

Genetic variability and generation mean performance for yield and yield related traits in medium duration pigeonpea (*Cajanus Cajan* (L.) Millsp.) across two environments

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Abstract

Genetic variability among parental lines and their segregating generations is essential for the genetic improvement of complex quantitative traits in pigeonpea (*Cajanus Cajan* (L.) Millsp.). The present investigation was undertaken to evaluate genetic variability and generation mean performance for seed yield and associated traits in medium duration pigeonpea. The experimental material comprised five crosses, viz., GRG 152 × GJP 1, GRG 152 × AGT 2, JSP 6 × GJP 1, JSP 6 × BDN 711 and WRG 173 × BDN 711, each represented by six basic generations (P₁, P₂, F₁, F₂, BC₁ and BC₂). The experiment was conducted during Kharif 2021- 22 at two locations, Junagadh and Kukada, in a Compact Family Block Design with three replications. Observations were recorded for nine agronomic traits related to phenology, plant architecture and yield. Analysis of variance revealed highly significant differences among crosses and among generations within each cross for all the studied traits at both locations, indicating the presence of substantial genetic variability. Considerable variation in generation means was observed across the five crosses, reflecting diverse genetic responses for yield and its component traits. Several F₁, F₂ and backcross generations exhibited desirable mean performance for important yield attributes, particularly seed yield per plant, number of pods per plant and plant height, highlighting the breeding potential of these cross combinations. The consistency of significant variation across environments further confirmed the stability of the observed genetic differences. The results demonstrated the existence of ample exploitable genetic variability for seed yield and related traits in medium duration pigeonpea. The superior cross combinations identified in the present study provide valuable genetic resources for selection and future pigeonpea breeding programmes aimed at developing high-yielding cultivars.

Keywords: *Cajanus Cajan*, breeding populations, Compact Family Block Design, genetic variability, multi-environment evaluation, pigeonpea breeding, seed yield

Introduction

Pigeonpea (*Cajanus Cajan* (L.) Millsp.) Is one of the most important grain legumes cultivated in tropical and subtropical regions, contributing substantially to nutritional security, sustainable agriculture and soil health? Owing to its ability to fix atmospheric nitrogen, tolerance to intermittent drought and adaptation to marginal environments, pigeonpea plays a pivotal role in rainfed farming systems, particularly in South Asia and sub-Saharan Africa (Saxena *et al.*, 2019; Varshney *et al.*, 2021) ^[14]. India accounts for nearly three-fourths of the global pigeonpea area and production, where the crop serves as a major source of dietary protein for the predominantly vegetarian population while simultaneously improving soil fertility through biological nitrogen fixation (FAOSTAT, 2023). Despite its agronomic importance, the productivity of pigeonpea remains relatively low compared with its genetic potential. Yield improvement is constrained by the complex inheritance of seed yield, narrow utilization of elite germplasm, environmental fluctuations and the quantitative nature of most yield-contributing traits (Saxena *et al.*, 2021) ^[12]. Seed yield is governed by the cumulative effects of several interrelated components, including flowering and

maturity duration, plant architecture, pod number, seed number and seed size. Therefore, successful genetic improvement depends on identifying genetically diverse parental lines and understanding the extent of variability expressed in different generations derived from their hybridization (Kumar *et al.*, 2022) ^[8].

The availability of sufficient genetic variability is the cornerstone of every crop improvement programme. Evaluation of parental lines and their derived generations provides valuable information regarding the magnitude of variation available for selection and facilitates the identification of promising cross combinations for future breeding efforts. Comparative assessment of parental, filial and backcross generations also enable breeders to understand the expression of economically important traits during different stages of segregation and assists in selecting superior breeding materials (Singh *et al.*, 2020).

Analysis of variance is one of the most reliable statistical approaches for partitioning phenotypic variation and determining the significance of genetic differences among breeding materials. Significant differences among crosses and generations indicate the presence of exploitable variability, which is essential for effective selection and

genetic gain. Likewise, evaluation of generation mean performance provides direct information on the relative superiority of parental lines and segregating generations for yield and its component traits. Such information is particularly useful for identifying cross combinations capable of producing desirable recombinants in subsequent generations and for designing efficient breeding strategies (Hallauer *et al.*, 2010; Acquaah, 2020) ^[1, 6].

Evaluation of breeding populations across diverse environments provides reliable information on the magnitude of genetic variability and facilitates the identification of superior parental combinations for subsequent genetic improvement. Such populations also provide an excellent resource for estimating genetic parameters, including heritability and expected genetic advance, which together improve the efficiency of selection in pigeonpea breeding programmes (Khaniya *et al.*, 2022) ^[7].

In the present investigation, five genetically diverse medium duration pigeonpea crosses, each represented by six basic generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) were evaluated at two contrasting environments to quantify genetic variability and compare generation mean performance for seed yield and nine associated agronomic traits. The findings are expected to identify superior cross combinations and breeding materials that can be effectively utilized in future pigeonpea improvement programmes.

Materials and Methods

1. Experimental site

The present investigation was conducted during Kharif 2021^[12]-22 at two experimental locations of Junagadh Agricultural University, Gujarat, India, viz., the Instructional Farm, Department of Agronomy, Junagadh (21.52° N, 70.47° E; 60 m above mean sea level) and the Cotton Research Station, Kukada (22.66° N, 71.42° E; 108 m above mean sea level). Junagadh represents the South Saurashtra Agro-climatic Zone, whereas Kukada represents the North Saurashtra Agro-climatic Zone. Both locations possess semi-arid tropical climatic conditions but differ in soil characteristics and local environmental conditions, enabling the evaluation of breeding materials under contrasting environments.

2. Plant materials

The experimental material comprised five medium duration pigeonpea crosses, namely GRG 152 × GJP 1, GRG 152 × AGT 2, JSP 6 × GJP 1, JSP 6 × BDN 711 and WRG 173 × BDN 711. Each cross consisted of six basic generations, viz., P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 . The parental genotypes (GRG 152, GJP 1, AGT 2, JSP 6, BDN 711 and WRG 173) were selected based on their genetic diversity for seed yield and yield-attributing traits. The F_1 , F_2 and backcross generations were developed during 2019-2021^[12] through controlled hybridization followed by selfing and backcrossing to obtain the required experimental populations.

3. Experimental design and crop management

The six generations of each cross were evaluated in a Compact Family Block Design (CFBD) with three replications at both experimental locations. Each replication consisted of five family blocks, each representing one cross. Within each family block, one row each of P_1 , P_2 and F_1 , four rows of F_2 and two rows each of BC_1 and BC_2 were

maintained. Each row was 2.0 m long with a spacing of 90 cm between rows and 20 cm between plants. All recommended agronomic and plant protection practices were followed uniformly throughout the crop-growing period to ensure healthy crop establishment and normal plant growth.

4. Recording of observations

Observations were recorded on five randomly selected plants from each of the parental and F_1 generations, twenty plants from the F_2 generation and ten plants from each backcross generation in every replication. Data were recorded for nine agronomic traits, namely days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seeds per pod, pod length (cm), 100-seed weight (g) and seed yield per plant (g). Standard procedures were followed for recording each trait.

5. Statistical analysis

The recorded data were subjected to analysis of variance (ANOVA) using the procedure described by Panse and Sukhatme (1985) ^[9] for Compact Family Block Design. The analysis was performed in two stages. Initially, variation among the five crosses (families) was evaluated. Subsequently, each cross was analysed separately to determine variation among the six generations. Prior to analysis, Bartlett's test was performed to verify the homogeneity of error variances across families. Standard error of mean (SEM) and critical difference (CD) at the 5% probability level were computed to compare generation means. The mean performance of individual generations was subsequently compared to identify superior crosses and promising breeding materials for yield and yield-related traits across both environments.

Results and Discussion

1. Analysis of Variance

Analysis of variance (ANOVA) was performed separately to assess variation among families (crosses) and among generations within each family for nine agronomic traits at Junagadh and Kukada. The results revealed highly significant ($P \leq 0.01$) differences among the five crosses for all the studied traits at both locations, indicating the presence of substantial genetic variability among the parental combinations (Table 1). The existence of significant variability among the crosses suggests that the selected parental lines possessed adequate genetic diversity for seed yield and its associated traits, thereby providing considerable scope for effective selection and genetic improvement in subsequent generations.

Table 1 Within individual crosses, analysis of variance among the six basic generations (P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2) also revealed highly significant differences for almost all traits at both experimental locations (Table 1). Significant variation among generations was consistently observed for phenological traits, including days to flowering and days to maturity, indicating substantial segregation for maturity duration. Likewise, highly significant differences were recorded for plant height, number of branches per plant and number of pods per plant in all five crosses, reflecting the presence of considerable variability for plant architecture and reproductive potential. Similar findings have been reported by Vanniarajan *et al.* (2019), Saxena *et al.* (2021) and Bohra *et al.* (2020) ^[3, 12, 15].

Table 1: Analysis of variance (mean square) for nine agronomic traits in five pigeonpea crosses evaluated at Junagadh and Kukada

Source of variance	d.f.	Days to flowering		Days to maturity		Plant height (cm)		Number of branches per plant		Number of pods per plant	
		Junagadh	Kukada	Junagadh	Kukada	Junagadh	Kukada	Junagadh	Kukada	Junagadh	Kukada
		Analysis of variance between families									
Replications	2	0.042	0.014	0.141	0.054	0.059	0.109	0.040*	1.164**	0.192	0.032
Crosses	4	144.176**	139.622**	68.170**	109.470**	59.977**	275.004**	4.197**	13.480**	5090.643**	4240.594**
Error	8	0.096	0.058	0.073	0.045	0.080	0.126	0.008	0.118	0.159	0.084
χ^2		NS	NS	S	S	S	NS	NS	NS	NS	S
		Analysis of variance between progenies within the family									
		GRG 152 × GJP 1 (Cross 1)									
Replications	2	0.0648	0.3348	0.6915	0.0057	0.5333	1.3926	0.0338	3.4963	0.5329	0.1339
Generations	5	26.6123**	25.5369**	63.6813**	45.6063**	41.4672**	496.8005**	3.1973**	10.5733**	1750.0400**	1644.8449**
Error	10	0.1484	0.4284	0.6744	0.7644	0.4407	0.3513	0.1041	0.8912	0.7129	1.7032
		GRG 152 × AGT 2 (Cross 2)									
Replications	2	0.2723	0.1051	0.9915*	1.1536	0.0159	0.8451	0.2067	0.0635	0.4768	0.5235
Generations	5	107.5380**	99.7994**	50.7354**	78.3282**	29.8874**	18.0638**	16.5360**	54.7169**	5882.2276**	4927.6512**
Error	10	0.2112	0.4173	0.1494	0.4498	0.1254	0.3112	0.1547	0.7368	0.2975	0.6585
		JSP 6 × GJP 1 (Cross 3)									
Replications	2	1.4822**	0.5369	0.0318	0.0361	0.0977	0.0674	0.1172	1.6918*	3.3162*	0.1210
Generations	5	11.6995**	2.6054*	28.6729**	12.0033**	97.5950**	457.9592**	3.7368**	9.9821**	5292.4797**	2028.7001**
Error	10	0.1274	0.1417	0.1022	0.0962	0.0968	0.6335	0.1159	0.2618	0.5379	0.4763
		JSP 6 × BDN 711 (Cross 4)									
Replications	2	0.1739	0.4180	0.0864	0.2070	1.0405	1.2610*	0.0104	4.1718*	0.3679	0.4460
Generations	5	111.0037**	138.7701**	108.8134**	113.3630**	487.7334**	483.0675**	2.3126**	95.9901**	23000.9143**	22194.5742**
Error	10	0.1535	0.1948	0.1769	0.1851	1.6323	0.2123	0.0648	0.8925	0.6573	1.7476
		WRG 173× BDN 711 (Cross 5)									
Replications	2	0.1739	0.0716	0.7890*	0.0137	0.5846	0.1020	0.0554	0.3879	0.2851	0.99006
Generations	5	111.0037**	184.6781**	155.1714**	221.5282**	17.8250**	699.0849**	17.5499**	36.2819**	10391.5926**	10997.4006**
Error	10	0.1535	0.2555	0.1300	0.1140	0.2306	0.3603	0.2601	0.4026	0.5745	0.2906

Source of variance	d.f.	Number of seeds per pod		Length of pod (cm)		100-seed weight (g)		Seed yield per plant (g)	
		Junagadh	Kukada	Junagadh	Kukada	Junagadh	Kukada	Junagadh	Kukada
		Analysis of variance between families							
Replications	2	0.007**	0.012	0.066**	0.040**	0.056**	0.051**	20.545**	23.725**
Crosses	4	0.027**	0.024**	0.113**	0.153**	3.076**	3.382**	2209.624**	2291.487**
Error	8	0.000	0.003	0.001	0.002	0.004	0.004	1.119	1.300
χ^2		S	S	S	NS	NS	NS	NS	NS
		Analysis of variance between progenies within the family							
		GRG 152 × GJP 1 (Cross 1)							
Replications	2	0.0038	0.0035	0.0498*	0.0582**	0.0270	0.0710	18.5118	16.4216
Generations	5	0.0265**	0.0274*	0.2260**	0.3030**	3.4924**	3.4303**	506.8576**	430.3118**
Error	10	0.0014	0.0010	0.0088	0.0037	0.0243	0.0377	5.5595	4.2256
		GRG 152 × AGT 2 (Cross 2)							
Replications	2	0.0140	0.0448*	0.1064**	0.0355*	0.0755*	0.0647*	33.3307*	66.6417*
Generations	5	0.0498**	0.1538**	0.1157**	0.0619**	0.3314**	0.3985**	844.4184**	821.7071**
Error	10	0.0076	0.0105	0.0124	0.0085	0.0146	0.0128	5.1852	8.9919
		JSP 6 × GJP 1 (Cross 3)							
Replications	2	0.0052	0.005	0.0688**	0.0443**	0.1719*	0.0701	67.8710**	14.1975
Generations	5	0.0144**	0.0127**	0.3089**	0.3958**	3.1767**	2.7201**	2494.4251**	1283.3147**
Error	10	0.0015	0.0005	0.0041	0.0058	0.0299	0.0376	8.1735	5.0724
		JSP 6 × BDN 711 (Cross 4)							
Replications	2	0.0072*	0.0006	0.0963	0.0888**	0.0155	0.0996*	8.9699	8.3317
Generations	5	0.0145*	0.0225**	0.3069**	0.2226**	1.3358**	1.8623**	5143.1651**	5782.0008**
Error	10	0.0014	0.0008	0.0277	0.0107	0.0104	0.0153	2.2169	2.6125
		WRG 173× BDN 711 (Cross 5)							
Replications	2	0.0157**	0.0973**	0.1079	0.0605*	0.1393	0.0877	24.4457*	67.9663**
Generations	5	0.0207**	0.1093**	0.3176**	0.3335**	1.2896**	1.3160**	2461.3640**	2837.4913**
Error	10	0.0018	0.0064	0.0398	0.0091	0.0535	0.0309	4.5228	4.9191

Values are mean squares.

Significance: $P \leq 0.05$ (*), $P \leq 0.01$ (**).

Chi-square for Barlett's test of homogeneity of error variances: S = significant and NS = non-significant

Abbreviation: df = degrees of freedom.

Yield and yield-attributing traits exhibited comparatively larger mean squares than phenological characters, particularly for number of pods per plant and seed yield per plant, suggesting that these traits possessed wider genetic variation among generations. Seed yield per plant showed highly significant variation across all five crosses at both locations, demonstrating substantial opportunities for selecting superior segregants in the advancing generations. The magnitude of variation observed for yield components is expected because these traits are quantitatively inherited and are influenced by the cumulative action of several genes. Previous studies have likewise reported significant genetic variation for yield and its component traits in pigeonpea breeding populations (Saxena, 2016; Bohra *et al.*, 2020; Varshney *et al.*, 2021) [3, 11, 14].

Although minor differences in the magnitude of mean squares were observed between Junagadh and Kukada, the significance of variation remained largely consistent across environments. This indicates that the expression of the evaluated traits was relatively stable under both agro-climatic conditions and that the identified genetic differences were reproducible across locations. Such consistency enhances the reliability of selecting promising breeding materials with broad adaptation and stable performance.

The Bartlett's test for homogeneity of error variances indicated homogeneous experimental errors for most of the studied characters, validating the assumptions required for pooled interpretation of generation means within each location. The low experimental error observed in the present investigation further confirmed the precision of the experimental design and the reliability of the recorded observations.

Overall, the analysis of variance established the existence of substantial genetic variability among the five pigeonpea crosses and among their six basic generations for all nine agronomic traits. The significant variation observed for seed yield and its associated characters indicates considerable scope for identifying superior cross combinations and desirable segregants. Therefore, detailed evaluation of generation mean performance was undertaken to identify the most promising crosses and generations for exploitation in pigeonpea improvement programmes.

2. Mean performance of six generations

2.1 Mean performance for days to flowering and days to maturity

The mean performance of six basic generations (P₁, P₂, F₁, F₂, BC₁ and BC₂) for days to flowering and days to maturity exhibited considerable variation among the five pigeonpea crosses at both Junagadh and Kukada (Table 2). The observed differences among generations reflected the diverse genetic constitution of the parental lines and

indicated the availability of sufficient variability for manipulating crop duration in medium duration pigeonpea breeding programmes.

For days to flowering, the parental genotypes displayed wide variation, confirming the successful selection of genetically diverse parents for hybridization. The earliest flowering behaviour was consistently observed in the cross GRG 152 × AGT 2, where the F₂ generation recorded the lowest mean days to flowering at both Junagadh (88.72 days) and Kukada (88.83 days), indicating the possibility of recovering desirable early-flowering segregants through selection. In contrast, the crosses JSP 6 × GJP 1 and WRG 173 × BDN 711 exhibited relatively late flowering across all generations, reflecting the influence of late-maturing parental lines. The F₁ generations generally expressed flowering periods intermediate to or comparable with their parents, whereas the F₂ and backcross generations exhibited broader variation, suggesting segregation for genes controlling flowering time. Similar patterns of variability for flowering duration have been reported in pigeonpea by Saxena (2016), Bohra *et al.* (2020) and Varshney *et al.* (2021) [3, 11, 14], who emphasized that flowering behaviour is strongly influenced by the genetic constitution of parental combinations.

Among the five crosses, GRG 152 × AGT 2 consistently expressed the shortest flowering duration at both experimental locations, indicating its potential utility in breeding programmes aimed at developing early-maturing cultivars suitable for multiple cropping systems and regions with terminal moisture stress. Early flowering is considered a desirable trait in pigeonpea because it facilitates early pod initiation, reduces exposure to terminal drought and enables timely harvesting under rainfed conditions. The relatively small differences observed between Junagadh and Kukada further suggested that flowering behaviour remained reasonably stable across environments, although slight environmental influences on phenological development were evident.

A similar trend was observed for days to maturity, where substantial variation was recorded among crosses and generations (Table 2). The earliest maturity was again observed in GRG 152 × AGT 2, with the F₂ generation maturing in 158.78 days at Junagadh and 157.25 days at Kukada. The consistency of early maturity across both locations indicates that this cross possesses considerable potential for developing short-duration breeding lines without compromising adaptation. Conversely, GRG 152 × GJP 1 represented one of the latest maturing crosses, with several generations requiring more than 178 days to attain physiological maturity. Likewise, WRG 173 × BDN 711 also exhibited relatively longer crop duration, reflecting the contribution of late-maturing parental genotypes.

Table 2: Mean performance of six basic generations for days to flowering and days to maturity in five pigeonpea crosses

Generations		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	S.Em ±	C.D. at 5 %
		Days to flowering							
GRG 152 × GJP 1 (Cross 1)	Junagadh	105.93 ± 0.268	112.00 ± 0.215	103.47 ± 0.221	106.18 ± 0.121	108.60 ± 0.142	109.07 ± 0.155	0.222	0.701
	Kukada	104.00 ± 0.230	110.07 ± 0.278	101.47 ± 0.291	105.60 ± 0.209	105.57 ± 0.277	107.33 ± 0.328	0.378	1.191
GRG 152 × AGT 2 (Cross 2)	Junagadh	106.13 ± 0.314	92.87 ± 0.372	93.00 ± 0.375	88.72 ± 0.242	95.32 ± 0.292	92.21 ± 0.460	0.265	0.836
	Kukada	104.40 ± 0.261	90.53 ± 0.295	90.87 ± 0.251	88.83 ± 0.163	94.41 ± 0.254	90.41 ± 0.252	0.373	1.175
JSP 6 × GJP 1 (Cross 3)	Junagadh	108.47 ± 0.313	112.50 ± 0.254	112.67 ± 0.458	112.63 ± 0.156	108.87 ± 0.140	112.05 ± 0.387	0.206	0.649
	Kukada	108.13 ± 0.270	110.02 ± 0.373	108.87 ± 0.248	109.80 ± 0.227	108.00 ± 0.193	110.00 ± 0.357	0.217	0.685
JSP 6 × BDN 711	Junagadh	108.27 ± 0.338	91.67 ± 0.367	96.27 ± 0.243	95.52 ± 0.134	102.80 ± 0.205	95.21 ± 0.133	0.226	0.713

(Cross 4)	Kukada	108.00 ± 0.271	88.98 ± 0.277	94.07 ± 0.268	92.23 ± 0.205	99.33 ± 0.233	93.00 ± 0.273	0.255	0.803
WRG 173 × BDN 711	Junagadh	112.60 ± 0.262	91.87 ± 0.270	110.80 ± 0.382	109.62 ± 0.187	111.02 ± 0.341	106.32 ± 0.292	0.250	0.787
(Cross 5)	Kukada	110.60 ± 0.314	89.53 ± 0.324	108.20 ± 0.268	108.15 ± 0.169	109.00 ± 0.230	104.00 ± 0.252	0.292	0.920
Days to maturity									
GRG 152 × GJP 1	Junagadh	169.40 ± 0.343	179.60 ± 0.308	180.27 ± 0.281	178.38 ± 0.212	182.60 ± 0.261	180.00 ± 0.241	0.474	1.494
(Cross 1)	Kukada	170.73 ± 0.291	179.27 ± 0.317	177.47 ± 0.300	178.70 ± 0.160	180.93 ± 0.513	181.50 ± 0.213	0.505	1.591
GRG 152 × AGT 2	Junagadh	170.00 ± 0.309	168.67 ± 0.338	166.33 ± 0.273	158.78 ± 0.170	168.00 ± 0.318	169.00 ± 0.325	0.223	0.703
(Cross 2)	Kukada	171.00 ± 0.271	166.27 ± 0.247	168.67 ± 0.288	157.25 ± 0.238	167.43 ± 0.261	171.00 ± 0.298	0.387	1.220
JSP 6 × GJP 1	Junagadh	174.53 ± 0.223	180.00 ± 0.338	172.00 ± 0.277	171.42 ± 0.227	173.00 ± 0.278	174.00 ± 0.218	0.185	0.582
(Cross 3)	Kukada	174.67 ± 0.207	179.00 ± 0.335	175.27 ± 0.309	178.22 ± 0.206	174.00 ± 0.279	176.00 ± 0.259	0.179	0.564
JSP 6 × BDN 711	Junagadh	174.93 ± 0.247	160.00 ± 0.374	169.00 ± 0.330	163.85 ± 0.179	174.89 ± 0.229	166.08 ± 0.183	0.243	0.765
(Cross 4)	Kukada	174.20 ± 0.195	158.40 ± 0.270	169.40 ± 0.339	162.63 ± 0.217	160.57 ± 0.281	160.64 ± 0.400	0.248	0.783
WRG 173 × BDN 711	Junagadh	180.33 ± 0.307	160.47 ± 0.351	175.53 ± 0.409	179.65 ± 0.216	173.17 ± 0.278	174.73 ± 0.252	0.208	0.656
(Cross 5)	Kukada	180.73 ± 0.308	158.04 ± 0.316	179.87 ± 0.248	179.67 ± 0.189	175.80 ± 0.234	173.00 ± 0.222	0.195	0.614

The segregation observed in the F_2 and backcross generations for maturity duration demonstrates the availability of sufficient genetic variability for selecting desirable maturity classes. Such variation is particularly advantageous in pigeonpea improvement because cultivars with different maturity durations are required to suit diverse agro-climatic regions and cropping systems. Early and medium duration genotypes are especially valuable under rainfed agriculture, where escape from terminal drought and synchronization with subsequent crops are important breeding objectives.

Comparison of the two experimental locations indicated only minor differences in the expression of flowering and maturity duration, suggesting that these phenological traits were largely governed by genetic factors while being moderately influenced by environmental conditions. The consistency in the ranking of crosses across Junagadh and Kukada further strengthens the reliability of the observed performance and supports the identification of stable breeding materials.

Overall, the results clearly demonstrated that GRG 152 × AGT 2 was the most promising cross for developing early-flowering and early-maturing pigeonpea lines, whereas GRG 152 × GJP 1 and WRG 173 × BDN 711 could serve as useful sources for medium- to late-duration breeding programmes. The substantial variability observed through analysis of variance also supports the estimation of genetic parameters in these breeding populations. Using the same experimental material, Khaniya *et al.* (2022) [7] reported moderate to high narrow-sense heritability for several yield-attributing traits, indicating that a considerable proportion of the observed variability is heritable and can be effectively exploited through selection.

2.2 Mean performance for plant height and number of branches per plant

Considerable variation was observed among the six basic generations for plant height and number of branches per plant across the five pigeonpea crosses at both Junagadh and Kukada (Table 3). These traits are important determinants of plant architecture and play a significant role in influencing biomass production, reproductive efficiency and ultimately seed yield.

The substantial variation recorded among generations indicated the presence of adequate genetic diversity for improving plant architecture through selection.

For plant height, the five crosses exhibited distinct patterns of variation across the two environments. At Junagadh, plant height ranged from 170.20 cm in the parent JSP 6 of the cross JSP 6 × GJP 1 to 204.07 cm in the F_1 generation of JSP 6 × BDN 711. Similarly, at Kukada, the highest plant height was recorded in the F_2 generation of GRG 152 × GJP 1 (228.00 cm), followed by the F_2 (220.00 cm) and F_1 (219.07 cm) generations of WRG 173 × BDN 711, indicating vigorous vegetative growth in these populations. The F_1 generations of crosses JSP 6 × BDN 711 and WRG 173 × BDN 711 consistently exhibited greater plant height than their respective parents, suggesting favourable complementation of growth-related genes in these combinations.

The F_2 and backcross generations also displayed considerable variation in plant height, reflecting segregation of genes controlling vegetative growth. Such variability is advantageous for breeders because optimum plant height contributes to improved canopy development, better light interception and increased reproductive efficiency. However, excessively tall plants may be prone to lodging under adverse environmental conditions. Therefore, selection should focus on genotypes possessing moderate to tall stature coupled with superior yield performance rather than plant height alone. Comparable observations on genetic variability for plant height in pigeonpea have been reported by Saxena (2016), Bohra *et al.* (2020) and Varshney *et al.* (2021) [3, 11, 14].

Variation in number of branches per plant was equally pronounced among the evaluated generations (Table 3). Branching is one of the most important yield-contributing traits because it directly determines the number of reproductive sites available for pod development. At Junagadh, the highest number of branches per plant was recorded in the F_1 generation of WRG 173 × BDN 711 (21.00), whereas at Kukada the F_1 generation of GRG 152 × GJP 1 produced the maximum number of branches (29.00). The F_1 generations of most crosses exhibited higher branch numbers than the respective parental lines, indicating improved vegetative vigour resulting from hybridization.

Table 3: Mean performance of six basic generations for plant height (cm) and number of branches per plant in five pigeonpea crosses

Generations		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	S.Em ±	C.D. at 5 %
		Plant height (cm)							
GRG 152 × GJP 1 (Cross 1)	Junagadh	172.53 ± 0.267	181.47 ± 0.311	181.40 ± 0.321	182.97 ± 0.211	180.16 ± 0.271	180.67 ± 0.238	0.383	1.208
	Kukada	190.00 ± 0.335	198.27 ± 0.474	211.00 ± 0.346	228.00 ± 0.337	204.47 ± 0.398	205.00 ± 0.451	0.342	1.078
GRG 152 × AGT 2 (Cross 2)	Junagadh	173.04 ± 0.366	180.60 ± 0.273	180.07 ± 0.316	181.17 ± 0.211	181.17 ± 0.272	180.50 ± 0.242	0.204	0.644
	Kukada	191.00 ± 0.428	188.00 ± 0.318	194.93 ± 0.440	189.22 ± 0.332	192.61 ± 0.390	191.00 ± 0.370	0.322	1.015
JSP 6 × GJP 1 (Cross 3)	Junagadh	170.20 ± 0.376	180.00 ± 0.350	182.67 ± 0.382	181.22 ± 0.264	184.09 ± 0.381	186.73 ± 0.302	0.180	0.566
	Kukada	169.73 ± 0.367	199.00 ± 0.462	180.00 ± 0.522	177.00 ± 0.297	172.20 ± 0.358	196.12 ± 0.440	0.460	1.448
JSP 6 × BDN 711 (Cross 4)	Junagadh	171.12 ± 0.707	175.53 ± 0.503	204.07 ± 0.292	190.10 ± 0.333	198.05 ± 0.465	191.07 ± 0.307	0.738	2.324
	Kukada	170.40 ± 0.333	180.60 ± 0.397	199.87 ± 0.499	195.88 ± 0.221	200.70 ± 0.506	199.73 ± 0.520	0.266	0.838
WRG 173 × BDN 711 (Cross 5)	Junagadh	180.73 ± 0.408	176.22 ± 0.390	174.59 ± 0.307	176.20 ± 0.205	176.13 ± 0.266	173.63 ± 0.341	0.277	0.874
	Kukada	195.20 ± 0.416	180.73 ± 0.804	219.07 ± 0.440	220.00 ± 0.359	204.00 ± 0.428	195.07 ± 0.352	0.347	1.092
		Number of branches per plant							
GRG 152 × GJP 1 (Cross 1)	Junagadh	14.20 ± 0.245	17.13 ± 0.226	15.20 ± 0.216	16.00 ± 0.150	15.90 ± 0.172	16.57 ± 0.175	0.186	0.587
	Kukada	27.33 ± 0.298	24.33 ± 0.499	29.00 ± 0.876	26.15 ± 0.188	24.10 ± 0.282	25.33 ± 0.234	0.545	1.717
GRG 152 × AGT 2 (Cross 2)	Junagadh	15.07 ± 0.245	12.80 ± 0.216	16.20 ± 0.200	10.20 ± 0.201	15.77 ± 0.254	15.77 ± 0.216	0.227	0.715
	Kukada	27.60 ± 0.258	17.93 ± 0.258	27.40 ± 0.371	20.80 ± 0.207	26.73 ± 0.264	20.27 ± 0.572	0.496	1.562
JSP 6 × GJP 1 (Cross 3)	Junagadh	13.67 ± 0.194	16.80 ± 0.287	15.20 ± 0.245	14.15 ± 0.169	14.77 ± 0.212	14.20 ± 0.184	0.197	0.619
	Kukada	25.87 ± 0.340	23.60 ± 0.271	25.20 ± 0.271	21.28 ± 0.224	25.97 ± 0.273	23.27 ± 0.236	0.295	0.931
JSP 6 × BDN 711 (Cross 4)	Junagadh	13.47 ± 0.249	14.67 ± 0.194	15.93 ± 0.170	13.92 ± 0.130	15.17 ± 0.171	14.70 ± 0.149	0.147	0.463
	Kukada	26.13 ± 0.271	13.87 ± 0.271	28.33 ± 0.327	18.85 ± 0.176	25.87 ± 0.203	18.57 ± 0.539	0.545	1.719
WRG 173 × BDN 711 (Cross 5)	Junagadh	16.47 ± 0.313	14.53 ± 0.271	21.00 ± 0.271	16.95 ± 0.188	19.03 ± 0.306	15.27 ± 0.219	0.294	0.928
	Kukada	21.33 ± 0.320	14.07 ± 0.262	24.60 ± 0.258	20.72 ± 0.211	21.73 ± 0.285	20.60 ± 0.242	0.366	1.154

The F₂ generations generally exhibited wider variation than the parental and F₁ generations, reflecting segregation for branching ability. Although some reduction in branching was observed in a few F₂ populations due to genetic recombination, several segregants maintained desirable branch numbers, indicating the possibility of recovering superior recombinants through selection. The backcross generations also demonstrated intermediate performance depending on the recurrent parent, further confirming the contribution of parental genetic background to branching behaviour.

Comparison between Junagadh and Kukada revealed that plants generally produced greater height and a higher number of branches at Kukada than at Junagadh. This trend suggests that the environmental conditions prevailing at Kukada were comparatively more favourable for vegetative growth. Nevertheless, the relative ranking of the crosses remained largely similar across locations, indicating that the observed differences were predominantly governed by genetic factors rather than environmental variation.

Among the evaluated crosses, JSP 6 × BDN 711 and WRG 173 × BDN 711 were identified as promising sources for improving plant height, whereas GRG 152 × GJP 1 and WRG 173 × BDN 711 consistently exhibited superior branching ability. These crosses may therefore serve as valuable genetic resources for developing pigeonpea genotypes with improved plant architecture and enhanced yield potential.

The substantial variation observed for plant height and number of branches per plant demonstrates the availability of exploitable genetic variability within the evaluated breeding populations. Such variability provides an effective opportunity for selecting desirable segregants possessing favourable plant architecture, which is expected to contribute positively to seed yield improvement in subsequent generations.

2.3 Mean performance for number of pods per plant and number of seeds per pod

The mean performance of the six basic generations for number of pods per plant and number of seeds per pod exhibited substantial variation among the five pigeonpea crosses at both Junagadh and Kukada (Table 4). These traits are major determinants of seed yield and therefore play a crucial role in the selection of superior breeding materials. The observed variation among generations indicates the presence of adequate genetic diversity that can be effectively exploited for yield improvement.

Among the evaluated traits, number of pods per plant exhibited the widest range of variation across the five crosses. At Junagadh, the highest pod number was recorded in the BC₂ generation of JSP 6 × GJP 1 (333.67 pods plant⁻¹), followed by the F₁ generation of JSP 6 × BDN 711 (319.47 pods plant⁻¹) and the BC₁ generation of JSP 6 × GJP 1 (309.43 pods plant⁻¹). A similar trend was observed at Kukada, where the BC₁ generation of JSP 6 × GJP 1 produced the highest number of pods per plant (310.07), closely followed by the F₁ generation of JSP 6 × BDN 711 (309.40) and the BC₂ generation of GRG 152 × GJP 1 (300.43). These findings clearly indicate the superior reproductive potential of these cross combinations.

The F₁ generations of several crosses demonstrated appreciable improvement in pod number over their respective parents, suggesting favourable complementation of genes controlling reproductive development. The F₂ and backcross generations exhibited wider variation than the parental and F₁ generations, reflecting segregation and recombination of favourable alleles governing pod production. Particularly, the crosses JSP 6 × GJP 1 and GRG 152 × GJP 1 consistently produced higher pod numbers in the segregating generations, indicating their suitability for selecting superior recombinant lines. Since the number of pods per plant contributes directly to final seed yield, these crosses deserve greater emphasis in future breeding programmes.

In contrast, comparatively lower pod numbers were observed in WRG 173 × BDN 711, particularly in the F₂ generation, while GRG 152 × AGT 2 exhibited moderate pod production across generations. These differences may be attributed to the genetic constitution of the parental lines and their combining ability for reproductive traits. Similar observations regarding substantial genetic variability for pod number have been reported by Saxena (2016), Bohra *et al.* (2020), Singh *et al.* (2021) and Varshney *et al.* (2021)^[3, 11, 12, 14], who emphasized that pod number is among the most important components contributing to yield improvement in pigeonpea.

The trait number of seeds per pod showed comparatively narrower variation than pod number, indicating relatively greater genetic stability across generations. Nevertheless, significant differences among the evaluated generations were evident at both locations (Table 4). At Junagadh, the highest mean number of seeds per pod was recorded in the AGT 2 parent of GRG 152 × AGT 2 (4.25), while the F₁ generation of JSP 6 × BDN 711 (4.00) and the F₂ generation of JSP 6 × GJP 1 (4.01) also exhibited superior performance. At Kukada, the AGT 2 parent again recorded the highest value (4.43), whereas the F₁ generation of JSP 6 × BDN 711 (4.23) and the F₂ generation of the same cross (4.14) maintained relatively higher seed numbers per pod.

Table 4: Mean performance of six basic generations for number of pods per plant and number of seeds per pod in five pigeonpea crosses

Generations		P ₁		P ₂		F ₁		F ₂		BC ₁		BC ₂		S.Em ±	C.D. at 5 %
		Number of pods per plant													
GRG 152 × GJP 1 (Cross 1)	Junagadh	258.40	± 0.471	262.80	± 0.429	245.20	± 0.499	288.50	± 0.623	296.10	± 0.963	306.40	± 0.793	0.487	1.536
	Kukada	253.13	± 0.568	265.67	± 0.471	238.33	± 0.411	280.13	± 0.428	290.43	± 0.511	300.43	± 0.527	0.753	2.374
GRG 152 × AGT 2 (Cross 2)	Junagadh	259.33	± 0.455	172.27	± 0.462	182.60	± 0.452	199.03	± 0.467	281.37	± 0.414	240.27	± 0.644	0.315	0.992
	Kukada	254.73	± 0.540	170.53	± 0.548	200.87	± 0.501	203.93	± 0.425	280.50	± 0.445	241.00	± 0.530	0.468	1.476
JSP 6 × GJP 1 (Cross 3)	Junagadh	230.07	± 0.435	261.40	± 0.558	252.13	± 0.572	235.00	± 0.679	309.43	± 1.288	333.67	± 0.865	0.423	1.334
	Kukada	245.07	± 0.537	263.87	± 0.455	263.27	± 0.429	238.58	± 0.509	310.07	± 0.621	281.63	± 0.573	0.398	1.255
JSP 6 × BDN 711 (Cross 4)	Junagadh	230.80	± 0.510	67.73	± 0.353	319.47	± 0.606	280.13	± 0.544	256.63	± 0.704	200.33	± 0.703	0.468	1.475
	Kukada	244.67	± 0.497	67.53	± 0.320	309.40	± 0.629	238.47	± 0.484	293.07	± 0.925	224.73	± 0.806	0.763	2.405
WRG 173× BDN 711 (Cross 5)	Junagadh	239.00	± 0.657	67.27	± 0.316	199.93	± 0.846	160.63	± 0.335	202.60	± 0.639	180.20	± 0.677	0.438	1.379
	Kukada	237.00	± 0.535	66.27	± 0.383	208.40	± 0.403	160.63	± 0.502	209.73	± 0.595	189.53	± 0.625	0.311	0.981
		Number of seeds per pod													
GRG 152 × GJP 1 (Cross 1)	Junagadh	3.86	± 0.004	3.95	± 0.006	3.92	± 0.004	3.78	± 0.013	3.74	± 0.022	3.73	± 0.018	0.021	0.068
	Kukada	4.08	± 0.005	4.01	± 0.053	4.03	± 0.043	4.01	± 0.024	3.93	± 0.014	3.81	± 0.012	0.018	0.057
GRG 152 × AGT 2 (Cross 2)	Junagadh	3.87	± 0.034	4.25	± 0.052	4.13	± 0.016	4.08	± 0.019	4.04	± 0.025	3.98	± 0.024	0.050	0.159
	Kukada	4.07	± 0.032	4.43	± 0.040	4.15	± 0.020	3.75	± 0.015	3.96	± 0.021	3.98	± 0.030	0.059	0.186
JSP 6 × GJP 1 (Cross 3)	Junagadh	3.85	± 0.023	3.87	± 0.029	3.92	± 0.020	4.01	± 0.017	3.81	± 0.031	3.88	± 0.017	0.022	0.070
	Kukada	3.99	± 0.033	4.01	± 0.005	4.05	± 0.004	4.10	± 0.005	3.98	± 0.005	3.91	± 0.004	0.013	0.042
JSP 6 × BDN 711 (Cross 4)	Junagadh	3.84	± 0.023	3.99	± 0.017	4.00	± 0.021	4.04	± 0.016	3.98	± 0.018	4.00	± 0.021	0.022	0.068
	Kukada	3.99	± 0.026	4.09	± 0.028	4.23	± 0.018	4.14	± 0.021	4.02	± 0.027	4.12	± 0.034	0.016	0.051
WRG 173× BDN 711 (Cross 5)	Junagadh	3.84	± 0.031	3.94	± 0.028	3.95	± 0.014	3.74	± 0.014	3.83	± 0.019	3.78	± 0.021	0.025	0.077
	Kukada	3.99	± 0.028	4.07	± 0.019	3.82	± 0.013	3.55	± 0.017	3.98	± 0.026	3.76	± 0.030	0.046	0.146

Unlike pod number, the differences among generations for seeds per pod were relatively small, suggesting that this trait is more genetically conserved and less influenced by segregation. Even so, the consistent superiority of certain generations in JSP 6 × BDN 711 and GRG 152 × AGT 2 indicates the possibility of improving seed number through appropriate parental selection. Because seed yield is determined by the combined effects of pod number, seed number and seed weight, simultaneous improvement of these traits is expected to enhance overall productivity. Comparison of the two environments indicated that the ranking of superior crosses remained largely consistent, although slight differences in the magnitude of trait expression were observed. This consistency demonstrates that the evaluated breeding materials possessed stable reproductive performance under contrasting agro-climatic conditions. The comparatively higher pod production recorded at Kukada in several cross combinations may be attributed to favourable environmental conditions supporting enhanced flowering, pod setting and reproductive development.

Overall, JSP 6 × GJP 1 emerged as the most promising cross for improving number of pods per plant, whereas JSP 6 × BDN 711 and GRG 152 × AGT 2 exhibited superior performance for number of seeds per pod. The substantial variability observed for these important yield components provides considerable opportunities for identifying elite segregants capable of producing higher seed yield in subsequent generations. These findings further support the potential utilization of these cross combinations in pigeonpea breeding programmes aimed at developing high-yielding cultivars with improved reproductive efficiency.

2.4 Mean performance for pod length and 100-seed weight

Pod length and 100-seed weight are important yield-attributing traits that directly influence seed development, market preference and overall grain yield in pigeonpea. The mean performance of the six basic generations for these traits varied considerably among the five crosses at both Junagadh and Kukada (Table 5), indicating the presence of sufficient genetic variability for their improvement through selection.

Table 5: Mean performance of six basic generations for length of pod (cm) and 100-seed weight (g) in five pigeonpea crosses

Generations		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	S.Em ±	C.D. at 5 %
		Length of pod (cm)							
GRG 152 × GJP 1 (Cross 1)	Junagadh	5.45 ± 0.020	5.60 ± 0.033	5.91 ± 0.011	5.27 ± 0.018	5.99 ± 0.045	5.75 ± 0.045	0.054	0.170
	Kukada	5.62 ± 0.037	6.11 ± 0.030	6.37 ± 0.027	5.77 ± 0.021	6.40 ± 0.039	6.18 ± 0.030	0.035	0.111
GRG 152 × AGT 2 (Cross 2)	Junagadh	5.28 ± 0.092	5.12 ± 0.059	4.86 ± 0.086	5.40 ± 0.022	5.16 ± 0.034	4.99 ± 0.033	0.064	0.203
	Kukada	5.59 ± 0.031	5.44 ± 0.045	5.24 ± 0.036	5.63 ± 0.022	5.51 ± 0.039	5.38 ± 0.040	0.053	0.169
JSP 6 × GJP 1 (Cross 3)	Junagadh	5.17 ± 0.062	5.57 ± 0.076	5.80 ± 0.032	5.50 ± 0.020	4.89 ± 0.030	5.31 ± 0.035	0.037	0.116
	Kukada	5.50 ± 0.040	6.06 ± 0.046	6.08 ± 0.019	5.44 ± 0.021	5.16 ± 0.036	5.62 ± 0.043	0.044	0.139
JSP 6 × BDN 711 (Cross 4)	Junagadh	5.12 ± 0.071	5.92 ± 0.086	5.54 ± 0.031	5.56 ± 0.022	5.11 ± 0.174	5.68 ± 0.026	0.096	0.303
	Kukada	5.53 ± 0.041	6.20 ± 0.039	5.75 ± 0.039	5.68 ± 0.019	5.62 ± 0.056	6.10 ± 0.037	0.060	0.188
WRG 173 × BDN 711 (Cross 5)	Junagadh	4.89 ± 0.068	5.85 ± 0.091	5.19 ± 0.194	5.20 ± 0.026	5.43 ± 0.030	5.47 ± 0.037	0.115	0.363
	Kukada	5.14 ± 0.038	6.18 ± 0.035	5.68 ± 0.037	5.70 ± 0.021	5.82 ± 0.029	5.73 ± 0.058	0.055	0.174
		100-seed weight (g)							
GRG 152 × GJP 1 (Cross 1)	Junagadh	11.61 ± 0.072	14.66 ± 0.053	13.41 ± 0.113	12.15 ± 0.039	13.05 ± 0.098	12.44 ± 0.108	0.090	0.283
	Kukada	11.80 ± 0.018	14.66 ± 0.038	13.37 ± 0.038	12.02 ± 0.034	12.41 ± 0.074	12.39 ± 0.040	0.112	0.353
GRG 152 × AGT 2 (Cross 2)	Junagadh	11.63 ± 0.030	12.37 ± 0.064	12.52 ± 0.049	12.09 ± 0.029	11.84 ± 0.040	11.97 ± 0.041	0.070	0.220
	Kukada	11.84 ± 0.026	12.42 ± 0.027	12.77 ± 0.029	12.12 ± 0.038	11.98 ± 0.059	12.59 ± 0.036	0.065	0.206
JSP 6 × GJP 1 (Cross 3)	Junagadh	13.08 ± 0.124	14.68 ± 0.049	15.77 ± 0.042	13.46 ± 0.040	15.23 ± 0.085	14.66 ± 0.078	0.100	0.315
	Kukada	13.52 ± 0.020	14.69 ± 0.032	16.03 ± 0.050	14.58 ± 0.054	15.41 ± 0.064	13.78 ± 0.083	0.112	0.353
JSP 6 × BDN 711 (Cross 4)	Junagadh	13.11 ± 0.077	11.47 ± 0.074	11.74 ± 0.050	11.64 ± 0.040	12.07 ± 0.038	12.79 ± 0.073	0.059	0.185
	Kukada	13.55 ± 0.040	11.47 ± 0.023	11.77 ± 0.026	11.72 ± 0.037	12.26 ± 0.045	12.80 ± 0.053	0.071	0.225
WRG 173 × BDN 711 (Cross 5)	Junagadh	11.65 ± 0.087	11.52 ± 0.040	13.35 ± 0.101	12.26 ± 0.055	12.49 ± 0.090	12.23 ± 0.074	0.133	0.421
	Kukada	11.85 ± 0.039	11.48 ± 0.030	13.36 ± 0.064	11.72 ± 0.045	12.21 ± 0.068	12.08 ± 0.046	0.102	0.320

For pod length, considerable differences were observed among the evaluated generations across all five crosses. At Junagadh, the maximum pod length was recorded in the BC₁ generation of GRG 152 × GJP 1 (5.99 cm), followed by the F₁ generation of the same cross (5.91 cm), indicating superior expression of this trait in the hybrid and backcross populations. Similarly, at Kukada, the BC₁ generation of GRG 152 × GJP 1 produced the longest pods (6.40 cm), followed by the F₁ generation (6.37 cm) and BC₂ generation (6.18 cm). These observations demonstrate the consistent superiority of this cross for pod length across both environments.

The F₁ generations generally exhibited longer pods than their respective parental lines in most crosses, suggesting favourable complementation of genes controlling pod development. The segregating generations (F₂, BC₁ and BC₂) displayed appreciable variation, reflecting recombination of favourable alleles governing this trait. However, the magnitude of variation for pod length was relatively smaller than that observed for pod number, indicating comparatively higher stability of this character. Similar findings have been reported by Saxena (2016), Bohra *et al.* (2020) and Varshney *et al.* (2021)^[3, 11, 14], who observed moderate genetic variability for pod length in pigeonpea breeding populations.

Although pod length alone contributes only indirectly to seed yield, longer pods generally accommodate a greater number of well-developed seeds and therefore contribute positively to grain productivity. The consistently superior performance of GRG 152 × GJP 1 across both locations suggests that this cross possesses favourable alleles for improving pod morphology and may serve as a useful donor in breeding programmes targeting enhanced pod characteristics.

Substantial variation was also observed for 100-seed weight, one of the most important economic traits determining grain quality and market value. The parental lines exhibited marked differences in seed weight, which were reflected in

their derived generations. Across both locations, the cross GRG 152 × GJP 1 consistently maintained comparatively higher seed weight in the parental and hybrid generations, whereas GRG 152 × AGT 2 and JSP 6 × GJP 1 exhibited moderate to high values depending on the generation. The F₁ generations of several crosses expressed desirable seed weight, while the segregating populations displayed wider variability due to genetic recombination.

The F₂ and backcross generations demonstrated considerable variation in 100-seed weight, indicating the possibility of selecting transgressive segregants with desirable seed size. Such variability is particularly valuable because seed weight is a relatively stable trait with moderate to high heritability and is less influenced by environmental fluctuations than several other yield components. Improvement in seed weight not only enhances grain yield but also increases consumer preference and commercial value, especially in medium duration pigeonpea cultivars.

Comparison between Junagadh and Kukada indicated only slight environmental influences on pod length and seed weight, with the relative ranking of the superior crosses remaining largely unchanged across locations. This consistency suggests that the expression of these traits is predominantly governed by genetic factors and that the identified superior crosses possess stable performance under contrasting agro-climatic conditions.

Overall, GRG 152 × GJP 1 emerged as the most promising cross for improving pod length, while several generations of GRG 152 × GJP 1, GRG 152 × AGT 2 and JSP 6 × GJP 1 exhibited desirable performance for 100-seed weight. The considerable variability observed for these traits provides valuable opportunities for selecting superior breeding materials possessing favourable pod morphology and seed characteristics. Improvement of pod length in combination with optimum seed weight is expected to contribute positively to grain yield and enhance the development of high-performing pigeonpea cultivars.

2.5 Mean performance for seed yield per plant

Seed yield per plant is the ultimate expression of the combined effects of several yield-contributing traits and is considered the most important criterion for the selection of superior genotypes in pigeonpea breeding programmes. The

mean performance of the six basic generations for seed yield per plant revealed considerable variation among the five crosses at both Junagadh and Kukada (Table 6), indicating the presence of substantial genetic diversity that can be effectively exploited for genetic improvement.

Table 6: Mean performance of six basic generations for seed yield per plant (g) in five pigeonpea crosses

Generations		P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂	S.Em	C.D. at 5
		Seed yield per plant (g)						±	%
GRG 152 × GJP 1 (Cross 1)	Junagadh	115.74 ± 0.794	152.19 ± 0.698	128.91 ± 1.182	132.53 ± 0.658	144.51 ± 1.375	142.13 ± 1.576	1.361	4.289
	Kukada	121.84 ± 0.446	156.16 ± 2.043	128.45 ± 1.461	135.03 ± 0.886	141.61 ± 0.996	141.86 ± 0.770	1.187	3.740
GRG 152 × AGT 2 (Cross 2)	Junagadh	116.82 ± 1.041	90.46 ± 1.007	94.53 ± 0.608	98.14 ± 0.539	134.52 ± 1.093	114.31 ± 0.789	1.315	4.142
	Kukada	122.93 ± 1.137	93.75 ± 0.826	106.51 ± 0.784	92.70 ± 0.562	132.96 ± 1.045	120.73 ± 1.091	1.731	5.455
JSP 6 × GJP 1 (Cross 3)	Junagadh	115.84 ± 1.165	148.49 ± 1.060	155.84 ± 0.983	126.87 ± 0.780	179.59 ± 2.112	189.86 ± 1.495	1.651	5.201
	Kukada	132.17 ± 1.012	155.28 ± 0.543	170.96 ± 0.755	142.64 ± 0.633	190.03 ± 0.889	151.77 ± 0.970	1.300	4.097
JSP 6 × BDN 711 (Cross 4)	Junagadh	116.17 ± 0.808	31.01 ± 0.324	149.93 ± 0.962	131.74 ± 0.587	123.34 ± 0.965	102.60 ± 1.047	0.860	2.709
	Kukada	132.26 ± 0.818	31.69 ± 0.212	154.05 ± 0.959	115.69 ± 0.709	144.46 ± 1.146	118.44 ± 1.006	0.933	2.940
WRG 173 × BDN 711 (Cross 5)	Junagadh	106.89 ± 1.370	30.54 ± 0.231	105.42 ± 1.146	73.75 ± 0.475	96.81 ± 0.765	83.39 ± 0.860	1.228	3.869
	Kukada	112.19 ± 0.701	30.59 ± 0.235	106.38 ± 0.643	66.81 ± 0.491	101.85 ± 0.843	86.14 ± 0.768	1.281	4.035

Marked differences in seed yield were observed among the parental lines, F₁ hybrids, F₂ populations and backcross generations, reflecting the diverse genetic constitution of the selected parental genotypes. In general, the F₁ generations of several crosses exhibited superior seed yield compared with their respective parents, suggesting favourable interactions among the parental genomes. The segregating generations (F₂, BC₁ and BC₂) displayed wider variability in seed yield, indicating extensive genetic recombination and the possibility of recovering high-yielding transgressive segregants through selection.

Among the evaluated cross combinations, JSP 6 × BDN 711 emerged as one of the most promising crosses for seed yield improvement. The F₁ generation consistently exhibited outstanding performance across both environments, demonstrating the favourable combining ability of the two parental lines for yield and associated traits. Likewise, JSP 6 × GJP 1 and GRG 152 × GJP 1 also produced superior-performing generations with desirable seed yield, largely attributable to their higher number of pods per plant, improved plant architecture and favourable reproductive characteristics. These findings suggest that the superior performance of these crosses resulted from the cumulative contribution of several yield components rather than from any single trait.

The F₂ populations exhibited comparatively greater variability than the parental and F₁ generations, which is expected because segregation generates a wide range of recombinant genotypes. Such variability provides an excellent opportunity for identifying elite segregants possessing favourable combinations of yield-contributing traits. Similarly, the BC₁ and BC₂ generations demonstrated intermediate to high seed yield depending on the recurrent parent involved, indicating that both parental backgrounds contributed useful alleles for yield improvement.

Comparison between the two experimental locations revealed slight differences in the magnitude of seed yield; however, the relative ranking of the superior crosses remained largely unchanged. This consistency indicates that the high-yielding cross combinations expressed stable performance under contrasting agro-climatic conditions and

that the observed differences were primarily governed by genetic factors. The stable expression of seed yield across locations enhances the breeding value of these crosses and supports their utilization in future selection programmes.

Seed yield is a complex quantitative trait governed by the collective influence of phenological, morphological and reproductive characters. In the present investigation, crosses exhibiting superior seed yield generally possessed favourable values for important yield components such as number of pods per plant, plant height, branching ability and seed size. This observation confirms that simultaneous improvement of multiple component traits is essential for achieving sustained genetic gain in pigeonpea. Similar relationships between seed yield and its component traits have been reported by Saxena (2016), Bohra *et al.* (2020), Saxena *et al.* (2021) and Varshney *et al.* (2021) [3, 11, 12, 14], who emphasized that effective selection should focus on the overall performance of yield-related characters rather than on individual traits alone.

Overall, the substantial variation observed for seed yield per plant among the six basic generations demonstrated the availability of considerable exploitable genetic variability within the evaluated breeding populations. The superior performance of JSP 6 × BDN 711, JSP 6 × GJP 1 and GRG 152 × GJP 1 suggests that these crosses possess high breeding potential and may serve as valuable genetic resources for developing improved medium duration pigeonpea cultivars. The promising segregating populations identified in the present study provide an excellent foundation for further selection and advancement in pigeonpea breeding programmes aimed at enhancing productivity and yield stability across diverse environments.

3. Identification of superior crosses and breeding implications

The comparative evaluation of five medium duration pigeonpea crosses across six basic generations and two contrasting environments revealed considerable differences in their performance for phenological, morphological and yield-related traits. The observed variation among generations demonstrated the effectiveness of selecting

genetically diverse parents for hybridization and confirmed the availability of substantial exploitable variability for crop improvement. Evaluation across both Junagadh and Kukada

Further strengthened the reliability of the results by identifying cross combinations that expressed stable performance under different agro-climatic conditions.

Table 7: Summary of superior cross combinations for important agronomic traits

Trait	Best cross	Superior generation	Breeding implication
Days to flowering	GRG 152 × AGT 2	F ₂	Early flowering
Days to maturity	GRG 152 × AGT 2	F ₂	Early maturity
Plant height (cm)	JSP 6 × BDN 711	F ₁	Vigorous growth
Branches per plant	WRG 173 × BDN 711	F ₁	Improved plant architecture
Pods per plant	JSP 6 × GJP 1	BC ₂	Higher reproductive efficiency
Seeds per pod	GRG 152 × AGT 2	Parent/ F ₁	Improved seed setting
Pod length (cm)	GRG 152 × GJP 1	BC ₁	Better pod morphology
100-seed weight (g)	GRG 152 × GJP 1	F ₁	Bold seed size
Seed yield per plant (g)	JSP 6 × BDN 711	F ₁	High-yielding cross

Among the evaluated crosses, GRG 152 × AGT 2 proved to be the most promising source for improving earliness. This cross consistently recorded the lowest values for days to flowering and days to maturity, particularly in the F₂ generation at both locations, indicating its suitability for developing early-maturing cultivars. Earliness is an important breeding objective in pigeonpea because it enables crop escape from terminal drought, facilitates multiple cropping systems and ensures timely harvesting under rainfed conditions. Therefore, this cross may serve as an excellent donor for breeding programmes targeting short- and medium duration pigeonpea cultivars.

The crosses JSP 6 × BDN 711 and WRG 173 × BDN 711 exhibited superior vegetative growth, particularly for plant height, whereas GRG 152 × GJP 1 and WRG 173 × BDN 711 consistently expressed desirable branching ability. Since plant architecture strongly influences canopy development, photosynthetic efficiency and reproductive potential, these crosses may provide valuable genetic resources for improving plant type in future breeding programmes. The expression of favourable plant height together with higher branching ability suggests the accumulation of complementary alleles governing vegetative growth.

Among all the evaluated yield components, number of pods per plant exhibited the greatest variability and emerged as the principal contributor to superior seed yield. The cross JSP 6 × GJP 1 consistently produced the highest pod numbers in the BC₁ and BC₂ generations across both environments, indicating its exceptional reproductive potential. Similarly, JSP 6 × BDN 711 also demonstrated remarkable pod production, particularly in the F₁ generation. The consistent superiority of these crosses indicates that they possess favourable gene combinations controlling pod development and reproductive efficiency.

For pod morphology and grain characteristics, GRG 152 × GJP 1 expressed comparatively superior performance for pod length, while several generations of GRG 152 × GJP 1, GRG 152 × AGT 2 and JSP 6 × GJP 1 maintained desirable 100-seed weight. Improvement in these traits is particularly important because seed size directly influences grain quality, market preference and commercial acceptance of pigeonpea cultivars. The stable expression of these traits across both locations further enhances their breeding value. Seed yield per plant, being the ultimate expression of the combined influence of all yield-contributing traits, clearly differentiated the breeding potential of the evaluated crosses. The cross JSP 6 × BDN 711 emerged as one of the

most promising combinations owing to its superior performance for seed yield and several associated characters. Likewise, JSP 6 × GJP 1 and GRG 152 × GJP 1 consistently exhibited favourable performance across multiple yield components, demonstrating balanced expression of both vegetative and reproductive traits. These crosses therefore represent valuable breeding materials for developing high-yielding medium duration pigeonpea cultivars.

An important outcome of the present investigation was the consistent performance of the superior crosses across both Junagadh and Kukada. Although minor environmental effects on trait expression were observed, the relative ranking of the cross combinations remained largely unchanged. This stability indicates that the observed superiority was primarily governed by genetic factors rather than environmental fluctuations and enhances confidence in the utilization of these crosses for future breeding programmes.

The wider variation observed in the F₂ and backcross generations compared with the parental and F₁ generations indicates the occurrence of extensive genetic recombination and segregation. Such populations constitute valuable breeding material because they provide opportunities for selecting transgressive segregants possessing favourable combinations of earliness, plant architecture, reproductive efficiency and seed yield. Consequently, these generations should receive greater emphasis during pedigree selection and subsequent advancement.

Based on the overall performance across all evaluated traits, GRG 152 × AGT 2 may be recommended as a valuable source for earliness, JSP 6 × GJP 1 for enhanced pod production and reproductive efficiency, JSP 6 × BDN 711 for high seed yield potential and GRG 152 × GJP 1 for favourable pod characteristics and balanced agronomic performance. These crosses provide a strong genetic foundation for developing improved medium duration pigeonpea cultivars with enhanced productivity and adaptation under diverse agro-climatic conditions.

The present findings clearly demonstrate that the evaluation of six basic generations under contrasting environments is an effective approach for identifying superior parental combinations and promising breeding populations. The cross combinations identified in this study may be effectively utilized in future pigeonpea improvement programmes aimed at enhancing yield potential, adaptability and overall breeding efficiency.

4. Overall discussion

The present investigation demonstrated the existence of substantial genetic variability among five medium duration pigeonpea crosses and their six basic generations for all nine agronomic traits evaluated across two contrasting environments. The significant differences observed among the crosses and generations through analysis of variance confirmed that the selected parental lines possessed sufficient genetic diversity to generate broad phenotypic variation, thereby providing considerable opportunities for effective selection and crop improvement. The consistency of significant variation at both Junagadh and Kukada further suggested that the observed differences were predominantly governed by genetic factors, although environmental conditions moderately influenced the magnitude of trait expression.

The mean performance of the evaluated generations clearly illustrated that different parental combinations contributed distinct genetic advantages for different groups of traits. The cross GRG 152 $\times$ AGT 2 consistently exhibited superior performance for earliness, indicating its suitability for developing short- and medium duration pigeonpea cultivars adapted to rainfed and multiple cropping systems. In contrast, JSP 6 $\times$ GJP 1 excelled for reproductive traits, particularly number of pods per plant, whereas JSP 6 $\times$ BDN 711 exhibited superior seed yield performance. Likewise, GRG 152 $\times$ GJP 1 demonstrated favourable pod characteristics and balanced performance across several agronomic traits. These observations indicate that no single cross was superior for all characters; rather, each cross possessed unique breeding value that could be effectively exploited depending on the breeding objective.

The superior performance of several F_1 generations for plant height, branching ability, pod production and seed yield suggests favourable interactions among parental genomes, resulting in improved expression of economically important traits. On the other hand, the wider variation observed in the F_2 and backcross generations reflects segregation and recombination of favourable alleles, creating opportunities for identifying transgressive segregants with desirable combinations of agronomic characters. The present findings are further supported by our earlier investigation using the same set of five crosses, which revealed moderate to high narrow-sense heritability for several yield-related traits, particularly number of branches per plant, number of seeds per pod and seed yield in specific cross combinations (Khaniya *et al.*, 2022) [7]. The combined evidence indicates that these populations possess both substantial phenotypic variability and exploitable additive genetic variation, thereby enhancing their usefulness for effective selection in pigeonpea improvement programmes. Such populations constitute valuable breeding materials because they allow simultaneous improvement of multiple quantitative traits through systematic selection. Similar observations have been reported by Saxena (2016), Bohra *et al.* (2020) and Varshney *et al.* (2021) [3, 11, 14], who emphasized the importance of exploiting segregating populations for genetic improvement in pigeonpea.

Among the yield-contributing traits, number of pods per plant exhibited the widest range of variation across the evaluated generations and appeared to be one of the major determinants of seed yield. Crosses expressing higher pod production generally recorded superior seed yield, indicating the strong contribution of reproductive efficiency

to final productivity. Plant height, branching ability, pod length and seed weight also contributed positively to overall yield performance, although their relative importance varied among the cross combinations. These findings highlight the complex quantitative nature of seed yield and demonstrate that improvement of yield requires simultaneous selection for multiple component traits rather than reliance on a single character.

Evaluation of the breeding materials under two contrasting agro-climatic environments enhanced the reliability of the present investigation by allowing assessment of the stability of trait expression. Although slight differences in the magnitude of individual traits were observed between Junagadh and Kukada, the relative ranking of the superior crosses remained largely consistent across locations. Such consistency suggests that the identified cross combinations possess broad adaptability and may perform reliably under diverse environmental conditions. Multi-location evaluation is therefore an important component of pigeonpea breeding programmes because it facilitates the identification of stable breeding materials suitable for wider cultivation.

The present investigation provides valuable information for future pigeonpea improvement programmes. Based on overall performance, GRG 152 $\times$ AGT 2 may be utilized for improving earliness, JSP 6 $\times$ GJP 1 for enhancing reproductive efficiency, JSP 6 $\times$ BDN 711 for increasing seed yield potential and GRG 152 $\times$ GJP 1 for improving pod characteristics and overall agronomic performance. The substantial variability observed in the F_2 and backcross populations further indicates that these generations should be emphasized during pedigree selection for recovering elite recombinant lines combining desirable maturity, favourable plant architecture and high yield.

Overall, the results confirm that the evaluation of six basic generations across contrasting environments is an effective strategy for identifying superior parental combinations and promising breeding populations in pigeonpea. The crosses identified in the present study constitute valuable genetic resources for the development of high-yielding, medium duration cultivars with improved adaptation and productivity. Furthermore, the variability documented in this investigation provides a strong foundation for subsequent studies on gene action, generation mean analysis and breeding strategies aimed at accelerating genetic improvement in pigeonpea.

Conclusion

The present investigation demonstrated the existence of substantial genetic variability among five medium duration pigeonpea crosses and their six basic generations for all nine agronomic traits evaluated under two contrasting agro-climatic environments. The highly significant differences observed through analysis of variance confirmed the effectiveness of the selected parental combinations in generating broad genetic variation for seed yield and its associated traits. The consistency of trait expression across Junagadh and Kukada further indicated the stability and reliability of the evaluated breeding materials.

Evaluation of generation mean performance revealed distinct genetic potential among the five crosses for different breeding objectives. GRG 152 $\times$ AGT 2 emerged as the most promising cross for improving earliness through reduced days to flowering and maturity, whereas JSP 6 $\times$ GJP 1 exhibited superior reproductive efficiency with a

higher number of pods per plant. JSP 6 × BDN 711 consistently demonstrated superior seed yield performance, while GRG 152 × GJP 1 showed desirable pod characteristics and balanced agronomic performance across environments. The wider variation observed in the F₂ and backcross generations indicates the presence of favourable recombination and provides excellent opportunities for identifying superior transgressive segregants through selection.

The results further demonstrated that seed yield improvement in pigeonpea depends on the simultaneous enhancement of several yield-contributing traits rather than on any single character. Superior seed yield was generally associated with favourable plant architecture, increased branching, higher pod number, desirable pod characteristics and optimum seed weight, highlighting the importance of integrated selection for multiple traits during varietal improvement.

Overall, the present study identified several promising cross combinations with high breeding potential for the development of improved medium duration pigeonpea cultivars. In particular, GRG 152 × AGT 2, JSP 6 × GJP 1, JSP 6 × BDN 711 and GRG 152 × GJP 1 constitute valuable genetic resources for future breeding programmes. The information generated in this investigation provides a strong foundation for the effective selection of superior breeding materials and will also facilitate subsequent studies on gene action and breeding strategies aimed at accelerating genetic improvement and enhancing productivity in pigeonpea. These findings complement earlier estimates of narrow-sense heritability and genetic advance obtained from the same breeding populations (Khaniya *et al.*, 2022) ^[7], thereby providing a comprehensive understanding of the genetic architecture of yield and its component traits in medium duration pigeonpea.

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