0.049	0.0042	0.0036	-0.0094	0.001	-0.0055	0.0073	-0.0152
Days to 50% flowering	rg	0.0025	0.0037	-0.0247	-0.0276	-0.0204	-0.0112	-0.0036	0.0014	-0.0033	0.0008	-0.0011	0.107
	rp	-0.001	-0.0018	0.0119	0.0134	0.0098	0.0027	0.0014	-0.0005	0.0015	-0.0013	0.0002	0.0868
Days to maturity	rg	0.002	0.01	-0.0361	-0.0331	-0.0448	0.0036	0.0021	0.0047	-0.0009	-0.0004	0.0006	0.0153
	rp	0.0035	0.0132	-0.043	-0.0398	-0.0542	0.0059	0.0009	0.005	-0.0008	0.0001	0.0032	-0.0046
Plant height (cm)	rg	0.1506	0.2776	0.0723	0.1406	-0.0276	0.3476	0.1614	0.1383	0.1954	0.0297	-0.0724	0.508**
	rp	0.0187	0.0421	0.0052	0.0159	-0.0084	0.0775	0.0268	0.0247	0.0288	0.0246	-0.0079	0.409*
Primary branches per plant	rg	-0.2327	-0.4047	-0.0367	-0.0697	0.0248	-0.2455	-0.5287	-0.4867	-0.4592	-0.0346	0.2558	0.812**
	rp	-0.069	-0.1049	-0.0105	-0.0184	0.003	-0.0624	-0.1808	-0.1505	-0.1473	-0.0296	0.073	0.673**
Secondary branches per plant	rg	0.9195	1.3939	-0.2866	-0.0934	-0.1871	0.714	1.6519	1.7944	1.7175	0.5332	-0.9227	0.952**
	rp	0.0798	0.1084	-0.0242	-0.0056	-0.0145	0.0503	0.1316	0.1581	0.1451	0.029	-0.0708	0.814**
No. of Pods per plant	rg	-0.3546	-0.4341	-0.0104	-0.066	-0.0107	-0.3064	-0.4734	-0.5217	-0.545	-0.2438	0.2744	0.645**
	rp	0.464	0.5132	0.0124	0.0832	0.0107	0.2755	0.603	0.6797	0.7403	0.2358	-0.3529	0.907**
No. of Seeds per pod	rg	0.2249	0.1347	-0.0147	-0.008	0.0024	0.025	0.0192	0.0871	0.1311	0.293	-0.0789	0.655**
	rp	0.0342	0.0181	-0.0068	-0.0073	-0.0002	0.0242	0.0125	0.014	0.0243	0.0764	-0.0115	0.404*
100 seed weight (g)	rg	0.0514	0.0451	0.0174	0.0045	0.0015	0.024	0.0558	0.0593	0.058	0.031	0.1153	0.620**
	rp	0.0273	0.0199	0.0083	0.0008	0.0042	0.0071	0.0283	0.0313	0.0334	0.0106	0.07	0.483**

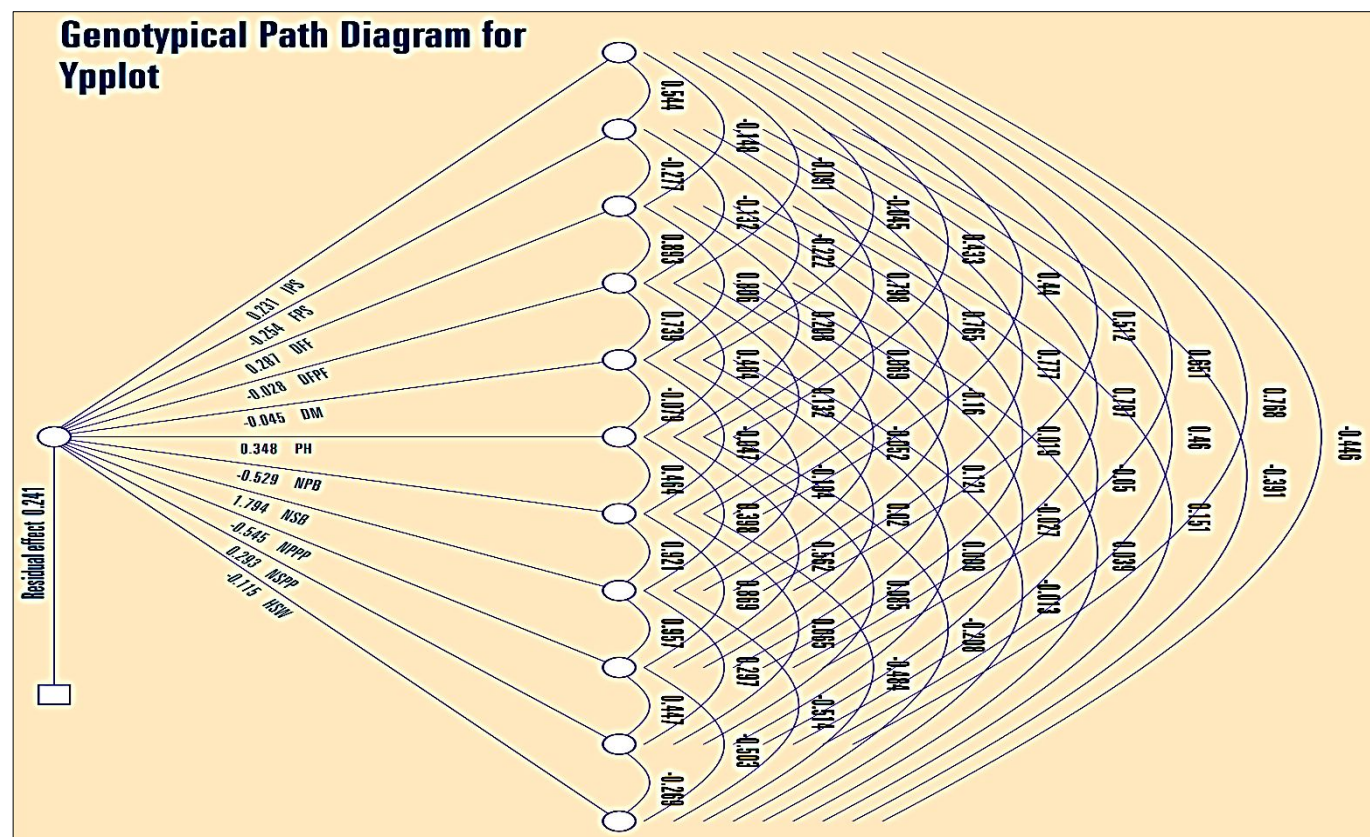


Fig 1: Genotypical Path Diagram for Yield per Plant (Ypplot) Showing Direct and Indirect Effects of Yield-Contributing Traits

Conclusion

The experimental material analysed shows sufficient genetic variety, implying that there is enough of potential to generate genotypes that mature early and yield well. Based on mean performance, TRG 47, TRG 59, LRG 721, and TRG 59 were recognized as elite genotypes for increasing production while maintaining quality. The traits with greater estimations of heritability and genetic progress were the number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and yield per plot.

This means that these attributes are heavily influenced by additive genes and can be significantly enhanced by phenotypic selection. Because the traits initial plant stand, final plant stand, plant height, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, and 100 seed weight all had a significant positive relationship with yield, opting for these traits would be beneficial for increasing yield in redgram. Therefore, to devise a suitable selection criterion for yield enhancement in future pigeonpea breeding programmes these traits must be prioritized.

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