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ASSESSMENT OF GENETIC VARIABILITY AND SELECTION POTENTIAL FOR PLANT HEIGHT IN PIGEONPEA (*CAJANUS CAJAN* L. MILLSPAUGH) DURING OFF-SEASON (*RABI*) CULTIVATION

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ABSTRACT

Pigeonpea (*Cajanus cajan* L. Millspaugh) is a nutritionally rich, climate-resilient legume widely cultivated in tropical and subtropical regions. This study emphasized 250 genotypes from the Pigeonpea International Genome-Wide Association Panel (PI-GAP) to assess genetic variability and selection potential for plant height under off-season (*rabi*). The trial was carried out at ICRISAT, Patancheru, employing alpha lattice design. Analysis of variance showed highly significant differences, for plant height, among the tested entries. The trait's high heritability and genetic advancement suggested strong genetic control and little environmental effect. Analysis of kurtosis and skewness revealed a platykurtic and right-skewed distribution, which signifies a flatter curve with asymmetry. The results from the study indicate that additive genetic effects predominantly govern plant height in *rabi* and can be effectively improved through direct selection. These findings offer valuable insights for breeding programs aiming to enhance genetic gain and productivity under off-season cultivation.

***Keywords* :** Off-season, Plant height, Selection, Variability.

Introduction

The pigeonpea or *Cajanus cajan* (L.) Millspaugh, is a vital food and economic crop throughout the world's tropical and subtropical climates (Nyirenda Yohane *et al.*, 2020). It can be cultivated in various cropping systems and provides protein-rich nutrition with fewer inputs; it is critical for subsistence agriculture (Sreelakshmi *et al.*, 2011). Pigeonpea through symbiosis with *Rhizobium* bacterial species, may fix nitrogen from the atmosphere in the soils, fertilizing agricultural lands with as much as 200 kg of nitrogen per hectare (Kwena *et al.*, 2019). The pigeonpea seeds contain protein (21–28%), vitamins, and mineral elements like phosphorus (0.56-0.72%), zinc (2.3–2.5%), potassium and magnesium, as well as being a good source of carbohydrates (57.3–58.7%), crude fibres (1.2–8.1%), and lipids (0.6–3.8%), which make it crucial for vegetarian diet (Phatak *et al.*, 1993). Pigeonpea is also rich in essential amino acids like arginine (13.51 g/kg), tyrosine (14.77 g/kg) and leucine (16.48 g/kg) (Ade-Omowaye *et al.*, 2015).

Usually, Pigeonpea is cultivated as a kharif crop, but initially, in the late 1970s, the potential of pigeonpea as a post-rainy/ *rabi* crop was tested in peninsular India (Narayanan and Sheldrake, 1979; Narayanan and Murthy, 1980). Due to the effects of low temperatures and short photoperiods, the ideal plant population for the *rabi* crop is three to four times larger than that typically utilized in kharif (Narayanan *et al.*, 1980). Given the crop's adaptability and nutritional value, understanding how off-season (*rabi*) cultivation influences key agronomic traits like plant height is essential for enhancing genetic gain through selection and ensuring sustainable productivity across diverse growing conditions.

Material and Methods

The current study was conducted in experimental fields of ICRISAT, Patancheru, in the *rabi* season 2023. The study's material consisted of 250 lines of Pigeonpea, which were part of the Pigeonpea International Genome-Wide Association Panel (PI-GAP). The material was sown in an alpha lattice design, with two replications. Each replication consisted of a row 2m in length. The material was planted in the Vertisol soil, with a 60 x 20 cm spacing. The experiment consisted of 500 plots, with 25 blocks for each replication, and each block accommodated 10 plots. The 250 lines were evaluated for genetic variability, heritability and genetic advance for the trait, plant height (cm) in off-season cultivation. The recommended agronomic and pest management practices were followed to cultivate a healthy crop. Each genotype's plant height was recorded by randomly selecting five plants in each replication.

An analysis of variance (ANOVA) was performed based on the methods described by Panse and Sukhatme (1967). The genotypic and phenotypic coefficients of variation were determined following Burton's (1952) approach. Heritability was estimated using the technique proposed by Lush (1940), while genetic advance was calculated according to the methodology outlined by Johnson *et al.* (1955). The selection differential and expected genetic gain were estimated based on the methods suggested by Lush (1937); Lerner and Cruden (1947). Skewness and Kurtosis for the frequency distribution was adopted as outlined by Joanes and Gill (1998). The data was analyzed completely using the R package version 4.5.0. The packages utilized for the analysis are "lme4"- for mixed-effect models, "lmerTest"- for hypothesis testing, "ggplot2"- for visualization plots and "dplyr"- for summarizing the data.

Results and Discussion

Descriptive Statistics, Frequency Distribution and ANOVA

The degree of variance among the genotypes for the trait, Plant Height, under investigation was revealed *via* descriptive statistical analysis (Table 1). The mean performance over all genotypes was indicated by the mean value, which was measured at 141 cm. The trait exhibited a wide range of genetic variation, ranging from a minimum of 30.3 cm to a maximum of 287 cm. Sharma *et al.* (2024) worked on a mini core collection of pigeonpea for the genetic diversity in the *kharif* season and have reported that the range of the plant height was 190, whereas, in rabi for the PI-GAP, the range obtained is more than 250. The standard deviation (SD) was 62.1 cm, indicating the degree of dispersion around the mean. The data distribution is right-skewed to some extent, with specific genotypes showing very high values, corresponding to a positive skewness of 0.41. Kumawat *et al.* (2012) reported a negative skewness for plant height in contrary to what is obtained in this current study, when they worked on $F_{2:3}$ population. In contrast to a normal distribution, the negative kurtosis value of -0.87 indicates a comparatively flat distribution with lighter tails, which may indicate fewer extreme outliers than would be predicted under normality.

Table 1: Descriptive statistics, Skewness and Kurtosis for Plant Height

Statistic	Value
Mean	141 cm
Minimum	30.3 cm
Maximum	287 cm
SD	62.1 cm
Skewness	0.41 [Slight positive skew (more lower values)]
Kurtosis	-0.87 [Platykurtic (flatter than normal)]

A visual representation of how genotypes are distributed across various value ranges for the trait under investigation was made possible by the frequency distribution analysis (Figure 1). The Plant Height ranged from 30 cm to 280 cm and were classified into group intervals or bins of width 10. There were 43 and 37 genotypes in the [100–110] and [110–120] bins, respectively, which were the most prevalent mid-range intervals. This implies that moderate trait expression was present in the majority of genotypes. The [70–80] (30 genotypes), [90–100] (35 genotypes), and [130–140] bin similarly had a consistent number of genotypes (34 genotypes). Conversely, seven genotypes were found in the [30–40] and [270–280] bins, representing the extreme ends of the distribution. This suggests the existence of a small number of extreme performers. The frequency distribution shows significant phenotypic variation in the population, which is necessary for an efficient breeding program selection.

The Analysis of Variance was calculated using a linear mixed model, considering the genotype as a fixed effect, whereas the replication and block are accounted for as random effects (Table 2). A high F-value of 105.93 indicates a significant difference among the genotypes and considerably less difference within the genotypes can be inferred. The p-value is extremely small, implying that the variation among the genotypes is highly statistically significant ($p<0.001$). Tuntun *et al.* (2022) and Gaur *et al.* (2020) also reported considerable variation in plant height.

Table 2: ANOVA for Plant Height variability in the *rabi*

Source	Sum Sq	Mean Sq	Num DF	Den DF	F value	Pr (>F)	Significance
Genotype	1,802,698	7,239.8	249	170.04	105.93	< 2.2e-16	***

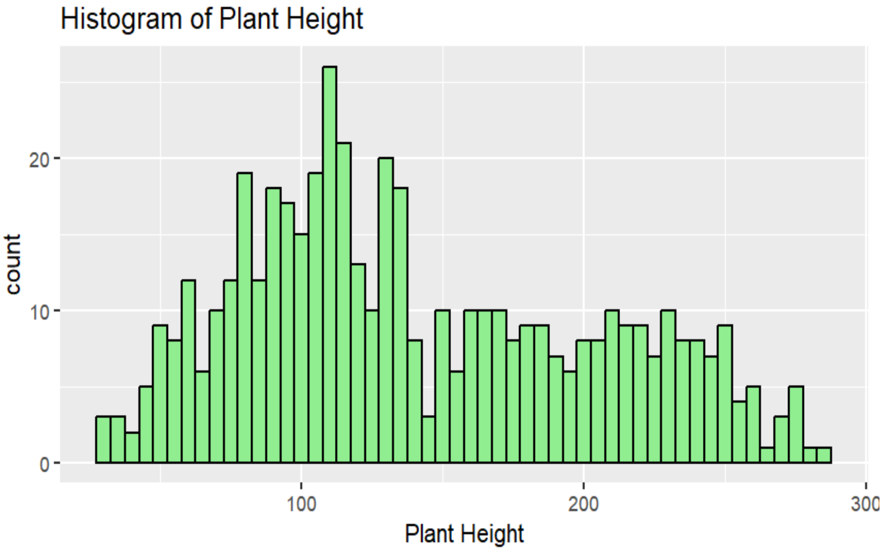

Fig. 1: Histogram for frequency distribution of plant height in *rabi*

Performance of Top and Bottom Ten Genotypes

The mean for the individual genotypes was evaluated to identify the significant differences in Plant Height. The genotypes and their mean plant height for the top ten and bottom ten entries are presented in Table 3. The top ten genotypes with higher plant height values varied from 250 cm to 278 cm. The highest was noted in the genotype ICP 11281, which had a height of 278cm, followed by ICP 7507 (274 cm), ICP 6859 (273 cm), and ICP 11238 (271 cm). The means for the bottom ten genotypes ranged from 31.2 cm to 50.2 cm. ICP 6370 (31.2 cm) and ICP 10904 (32.6 cm) recorded the lowest height.

Table 3: Top and Bottom Performing Lines

Rank	Top Performing Lines	Mean PH	Bottom Performing Lines	Mean PH
1	ICP 11281 (G30)	278.0	ICP 11543 (G37)	50.2
2	ICP 7507 (G198)	274.0	ICP 15021 (G101)	49.2
3	ICP 6859 (G166)	273.0	ICP 15599 (G109)	48.7
4	ICP 11238 (G27)	271.0	ICP 8817 (G224)	47.7
5	ICP 11230 (G26)	268.0	ICP 15014 (G100)	45.4
6	ICP 11833 (G44)	268.0	ICP 15597 (G108)	45.2
7	ICP 8144 (G208)	268.0	ICP 14444 (G86)	43.0
8	ICP 10880 (G17)	256.0	ICP 11613 (G39)	35.8
9	ICP 655 (G161)	251.0	ICP 10904 (G20)	32.6
10	ICP 8921 (G228)	250.0	ICP 6370 (G159)	31.2

The box plots of the top and the bottom ten genotypes, the narrow interquartile range genotypes show stability, and the wider genotypes show existing variability within the genotype, as suggested by Williamson *et al.* (1989). Genotypes that show stability in the constructed box plots are ICP 6370, ICP 10904, ICP 8817, ICP 11613, ICP 655, ICP 6859, ICP 10880 and ICP 11238 (Figure 2). Along with the box plots, violin plots were constructed to check the distribution density for the top ten and bottom ten entries. Among the top 10 genotypes, the violin plots revealed a narrow and concentrated distribution around higher mean values, indicating both high performance and consistency, as outlined by Hintze and Nelson (1998). The top performing genotypes which exhibit the distribution of the values around the median with less variation are ICP 655 and ICP 10880 (Figure 3). On contrary, the bottom 10 genotypes have shown broader violin shapes, implying greater variability in their performance (Figure 4). The entries which are included in the bottom 10 and that have consistent performance are ICP 10904 and ICP 8817.

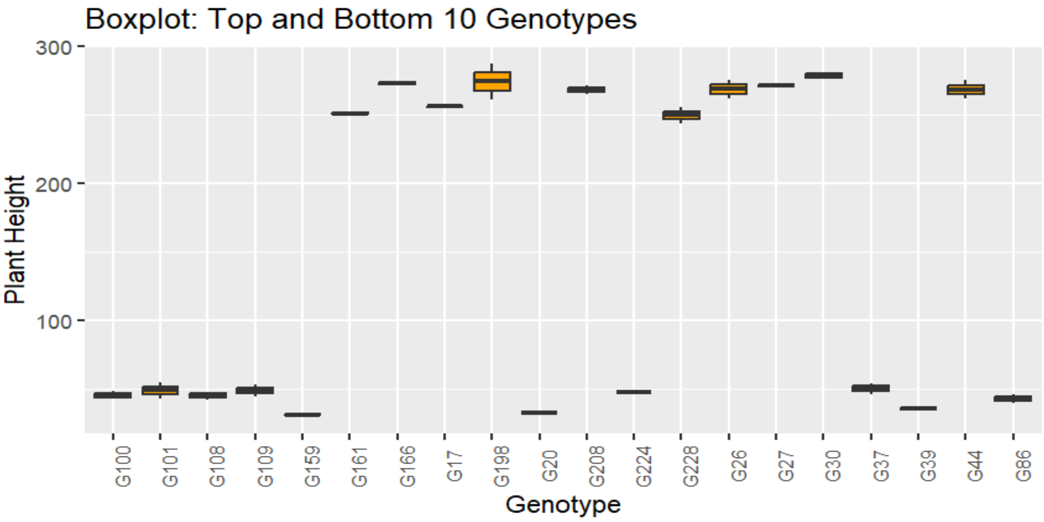

Fig. 2 : Box plot of top and bottom ten genotypes for plant height in *rabi.*

Fig. 3 : Violin plot for top ten genotypes

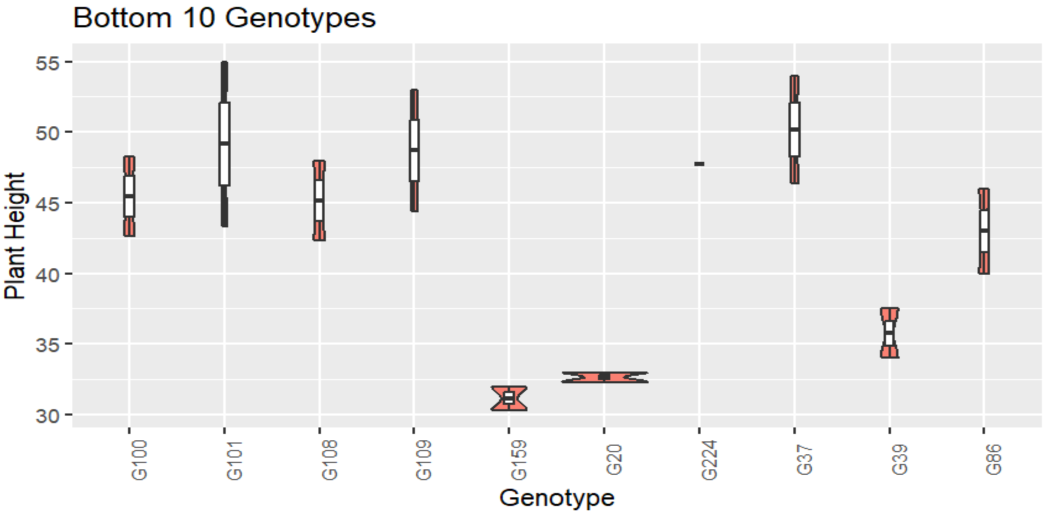

Fig. 4 : Violin plot for the bottom ten genotypes

Genetic Parameters and Selection Indices

The genetic parameters revealed greater variability for the trait, plant height in the current study (Table 4). The Genotypic Coefficient of Variation (GCV) was 42.35, while the Phenotypic Coefficient of Variation (PCV) was 42.75, which indicated that the variation observed is due to genetics. There is a very minimal influence of the environment. The broad-sense heritability was recorded as 98.13%, which is high, indicating that the prevalent variation observed phenotypically is backed by the genetic make-up of the lines. Parre and Raje (2022) also reported high heritability for plant height in the recombinant inbred lines. The Genetic Advance (GA) was 123.35, and the genetic advance as a percentage of the mean (GAM) was 87.25%, indicating the potential for considerable improvement through phenotypic selection. High heritability combined with high GAM shows that the variability in the genotypes is strongly genetic and selection can be effective, as Patel *et al.* (2021) reported. The selection differential was calculated as 120.24, and the expected genetic gain was 117.99, emphasizing that selection of superior genotypes based on phenotypic performance will likely result in genetic improvement in subsequent generations. These findings cumulatively suggest that the plant height in this study is under strong additive genetic control and can be efficiently improved through direct selection strategies in pigeonpea breeding programs.

Table 4: Genetic Parameters and Selection Indices

Parameter	Value
GCV (%)	42.35
PCV (%)	42.75
Heritability (%)	98.13
Genetic Advance (cm)	123.35
GAM (%)	87.25
Selection Differential (cm)	120.24
Expected Genetic Gain (cm)	117.99

Conclusion

In conclusion, the study demonstrated substantial genetic variability for plant height among PI-GAP pigeonpea genotypes under *rabi* conditions. The high heritability and genetic advance highlight the trait's amenability to improvement through selection. The observed distribution patterns further confirm the predominance of additive gene action. These results provide a strong foundation for breeding strategies aimed at enhancing pigeonpea performance in the off-season.

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