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**VD Waghmare**  
M.Sc. Scholar, College of  
Agriculture Badnapur, Department  
of Genetics & Plant Breeding,  
VNMKV, Parbhani, Maharashtra,  
India

**PJ Shedge**  
M.Sc. Scholar, College of  
Agriculture Badnapur, Department  
of Genetics & Plant Breeding,  
VNMKV, Parbhani, Maharashtra,  
India

**PS.Zine**  
M.Sc. Scholar, College of  
Agriculture Badnapur, Department  
of Agronomy, VNMKV, Parbhani,  
Maharashtra, India

**Corresponding Author:**  
**VD Waghmare**  
M.Sc. Scholar, College of  
Agriculture Badnapur, Department  
of Genetics & Plant Breeding,  
VNMKV, Parbhani, Maharashtra,  
India

## Heterosis and genetic parameters for yield-related traits in pigeonpea (*Cajanus cajan* (L.) Millsp.)

VD Waghmare, PJ Shedge and PS Zine

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### Abstract

The present study on “Heterosis and Genetic Parameters for Yield-Related Traits in pigeonpea (*Cajanus cajan* (L.) Millsp.)” was conducted during *Kharif 2018* using three crosses — *BDN 708* × *BDN 2014-1*, *BDN 711* × *BDN 2010-1*, and *BSMR 853* × *PUSA 2001* — along with the standard check *BDN 716*. Significant heterosis was observed for most yield and yield-related traits, indicating ample genetic variability. The cross *BDN 711* × *BDN 2010-1* exhibited the highest positive heterosis for seed yield per plant and number of pods per plant, while *BSMR 853* × *PUSA 2001* showed desirable heterosis for earliness and number of seeds per pod. Negative heterosis for days to flowering and maturity suggested potential for developing early maturing genotypes. Overall, *BDN 711* × *BDN 2010-1* emerged as the most promising cross for yield improvement in pigeonpea.

**Keywords:** *Cajanus cajan*, gene action, heterosis, yield components

### Introduction

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is a major grain legume of the tropics and subtropics, valued for its multipurpose use as food, feed, fodder, and fuel. Belonging to the family *Leguminosae*, it is a hardy, drought-tolerant, and widely adaptable crop with a maturity range of 90-300 days. In India, it occupies about 4.45 million ha with a production of 4.18 million tonnes and productivity of 937 kg/ha (Anonymous, 2019), ranking second after chickpea. Nutritionally, pigeonpea is rich in protein (17.9-24.3%), carbohydrates, and essential amino acids, and plays a key role in soil fertility improvement through biological nitrogen fixation. Despite its significance, productivity remains low due to limited genetic gain in yield improvement.

Understanding the genetic basis of yield and its components is essential for developing high-yielding varieties. Generation mean analysis helps partition genetic effects into additive, dominance, and epistatic components, thereby guiding effective breeding strategies. Hence, the present study entitled “Heterosis and Genetic Parameters for Yield-Related Traits in pigeonpea (*Cajanus cajan* (L.) Millsp.)” was undertaken to assess the nature and magnitude of gene action governing yield and related traits.

### Materials and Methods

#### 1. Experimental materials

The present investigation entitled “Generation mean analysis for yield and its component traits in pigeonpea (*Cajanus cajan* (L.) Millsp.)” was carried out during *Kharif 2018-2019* at Agricultural Research Station, Badnapur experimental field.

The experimental material used for present investigation comprised of six generations ( $P_1$ ,  $P_2$ ,  $F_1$ ,  $F_2$ ,  $BC_1$  and  $BC_2$ ) derived from three crosses involving six parents viz. *BDN 708*, *BDN 711*, *BSMR 853*, *BDN 2014-1*, *BDN 2010-1* and *PUSA 2001* along with standard check *BDN 716*. The characteristic of parents are listed in Table (1.1).

**Table 1:** Characters of the parental lines

| Sr. No. | Parents    | Characters                            |
|---------|------------|---------------------------------------|
| 1       | BDN 708    | Resistant to wilt                     |
| 2       | BDN 711    | Earliness                             |
| 3       | BSMR 853   | Resistant to Sterility Mosaic Disease |
| 4       | BDN 2014-1 | White flowered mutant                 |
| 5       | BDN 2010-1 | More no. of pods, high yielding       |
| 6       | PUSA 2001  | Extra earliness                       |

**Table 2:** Detail of six generation developed for generation mean analysis study

| Generations     | Cross-1                             | Cross-2                             | Cross-3                            |
|-----------------|-------------------------------------|-------------------------------------|------------------------------------|
| P <sub>1</sub>  | BDN 708                             | BDN 711                             | BSMR 853                           |
| P <sub>2</sub>  | BDN 2014-1                          | BDN 2010-1                          | PUSA 2001                          |
| F <sub>1</sub>  | (BDN 708 x BDN 2014-1)              | (BDN 711 x BDN 2010-1)              | (BSMR 853 X PUSA 2001)             |
| F <sub>2</sub>  | Self on F <sub>1</sub>              | Self on F <sub>1</sub>              | Self on F <sub>1</sub>             |
| BC <sub>1</sub> | (BDN 708 x BDN 2014-1) x BDN 708    | (BDN 711 x BDN 2010-1) x BDN 711    | (BSMR 853 x PUSA 2001) X BSMR 853  |
| BC <sub>2</sub> | (BDN 708 x BDN 2014-1) x BDN 2014-1 | (BDN 711 x BDN 2010-1) x BDN 2010-1 | (BSMR 853 x PUSA 2001) X PUSA 2001 |

Check: BDN 716

## 2.1 Crossing programme

During *kharif* 2017 parental materials were sown to undertake crossing programme. Female lines were crossed with each male line viz. BDN 2014-1, BDN 2010-1, PUSA 2001.

## 2.2 Design and Layout

The experiment consisted of three F<sub>1</sub>'s and six parents.

The detail of experiment is given below:

1. Design: RBD (Randomized Block Design)
2. No. of replication: Two (Two rows each of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, BC<sub>1</sub>, BC<sub>2</sub> and four rows for F<sub>2</sub> generation)
3. Treatments: 19(3F<sub>1</sub> + 3BC<sub>1</sub> + 3BC<sub>2</sub> + 3F<sub>2</sub> + 6 parents + 1Check)
4. Plot size: 1.80 x 4.00 m<sup>2</sup> (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, BC<sub>1</sub>, BC<sub>2</sub> generations): 3.60 x 4.00 m<sup>2</sup> (F<sub>2</sub> generations)
5. Spacing: 90 x 20 cm<sup>2</sup>
6. Fertilizer dose: 20:50:00 NPK (kg/ha).
7. Season: *Kharif* 2018-19.
8. Location: Agricultural Research Station, Badnapur
9. Check: BDN 716

## 2.3 Testing of six generation of crosses

During *kharif* 2018, six generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of three crosses along with one check were sown in Randomized Block Design with two replications on 10<sup>th</sup> July 2018. Each replication consisted of six generation (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>) of three crosses along with one check. Each genotype was represented by two rows in each replication. The experimental plot size was 1.80 x 4.00 m<sup>2</sup> (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, BC<sub>1</sub>, BC<sub>2</sub> generations) and 3.60 x 4.00 m<sup>2</sup> (F<sub>2</sub> generation) spaced 90 cm apart with 20 cm plant to plant distance.

## 3. Collection of experimental data

Observations were recorded on randomly selected five plants in parents, F<sub>1</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations and 20 plants in F<sub>2</sub> generations in each replication. Data on following characters were recorded.

### a. Days to 50% flowering

The number of days required from sowing to flowering of 50% plants in each generation was recorded.

### b. Days to maturity

The number of days required from sowing to maturity of crops

The following three F<sub>1</sub>'s was developed using above parental lines in *kharif* 2017.

1. BDN 708 × BDN 2014-1
2. BDN 711 × BDN 2010-1
3. BSMR 853 × PUSA 2001

## 2. Experimental details

The field experiment was conducted at Agricultural Research Station, Badarpur experimental field during *kharif* 2018-19.

was recorded.

### c. Plant height (cm)

At maturity, plant height was measured from base of the plant to tip of the main stem.

### d. Number of primary branches per plant

The main fruiting branches per plant developed on main shoot were recorded per plant at maturity. Total effective branches on the main stem were recorded.

### e. Number of secondary branches per plant

At maturity, the total number of branches was developed on primary branches counted per plant. Total effective branches on the primary branches were recorded.

### f. Number of pods per plant

The number of pods retained on plants at the time of harvest was recorded.

### g. No. of seeds per pod

The number of seeds in each of 10 pods of selected five plants was recorded and average was worked out as number of seeds per pods on each plant.

### h. Pod length (cm)

The length in each of 10 pods of selected five plants was recorded in cm and average was worked out as pod length on each plant.

### i. 100 seed weight (g)

Healthy 100 seeds were counted and weight recorded in grams.

### j. Seed yield per plant (g)

The grain yield was recorded in grams (g) per plant.

## 4. Statistical analysis

### 4.1. Analysis of variance for treatment differences

To test the significance of differences between treatments, the analysis of variance for Randomized Block Design (RBD) was carried out as per procedure given by Panse and Sukhatme (1967) for all metric characters under study as below,

**Table 3:** Analysis of variance

| Source of variation | d.f.       | S.S. | MS  | Expected mean sum of squares | F value |
|---------------------|------------|------|-----|------------------------------|---------|
| Replications        | (r-1)      | SSr  | MSr | $\sigma^2_e + t \sigma^2_r$  | MSr/MSe |
| Treatments          | (t-1)      | SSt  | MSt | $\sigma^2_e + r \sigma^2_t$  | MSt/MSe |
| Error               | (r-1)(t-1) | SSe  | MSe | $\sigma^2_e$                 |         |

Where,

r = Number of replications.

t = Number of treatments.

d.f. = Degrees of freedom.

S.S. = Sum of square.

SSr = Replication sum of square

SSt = Treatment sum of square

SSe = Error sum of square

MS = Mean sum of squares.

MSr = Replication mean sum of squares.

MSt = Treatment mean sum of squares.

MSe = Error sum mean of squares.

Standard error (SE), critical difference (CD) and coefficient of variation (CV) were calculated as follows,

$$SE (\pm) = \sqrt{2MSe / r}$$

$$CD = SE \times \sqrt{2 \times 't'}$$

$$CV (\%) = \frac{\sigma}{\bar{x}} \times 100$$

Where,

MSe: Error mean square

t: Table 't' value at error degrees of freedom at 5 and 1 per cent level.

r: Number of replication

$\sigma$ : Standard deviation

$\bar{x}$ : Mean

$$SD = \frac{x \sqrt{\sum (x - \bar{x})^2}}{n-1}$$

#### 4.2 Estimation of Heterosis

Heterobeltiosis was measured as the proportion of the deviation of the mean value from the better parent value and standard heterosis from the value of standard check. The  $F_1$  hybrids performance will be calculated as the heterosis over standard checks and better parent as per Fonesca and Patterson (1968).

$$1. \text{ Heterobeltiosis} = \left[ \frac{\overline{F_1 - BP}}{\overline{BP}} \right] \times 100$$

$$2. \text{ Standard Heterosis} = \left[ \frac{\overline{F_1 - SC}}{\overline{SC}} \right] \times 100$$

Where,

$\overline{F_1}$ : Average performance of  $F_1$  hybrid.

$\overline{BP}$ : Mean values of Better parent.

$\overline{SC}$ : Mean values of standard check.

Mean heterobeltiosis and standard heterosis was worked out for all the characters by summing up the heterotic effects of all the hybrids and dividing it by the total number of hybrid

combinations.

#### Test of significance

The heterosis was tested by least significant difference at 5 per cent and at 1 per cent level of significance for error degrees of freedom as follows,

For testing heterosis over better parents and standard check

$$SE (d) (BP) = \sqrt{2MSe / r}$$

$$SE (d) (SC) = \sqrt{2MSe / r}$$

Where,

MSe = Error variance

r = Number of replications

Estimation of t value for all hybrids

$$1. \text{ t value for heterobeltiosis} = \frac{\overline{F_1 - BP}}{\overline{SE}}$$

$$2. \text{ t value for standard heterosis} = \frac{\overline{F_1 - SC}}{\overline{SE}}$$

#### Critical difference

CD = SE (d) x 't' (at error d.f. at 5 and 1 per cent level of significance). Heterosis was considered significant when ( $F_1 - BP$ ) or ( $F_1 - SC$ ) was higher than critical difference.

#### Results and Discussion

The findings of the present study as well as relevant discussion have been presented under following heads.

#### 5. Heterosis

Results of per cent heterosis over better parent (BP), Standard check (SC) and inbreeding depression are presented for each other in Table 4.3.

##### 5.1. Days to 50 per cent flowering

The heterosis over better parent was in the range of -10.04 per cent (BSMR 853 X PUSA 2001) to 1.86 per cent (BDN 708 X BDN 2014-1) and over standard check viz. BDN 716 it was in the range of -4.18 per cent (BSMR 853 X PUSA 2001) to 3.25 per cent (BDN 711 X BDN 2010-1). The negative heterosis was desirable for days to 50 per cent flowering. The heterosis over better parent was significant and negative in the crosses BDN 711 X BDN 2010-1 and BSMR 853 X PUSA 2001. However, heterosis over standard check viz. BDN 716 was significant and positive in the cross BDN 711 X BDN 2010-1, while significant and negative in the cross BSMR 853 X PUSA 2001.

##### 5.2. Days to maturity

The heterosis over better parent was in the range of -3.52 per cent (BDN 708 X BDN 2014-1) to -1.22 per cent (BDN 711 X BDN 2010-1) and over standard check viz. BDN 716 it was in the range of -2.42 per cent (BDN 711 X BDN 2010-1) to 6.96 per cent BSMR 853 X PUSA 2001.

##### 5.3. Plant height (cm)

The heterosis over better parent was in the range of -12.94 per cent (BSMR 853 X PUSA 2001) to 1.03 per cent (BDN 708 X BDN 2014-1) and over standard check viz. BDN 716 it was in the range of -18.66 per cent (BDN 711 X BDN 2010-1) to -13.71 per cent (BDN 708 X BDN 2014-1).

#### 5.4. Number of primary branches per plant

The heterosis over better parent was in the range of -18.68 per cent (BDN 711 X BDN 2010-1) to -6.70 per cent (BDN 708 X BDN 2014-1) and over standard check viz. BDN 716 it was in the range of -11.90 per cent (BDN 711 X BDN 2010-1) to 13.09 per cent (BSMR 853 X PUSA 2001).

#### 5.5. Number of secondary branches per plant

The heterosis over better parent was in the range of -12.98 per cent (BDN 711 X BDN 2010-1) to 3.00 per cent (BSMR 853 X PUSA 2001) and over standard check viz. BDN 716 it was in the range of -17.64 per cent (BDN 708 X BDN 2014-1) to -13.44 per cent (BSMR 853 X PUSA 2001).

#### 5.6. Number of pods per plant

The heterosis over better parent was in the range of -19.24 per cent (BSMR 853 X PUSA 2001) to 30.38 per cent (BDN 711 X BDN 2010-1) and over standard check viz. BDN 716 it was in the range of 27.19 per cent (BSMR 853 X PUSA 2001) to 36.76 per cent (BDN 708 X BDN 2014-1).

#### 5.7. Number of seeds per pod

The heterosis over better parent was in the range of 0.00 per cent (BDN 711 X BDN 2010-1) to 23.33 per cent (BSMR 853 X PUSA 2001) and over standard check viz. BDN 716 it was in the range of 19.35 per cent (BSMR 853 X PUSA 2001) to 29.03 per cent (BDN 711 X BDN 2010-1).

#### 5.8. Pod length (cm)

The heterosis over better parent was in the range of -3.67 per cent (BDN 711 X BDN 2010-1) to 1.81 per cent (BSMR 853 X PUSA 2001) and over standard check viz. BDN 716 it was in the range of -5.08 per cent (BSMR 853 X PUSA 2001) to 5.08 per cent (BDN 711 X BDN 2010-1).

#### 5.9. 100-Seed weight (gm)

The heterosis over better parent was in the range of -11.53 per cent (BSMR 853 X PUSA 2001) to 2.16 per cent (BDN 708 X BDN 2014-1) and over standard check viz. BDN 716 it was in the range of -26.31 per cent (BSMR 853 X PUSA 2001) to -19.07 per cent (BDN 711 X BDN 2010-1).

#### 5.10. Seed yield per plant

The heterosis over better parent was in the range of -24.14 per cent (BSMR 853 X PUSA 2001) to 27.82 per cent (BDN 711 X BDN 2010-1) and over standard check viz. BDN 716 it was in the range of 7.96 per cent (BSMR 853 X PUSA 2001) to 30.29 per cent (BDN 711 X BDN 2010-1).

**Table 4:** Heterosis for different characters in three crosses of pigeonpea

| Characters and cross                                                                              | Per cent heterosis over        |                                  |
|---------------------------------------------------------------------------------------------------|--------------------------------|----------------------------------|
|                                                                                                   | BP                             | SC                               |
| 1) Days to 50% flowering<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001  | 1.86<br>-5.12**<br>-10.04**    | 1.86<br>3.25*<br>-4.18**         |
| 2) Days to maturity<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001       | -3.52*<br>-1.22<br>-2.48       | -0.60<br>-2.42<br>6.96**         |
| 3) Plant height (cm)<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001      | 1.03<br>-0.36<br>-12.94**      | -13.71**<br>-18.66**<br>-14.99** |
| 4) No. primary branches<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001   | -6.70**<br>-18.68**<br>-7.76** | -8.33**<br>-11.90**<br>13.09**   |
| 5) No. secondary branches<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001 | -7.98**<br>-12.98**<br>3.00*   | -17.64**<br>-15.54**<br>-13.44** |

**Table 4:** Contd...

| Characters and cross                                                                            | Per cent heterosis over        |                                  |
|-------------------------------------------------------------------------------------------------|--------------------------------|----------------------------------|
|                                                                                                 | BP                             | SC                               |
| 6) Number of pods/plant<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001 | 22.25**<br>30.38**<br>-19.24** | 36.76**<br>33.68**<br>27.19**    |
| 7) Number of seeds/pod<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001  | 8.33**<br>0.00<br>23.33**      | 25.80**<br>29.03**<br>19.35**    |
| 8) Pod length (cm)<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001      | -2.88*<br>-3.67*<br>1.81       | -3.05*<br>5.08**<br>-5.08**      |
| 9) 100-seed weight (gm)<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001 | 2.16<br>-1.16<br>-11.53**      | -25.00**<br>-19.07**<br>-26.31** |
| 10) Seed yield/plant<br>BDN 708 X BDN 2014-1<br>BDN 711 X BDN 2010-1<br>BSMR 853 X PUSA 2001    | 21.94**<br>27.82**<br>-24.14** | 27.57**<br>30.29**<br>7.96**     |

\* -Significant at 5% level of significance

\*\* -Significant at 1% level of significance

SC = Standard check BDN 71

#### 6. Conclusion

The study on heterosis and inbreeding depression among three pigeon pea crosses — *BDN 708 × BDN 2014-1*, *BDN 711 ×*

*BDN 2010-1*, and *BSMR 853 × PUSA 2001* — revealed considerable variability in the magnitude and direction of heterosis for different yield and yield-contributing traits.

Significant and desirable negative heterosis was observed for days to 50% flowering in the crosses *BDN 711* × *BDN 2010-1* and *BSMR 853* × *PUSA 2001*, indicating their potential for developing early maturing genotypes. For days to maturity, heterosis values were negative over both the better parent and standard check, suggesting scope for developing early varieties. For plant height, most crosses exhibited negative heterosis, which could be desirable for developing dwarf and lodging-resistant plant types. The cross *BSMR 853* × *PUSA 2001* showed a favourable trend for number of secondary branches per plant, while *BDN 708* × *BDN 2014-1* and *BDN 711* × *BDN 2010-1* exhibited higher heterotic response for number of pods per plant and seed yield per plant.

Marked heterosis was observed for seed yield per plant, particularly in *BDN 711* × *BDN 2010-1*, which recorded the highest positive heterosis over both better parent and standard check, indicating this cross as a promising combination for yield improvement. Similarly, *BSMR 853* × *PUSA 2001* exhibited desirable heterosis for number of seeds per pod, while *BDN 708* × *BDN 2014-1* showed positive heterosis for 100-seed weight and pod length.

Overall, the cross *BDN 711* × *BDN 2010-1* emerged as the most superior hybrid combination with significant positive heterosis for several yield-attributing traits and overall seed yield. This suggests its potential utility in future breeding programs aimed at improving productivity and earliness in pigeon pea.

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