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EFFECT OF SELECTION RESPONSE FOR YIELD RELATED TRAITS IN EARLY GENERATION OF FABA BEAN (*VICIA FABA* L.)

Anjali Kumari Jha¹, Ashish Ranjan^{2*}, Anuj Kumar Choudhary¹, Ajay Bhardwaj³, Raj Bhawan Verma³ and Abhishek Kumar³

¹Department of Horticulture (Vegetable & Floriculture), Bihar Agricultural University, Sabour, Bhagalpur, Bihar, India

²Department of Horticulture, Bhola Paswan Shastri Agricultural College, Purnea, Bihar, India

³Department of Plant Breeding & Genetics, Bhola Paswan Shastri Agricultural College, Purnea, Bihar, India

*Corresponding author E-mail: aranjan1978@gmail.com

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ABSTRACT

The present experiment was carried out at the research farm of Bhola Paswan Shastri Agricultural College Purnea, Bihar, India, during *rabi* season of 2022-23 to investigate the selection response for yield related traits in early generations in faba bean. In the current study, genetic interactions were investigated in the F₃ generations of eight faba bean (*Vicia faba* L.) hybrids. The majority of the traits investigated were positively skewed and controlled by many genes, indicating quantitative inheritance. While in cross combination Bak-1 × Bak-20 non-skewed and platykurtic distribution was observed for number of seeds per pod at edible stage. The variance, skewness, and kurtosis of all the crosses indicate high level of heterozygosity. All of the crosses outperformed the parents and the national check in terms of producing high-yielding segregants that demonstrated parental diversity. Pod yield per plant and other associated characters, such as number of pods per plant and number of seeds per pod, are controlled by complementary action of multiple genes. Overall, three lines from each cross with superior pod yield were identified, which could be used for varietal development.

Keywords: Faba bean, *Vicia faba* L., skewness, kurtosis, segregation.

Introduction

The faba bean (*Vicia faba* L.), commonly known as horse bean or broad bean, is a significant minor legume crop extensively cultivated in India, particularly in the North-eastern region. It is predominantly harvested for its dry seeds, which are used as food, while fresh seeds and tender pods are consumed as vegetables. Faba bean is a rich source of essential nutrients, including proteins, carbohydrates, starch, total sugars, vitamins, and minerals (Duranti *et al.*, 2008). Moreover, it contains L-dopa in various parts, a natural compound used in the treatment of Parkinson's disease (Duranti, 2006). However, its consumption is limited by the presence of certain antinutritional factors such as phytic acid, tannins, phenols, trypsin inhibitors, vicine, and convicine, which are associated with hemolytic anemia, a condition

known as favism. Faba bean plays a crucial role in sustainable agriculture by contributing to crop diversity and engaging in biological nitrogen fixation through symbiosis with specific rhizobia bacteria, thereby reducing the need for synthetic fertilizers in cultivation. Although the area under faba bean cultivation in India remains small, it ranks seventh among legume crops globally, following major crops like soybean, groundnut, and common bean.

The global productivity of faba bean remains low, primarily due to the crop's narrow genetic base, which makes it susceptible to various biotic and abiotic stresses (Toker and Mutlu, 2011). Variability is essential for the success of any selection process (Andrade, 2019), as progress in breeding programs relies on the amount of variability present in the population (Vinithashri *et al.*, 2019). To enhance faba

bean production, understanding the inheritance patterns of yield and its components is crucial. Genetic variability parameters provide significant value in identifying superior segregants for yield and related traits. Standard measures of variability, such as range, variance, and standard error, are commonly employed to evaluate variability and gene action for desirable traits. Furthermore, information on the frequency distribution of various traits is vital for selecting plants with desirable trait expression (Dinesh *et al.*, 2018). Breeding for higher yield is a primary objective in crop improvement programs (Woyann *et al.*, 2019).

Since yield is polygenically controlled and highly influenced by environmental factors (Santos *et al.*, 2014), selection based solely on yield may not be effective. Therefore, yield improvement can be achieved through indirect selection of component traits (Luz *et al.*, 2011) that are highly heritable and strongly correlated with yield. The distribution properties of skewness and kurtosis provide insights into the nature of gene action and the number of genes controlling each trait, respectively. Consequently, the present study aimed to examine the genetics of different traits in association with yield and its component traits, utilizing third and fourth-degree statistics in the early generations of eight different faba bean crosses.

Material and Methods

The research was conducted at the experimental farm of Bholu Paswan Shastri Agricultural College, Purnea, Bihar, India. The study material comprised F₃ generations from eight faba bean crosses, specifically Bak-1 × Bak-5, Bak-1 × Bak-11, Bak-1 × Bak-20, Bak-2 × Bak-5, Bak-2 × Bak-11, Bak-2 × Bak-20, Bak-12 × Bak-5, and Bak-16 × Bak-20, along with the parent lines and a national check variety, Vikrant. The plants were cultivated under field conditions during the *rabi* season of 2022-23, adhering to standard crop

management practices to ensure healthy growth. Seeds were sown in the first week of November, with a spacing of 45 x 15 cm between plants. A total of 640 plants were selected for the study, with 80 plants from each cross. Observations were made on 13 quantitative traits, including days to flowering, days to first pod picking, plant height (cm), number of branches, internodal length, node of the first flower, pod length (cm), pod diameter (cm), number of fruit clusters per plant, number of pods per plant, pod yield per plant (g), number of seeds per pod, and harvesting span. Data were recorded from individual F₃ plants and from five randomly selected plants of each parent and the national check. The range and variance of yield and associated traits were determined using an analysis toolkit in Microsoft Excel. Skewness (K3) and third-degree statistics, along with kurtosis (K4) and fourth-degree statistics, were calculated using Minitab software to analyze the nature of trait distributions.

Additionally, the yield of the 640 F₃ progenies was compared to that of the best check cultivar, Vikrant, which was grown in the field alongside the test lines. F₃ progenies exhibiting higher pod yield per plant than their respective parents and the check cultivar were selected for further evaluation. The standard error of the mean (SE), standard deviation, and variance were analyzed using the formula provided by Jasani *et al.* (2018).

Results and Discussion

The range demonstrated considerable variability both among and within the F₃ populations for all thirteen quantitative traits across the crosses (Table 1). This variability can be attributed to the broad differences among F₂ plants and the presence of heterozygosity at several loci where the parents exhibited genetic differences.

Table 1: Range of thirteen traits in eight populations of faba bean

| Genotypes | Bak-1 × Bak-5 | Bak-1 × Bak-11 | Bak-1 × Bak-20 | Bak-2 × Bak-5 | Bak-2 × Bak-11 | Bak-2 × Bak-20 | Bak-12 × Bak-5 | Bak-16 × Bak-20 |
|---------------|---------------|----------------|----------------|---------------|----------------|----------------|----------------|-----------------|
| Traits | Range | | | | | | | |
| PH | 22-57 | 28-60 | 23-66 | 31-79 | 33-71 | 29-68 | 42-77 | 40-88 |
| NB | 2-13 | 2-23 | 2-10 | 2-10 | 2-12 | 2-13 | 2-9 | 2-12 |
| IL | 2.70-4.40 | 2.30-4.40 | 2.80-4.60 | 2.00-6.50 | 2.20-6.00 | 2.00-4.30 | 1.80-4.30 | 2.00-4.80 |
| NFF | 1-5 | 1-5 | 1-6 | 2-8 | 2-6 | 2-6 | 1-5 | 1-9 |
| DFF | 60-101 | 56-87 | 52-87 | 44-108 | 47-86 | 46-88 | 43-78 | 47-88 |
| DPP | 99-115 | 96-114 | 99-112 | 99-115 | 89-115 | 94-117 | 92-112 | 103-114 |
| NFCP | 0-10 | 0-11 | 0-11 | 0-14 | 0-9 | 0-8 | 0-14 | 0-20 |
| NPP | 10-55 | 5-75 | 6-62 | 6-77 | 8-48 | 6-55 | 10-55 | 6-61 |
| PL | 4.82-6.20 | 4.14-5.92 | 4.26-6.08 | 3.37-6.39 | 4.22-6.86 | 4.45-5.95 | 4.20-6.00 | 3.98-7.18 |

| | | | | | | | | |
|--------|--------------|-----------|--------------|--------------|--------------|--------------|--------------|--------------|
| PD | 0.87-1.18 | 0.86-1.12 | 0.88-1.03 | 0.89-1.04 | 0.84-1.08 | 0.84-1.04 | 0.87-1.06 | 0.89-1.24 |
| HS | 4-17 | 2-13 | 2-13 | 3-19 | 2-16 | 2-10 | 2-18 | 4-17 |
| NSPPES | 1.40-3.60 | 1.40-3.60 | 1.60-3.20 | 1.80-3.40 | 1.60-3.20 | 1.80-3.80 | 1.80-3.20 | 2.20-3.80 |
| PY | 26.97-129.29 | 10.12-171 | 16.93-125.05 | 18.90-130.40 | 12.60-120.96 | 13.50-104.40 | 14.40-109.33 | 17.36-135.12 |

PH: Plant height (cm), NB: No. of branches per plant, IL: Internodal length (cm), NFF: Node of first flower, DFF: Days to first flowering, DPP: Days to first pod picking, NFCP: No. of fruit cluster per plant, NPP: No. of pods per plant, PL: Green pod length (cm), PD: Pod diameter (cm), HS: Harvesting span, NSPPES: No. of seeds per pod at edible stage, PY: Green pod yield per plant (g)

Skewness and kurtosis in F₃ population of Bak-1 × Bak-5

The range of all the traits revealed a highly significant difference for key characteristics such as the number of branches per plant, plant height, number of pods per plant, and pod yield per plant across the crosses, indicating substantial variability in all the studied traits. The analysis of trait distribution using skewness and kurtosis provides valuable insights into the nature of gene action and the number of genes controlling the traits (Govintharaj *et al.*, 2018). Positive skewness is typically linked to complementary gene action, while negative skewness indicates duplicate (additive × additive) gene interactions. Kurtosis tends to be negative or close to zero (platykurtic) in the absence of gene interaction but becomes positive (leptokurtic) when gene interaction is present (Ramadhan *et al.*, 2018). Understanding gene interactions is essential for improving selection efficiency in breeding programs.

Positive skewness combined with a platykurtic distribution suggested the involvement of dominance-based complementary gene interaction and a large number of genes with decreasing effects in the inheritance of traits such as the number of branches per plant, internodal length (cm), node of the first flower, number of pods per plant, pod length (cm), pod diameter (cm), harvesting span, number of seeds per pod at the edible stage, and green pod yield per plant (g) in the cross Bak-1 × Bak-5. Similar results were observed for traits such as plant height (cm), number of branches per plant, node of the first flower, days to first flowering, pod diameter (cm), harvesting span, and green pod yield per plant (g) in the cross Bak-1 × Bak-11, and for traits like the number of branches per plant, node of the first flower, number of pods per plant, pod length (cm), harvesting span, number of seeds per pod at the edible stage, and green pod yield per plant (g) in Bak-1 × Bak-20. This pattern continued with traits such as the number of branches per plant, internodal length (cm), node of the first flower, days to first flowering, days to first pod picking, number of pods per plant, harvesting span, number of seeds per

pod at the edible stage, and green pod yield per plant (g) in the cross Bak-2 × Bak-5, and for plant height (cm), number of branches per plant, internodal length (cm), node of the first flower, number of pods per plant, pod diameter (cm), harvesting span, number of seeds per pod at the edible stage, and green pod yield per plant (g) in Bak-2 × Bak-11. Furthermore, internodal length (cm), node of the first flower, days to first flowering, number of fruit clusters per plant, number of pods per plant, pod length (cm), pod diameter (cm), number of seeds per pod at the edible stage, and harvesting span in Bak-2 × Bak-20, and traits such as plant height (cm), number of branches per plant, internodal length (cm), node of the first flower, days to first flowering, days to first pod picking, number of pods per plant, number of seeds per pod at the edible stage, and harvesting span in Bak-12 × Bak-5 showed similar inheritance patterns. The same was observed for plant height (cm), node of the first flower, days to first flowering, number of pods per plant, and green pod yield per plant (g) in the cross Bak-16 × Bak-20. These traits exhibit dominant and dominance-based complementary epistasis in their inheritance, suggesting that intensive selection is necessary to achieve significant genetic improvements in these traits.

On the other hand, positive skewness and leptokurtic distribution were found for traits such as the number of branches per plant, number of fruit clusters per plant, number of pods per plant, and green pod yield per plant (g) in Bak-1 × Bak-11, number of fruit clusters per plant in Bak-1 × Bak-20, number of fruit clusters per plant in Bak-2 × Bak-5, number of fruit clusters per plant and pod length (cm) in Bak-2 × Bak-11, the number of branches per plant in Bak-2 × Bak-20, the number of seeds per pod at the edible stage in Bak-12 × Bak-5, and the number of branches per plant and number of fruit clusters per plant in Bak-16 × Bak-20, indicating the presence of complementary gene interactions. These traits are governed by a few dominant genes, most of which have increasing effects.

Negative skewness and a platykurtic distribution were observed for traits like plant height (cm), days to

first flowering, and days to first pod picking in Bak-1 × Bak-5, and for internodal length (cm), days to first pod picking, pod length (cm), and the number of seeds per pod at the edible stage in Bak-1 × Bak-11. In Bak-1 × Bak-20, traits such as plant height (cm), internodal length (cm), days to first flowering, days to first pod picking, and pod diameter (cm) showed negative skewness. Similarly, for Bak-2 × Bak-5, plant height (cm), pod length (cm), and pod diameter (cm) exhibited negative skewness, while days to first flowering and days to first pod picking showed this pattern in Bak-2 × Bak-11. Traits like plant height (cm) and days to first pod picking in Bak-2 × Bak-20, pod length (cm), pod diameter (cm), and the number of seeds per pod at the edible stage in Bak-12 × Bak-5, and days to first pod picking, pod length (cm), pod diameter (cm), harvesting span, and the number of seeds per pod at the edible stage in Bak-16 × Bak-20, suggested the involvement of a large number of genes,

most of which exhibited duplicate inheritance and dominance with increasing effects. Under mild selection, utilizing the existing variability, rapid genetic gains can be achieved for all these traits exhibiting duplicate gene action.

The number of seeds per pod at the edible stage in the cross combination Bak-1 × Bak-20 exhibited a non-skewed and platykurtic distribution, indicating that the inheritance of this trait is governed by a few segregating genes, with most showing a decreasing effect and dominance-based complete interaction. To achieve maximum genetic gain for these traits, intense selection would be necessary. Similar findings were previously reported by Chandrakant *et al.* (2015) in dolichos bean, Prabhu *et al.* (2015), Ajay *et al.* (2016) in pigeon pea, Sumathi *et al.* (2018) in maize, Mariyammal *et al.* (2019) in green gram, Kamdar *et al.* (2020) in groundnut, and Kanavi *et al.* (2020) in green gram.

Table 2: Skewness and kurtosis in F₃ Population of Bak-1 × Bak-5 and Bak-1 × Bak-11

| F ₃ Population | | | | | | | |
|---------------------------|--------|----------|----------|----------|----------------|----------|----------|
| Bak-1 × Bak-5 | | | | | Bak-1 × Bak-11 | | |
| S.No. | Traits | Skewness | Kurtosis | Variance | Skewness | Kurtosis | Variance |
| 1. | PH | -0.05 | -0.12 | 46.46 | 0.25 | -0.62 | 62.50 |
| 2. | NB | 0.66 | -0.09 | 6.79 | 2.82 | 12.19 | 10.53 |
| 3. | IL | 0.07 | -0.53 | 0.16 | -0.13 | -1.03 | 0.30 |
| 4. | NFF | 0.53 | -0.68 | 1.11 | 0.76 | 0.10 | 1.22 |
| 5. | DFF | -1.13 | 1.69 | 64.00 | 0.28 | -0.82 | 78.42 |
| 6. | DPP | -0.18 | -0.48 | 14.52 | -0.09 | -0.26 | 13.47 |
| 7. | NFCP | 1.15 | 1.31 | 4.85 | 1.96 | 5.24 | 4.15 |
| 8. | NPP | 0.48 | 0.38 | 81.19 | 1.84 | 3.97 | 182.04 |
| 9. | PL | 0.22 | -0.44 | 0.11 | -0.53 | 0.57 | 0.13 |
| 10. | PD | 0.61 | 1.05 | 0.00 | 0.84 | 0.61 | 0.00 |
| 11. | HS | 0.06 | -0.73 | 9.12 | 0.62 | -0.38 | 7.54 |
| 12. | NSPPES | 0.01 | -0.11 | 0.17 | 0.31 | 0.52 | 0.18 |
| 13. | PY | 0.14 | -0.40 | 555.43 | 1.96 | 4.54 | 932.98 |

Skewness: positive (+) and negative (-), Kurtosis value less than 3 indicates platykurtic, more than 3 leptokurtic and three indicates mesokurtic

Table 3: Skewness and kurtosis in F₃ Population of Bak-1 × Bak-20 and Bak-2 × Bak-5

| F ₃ Population | | | | | | | |
|---------------------------|--------|----------|----------|----------|---------------|----------|----------|
| Bak-1 × Bak-20 | | | | | Bak-2 × Bak-5 | | |
| S.No. | Traits | Skewness | Kurtosis | Variance | Skewness | Kurtosis | Variance |
| 1. | PH | -0.05 | -0.35 | 84.33 | -0.13 | -0.47 | 91.58 |
| 2. | NB | 0.73 | -0.19 | 4.51 | 0.42 | -0.22 | 3.48 |
| 3. | IL | -0.19 | -0.90 | 0.26 | 0.79 | 0.18 | 0.91 |
| 4. | NFF | 0.49 | 0.27 | 1.27 | 0.91 | 0.49 | 1.75 |
| 5. | DFF | -0.10 | -0.78 | 64.92 | 0.29 | 0.69 | 145.43 |
| 6. | DPP | -0.24 | -1.07 | 14.27 | 0.22 | -0.60 | 17.10 |
| 7. | NFCP | 2.87 | 13.43 | 2.59 | 1.81 | 5.91 | 5.57 |
| 8. | NPP | 1.09 | 1.29 | 130.59 | 1.15 | 1.74 | 193.65 |
| 9. | PL | 0.46 | 2.77 | 0.07 | -0.87 | 1.03 | 0.37 |
| 10. | PD | -0.46 | 0.40 | 0.00 | -0.28 | -0.46 | 0.00 |
| 11. | HS | 0.33 | -0.10 | 5.34 | 0.04 | -0.72 | 19.22 |
| 12. | NSPPES | 0.00 | -0.77 | 0.13 | 1.15 | 1.03 | 0.13 |
| 13. | PY | 0.99 | 0.86 | 531.24 | 1.09 | 1.48 | 525.36 |

Table 4: Skewness and kurtosis in F₃ Population of Bak-2 × Bak-11 and Bak-2 × Bak-20

| F ₃ Population | | | | | | | |
|---------------------------|--------|----------|----------|----------|----------------|----------|----------|
| Bak-2 × Bak-11 | | | | | Bak-2 × Bak-20 | | |
| S.No. | Traits | Skewness | Kurtosis | Variance | Skewness | Kurtosis | Variance |
| 1. | PH | 0.19 | 0.08 | 57.69 | -0.65 | 0.72 | 45.69 |
| 2. | NB | 1.36 | 2.99 | 3.62 | 1.67 | 5.88 | 3.17 |
| 3. | IL | 1.13 | 1.71 | 0.50 | 0.58 | 0.35 | 0.23 |
| 4. | NFF | 1.02 | 0.99 | 0.92 | 0.98 | 2.08 | 0.59 |
| 5. | DFP | -0.07 | -0.04 | 75.18 | 0.05 | -0.51 | 112.97 |
| 6. | DPP | -0.51 | 0.34 | 27.17 | -0.62 | -0.17 | 27.87 |
| 7. | NFCP | 2.02 | 5.93 | 2.79 | 1.32 | 1.32 | 3.58 |
| 8. | NPP | 1.20 | 1.46 | 76.42 | 1.18 | 0.74 | 141.39 |
| 9. | PL | 1.26 | 3.92 | 0.19 | 0.41 | -0.39 | 0.11 |
| 10. | PD | 0.50 | -0.10 | 0.00 | 0.35 | -1.16 | 0.00 |
| 11. | HS | 1.21 | 1.57 | 8.17 | 1.14 | 2.12 | 2.59 |
| 12. | NSPPES | 0.02 | 0.05 | 0.09 | 1.71 | 4.91 | 0.11 |
| 13. | PY | 1.14 | 1.78 | 408.77 | 0.87 | -0.09 | 516.02 |

Table 5: Skewness and kurtosis in F₃ Population of Bak-1 2× Bak-5 and Bak-16× Bak-20

| F ₃ Population | | | | | | | |
|---------------------------|--------|----------|----------|----------|-----------------|----------|----------|
| Bak-12 × Bak-5 | | | | | Bak-16 × Bak-20 | | |
| S.No. | Traits | Skewness | Kurtosis | Variance | Skewness | Kurtosis | Variance |
| 1. | PH | 0.64 | 1.25 | 36.67 | 0.38 | 0.18 | 91.29 |
| 2. | NB | 0.49 | -0.09 | 3.45 | 0.77 | -0.08 | 6.60 |
| 3. | IL | 0.39 | -0.55 | 0.37 | 0.36 | -0.44 | 0.34 |
| 4. | NFF | 0.40 | -0.24 | 0.92 | 1.50 | 2.30 | 2.65 |
| 5. | DFP | 0.69 | -0.18 | 68.22 | 0.67 | -0.30 | 100.71 |
| 6. | DPP | 0.11 | -0.67 | 21.98 | -0.49 | 0.13 | 4.74 |
| 7. | NFCP | 2.47 | 9.94 | 4.79 | 2.73 | 10.15 | 11.42 |
| 8. | NPP | 0.93 | 0.52 | 93.79 | 0.13 | -0.54 | 157.57 |
| 9. | PL | -0.03 | -0.48 | 0.17 | -0.18 | 0.32 | 0.33 |
| 10. | PD | -0.52 | -0.03 | 0.00 | -0.22 | 0.16 | 0.00 |
| 11. | HS | 0.75 | 0.04 | 15.26 | -0.45 | 0.50 | 6.27 |
| 12. | NSPPES | 0.38 | -0.46 | 0.12 | 1.49 | 2.70 | 0.10 |
| 13. | PY | 0.69 | 0.41 | 384.54 | 0.04 | -0.94 | 960.66 |

Selection of superior lines

All the 640 F₃ progenies were classified to identify superior lines with higher pod yield per plant when compared with the yield of parents and check cultivars. On the basis of yield best three lines were selected among 80 plants from each cross. Considering all the important and yield attributing traits, on which

selection is based, best three segregants in the cross combination Bak-1 × Bak-5, *viz.* plant numbers 38, 54 and 36 that produced pods more than 120 g per plant with greater than 50 pods per plant along with more than 3.00 number of seeds per pod were identified as a best segregants.

Table 6: Selected segregants on the basis of yield attributing traits in Bak-1 × Bak-5 and Bak-1 × Bak-11

| Traits | Bak-1 × Bak-5 | | Segregants | | | Bak-1 × Bak-11 | | Segregants | | |
|--------|---------------|------------|--------------|--------------|--------------|----------------|------------|-------------|--------------|--------------|
| | Parents mean | Check mean | Plant No. 38 | Plant No. 54 | Plant No. 36 | Parents mean | Check mean | Plant No. 1 | Plant No. 28 | Plant No. 57 |
| PY | 76.39 | 68.85 | 129.29 | 127.35 | 124.97 | 77.65 | 68.85 | 171.00 | 152.76 | 131.80 |
| NPP | 39.00 | 37.92 | 55 | 51 | 50 | 40.00 | 37.92 | 75 | 67 | 57 |
| NSPPES | 2.30 | 2.92 | 3.60 | 3.30 | 3.20 | 2.31 | 2.92 | 3.00 | 2.60 | 2.40 |
| NFCP | 2.70 | 4.89 | 10 | 9 | 3 | 2.15 | 4.89 | 7 | 11 | 5 |

Table 7: Selected segregants on the basis of yield attributing traits in Bak-1 × Bak-20 and Bak-2 × Bak-5

| Bak-1 × Bak-20 | | | Segregants | | | Bak-2 × Bak-5 | | Segregants | | |
|----------------|--------------|------------|--------------|-------------|--------------|---------------|------------|--------------|--------------|--------------|
| Traits | Parents mean | Check mean | Plant No. 32 | Plant No. 1 | Plant No. 11 | Parents mean | Check mean | Plant No. 16 | Plant No. 14 | Plant No. 13 |
| PY | 74.65 | 68.85 | 125.05 | 115.18 | 105.35 | 66.25 | 68.85 | 130.40 | 126.40 | 117.80 |
| NPP | 39.50 | 37.92 | 62 | 53 | 52 | 33.50 | 37.92 | 77 | 68 | 61 |
| NSPPES | 2.28 | 2.92 | 2.20 | 3.20 | 2.80 | 2.26 | 2.92 | 3.40 | 3.30 | 3.00 |
| NFCP | 2.65 | 4.89 | 11 | 7 | 5 | 1.90 | 4.89 | 6 | 4 | 8 |

Table 8: Selected segregants on the basis of yield attributing traits in Bak-2 × Bak-11 and Bak-2 × Bak-20

| Bak-2 × Bak-11 | | | Segregants | | | Bak-2 × Bak-20 | | Segregants | | |
|----------------|--------------|------------|--------------|-------------|--------------|----------------|------------|--------------|--------------|--------------|
| Traits | Parents mean | Check mean | Plant No. 37 | Plant No. 1 | Plant No. 38 | Parents mean | Check mean | Plant No. 24 | Plant No. 32 | Plant No. 30 |
| PY | 67.51 | 68.85 | 120.96 | 93.30 | 93.24 | 64.51 | 68.85 | 104.40 | 102.60 | 100.80 |
| NPP | 34.50 | 37.92 | 48 | 37 | 37 | 34.00 | 37.92 | 55 | 54 | 53 |
| NSPPES | 2.27 | 2.92 | 2.80 | 2.00 | 2.00 | 2.24 | 2.92 | 3.40 | 3.20 | 3.80 |
| NFCP | 1.35 | 4.89 | 8 | 3 | 5 | 1.85 | 4.89 | 8 | 4 | 6 |

Table 9: Selected segregants on the basis of yield attributing traits in Bak-12 × Bak-5 and Bak-16 × Bak-20

| Bak-12 × Bak-5 | | | Segregants | | | Bak-16 × Bak-20 | | Segregants | | |
|----------------|--------------|------------|-------------|--------------|--------------|-----------------|------------|--------------|--------------|--------------|
| Traits | Parents mean | Check mean | Plant No. 1 | Plant No. 65 | Plant No. 35 | Parents mean | Check mean | Plant No. 53 | Plant No. 74 | Plant No. 51 |
| PY | 78.73 | 68.85 | 109.33 | 98.10 | 97.74 | 86.12 | 68.85 | 135.12 | 130.88 | 129.12 |
| NPP | 47.50 | 37.92 | 55 | 50 | 49 | 49.50 | 37.92 | 61 | 58 | 57 |
| NSPPES | 2.33 | 2.92 | 3.20 | 2.80 | 2.60 | 2.63 | 2.92 | 3.20 | 3.80 | 3.40 |
| NFCP | 2.30 | 4.89 | 7 | 5 | 3 | 2.75 | 4.89 | 11 | 6 | 3 |

In the cross combination Bak-1 × Bak-11, plant numbers 1, 28, and 57 were identified as superior, producing over 130 g per plant, with more than 55 pods per plant, over 2.20 seeds per pod. Similarly, in the Bak-1 × Bak-20 cross combination, plant numbers 32, 1, and 11 were identified as the best segregants, yielding over 100 g per plant with more than 50 pods, over 2.20 seeds per pod. In the cross combination Bak-2 × Bak-5, plant numbers 16, 14, and 13 were identified for producing over 115 g per plant, with more than 60 pods, over 3.00 seeds per pod. For the Bak-2 × Bak-11 combination, plant numbers 37, 1, and 38 were identified for producing more than 90 g per plant, with over 35 pods, more than 1.90 seeds per pod. In the cross combination Bak-2 × Bak-20, plant numbers 24, 32, and 30 were recognized as the best segregants, producing more than 100 g per plant with over 50 pods, more than 3.00 seeds per pod. In the Bak-12 × Bak-5 cross, plant numbers 1, 65, and 35 were identified for producing over 97 g per plant, with more than 48 pods, over 2.50 seeds per pod. Similarly, in the Bak-16 × Bak-20 cross combination, plant numbers 53, 74, and 51 were recognized for producing over 125 g per plant, with more than 60 pods, over 3.00 seeds per pod. These lines will undergo further

testing to confirm their yield stability over time and their potential for future use. Previous studies in chickpea have demonstrated that superior lines derived from transgressive segregation exhibit higher progeny values compared to their parents (Koseoglu *et al.*, 2017; Ceylan *et al.*, 2019). Genetic research suggests that transgressive segregation typically arises from the combination of alleles from both parents, with complementary gene effects distributed among them (Risenberg *et al.*, 1999). In F₃ generations, transgressive segregants may result from dominance × dominance and additive × additive interactions, which are fixable due to the recombination of genes with positive effects. This phenomenon has been previously observed in lentils for seed yield per plant (Chahota *et al.*, 2007), peanuts for mature pod weight and grain weight per plant (Shreya *et al.*, 2017), rice for flowering days (Koide *et al.*, 2019), and pigeon pea for earliness (Srivastava & Saxena, 2019).

Conclusion

The process of hybridization and recombination generated substantial genetic variability in the faba bean F₃ populations analyzed. Rare gene combinations in segregating generations, accompanied by additive

gene action, resulted in extreme phenotypes that surpassed the values of the parent plants. A high degree of variability in traits was observed in the F₃ generation, attributed to heterozygosity. The majority of the traits studied exhibited positive skewness and were controlled by multiple genes, indicating quantitative inheritance. Based on yield performance in comparison to the parents and the check cultivar, a total of twenty-four superior progenies were identified within the F₃ population, each demonstrating higher pod yield per plant than both the parents and the respective check cultivars.

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