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## Research Article

# Evaluation of quantitative traits distribution in $F_2$ backcross population of purple wingedbean [*Psophocarpus tetragonolobus* (L.) DC] and its application in selection

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**Abstract**

Wingedbean [*Psophocarpus tetragonolobus* (L.) DC] is a nutritious legume vegetable with high potential for food diversification in Indonesia, yet its cultivation remains limited due to late maturity and unstable yield. Information on the distribution of quantitative traits, heritability, and genetic advance in segregating populations is essential to determine effective selection criteria in breeding programs. This study evaluated the distribution patterns, heritability, expected genetic advance, and selection limits of quantitative traits in a $BC_1F_2$ population of purple wingedbean. $BC_1F_2$ backcross population generated through selfing of $BC_1$ plants originating from the cross between $F_1$ (PLB 2.3 × MDM 1.2) and the recurrent parent MDM 1.2. Total of 161 plants were observed for quantitative traits, including flowering time, harvest age, yield components, and pod characteristics. Normality was tested using the Kolmogorov–Smirnov method, followed by skewness and kurtosis analysis for non-normally distributed traits. Results showed that only pod length and fresh pod weight per pod were normally distributed, while the remaining traits deviated from normal distribution, indicating segregation effects and possible influence of major genes, epistatic interactions, and environmental variation. Most traits exhibited high broad-sense heritability and high expected genetic advance, particularly number of flowers per plant, number of fresh pods, pod length, and pod weight per plant, suggesting good prospects for improvement through selection. Selection based on multiple yield-related traits identified several superior individuals with higher yield potential. These traits are recommended as effective selection criteria for developing early-maturing and high-yielding purple wingedbean varieties in subsequent generations.

**Keywords**: purple wingedbean, $BC_1F_2$ population, heritability, genetic advance

## INTRODUCTION

Wingedbean [*Psophocarpus tetragonolobus* (L.) DC] is a legume belonging to the Fabaceae family and is well known in Indonesia, although it is still rarely cultivated. This plant is a rich source of protein, carbohydrates, vitamins, minerals, and fiber (Tanzi *et al*., 2019). Therefore, wingedbean could be a good candidate for food diversification in Indonesia, particularly as a non-grain food source or vegetable (Sharma and Patel, 2017).

It has the advantage as a vegetable because every edible part of the plant contains high protein. Protein content in the flower is 2.8–5.6 g; leaves 5–7.6 g; young pods 1.9–4.3 g; fresh seeds 4.6–10.7 g; and tubers 3–15 g, per 100 g fresh weight (Handayani *et al*., 2015). Additionally, the fresh pods of the wingedbean plant are rich in vitamin A (Eagleton *et al*., 2023). Purple wingedbean is easily recognized by its striking purple color, which comes from

natural pigments called anthocyanins. These compounds are well known for their health benefits, such as functioning as antioxidants, reducing inflammation, and even helping to protect against cancer (Speer *et al*., 2020; Lakshmikanthan *et al*., 2024). Local verities cultivated by farmers generally take more than 100 days for the first flowers to appear. On the other hand, to date, only a few superior wingedbean varieties have been released by the government (Krisnawati, 2010). Therefore, to overcome the challenges in wingedbean cultivation, it is imperative to breed for wingedbean varieties that are early maturing and with high yields (Nentia *et al*., 2023).

Quantitative traits, which are characterized by continuous phenotypic variation, are controlled by many genes and influenced by environmental factors generally exhibit a normal distribution, indicating polygenic genetic control (Yulianah, 2021). Estimated heritability values and expected genetic progress are crucial for determining the effectiveness of selection (Satriawan *et al*., 2017), especially in segregation generations like $F_2$, which still exhibit high variability (Parari *et al*., 2022). However, research related to inheritance and the potential for improvement of agronomic traits in $BC_1F_2$ of purple wingedbeans is still limited. This study aims to evaluate the distribution pattern, heritability value, and expected genetic progress of quantitative traits in the $BC1F_2$ population of purple wingedbeans as a basis for selection in the development of early maturing and high-yielding superior varieties.

## MATERIALS AND METHODS

*Plant Material :* The experiment was conducted during the period from September 2024 to May 2025 at the Agrotechno Park of Brawijaya University, Jatikerto Village, Kromengan Subdistrict, Malang Regency, East Java. The $BC1F_2$ population used in the present study was derived from the $BC_1$ generation of the cross (PLB 2.3 x MDM 1.2 ) x MDM 1.2. The backcross $F_2$ population consisted of 161 plants, while the parental population consists of 30 plants each in PLB 2.3 plants and MDM 1.2. Planting in the $F_2$ backcross population, PLB 2.3, and MDM 1.2 were respectively laid out using the single plant method, wherein each plant was planted individually without replication, in the same environment, adopting a spacing of 1.5m x 1.25m.

Observations were recorded made on 10 quantitative characteristics, including days to flower, fresh pod harvest age, number of flowers per plant, number of flowers per stalks, number of fresh pods, pod length, pod width, fresh pod weight, pod weight per plant and fruit set, in each of the plants. The data were subjected to normality tests using the Kolmogorov-Smirnov test. For traits that did not follow a normal distribution, skewness and kurtosis tests were performed in the $F_2$ backcross population using IBM SPSS Version 25 software. The broad sense heritability and expected genetic advance were estimated as per Allard (1960).

The selection of the $F_2$ backcross population was determined by calculating the selection limit value was calculated using the formula according to (Novita *et al.,* 2022). The highest selection limit was used for the observed variables of flower number, fresh pod number, fresh pod weight per plant, and pod length. The lowest selection limit was used for the observed variables of days of flowering and fresh pod harvest age.

## RESULTS AND DISCUSSION

*Evaluation of Quantitative Character Variation*: Analysis of observations on 10 quantitative traits in the $F_2$ backcross population of wingedbean plants (**Table 1**) showed high phenotypic variability among individuals. The days to flowering was observed to range from 89–236 DAP and fresh pod harvest age ranged from 131–250 DAP (**Table 1**).

This variation reflects differences in genotype responses to the environment and the influence of genetic factors that vary among individuals (Farida *et al*., 2018). High rainfall during the growth period, reaching 372–475 mm/month (BMKG, 2024), also contributed to reduced fruit set due to flower drop. Heavy rain also has the potential to wash away pollen grains and damage the surface of flowers, thereby inhibiting the pollination process (Ngawit *et al*., 2023). In addition, Eagleton (2019) stated that several wingedbean accessions planted in areas with fertile environments and high rainfall showed a longer vegetative phase before flowering.

The number of flowers per stalk has a narrow range (3–7 flowers), but the number of flowers per plant varied greatly (**Table 2**), indicating a wide genetic potential for flowering with fairly high diversity. The number of fresh pods per plant ranged from 5–138 pods, pod length from 12.60–54.90 cm, and pod width from 0,71–8.25 cm, indicating moderate to low diversity (**Table 2**) in pod dimensions. Fresh pod weight varied from 0.52–47.14 g, while fresh pod weight per plant ranged from 16.02–4555.67 g. Fruit set showed a low average of 15.74%, with a range of 3.48–66.36%, attributed to environmental influences on reproductive success. This level of diversity also reflects the emergence of parental traits. This level of diversity also indicates the expression of parental traits. The wide variation observed in pod dimensions, fresh pod weight, and fruit set is associated with the segregation of parental traits in the $BC_1F_2$ population. The $F_1$ hybrid is characterized by early flowering, whereas the recurrent parent MDM 1.2 exhibits late flowering but superior pod weight, pod width, and pod length, which may contribute to the observed phenotypic diversity in the segregating population (Yulianah, 2021). However, apparent phenotypic variation does not always correspond to true genetic diversity, as it may be influenced by environmental factors (Mohanty *et al.,* 2013).

The traits used as selection criteria must be capable of being inherited to the next generation so that the selection

**Table 1. Mean, standard deviation, minimum, maximum, heritability and expected genetic advance value of F$_2$ backcross wingedbean population**

| S.No. | Traits | Mean ± Std. Deviation | Minimum | Maximum | h$^2_{bs}$(%) | Category | EGA | EGA (%) | Category |
|---|---|---|---|---|---|---|---|---|---|
| 1 | Days to flower | 178.15 ± 37.75 | 89 | 236 | 89.13 | High | 59.23 | 33.24 | High |
| 2 | Fresh pod harvest age (days) | 221.57 ± 21.13 | 131 | 250 | 63.96 | High | 23.72 | 10.70 | High |
| 3 | Number of flowers per stalk | 4.78 ± 1.04 | 3.00 | 7.00 | 16.87 | Low | 0.31 | 6.46 | Moderate |
| 4 | Number of flowers per plant | 407.35 ± 262.07 | 65.00 | 1350 | 78.08 | High | 360.13 | 88.41 | High |
| 5 | Number of fresh pods | 51.94 ± 25.93 | 5.00 | 138 | 90.48 | High | 41.29 | 79.50 | High |
| 6 | Pod length (cm) | 28.73 ± 5.03 | 12.60 | 39.89 | 77.47 | High | 9.38 | 32.05 | High |
| 7 | Pod width (cm) | 1.54 ± 0.31 | 0.71 | 2.43 | 74.58 | High | 0.95 | 51.00 | High |
| 8 | Fresh pod weight (g) | 24.59 ± 5.12 | 0.52 | 47.14 | 49.73 | Moderate | 4.48 | 18.23 | High |
| 9 | Pod weight per plant (g) | 1299.32 ± 768.28 | 16.02 | 4555.67 | 85.57 | High | 1157.08 | 89.05 | High |
| 10 | Fruit set (%) | 15.74 ± 9.83 | 3.48 | 66.36 | 11.27 | Low | 1.95 | 12.38 | High |

**Table 2. Normality test with Kormogorov-Smirnov F$_2$ backcross wingedbean population**

| S.No. | Traits | F$_2$ Backcross | |
|---|---|---|---|
| | | Significance | Data distribution |
| 1 | Days to flower | 0.00 | Not normal |
| 2 | Fresh pod harvest age | 0.00 | Not normal |
| 3 | Number of flowers per plant | 0.00 | Not normal |
| 4 | Number of fresh pods | 0.02 | Not normal |
| 5 | Number of flowers per stalk | 0.00 | Not normal |
| 6 | Pod length | 0.082* | Normal |
| 7 | Pod width | 0.019 | Not normal |
| 8 | Fresh pod weight | 0.079* | Normal |
| 9 | Pod weight per plant | 0.005 | Not normal |
| 10 | Fruit set | 0.00 | Not normal |

Remarks : * = Data are considered normally distributed when Sig. > 0.05. Significance values of 0.00 indicate p < 0.001 as rounded by the software output.

process can be carried out effectively. This can be analysed through the calculation of heritability values. Heritability values combined with expected genetic advance will provide better results in selection as compared to looking at heritability only (Riyanto *et al*., 2023).

The estimates of expected genetic advance (EGA) and heritability were high for most of the traits (**Table 1**), while for the number of flowers per stalk it was observed to be nd. High heritability coupled with high genetic advance reflects strong selection effectiveness, serving as a practical basis for selection in segregating populations and breeding programs (Govintharaj *et al*., 2018; Dutta *et al*., 2021). Fresh pod weight (g) exhibited moderate heritability accompanied by high genetic advance as a percentage of the mean (GAM), suggesting that the trait is predominantly governed by additive gene action with some degree of environmental influence. According to Patel *et al*. (2024), such traits can be effectively improved

through mass selection combined with progeny testing and pedigree selection. The number of flowers per stem and fruit set exhibited moderate heritability and EGA. Therefore, selection based on these traits could have less impact in the subsequent generations.

*Evaluation of quantitative character distribution:* A normality test using the Kolmogorov-Smirnov method was conducted to evaluate whether the quantitative character data followed a normal distribution. Based on the test results (**Table 2**), of the ten characters observed, only two , namely pod length and fresh pod weight per pod, showed a normal distribution (**Fig.1**), as indicated by a significance value > 0.05.

According to Allard (1995) in Sudharmawan *et al*. (2019), characters that follow a normal distribution are generally controlled by many genes (polygenic) with minor effects. A normality test using the Kolmogorov–Smirnov method
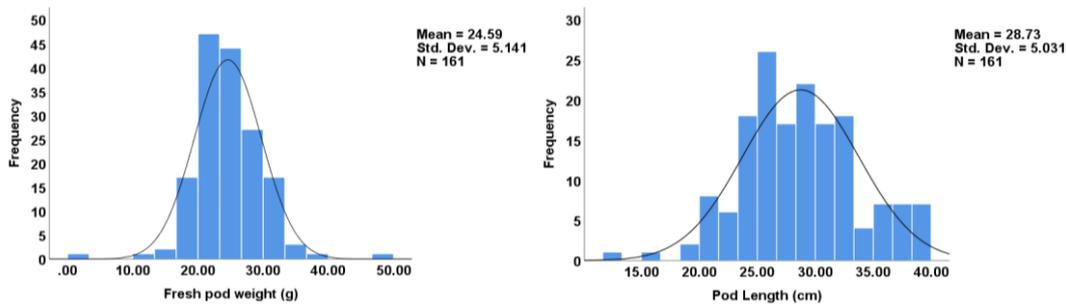
**Fig. 1. Normal distribution curve of fresh pod weight and pod length characters in the F$_2$ backcross population**

**Table 3. Skewness and kurtosis test of F$_2$ backcross wingedbean population**

| S.No. | Traits | F$_2$ Backcross | | | |
|-------|--------|------------------|---|---|---|
| | | *Skewness* | Data distribution | *Kurtosis* | Data distribution |
| 1 | Days to flower | -0.58 | Positively skewed | -1.02 | Platykurtic |
| 2 | Fresh pod harvest age | -1.53 | Positively skewed | 2.88 | Leptokurtic |
| 3 | Number of flowers per plant | 1.29 | Negatively skewed | 1.42 | Platykurtic |
| 4 | Number of flowers per stalk | 0.09 | Negatively skewed | -0.61 | Platykurtic |
| 5 | Number of fresh pods | 0.77 | Negatively skewed | 0.76 | platykurtic |
| 6 | Pod width | 0.51 | Negatively skewed | 0.27 | platykurtic |
| 7 | Pod weight per plant | 1.17 | Negatively skewed | 2.25 | Leptokurtic |
| 8 | Fruit set | 2.00 | Negatively skewed | 6.07 | Leptokurtic |

was conducted to evaluate whether the quantitative trait data followed a normal distribution. Based on the results (**Table 2**), only two out of ten traits, namely pod length and fresh pod weight per pod, showed a normal distribution (Sig. > 0.05), while the remaining traits deviated from normality. According to Allard (1995), as cited in Sudharmawan *et al.* (2019), quantitative traits with normal distribution patterns are generally controlled by many genes (polygenic) with minor effects. Deviation from normal distribution in segregating populations such as F$_2$ backcross may indicate the presence of major genes, epistatic interactions, or skewed segregation patterns. In addition, environmental variation may also contribute to increased phenotypic variability.

*Skewness and Kurtosis tests on quantitative characteristics:* Abnormal data often shows an uneven distribution pattern, for example, leaning too much to one side (skewed) or too sharp or flat (peaked or blunt). Data distribution that is not normal can be identified by testing skewness and kurtosis. The skewness analysis results showed that most characters have positive skewness values, indicating a left-skewed distribution (**Table 4**), with the exception of flowering age and fresh harvest age, which showed negative skewness or right-skewed distribution (**Fig. 2a and Fig. 2b.** This negative skewness suggests the presence of duplicate epistasis gene

action, *i.e.*, the interaction between two genes that can each produce similar phenotypes (Griffiths *et al.*, 2012). Conversely, positive skewness suggests complementary epistasis, where the expression of one gene depends on the presence of another gene with a specific function (Ardiarini *et al.*, 2022). This imbalance reinforces the suspicion that these traits are not yet genetically stable and are still undergoing segregation.

The results of kurtosis analysis (**Table 4**) showed that some characters (**Fig. 2b; Fig. 2g; Fig. 2h**) have a leptokurtic (peaked) distribution, while others (**Fig. 2a; Fig. 2c; Fig. 2d; Fig. 2e; Fig.2f**) show a platykurtic (blunt) distribution. A leptokurtic distribution indicates that the character is likely controlled by a few genes with large effects, causing the data to be concentrated around the mean value and only a few individuals to deviate (Sulistyowati *et al.*, 2016). Meanwhile, a platykurtic distribution indicates control by many additive genes that contribute small amounts to total variance, resulting in more even distribution and lower environmental influence (Roy, 2000; Lestari *et al.*, 2023 in Riyanto *et al.*, 2023). Thus, information on these distribution patterns is important for determining the appropriate selection approach in breeding (Herawati *et al.*, 2019). Based on kurtosis analysis, fresh pod harvest age, pod weight per plant, and fruit set exhibited

a leptokurtic distribution, indicating that most genotypes were clustered around the mean. This distribution pattern suggests limited scope for effective selection, particularly when accompanied by low genetic variability (Muthupriya *et al.*, 2016). Therefore, the non-normal distribution observed in most traits suggests that both genetic factors and environmental effects may play roles in shaping trait expression in this population.
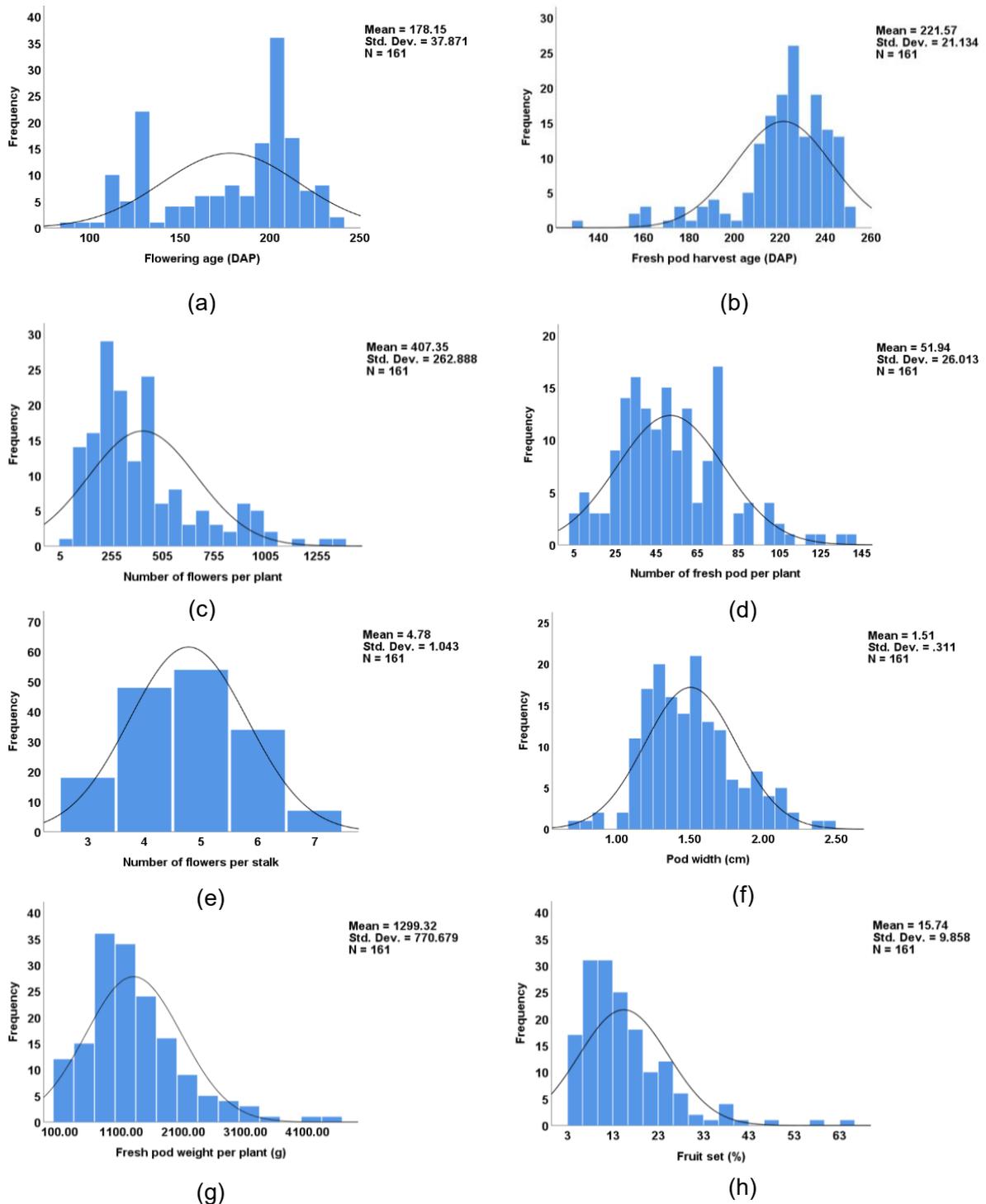


Fig. 2. (a) Flowering age; (b) Fresh pod harvest age; (c) Number of flowers per stalk; (d) Number of flowers per plant; (e) Number of fresh pods; (f) Pod width; (g) Pod weight per plant; (h) Fruit set

**Table 4. Performance of selected plants in F$_2$ backcross population of wingedbean**

| Selected plant | Traits | | | | |
|---|---|---|---|---|---|
| | Number of flower per plant | Number of fresh pod per plant | Pod length (cm) | Fresh pod weight (g) | Pod weight per plant (g) |
| 54 | 1170 | 123 | 28.44 | 24.44 | 3006.01 |
| 104 | 945 | 136 | 29.02 | 24.98 | 3396.65 |
| 133 | 774 | 138 | 38.40 | 33.01 | 4555.67 |
| 160 | 110 | 73 | 28.70 | 24.72 | 1804.39 |
| 164 | 870 | 74 | 37.10 | 34.11 | 2366.16 |
| 169 | 950 | 84 | 32.00 | 34.36 | 2886.55 |
| 170 | 462 | 77 | 39.89 | 38.11 | 2934.74 |
| 285 | 475 | 106 | 31.40 | 27.04 | 2865.90 |
| 319 | 1320 | 101 | 32.70 | 22.97 | 2319.54 |
| Selection limit | 868 | 97 | 37.20 | 33.61 | 2651 |

*Selected genotypes:* Based on the selection results (**Table 4**), the traits flowering age and fresh harvest age were not used as selection criteria in this study because the selection limit values obtained were still relatively high and far from the expected early maturing criteria, which was less than 80 days after planting (DAP). Therefore, selection based on these two characteristics is considered ineffective and not recommended for this generation, since the aim of the study was to get genotypes with an early harvest age.

Six individuals (codes 54, 104, 164, 169, and 319) were observed to produce above average number of flowers per plant as compared to the population mean. Five individuals (54, 104, 133, 285, and 319) were also selected based on higher pod number. Longest pods were observed in three individuals (codes 133 and 170) with a range of 37–39 cm, longer than the range of 10.0 – 25.70 cm (Chandel *et al.,* 1984) and 5–32 cm (Sukma *et al.,* 2015). The maximum fresh pod weight was observed in the individuals 164, 169, and 170, while the pod weight per plant was maximum in six individuals (codes 54, 104, 133, 169, 170, and 285).

Based on the results of this study on the BC$_1$F$_2$ population of purple wingedbean, only two quantitative traits, namely pod length and fresh pod weight per pod, exhibited normal distribution, while most other traits showed non-normal distribution with skewed and peaked patterns, indicating strong genetic segregation in this generation. Several traits, including days to flower, fresh pod harvest age, number of flowers per plant, number of fresh pods per plant, pod length, and pod weight per plant, showed high heritability and high expected genetic advance, suggesting that these traits are predominantly controlled by genetic factors and are responsive to selection. However, none of the indivisuals were observed to be early-maturing. Nevertheless, six individuals showed high yield potential based on pod weight per plant, namely genotypes 54,

104, 133, 169, 170, and 285, which can be considered as promising candidates for further selection and breeding in subsequent generations. Most quantitative traits in the F$_2$ backcross population of purple wingedbean showed non-normal distributions, except for pod length and fresh pod weight. Several traits with high heritability and expected genetic advance were identified as selection criteria. Six genotypes showed high yield potential based on fresh pod weight per plant. Further research is recommended to continue to the BC$_1$F$_3$ generation to increase genetic variability and improve the chances of obtaining early-maturing and high-yielding individuals.

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