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INHERITANCE STUDIES OF PLANT BRANCHING PATTERNS IN DIFFERENT CROSSES OF PIGEON PEA (*CAJANUS CAJAN* L.)

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ABSTRACT

In the pigeon pea (*Cajanus cajan*), the inheritance patterns of plant branching types were examined. The results showed that three branching classes erect, semi-spreading, and spreading affected yield. Semi-spreading patterns were seen in both the parental and F₁ generations. GRG-152 x C.G. Arhar 1 segregated into 26 erect, 96 semi-spreading, and 42 spreading plants (9:3:4 ratio) in the F₂ generation, indicating supplementary gene action. Rajeevlochan x C.G. Arhar 1 showed 136 erect, 275 semi-spreading and 26 spreading plants (9:6:1 ratio), suggesting polymeric gene action. Crosses GRG-152 x Rajeevlochan and its reciprocal i.e, Rajeevlochan x GRG-152 resulted in 12, 7 erect, 275, 214 semi-spreading and 50, 52 spreading plants (12:3:1 ratio), demonstrating masking gene action. Chi-square tests for the crosses (GRG-152 x C.G. Arhar 1, Rajeevlochan x C.G. Arhar 1, GRG-152 x Rajeevlochan, and Rajeevlochan x GRG-152) yielded values of 0.6103, 8.27, 8.6103 and 6.36 respectively, all below the critical value range of 0.025% to 0.005%, indicating the validity of the observed ratios. These discoveries about genetic pathways offer implications for breeding and yield optimization in pigeon pea.

Keywords: inheritance, supplementary ratio, pigeon pea, chi-square testing, Yates correction.

Introduction

Pigeon pea (*Cajanus cajan*) is a vital pulse crop, especially in India, contributing 40% of the nation's pulse production and 90% globally. It is mainly eaten in the form of a split pulse as 'dal'. Pigeon pea is also known as red gram, tuar and arhar. It grows well in semiarid climates and enriches soil by fixing nitrogen. It is grown on 5.2 million hectares worldwide, with 77% of the area in India. A yield of 3.34 quintals per hectare is achieved by growing pigeon pea on 4.04 million hectares in India. The three most important states are Gujarat (243.77 thousand hectares, 283.5 thousand tonnes), Uttar Pradesh (350 thousand hectares, 363.65 thousand tonnes), and Maharashtra (1175.8 thousand hectares, 925.55 thousand tonnes). Source: 2nd Advance estimates by the DA & FW, MoAFW, GOI, and the Project Coordinator Report 2023-24. Pigeon pea seeds are abundant in minerals, vital amino acids, and proteins (18–28%). Pigeon pea is an important crop, although it has difficulties such as inconsistent yields and limited research. Genetic

diversity, safeguarded in gene banks, is essential for breeding and adaptation, enhancing resilience and productivity (Rao and Rao, 2020; Govindaraj *et al.*, 2015). According to Saxena *et al.* (2017), meeting agricultural difficulties and improving varieties require an understanding of gene function and inheritance patterns.

Materials and Methods

The experiment comprising six generations (P₁, P₂, F₁, F₂, F₃, BC₁, and BC₂) of four crosses were laid out in a Random Block Design (RBD) with three replications at the experimental plots during Kharif 2021-22 at (21°16'N latitude and 81°36'N longitude and 298.56 m above MSL) Research Farms, College of Agriculture, IGKV, Raipur, Chhattisgarh, India. Seven generations within a block were randomly allotted to each plot. Each plot has seven generations randomly assigned to it inside a block. Two replications of the F₂ generations of each cross plus a single replication of the parents, F₁s, and backcrosses made up each plot.

Every row measured four metres in length, with a 20 cm x 60 cm inter- and intra-row spacing.

Three promising Pigeon Pea varieties GRG-152, Rajeevlochan, and Chhattisgarh Arhar-1—were crossed to obtain the F₁ crosses during *Kharif* 2020-21 (GRG-152 x CG-Arhar-I, GRG-152 x Rajeevlochan, Rajeevlochan x CG-Arhar-I). Parents were sown, additional F₁ crosses using the same parental material and backcrosses (BC₁ and BC₂) were carried out in the second year (2021–2022). In the third year, sowing included parents, F₁'s, F₂'s, F₃'s, BC₁, and BC₂'s.

Observations for non-metric trait like plant branching pattern was recorded in all generations of the four crosses. During *Kharif* 2021-22, morphological scoring for the trait plant branching pattern was done for all the generations/ population under study. To confirm the findings, more analysis of the scored data was done using the Goodness of Fit test.

Statistical analysis for agro-morphological traits Test for Goodness of fit:

Based on qualitative data, the chi-square test (χ^2) is used to assess whether observed values of a certain phenomenon differ significantly from expected values.

This test measures the discrepancy between observed and expected values and is a valuable tool for breeders to decide if the observed data fits well to an expected ratio or theoretical frequency distribution

(χ^2) Chi-square is measured as:

$$\chi^2 = \sum_{i=1}^n \frac{(O - E)^2}{E}$$

Where,

O=Observed frequency of the class,

E = Expected frequency of the respective class,

Σ =Summation of all classes.

i.e. H₀ : Null Hypothesis H₁ : Alternate Hypothesis

The computed chi-square value and the tabular value are compared in the chi-square test. The data is significant and the null hypothesis is rejected if the calculated value is higher than the tabulated value, suggesting a significant difference. In contrast, the data is deemed non-significant and the null hypothesis for the predicted ratio is accepted if the computed value is less than the tabulated value.



Fig. 1 : Plant Branching patterns; (a) erect type (b) semi-spreading type (c) spreading type

Result and Discussion

The inheritance patterns of plant branching types in pigeon pea (*Cajanus cajan*) were studied across various crosses, revealing significant insights into

genotype-phenotype relationships. Three branching classes namely erect, semi spreading and spreading were qualitatively recorded Table.1; impacting the source-sink relationship, harvesting methodology and yield in target crop.

In the cross GRG-152 x C.G. Arhar I, the plant branching pattern was observed across various generations. The plant branching patterns of the parental generations (P₁ and P₂) were found to belong to a semi spreading class. The F₁ generation showed semi-spreading type in every plant. The results of segregation for the F₂ generation included 42 spreading, 90 semi-spreading, and 26 erect plants. Due to the dominant allele of one of the two genes controlling the phenotype, this segregation corresponded well with the predicted 9:3:4 ratio, suggesting supplemental gene action. The observed ratio was valid, as evidenced by the estimated chi-square value of 0.6103 for this cross, which was less than the table value of 0.10%.

In the cross GRG-152 x Rajeevlochan, similar observations were made. Plant branching patterns in the P₁ and P₂ parental generations displayed a semi-spreading class. Every plant in the F₁ generation was a semi-spreading variety. Segregation was seen in the F₂ generation with 12 erect, 275 semi-spreading, and 50 spreading plants, all of which matched the predicted 12:3:1 ratio and suggested that one of the genes' dominant alleles was masking gene function. The expected ratio was validated by the computed chi-square value of 8.6103, which was smaller than the table value at 0.025% to 0.005%.

The parental generations (P₁ and P₂) in the Rajeevlochan x C.G. Arhar I cross likewise showed semi-spreading plant branching patterns. Semi-spreading plants belonged to the F₁ generation. Segregation produced 13 erect, 275 semi-spreading, and 26 spreading plants in the F₂ generation. This ratio matched the predicted 9:6:1, suggesting that many dominant genes were acting in polymeric gene activity. This cross's computed chi-square value was 8.27, which was smaller than the value in the table at 0.025% to 0.005%, confirming the observed ratio.

The parental generations (P₁ and P₂) in the Rajeevlochan x GRG-152 hybrid showed semi-spreading plant branching patterns. Plants of the F₁ generation were semi-spreading. 52 spreading, 214 semi-spreading, and 7 erect plants were produced via segregation in the F₂ generation. These results fit the predicted 12:3:1 ratio well, suggesting that one of the genes' dominant alleles was responsible for masking gene action. The observed ratio's validity was confirmed by the estimated chi-square value for this cross, which was 6.36 and smaller than the table value at 0.25% to 0.05%.

Cross Rajeevlochan X C.G. Arhar I and Cross C.G. Arhar I x Rajeevlochan - 12:3:1 (Masking gene action)

F₂-Punnet square

	AB	Ab	aB	ab
AB	AABB (ss)	AABb (ss)	AaBB (ss)	AaBb (ss)
Ab	AABb (ss)	AAbb (ss)	AaBb (ss)	Aabb (ss)
aB	AaBB (ss)	AaBb (ss)	aaBB (s)	aaBb (s)
ab	AaBb (ss)	Aabb (ss)	aaBB (s)	aabb (e)

2 dominant gene-SS

Here dominant - A masks B

Here recessive- Erect type

12: 3: 1

A_B_	SS	} 12	Semispreading type
A_bb	SS		
aa_B_	S -	3	Spreading type
aabb	E-	1	Erect type

Cross GRG-152 x C.G. Arhar 1 (9:3:4) Supplementary gene action.

F₂ – Punnet square

	AB	Ab	aB	ab
AB	AABB (ss)	AABb (ss)	AaBB (ss)	AaBb (ss)
Ab	AABb (ss)	AAbb (s)	AaBb (ss)	Aabb (s)
aB	AaBB (ss)	AaBb (ss)	aaBB (e)	aaBb (e)
ab	AaBb (ss)	Aabb (s)	aaBb (e)	Aabb (e)

A_B_ = 9 semi spreading type.

A_bb = 3 spreading type.

aaB_ = 3 erect type.

aabb = 1 erect type.

**Cross Rajeevlochan x C.G. Arhar 1 (9:6:1)
Polymeric gene action.**

F₂- Punnet square

	AB	Ab	aB	ab
AB	AABB (ss)	AABb (ss)	AaBB (ss)	AaBb (ss)
Ab	AABb (ss)	AAbb (s)	AaBb (ss)	Aabb (s)
aB	AaBB (ss)	AaBb (ss)	aaBB (s)	aaBb (s)
ab	AaBb (ss)	Aabb (s)	aaBb (s)	Aabb (e)

A_B_ = 9 semi-spreading type.

A_bb = 3 erect type.

aaB_ = 3 erect type.

aabb = 1 spreading type.

Conclusion

Understanding the inheritance of the qualitative traits is essential for supporting the breeding efforts

aimed at developing improved cultivars with desired agronomic traits. The investigation into the inheritance patterns on pigeonpea over the different crosses revealed significant segregation patterns in plant branching pattern traits across generations, indicating genetic regulation through supplementary, masking, and polymeric gene actions, supported by chi-square analysis for validating expected ratios. These findings emphasize the potential utility of these qualitative traits as morphological markers for germplasm characterization and hybrid confirmation in pigeonpea breeding programs. Thus, the genetic improvement in plant types with respect to the studied traits can be effectively brought in by efficient selection in segregating and subsequent generations. Improvement programs and the variations generated could be easily utilized for broadening the genetic base of the cultivated pigeonpea gene pool for improving yield *via* attributing traits.

Table 1: Inheritance pattern of branching in different crosses of pigeon pea

No	Crosses	F ₁ Expression	Observed Frequency in F ₂			Expected frequencies in F ₂			Expected ratio	Chi- square Cal. value	Chi- square Table Value	P- value range
			E	SS	S	E	SS	S				
1	GRG-152X C.G. Arhar I	Semi- Spreading	26	90	42	29.6	88.87	39.2	9:3:4	0.61	0.10	0.10-090
2	GRG-152 X Rajeevlochan	Semi- Spreading	12	275	50	21	252	63	12:3:1	8.61	9.21	0.10-0.025
3	Rajeevlochan X C.G. Arhar I	Semi- Spreading	13	275	26	163	245	27	9:6:1	8.27	9.21	0.025-0.01
4	Rajeevlochan X GRG-152	Semi- Spreading	7	214	52	17	204	51	12:3:1	6.36	7.37	0.10=0.05

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