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Heritability and Genetic Advance Analysis for Seed Yield and its Contributing Traits in Cowpea [*Vigna unguiculata* (L.) Walp]

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ABSTRACT: The present investigation was carried out during July 2020 to October 2021 at the Research Farm of Rajasthan Agricultural Research Institute, Durgapura to estimate heritability and genetic advance for seed yield and its contributing traits in Cowpea for four crosses. The experiment material consists of six generations *i.e.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses (Sel 152 Gujarat × CPD10, RC101 × TEML-84-1, CPD13 × GC3, IC8966 × CAZC10) involving eight diversified cultivars of cowpea. The evaluation trial was conducted during Kharif 2021 to evaluate all the six generations of each single cross in a randomized block design with three replications to observe 14 yield characteristics. The seed yield per plant showed exceptionally high broad-sense heritability in all crosses, particularly in IC8966 × CAZC-10 (91.63%).The high genetic advance observed (77.26% for IC8966 × CAZC-10) further emphasizes that this trait is largely governed by additive genetic factors, and selection for seed yield in this cross would likely be highly effective.

Keywords: Cowpea, heritability and genetic advance.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp] is a nutritionally rich, drought-tolerant legume cultivated widely in tropical and subtropical regions of the world, especially in Asia and Africa. In India, it serves as a vital component of farming systems due to its multipurpose uses-ranging from food grain, fodder, and green manure to soil fertility enhancement through biological nitrogen fixation. Cowpea grains are a valuable source of protein (23–25%), carbohydrates, vitamins, and essential amino acids, making it a key food security crop, particularly for resource-poor farmers (Singh *et al*., 2021). Despite its potential, the productivity of cowpea in many regions remains sub-optimal due to limitations in genetic improvement and low adoption of improved varieties. Enhancing seed yield and its contributing traits through breeding requires a thorough understanding of the underlying genetic architecture of these traits. Parameters such as heritability and genetic advance are essential tools for assessing the efficiency of selection in crop improvement programs. Heritability estimates the proportion of phenotypic variance attributable to genetic variance, whereas genetic advance indicates the expected improvement under selection pressure (Burton & DeVane 1953; Johnson *et al*., 1955).

The presence of significant variability in cowpea germplasm for traits such as days to flowering, plant height, number of pods per plant, seed size and seed yield per plant provides ample scope for genetic improvement. Estimating heritability along with genetic advance is crucial to determine the selection efficiency of these traits. High heritability coupled with high genetic advance indicates additive gene action and justifies selection-based breeding. On the other hand, low heritability and low genetic advance may suggest the predominance of non-additive gene effects or strong environmental influence (Falconer & Mackay 1996). Given the significance of cowpea in rainfed agriculture and marginal lands, it is imperative to identify and promote genotypes with high genetic potential for yield and other agronomic traits. This study aims to estimate the heritability and genetic advance of seed yield and its contributing traits across diverse cowpea crosses, thereby aiding breeders in devising efficient selection strategies for yield enhancement under varying environmental conditions.

MATERIAL AND METHOD

The experiment material consists of six generations *i.e.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 of four crosses (Sel 152 Gujarat × CPD10, RC101 × TEML-84-1, CPD13 × GC3, IC8966 × CAZC10) involving eight diversified cultivars of cowpea. The parental seed material for this research was collected from Division of Plant Breeding and Genetics, RARI, Durgapura. All the 4 F_1 crosses were raised during summer 2021 and allowed to self-pollination to produce F_2 population. Simultaneously, F_1's were backcrossed with their respective parents (P_1 and P_2) to get backcross generations (BC_1 and BC_2). The evaluation trial was conducted during Kharif 2021 to evaluate all the six generations of each single cross in a randomized block design with three replications. The following 14 significant yield characteristics were observed: Days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, 100-seed weight (g), seed yield per plant (g), biological yield per plant (g), harvest index (%) and protein content (%). The analysis of variance was performed using the treatment data to determine the genotypic variability. The broad and narrow sense heritability in percent was calculated by using formula suggested by Burton and Devane (1953) and estimation of expected genetic advance suggested by Johnson *et al*. (1955).

RESULT AND DISCUSSION

In crop improvement, the genetic component of variation is the cornerstone of effective breeding, as it is the only component that can be passed on to subsequent generations. The estimates of heritability were categorised as high (>50%), moderate (20 to 50%) and low (<20%) as per the standard given by Stansfield (1969). The values of expected genetic advance as percentage of mean for various characters is demarcated into three categories *viz*., low (<10%), moderate (10 to 20%) and high (>20%) as per the method given by Johnson *et al*. (1955).

The heritability estimates for days to 50% flowering were moderate to high in most crosses, with the highest broad-sense and narrow-sense heritability observed in the cross IC8966 × CAZC-10 (73.84% and 72.65% respectively) (Table 1). This finding aligns with the results of Pathak *et al.* (2017), who reported strong genetic control over flowering time in their crosses. However, the cross CPD13 × GC3 showed slightly lower narrow-sense heritability in this study suggests that non-additive genetic effects may play a role in the expression of this trait, which concurs with the observations of Khanpara *et al.* (2016), who also found that both additive and non-additive gene effects influenced flowering time in their study. For days to maturity, high heritability estimates were observed for both broad and narrow-sense heritability, especially in CPD13 × GC3 (85.20% broad sense and 79.09% narrow sense) and RC101 × TEML-84-1 (83.04% broad sense and 67.16% narrow sense) (Table 1). These findings are in agreement with those of Sabale *et al.* (2018), who reported high heritability for maturity traits in their crop improvement studies. However, despite the high heritability, the observed moderate genetic advance across all crosses suggests that the trait may not respond as effectively to selection, a result also noted by Santos *et al.* (2024), who attributed limited response to selection for maturity due to the influence of environmental factors.

In the case of plant height, high broad-sense heritability was observed in all crosses, particularly in Sel 152 Gujarat × CPD-10 (88.59%) and CPD13 × GC3 (88.34%). These results are consistent with findings by Swathi *et al*. (2024), who observed high heritability for plant height in their experiments. The high genetic advance (above 50%) in several crosses, particularly in IC8966 × CAZC-10 (63.70%) and Sel 152 Gujarat × CPD-10 (63.01%) (Table 1), indicates that plant height is primarily controlled by additive genetic factors, making it amenable to selection, as suggested by Vinay *et al*. (2022). These findings highlight the potential for significant genetic improvement in plant height through effective selection. For the number of primary branches per plant, moderate to high broad-sense heritability was observed, with the highest genetic advance recorded in CPD13 × GC3 (63.72%). This supports the conclusions of Khanpara *et al.* (2016), who identified high heritability for branch number in their work and suggested that this trait can be improved through selection. The strong genetic advance in certain crosses further corroborates the findings of Verma *et al.* (2019), who also observed that traits with high heritability and genetic advance can be effectively selected for in breeding programs. The number of clusters per plant showed moderate to high heritability, with the highest broad-sense heritability in Sel 152 Gujarat × CPD-10 (62.41%). This is consistent with the findings of Pathak *et al*. (2017), who reported moderate to high heritability for the number of clusters in their studies. The high genetic advance (65.42%) observed in this study indicates that the number of clusters is primarily influenced by additive genetic effects, supporting the conclusions of Swathi *et al*. (2024), who highlighted the potential for genetic improvement in this trait through selection.

The broad-sense heritability for number of pods per cluster was generally low to moderate, ranging from 19.45% (RC 101 × TEML-84-1) to 59.25% (IC8966 × CAZC-10). However, most of crosses showed high narrow-sense heritability, such as Sel 152 Gujarat × CPD 10 (89.57%), RC 101 × TEML-84-1 (78.12%), and CPD13 × GC 3 (75.06%). Crosses such as RC 101 × TEML-84-1 (111.02%), Sel 152 Gujarat × CPD 10 (95.51%), and CPD 13 × GC 3 (73.35%) demonstrated high genetic advance, implying that direct selection would be highly effective for improving the number of pods per cluster in these combinations.

Table 1: Estimates of heritability and genetic advance for days to 50 % flowering, days to maturity, plant height, number of primary branches per plant, number of cluster per plant, number of pods per cluster and number of pods per plant in four cowpea crosses.

Crosses	Heritability (Broad sense) (%)	Heritability (Narrow sense) (%)	Genetic advance	Genetic advance (% of mean)
Days to 50 % flowering				
Sel 152 Gujarat × CPD-10	49.16	38.47	1.59	4.37
RC-101 × TEML-84-1	68.68	42.21	2.47	6.18
CPD-13 × GC-3	69.93	31.09	1.97	4.28
IC8966 × CAZC-10	73.84	72.65	5.01	12.97
Day to maturity				
Sel 152 Gujarat × CPD-10	79.03	65.28	4.87	7.76
RC-101 × TEML-84-1	83.04	67.16	6.79	9.92
CPD-13 × GC-3	85.20	79.09	10.60	14.12
IC8966 × CAZC-10	67.19	34.52	3.19	5.06
Plant height				
Sel 152 Gujarat × CPD-10	88.59	57.69	23.08	63.01
RC-101 × TEML-84-1	76.31	42.38	17.31	28.25
CPD-13 × GC-3	88.34	47.00	14.13	47.10
IC8966 × CAZC-10	58.39	63.48	23.30	63.70
Number of primary branches per plant				
Sel 152 Gujarat × CPD-10	42.66	39.84	2.02	56.27
RC-101 × TEML-84-1	27.75	2.45	0.11	2.97
CPD-13 × GC-3	56.58	43.19	2.65	63.72
IC8966 × CAZC-10	59.95	30.81	1.68	45.57
Number of cluster per plant				
Sel 152 Gujarat × CPD-10	62.41	47.44	4.51	45.09
RC-101 × TEML-84-1	58.30	54.91	6.67	65.42
CPD-13 × GC-3	60.03	17.53	1.51	15.45
IC8966 × CAZC-10	43.64	25.03	1.88	21.53
Number of pods per cluster				
Sel 152 Gujarat × CPD-10	35.94	89.57	2.13	95.51
RC-101 × TEML-84-1	19.45	78.12	3.05	111.02
CPD-13 × GC-3	50.18	75.06	2.02	73.35
IC8966 × CAZC-10	59.25	8.27	0.28	9.11
Number of pods per plant				
Sel 152 Gujarat × CPD-10	67.16	45.62	9.64	43.98
RC-101 × TEML-84-1	57.22	75.42	19.08	71.25
CPD-13 × GC-3	54.23	35.79	8.47	31.83
IC8966 × CAZC-10	24.07	7.64	1.40	5.50

Both pod number per plant and pod length exhibited moderate to high heritability, with corresponding high genetic advance in most crosses (Table 1 & 2). IC8966 × CAZC-10 (44.65%) showed high genetic advance for pod length, which is consistent with findings by Verma *et al.* (2019) who reported a significant genetic component influencing pod length in their study. High heritability for both traits across most crosses suggests that selection would be effective, particularly for pod number per plant, where additive gene action predominates (Khanpara *et al*., 2016). The 100-seed weight showed exceptionally high broad-sense heritability in all crosses, particularly in CPD 13 × GC 3 (89.80%) (Table 2). The high genetic advance observed for Sel 152 Gujarat × CPD 10 (44.83%) and IC8966 × CAZC-10 (40.32%) implying that direct selection would be highly effective for improving this trait.

The seed yield per plant showed exceptionally high broad-sense heritability in all crosses, particularly in IC8966 × CAZC-10 (91.63%) (Table 2), aligning with the results of Vinay *et al.* (2022), who also found high heritability for seed yield in their crosses. The high genetic advance observed (77.26% for IC8966 × CAZC-10) further emphasizes that this trait is largely governed by additive genetic factors, and selection for seed yield in this cross would likely be highly effective, similar to findings by Santos *et al.* (2024). The harvest index demonstrated high broad-sense heritability, with significant genetic advance in crosses such as Sel 152 Gujarat × CPD-10 (64.25%) and RC101 × TEML-84-1 (68.89%), confirming the results of Sabale *et al.* (2018), who observed high heritability for harvest index in their research. The genetic advance and heritability values indicate that selection for this trait can be successful, particularly in crosses with strong additive genetic effects. For seed protein content, high broad-sense heritability was observed, with IC8966 × CAZC-10 showing the highest values (89.57%) (Table 2). Narrow-sense heritability was lower, indicating a greater role for non-additive gene effects, which aligns with the findings of Verma *et al.* (2019), who also reported lower narrow-sense heritability for protein content. This suggests that while selection may still be possible, the effectiveness of selection for protein content may be more limited due to the significant influence of non-additive genetic effects. The findings of this study corroborate and extend the results of previous studies by Khanpara *et al.* (2016); Pathak *et al*. (2017); Sabale *et al.* (2018); Verma *et al.* (2019); Vinay *et al*. (2022); Santos *et al.* (2024); Swathi *et al.* (2024). The results of this study indicate that traits such as plant height, seed yield, and harvest index are under strong genetic control and could be effectively improved through selection, particularly where additive genetic effects predominate. Traits like days to maturity and seed protein content, while heritable, may require more strategic selection strategies, as non-additive gene effects play a significant role in their expression. These findings provide valuable insights for crop improvement programs aiming to enhance productivity and nutritional quality.

Table 2: Estimates of heritability and genetic advance for pod length, number of seeds per pod, 100-seed weight, seed yield per plant, biological yield per plant, harvest index and seed protein content in four cowpea crosses.

Crosses	Heritability (Broad sense) (%)	Heritability (Narrow sense) (%)	Genetic advance	Genetic advance (% of mean)
Pod length				
Sel 152 Gujarat × CPD-10	72.89	60.48	4.45	35.69
RC-101 × TEML-84-1	61.13	42.26	2.46	21.03
CPD-13 × GC-3	78.15	52.46	3.89	30.56
IC8966 × CAZC-10	71.16	74.32	5.61	44.65
Number of seeds per pod				
Sel 152 Gujarat × CPD-10	61.90	15.40	1.40	11.63
RC-101 × TEML-84-1	46.11	21.47	1.89	16.76
CPD-13 × GC-3	52.69	35.21	2.91	25.93
IC8966 × CAZC-10	58.74	33.88	3.06	25.75
100-seed weight				
Sel 152 Gujarat × CPD-10	81.64	69.52	5.27	44.83
RC-101 × TEML-84-1	80.96	62.39	4.14	33.88
CPD-13 × GC-3	89.80	48.96	4.24	35.89
IC8966 × CAZC-10	58.36	54.36	5.38	40.32
Seed yield per plant				
Sel 152 Gujarat × CPD-10	80.68	55.27	9.32	35.13
RC-101 × TEML-84-1	35.61	24.16	4.80	16.02
CPD-13 × GC-3	78.01	38.57	7.37	23.85
IC8966 × CAZC-10	91.63	74.18	16.42	77.26
Biological yield per plant				
Sel 152 Gujarat × CPD-10	94.47	78.20	44.79	87.28
RC-101 × TEML-84-1	82.94	46.11	26.67	30.28
CPD-13 × GC-3	89.69	39.69	25.06	29.27
IC8966 × CAZC-10	90.62	64.74	39.24	54.33
Harvest index				
Sel 152 Gujarat × CPD-10	87.87	68.22	33.52	64.25
RC-101 × TEML-84-1	73.53	42.01	24.52	68.89
CPD-13 × GC-3	85.54	62.15	20.36	55.68
IC8966 × CAZC-10	90.67	78.68	27.69	53.06
Seed protein content				
Sel 152 Gujarat × CPD-10	82.56	42.82	2.19	9.47
RC-101 × TEML-84-1	61.38	53.00	3.41	15.06
CPD-13 × GC-3	83.12	79.73	3.76	15.42
IC8966 × CAZC-10	89.57	84.13	5.15	21.47

CONCLUSIONS

The high estimates of broad-sense heritability observed for key traits like seed yield per plant, plant height, and harvest index across several crosses suggest that these traits are predominantly governed by genetic factors and are less influenced by the environment. Notably, traits with high heritability coupled with high genetic advance—such as seed yield in IC8966 × CAZC-10 and plant height in Sel 152 Gujarat × CPD-10 indicate the predominance of additive gene action, making them ideal candidates for improvement through direct selection.

FUTURE SCOPE

The promising hybrids/genotypes identified in this study can be used in future breeding programs and direct selection based on characters studied would be effective in further improvement for developing high yielding varieties of cowpea.

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Conflict of Interest. None.

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