

Selection for early maturity in F4 families of winged bean based on descriptive statistical analysis and Genotype-by-Trait grouping

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Abstract. *Yulianah I, Kuswanto, Mubarak A, Prasasti OT. 2026. Selection for early maturity in F4 families of winged bean based on descriptive statistical analysis and Genotype-by-Trait grouping. Asian J Agric 10 (1): g100121. <https://doi.org/10.13057/asianjagric/g100121>.* The winged bean (*Psophocarpus tetragonolobus*) is a nutrient-rich tropical legume with the potential to enhance protein security in developing regions. However, its adoption is limited due to long growth duration and low yield. This study evaluated genetic variability, trait correlations, and genotype-trait relationships among 22 F4 winged bean families derived from the cross between PLB (early, high pod number) and MDM (late, large-seeded). This study used a row planting design. Ten plants were planted per genotype. Quantitative traits, including flowering age (FLA), fresh pod harvest age (FPHA), pod dimensions (PDL, PDW), pod weight (PWG), pods per plant (PPP), fresh pod weight per plant (FPWP), seeds per pod (SPP), and hundred-seed weight (HSW), were analyzed using descriptive statistics, Pearson correlation, and Genotype-by-Trait (G×T) analysis with Principal Component Analysis (PCA). Substantial phenotypic variability and transgressive segregation were observed, with several lines surpassing parental performance. PM 126.126 matched MDM's high yield (FPWP=825.9 g/plant), while PM 1.1 combined high yield (FPWP=825.9 g/plant) with early flowering (FLA=64.57 days). Correlation analysis revealed strong positive associations between flowering age and pod weight ($r=0.81$) and between pod weight and hundred-seed weight ($r=0.81$), indicating a coordinated development of late maturity, heavy pods, and large seeds. Negative correlations between the number of pods per plant and fresh pod weight ($r=-0.47$) and seed weight ($r=-0.43$) showed a yield component trade-off. PCA-based (G×T) analysis explained 84.0% of the total variation and classified genotypes into groups: high-yield types emphasizing pod/seed size (e.g., PM 126.126), high pod number types (PM 99.99), and balanced performers (PM 57.57). Three early-maturing genotypes PM 99.99, PM 1.1, and PM 131.131 combined early flowering (64.29-64.57 days) with competitive yields (FPWP=743.6-825.9 g/plant), demonstrating the effectiveness of advanced-generation selection for developing early, high-yielding winged bean cultivars for tropical farming systems.

Keywords: Correlation analysis, genetic variability, (G×T) with PCA, winged bean, yield components

INTRODUCTION

The winged bean (*Psophocarpus tetragonolobus*) is a multipurpose, leguminous crop adapted to tropical environments, valued for its exceptional nutritional composition and diverse agronomic uses (Eagleton 2020; Kumar and Rajalakshmi 2023). The seeds contain 30-40% protein, significantly exceeding that of common legumes such as soybean and mung bean, positioning the winged bean as a strategic crop for addressing protein malnutrition in developing countries (Boniface et al. 2024). However, the winged bean is still underutilized due to its long growth cycle (>100 days) and relatively low seed yields (Eagleton 2020; Kumar and Rajalakshmi 2023).

To enhance adoption, developing cultivars combining early maturity with high yield is essential. Early maturity shortens the production cycle, enables higher planting densities, increases farmer returns, and reduces exposure to unfavorable conditions. Variability in maturity traits allows selection of superior early-maturing families through systematic evaluation. A breeding-derived early-maturing cultivar would improve competitiveness.

Plant breeding depends on systematic evaluation and comparison of germplasm to identify genotypes with superior trait combinations. Descriptive statistics provide foundational tools for quantifying and understanding phenotypic variation within segregating populations (Eagleton 2020; Boniface et al. 2024; Ho et al. 2024). Key descriptive parameters—mean, Standard Deviation (SD), and Coefficient of Variation (CV)—characterize the distribution and relative magnitude of trait expression across genotypes.

The Coefficient of Variation ($CV = SD/mean \times 100$) is particularly valuable for comparing trait variability on a scale-independent basis, enabling researchers to identify traits with high selection potential (Kumar and Rajalakshmi 2023). High CV values for yield and maturity-related traits indicate substantial genetic or phenotypic diversity available for targeted selection (Shonde et al. 2023; Zewdu et al. 2024).

Understanding associations among traits is critical for effective selection. Phenotypic correlations quantify the linear relationship between pairs of traits and reveal whether genetic gains in one trait may affect other traits (Berhanu et al. 2023; Zhang et al. 2024). For early maturity breeding, identifying genotypes that combine short growth

cycles (early flowering, early maturity) with high seed yield requires knowledge of the phenotypic correlation between maturity and yield components.

Positive correlations between maturity-related traits (e.g., days to flowering and days to maturity) and negative correlations between maturity and yield components have been documented in various legumes, reflecting the biological trade-offs between life history strategies (Singh et al. 2019). Conversely, some yield components such as harvest index or thousand-seed weight may show positive correlations with early maturity, offering opportunities for simultaneous selection (Kumar and Rajalakshmi 2023). Correlation analysis helps identify genotypes with desirable trait combinations.

While correlation analysis shows pairwise relationships, Genotype-by-Trait ($G \times T$) clustering classifies genotypes based on overall trait profiles (Boniface et al. 2024). This integrates multiple traits, identifying genotypes performing well across desired characteristics.

For early maturity selection, $G \times T$ clustering evaluates maturity traits (days to flowering, 50% pod maturity), yield components (pod number, seed number, seed weight), and overall yield. Genotypes clustering together represent distinct phenotypic classes, helping select lines systematically (Shonde et al. 2023).

While many legume breeding studies focus on F2 and F3 populations, where genetic variability is high, the F4 generation offers distinct advantages for phenotypic evaluation and selection. By the F4 generation, increased homozygosity within families has stabilized most segregating loci, reducing segregation variance and environmental noise relative to earlier generations. This allows more reliable selection of superior families (Singh et al. 2019).

Additionally, the F4 generation retains sufficient heterogeneity among families to differentiate superior lines from less promising ones, making it an optimal stage for family-based selection decisions. Descriptive statistics and correlation analyses conducted in F4 populations thus provide more stable and representative indicators of likely breeding performance than earlier generations (Kumar and Rajalakshmi 2023).

This study evaluates F4 winged bean families derived from a cross between parental lines PLB 2.3 and MDM 1.2, extending prior selection for early maturity and high yield conducted in the F3 generation. By systematically assessing phenotypic trait distributions and correlations using descriptive statistics (mean, SD, CV), and by applying Genotype-by-Trait clustering to classify families into phenotypically distinct groups, this research aims to provide empirically sound criteria for selecting elite families. This integrated approach underscores the importance of combining descriptive statistical evidence with multivariate trait analysis to accelerate the development of competitive, early-maturing winged bean cultivars suited to diverse tropical farming systems (Kuswanto et al. 2024).

MATERIALS AND METHODS

Study area

The research was conducted from December 2023 to June 2024 at the Agrotechnopark Experimental Field of Brawijaya Universitas, Malang, East Java, Indonesia, which is located in Jatikerto Village, Kromengan District, Malang. The land utilized in this study is situated at an altitude of 321 meters above sea level.

Materials

The 22 F4 families of winged bean, derived from a cross between PLB 2.3 and MDM 1.2 and selected in the F3 generation, exhibited clear segregation for all measured traits (Table 1). The mean flowering age for the F4 population was 69.2 days after planting (DAP) with a range of 63 to 75 DAP. The fresh harvest age averaged 86.5 DAP (range: 80-93 DAP). The number of pods per plant and fresh pod weight per plant also showed considerable variation, with means of 94.5 pods (range: 79-110) and 1389 g (range: 998-1780 g), respectively. The observed ranges in the F4 families exceeded those of the parents, indicating successful segregation of the traits.

Methods

This study used a row planting design. Ten plants were planted per genotype. The seeds were soaked in warm water for 24 hours prior to planting, which was carried out in small polybags containing a planting medium consisting of soil and manure in a 1:1 ratio. Following a period of two weeks, the seedlings were transplanted to the field in the afternoon. Watering was conducted at regular intervals in the afternoon for the initial two weeks. Following a period of two weeks, irrigation was administered once weekly, contingent on the absence of precipitation. The process of weeding was conducted within a period of two weeks, with a focus on addressing any areas where plant material was absent. The fertilization process entailed the excavation of soil at a depth of 10 cm from the plants' immediate vicinity. The fertilization of each plant necessitates the application of 5 g of urea, 7.5 g of SP36, and 5 g of KCl, which is to be administered at the two-week mark following planting. During the flowering and pod formation stages, fertilization is conducted on a weekly basis using a NPK fertilizer at a dosage of 5 g per plant. The management of pests and diseases involves the utilization of chemical methods for moderate to high infestation levels, and mechanical methods for low infestation levels.

A quantitative observational study was conducted on a range of plant specimens within the designated plot. The observation variables encompassed several metrics, including flowering age (which is defined as the number of days from planting until 50% of plants flower for the first time), fresh pod harvest age (which is measured as the number of days from planting until fresh pods are ready for harvest), pod length, pod width, and fresh weight per pod (these variables were derived from an average of ten pods per plant), harvest frequency (defined as the number of harvests at 120 days after planting, with a four-day harvest interval), number of pods per plant (based on the number of

Pods at 120 days), pod weight per plant (calculated as the number of pods multiplied by the fresh weight per pod), number of seeds per pod (based on the average of 10 dry pods), weight of 100 seeds (based on a random sample of 100 seeds, with three replicates).

Data analysis

Mean

The Mean, or average, is the sum of all values divided by the number of values. Its formula is:

$$\text{Mean} = \frac{\sum_{i=1}^n x_i}{n}$$

Where: X_i is the value of the i -th data point; n is the total number of data points. The mean provides the central value of a dataset. It is the balance point where the sum of deviations from the mean is zero. However, the mean can be sensitive to extreme values (outliers).

Standard deviation

Standard deviation measures the spread or dispersion of data points around the mean. The formula for the population standard deviation is:

$$\sigma = \sqrt{\frac{\sum_{i=1}^n (x_i - \mu)^2}{n}}$$

Where: X_i is the value of the i -th data point; μ is the mean of the data, n is the total number of data points. Standard deviation quantifies the amount of variation or dispersion in a dataset. A higher standard deviation indicates that data points are spread out more widely from the mean, while a lower standard deviation means that data points are closer to the mean. In general, a large standard deviation suggests more variability in the data, and a small standard deviation suggests more consistency.

Coefficient of Variation (CV)

The coefficient of variation is the ratio of the standard deviation to the mean, expressed as a percentage. The formula is:

$$CV = \frac{\sigma}{\mu} \times 100\%$$

Where: σ is the standard deviation; μ is the mean. The CV allows you to compare the variability of datasets with different means. A higher CV indicates greater relative variability, and a lower CV indicates less relative variability. It is particularly useful when comparing datasets with different units or scales.

Pearson's product-moment correlation (r)

Pearson's correlation coefficient measures the strength and direction of the linear relationship between two variables. The formula is:

$$r = \frac{n \sum xy - \sum x \sum y}{\sqrt{[n \sum x^2 - (\sum x)^2][n \sum y^2 - (\sum y)^2]}}$$

Where: x and y are the data points of the two variables; n is the number of data pairs; \sum indicates the sum of the values. The correlation coefficient (r) ranges from -1 to +1. A value of +1 indicates a perfect positive linear relationship, while -1 indicates a perfect negative linear relationship. A value of 0 indicates no linear relationship. The closer the absolute value of r is to 1, the stronger the relationship between the two variables.

Table 1. 22 winged bean families from the F4 generation

Family code
PM.1.1
PM.2.2
PM.8.8
PM.10.10
PM.19.19
PM.33.33
PM.47.47
PM.57.57
PM.62.62
PM.82.82
PM.99.99
PM.100.100
PM.114.114
PM.118.118
PM.120.120
PM.126.126
PM.131.131
PM.145.145
PM.153.153
PM.155.155
PM.166.166
PM.193.193

Genotype-by-Trait

The Genotype-by-Trait (G×T) analysis was conducted using Principal Component Analysis (PCA) to evaluate the interrelationships among multiple agronomic traits and to discriminate genotypes based on their multivariate performance. A Genotype-by-Trait matrix, composed of mean values for each genotype across all measured traits, was used for the analysis. PCA was applied to reduce the dimensionality of the data, with principal components extracted based on eigenvalues greater than one. The first two principal components, which cumulatively explained the majority of the total variance, were retained for interpretation. Trait loadings were examined to determine the contribution of individual traits to each principal component, while genotype scores were computed to project each genotype into the multivariate space defined by the principal components. This PCA-based (G×T) approach facilitated the identification of major trait associations and the grouping of genotypes into distinct phenotypic clusters, providing a statistical foundation for multi-trait selection and genotype classification, even without the use of visual biplot representation.

RESULTS AND DISCUSSION

Genetic variation and agronomic performance of F4 winged bean progenies

Descriptive analysis was conducted to evaluate the variability and performance of agronomic traits among different generations of winged bean (*P. tetragonolobus*) (Table 2). The parameters measured included vegetative and reproductive characteristics that influence overall plant productivity. Mean values, standard deviations, and CV

were calculated for each trait to assess the degree of variation and stability across genotypes. The observed variation among traits indicates the potential for selection and genetic improvement in the evaluated populations.

Table 2. Genetic parameters for agronomic traits in winged bean

Generation	Parameters									
	FLA		FPHA		PDL		PDW		PWG	
	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV
MDM	77.50±1.31	1.69	92.50±1.20	1.29	21.68±1.67	7.7	2.52±0.04	1.63	26.57±0.57	2.14
PLB	64.14±1.07	1.67	84.86±0.69	0.81	15.34±0.91	5.96	1.99±0.09	4.67	12.69±1.14	8.98
PM 1.1	64.57±0.54	0.83	83.86±1.07	1.28	21.03±1.08	5.14	2.22±0.36	16.12	17.75±3.97	18.25
PM 2.2	70.50±0.54	0.76	85.00±0.00	0	21.19±1.56	7.35	2.00±0.44	22.15	19.27±3.24	17.28
PM 8.8	70.44±0.53	0.75	86.56±0.53	0.61	15.89±1.02	6.45	2.08±0.17	8.28	17.64±2.65	15.9
PM 10.10	70.63±0.52	0.73	85.63±0.52	0.61	18.63±1.43	7.69	2.09±0.32	15.47	17.19±3.20	19.18
PM 19.19	70.00±0.00	0	87.89±1.05	1.19	20.56±2.14	10.42	2.08±0.35	17	18.94±3.55	15.62
PM 33.33	72.38±0.52	0.72	88.00±0.00	0	19.19±2.42	12.61	1.67±0.40	23.67	21.20±2.23	13.77
PM 47.47	73.50±0.54	0.73	88.50±0.00	0	20.25±2.30	11.35	2.19±0.31	14.04	22.07±4.25	23.53
PM 57.57	75.00±0.00	0	90.00±0.00	0	18.69±1.39	7.44	1.83±0.18	9.96	22.96±3.41	16.64
PM 62.62	74.57±0.54	0.72	95.00±0.00	0	20.21±1.73	8.55	1.83±0.31	17.06	22.58±5.10	29.98
PM 82.82	69.50±0.54	0.77	91.00±0.00	0	16.81±1.79	10.66	1.83±0.32	17.43	15.82±1.66	14.01
PM 99.99	64.50±0.55	0.85	80.50±0.55	0.68	20.33±0.82	4.01	2.35±0.49	20.64	16.84±2.47	16.63
PM 100.100	75.00±0.00	0	89.00±1.07	1.22	18.88±1.83	9.68	1.94±0.32	16.51	20.46±7.24	37.22
PM 114.114	74.43±0.54	0.72	90.43±0.54	0.59	16.36±2.17	13.29	1.50±0.10	6.67	21.32±4.06	24.88
PM 118.118	75.00±0.00	0	88.50±0.00	0	19.48±2.31	11.88	2.04±0.28	13.59	22.86±5.64	29.89
PM 120.120	71.00±0.00	0	86.00±0.00	0	18.79±1.22	6.49	1.99±0.49	24.42	20.00±3.27	19.22
PM 126.126	73.50±0.54	0.73	87.00±0.00	0	18.44±1.24	6.71	2.19±0.26	11.84	21.74±9.13	40.18
PM 131.131	64.29±0.49	0.76	85.71±3.90	4.56	19.07±3.40	17.81	1.92±0.30	15.77	17.91±3.40	17.08
PM 145.145	69.43±0.54	0.77	85.57±0.54	0.63	19.50±2.35	12.03	2.19±0.37	16.96	18.72±3.72	18.22
PM 153.153	71.00±0.00	0	89.00±1.05	1.18	18.10±1.08	5.94	2.21±0.37	16.88	17.54±2.95	19.89
PM 155.155	70.57±0.54	0.76	90.00±0.00	0	17.14±1.80	10.48	2.21±0.24	10.89	19.02±3.54	21.66
PM 166.166	72.56±0.53	0.73	91.00±0.00	0	19.28±1.68	8.71	2.03±0.11	5.51	18.79±5.38	27.16
PM 193.193	72.00±0.00	0	89.88±1.55	1.75	20.81±6.08	29.2	1.55±0.08	4.9	17.83±4.61	29.11

Generation	Parameters							
	PPP		FPWP		SPP		HSW	
	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV	$\bar{x} \pm \text{stdv}$	CV
MDM	31.13±5.30	5.30	825.9±16.00	1.94	17.17±1.25	7.25	50.47±1.36	2.7
PLB	43.13±3.83	3.83	549.3±14.01	2.55	11.66±1.50	12.88	33.89±1.90	5.6
PM 1.1	34.17±4.98	4.98	825.9±11.00	1.33	11.57±2.37	20.48	39.40±1.43	3.3
PM 2.2	43.13±3.83	3.83	549.0±11.00	2.00	14.38±1.92	13.38	41.33±9.14	21.1
PM 8.8	38.80±4.12	4.12	773.0±11.00	1.42	12.22±1.64	13.43	39.60±5.95	15.42
PM 10.10	38.37±4.30	4.30	743.5±10.50	1.41	10.75±1.17	10.84	40.10±10.86	28.5
PM 19.19	42.03±3.93	3.93	744.5±11.00	1.48	13.22±2.59	19.57	39.20±7.13	16.13
PM 33.33	36.20±4.70	4.70	744.9±11.00	1.48	11.13±2.48	22.25	39.22±6.24	16.77
PM 47.47	34.80±4.60	4.60	725.9±11.00	1.52	13.88±1.73	12.45	42.81±9.18	22.5
PM 57.57	37.60±4.52	4.52	757.7±11.01	1.45	11.56±0.88	7.63	44.54±5.14	15.14
PM 62.62	41.63±4.20	4.20	775.6±11.02	1.42	12.29±0.95	7.74	44.37±5.51	13.82
PM 82.82	32.93±5.31	5.31	784.9±11.00	1.40	10.50±2.07	19.71	38.24±5.21	13.99
PM 99.99	40.87±4.16	4.16	775.7±11.01	1.42	12.67±1.51	11.89	35.00±5.25	13.12
PM 100.100	37.23±4.43	4.43	693.8±11.00	1.59	11.75±1.28	10.91	44.96±6.42	15.59
PM 114.114	38.47±4.29	4.29	549.0±11.00	2.00	10.29±1.50	14.54	41.64±4.43	12.78
PM 118.118	36.23±4.55	4.55	789.7±11.01	1.39	11.63±1.30	11.2	42.53±2.65	6.88
PM 120.120	38.87±4.24	4.24	779.7±11.00	1.41	11.57±1.62	13.98	41.14±6.18	16.21
PM 126.126	39.43±4.31	4.31	825.9±11.00	1.33	10.88±0.84	7.68	43.75±3.62	9.84
PM 131.131	32.93±5.01	5.01	743.6±11.02	1.48	12.43±1.40	11.24	38.37±4.49	11.69
PM 145.145	39.47±4.18	4.18	787.8±11.01	1.40	12.14±1.35	11.08	36.73±4.45	12.82
PM 153.153	37.67±4.38	4.38	739.8±11.00	1.49	11.20±2.44	21.79	42.68±4.53	10.61
PM 155.155	41.53±3.97	3.97	701.7±11.01	1.57	11.43±1.62	14.16	39.44±2.67	6.76
PM 166.166	37.57±4.39	4.39	705.9±11.00	1.56	12.33±2.00	16.22	38.39±6.82	17.77
PM 193.193	39.47±4.18	4.18	753.7±11.01	1.46	10.88±1.81	16.63	39.84±4.91	12.32

Note: The variables observed in this study were as follows. FLA: Flowering Age, FPHA: Fresh Pod Harvest Age, PDL: Pod Length, PDW: Pod Width, PWG: Pod Weight, PPP: Pods per Plant, FPWP: Fresh Pod Weight per Plant, SPP: Seeds per Pod, and HSW: 100-Seed Weight

The evaluation of genetic parameters in 22 F4 winged bean families derived from the MDM×PLB cross confirms successful trait recombination with substantial transgressive segregation. MDM, characterized by late maturity, produced large, heavy pods but fewer pods per plant, while early-maturing PLB yielded more numerous but smaller pods. Several F4 lines surpassed parental yields, with PM 126.126 matching MDM's high yield (825.9 g/plant) and PM 118.118 achieving near-parental yield with exceptional stability. Remarkable uniformity was observed in flowering and maturity traits, with PM 57.57, PM 118.118, and PM 120.120 showing zero CV for flowering days. All F4 families exhibited lower yield than the parental lines (Table 2).

Correlation analysis among agronomic and yield traits for F4 generation

Correlation analysis in the F4 generation of winged bean (*P. tetragonolobus*) was conducted to identify the relationships among key agronomic and yield-related traits. Understanding these associations in the segregating F4 population is crucial for determining which traits most strongly influence yield potential and can serve as effective selection criteria in early-generation breeding (Table 4 and Figure 1).

The correlation analysis revealed strong positive associations between flowering age (FLA) and pod weight (PWG) ($r=0.81$) and between PWG and hundred seed weight (HSW) ($r=0.81$), indicating coordinated development of late maturity, heavy pods, and large seeds. FLA also correlated strongly with fresh pod harvest age (FPHA) ($r=0.74$) and HSW ($r=0.73$). Pod dimensions (PDL and PDW) positively influenced seeds per pod (SPP) ($r=0.57$ each). Conversely, the number of pods per plant (NPP) showed negative correlations with fresh pod weight per plant (FPWP) ($r=-0.47$) and HSW ($r=-0.43$), revealing a trade-off between yield components. FPWP also correlated moderately with pod size traits (Figure 1).

Genotype-by-Traits

The Genotype-by-Trait (G×T) analysis was performed to visualize the relationships between genotypes and key agronomic traits in the F4 winged bean population. This analysis helps identify superior genotypes for specific traits and reveals the interrelationships among yield-related characteristics. The first two Principal Components (PC1 and PC2) explained 64.90% and 19.10% of the total variation, respectively, accounting for a combined 84% of the total variability in the dataset.

The Principal Component Analysis (PCA) results indicate that the first Principal Component (PC1) has an eigenvalue of 5.84, explaining 64.9% of the total variance in the dataset. This suggests that PC1 plays a dominant role in capturing the variation within the data. The second Principal Component (PC2), with an eigenvalue of 1.72, explains 19.1% of the variance, while the third component (PC3) explains only 7.5% (Table 3). Collectively, the first three components (PC1, PC2, and PC3) account for 91.5% of the total variance. The subsequent components (PC4 through PC9) contribute increasingly less, with their

eigenvalues significantly smaller. This indicates that the majority of the important information about variation in the data is captured by the first few components.

The trait loadings on PC1 and PC2 show the relationship between specific traits and the identified principal components. PC1, which is associated with production-related traits, shows positive loadings for traits such as FLA, FPHA, PWG, and FPWP, which are linked to key production characteristics, such as seed weight and fresh pod yield. In contrast, PC2 is more related to maturity, with high positive loadings on NPP (Number of Pods) and HSW (Hundred Seed Weight), indicating a link to the maturation process and seed characteristics. Traits like PDL (Pod Size) and SPP (Seeds per Pod) contribute to both components, reflecting the complex relationship between production and maturity. While these traits may not have as high a loading as PWG or FPWP, they still play a significant role in the overall variation explained by the components (Table 4).

The genotype scores for PC1 and PC2 indicate the relationship between different genotypes in terms of their production and maturity traits. MDM shows a high positive score on PC1 (2.85) and a negative score on PC2 (-1.92), placing it in Group A, characterized by high production and early maturity. PLB, with a negative PC1 score (-2.74) and a positive PC2 score (1.68), falls into Group D, indicating low production and late maturity (Table 5).

Genotypes such as PM 1.1 (PC1=1.23, PC2=-1.05) and PM 47.47 (PC1=0.68, PC2=-0.38) belong to Group B, which represents genotypes with moderate production and early maturity. Other genotypes, such as PM 2.2, PM 8.8, and PM 10.10, fall into Group C, which is characterized by moderate production and later maturity. Additionally, PM 62.62 (PC1=1.25, PC2=0.82) is in a transition between Group B and Group C, indicating a balance of both traits (Table 5).

The genotypes with intermediate positions, like PM 82.82 and PM 99.99, exhibit varying degrees of production and maturity, categorized in Group C/B and Group C, respectively (Table 5). These genotypes are important for breeding programs seeking to balance these traits. The clusters help identify genotypes that share similar characteristics in production and maturity, with Group B representing genotypes that balance both traits, while Group D includes those with the lowest production and highest maturity.

Table 3. PCA results - eigenvalues and variance proportions

Component	Eigenvalue	Proportion of variance	Cumulative proportion
PC1	5.84	64.9%	64.9%
PC2	1.72	19.1%	84.0%
PC3	0.68	7.5%	91.5%
PC4	0.41	4.6%	96.1%
PC5	0.20	2.2%	98.3%
PC6	0.09	1.0%	99.3%
PC7	0.04	0.4%	99.7%
PC8	0.02	0.2%	99.9%
PC9	0.01	0.1%	100.0%

Table 4. Trait loadings (character vectors)

Trait	PC1 loading	PC2 loading	Interpretation
FLA	0.35	-0.12	Production Component (PC1 positive) vs Maturity (PC2 negative)
FPHA	0.38	-0.08	Production Component
PDL	0.34	-0.45	Pod Size (opposite to PC2)
PDW	0.29	0.21	Pod Width
PWG	0.39	0.03	Seed Weight - main contributor to PC1
NPP	0.03	0.64	Number of Pods - main contributor to PC2
FPWP	0.40	0.15	Fresh Pod Yield - largest contributor to PC1
SPP	0.34	-0.19	Seeds per Pod
HSW	0.37	-0.49	Hundred Seed Weight (opposite to PC2)

Note: The variables observed in this study were as follows. FLA: Flowering Age, FPFA: Fresh Pod Harvest Age, PDL: Pod Length, PDW: Pod Width, PWG: Pod Weight, PPP: Pods per Plant, FPWP: Fresh Pod Weight per Plant, SPP: Seeds per Pod, and HSW: 100-Seed Weight

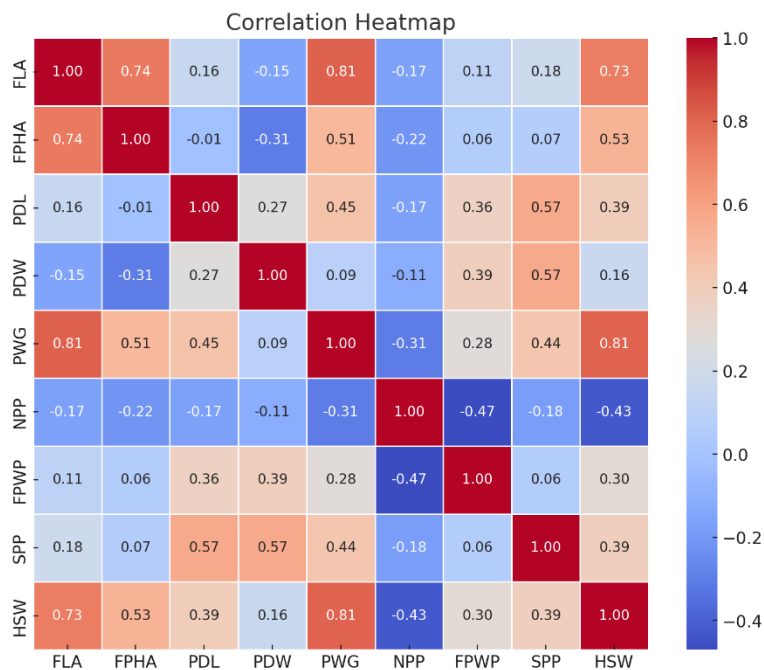


Figure 1. Heatmap of correlation among selected agronomic and yield traits in F4 generation of winged bean (*Psophocarpus tetragonolobus*). Note: The variables observed in this study were as follows. FLA: Flowering Age, FPFA: Fresh Pod Harvest Age, PDL: Pod Length, PDW: Pod Width, PWG: Pod Weight, PPP: Pods per Plant, FPWP: Fresh Pod Weight per Plant, SPP: Seeds per Pod, and HSW: 100-Seed Weight

Table 5. Genotype scores (PC1 and PC2)

Genotype	PC1 score	PC2 score	Cluster group
MDM	2.85	-1.92	Group A
PLB	-2.74	1.68	Group D
PM 1.1	1.23	-1.05	Group B
PM 2.2	0.18	1.41	Group C
PM 8.8	-0.42	0.56	Group C
PM 10.10	-0.31	0.62	Group C
PM 19.19	0.05	1.28	Group C
PM 33.33	-0.15	0.21	Group C
PM 47.47	0.68	-0.38	Group B
PM 57.57	0.92	-0.15	Group B
PM 62.62	1.25	0.82	Group B/C
PM 82.82	-0.58	-0.42	Group C/B
PM 99.99	-0.02	0.95	Group C

Genotype	PC1 score	PC2 score	Cluster group
PM 100.100	0.41	-0.88	Group B
PM 114.114	-1.86	0.34	Group D
PM 118.118	1.08	-0.02	Group B
PM 120.120	0.52	0.45	Group C
PM 126.126	1.42	0.28	Group B
PM 131.131	-0.71	-0.51	Group C/B
PM 145.145	0.28	0.38	Group C
PM 153.153	0.11	0.18	Group C
PM 155.155	-0.18	0.72	Group C
PM 166.166	0.01	0.05	Group C
PM 193.193	0.35	0.12	Group C

Discussion

Phenotypic variation and transgressive segregation in F4 winged bean families

The evaluation of 22 F4 winged bean families derived from the cross MDM×PLB revealed substantial phenotypic diversity and successful trait recombination through segregation and selection (Table 2). The parental genotypes exhibited complementary traits: MDM, the late-maturing parent (FLA=77.50 days; FPHA=92.50 days), produced larger pods (PDL=21.68 cm; PWG=26.57 g) and heavier seeds (HSW=50.47 g) but had fewer pods per plant (PPP=31.13). Conversely, PLB, the early-maturing parent (FLA=64.14 days; FPHA=84.86 days), produced a higher pod number (PPP=43.13) despite smaller pod dimensions (PDL=15.34 cm; PWG=12.69 g) and lighter seeds (HSW=33.89 g). This parental divergence provided a favorable genetic foundation for simultaneous selection of early maturity and high yield components (Mackay et al. 2021).

The F4 families demonstrated transgressive segregation, with multiple lines exhibiting superior or novel combinations of traits (Table 2). For instance, PM 118.118 achieved a high fresh pod weight per plant (FPWP=789.7 g/plant) while maintaining excellent stability (CV=1.39%) and a favorable combination of seed weight (HSW=42.53 g, CV=6.88%) and maturity uniformity (CV=0% for FLA & FPHA). Similarly, PM 1.1 combined high yield (FPWP=825.9 g/plant) with early flowering (FLA=64.57 days), and PM 100.100 showed good yield (FPWP=693.8 g/plant) with high seed weight (HSW=44.96 g). PM 126.126 matched the high-yield parent MDM (FPWP=825.9 g/plant) while offering improved pod number (PPP=39.43). These exceptional lines represent successful genetic recombination of parental traits, indicating that favorable alleles from both MDM (for seed and pod size) and PLB (for pod number and earliness) were combined through segregation (Bhadmus et al. 2023; Shonde et al. 2023). Transgressive segregation, where progeny traits exceed parental ranges results from complementary gene action and beneficial allele recombination. The presence of transgressive segregants strongly supports continuing selection in advanced generations for cultivar development (Acquaah 2012).

Many F4 families also demonstrated remarkable uniformity in critical agronomic traits (Table 2). For flowering age (FLA), PM 57.57, PM 118.118, PM 120.120, PM 153.153, and PM 193.193 exhibited zero coefficient of variation (CV=0%), indicating perfect phenotypic uniformity. For pod harvest age (FPHA), an even larger group including PM 2.2, PM 33.33, PM 47.47, PM 57.57, PM 62.62, PM 82.82, PM 118.118, PM 120.120, PM 126.126, PM 155.155, and PM 166.166 also showed CV=0%. Furthermore, all F4 families exhibited excellent yield stability, with CV for fresh pod weight per plant (FPWP) ranging from 1.33% to 2.00%, which is generally lower than the parental values (MDM: 1.94%; PLB: 2.55%). This high uniformity in key agronomic and yield traits is expected by the F4 generation due to reduced segregation variance and increased homozygosity from the F₂ baseline (~75% theoretical homozygous loci in F4

populations) (Falconer and Mackay 1996; Akinyosoye et al. 2025). Such stability is desirable for cultivar certification and predictable field performance, indicating these lines are approaching sufficient stability for potential release as commercial cultivars (Acquaah 2012).

Trait correlations and breaking the maturity-yield trade-off

Phenotypic correlation analysis in the F4 generation of winged bean (*P. tetragonolobus*) revealed a nuanced picture of trait associations that fundamentally reshapes breeding strategy for early-maturing, high-yielding winged bean cultivars. The strongest positive correlations identified were between flowering age (FLA) and pod weight (PWG) ($r=0.81$) and between PWG and hundred-seed weight (HSW) ($r=0.81$) (Figure 1). This exceptionally strong association between pod weight and seed size suggests coordinated resource allocation towards reproductive structures, contradicting the common trade-off between yield quantity and seed quality observed in many crops (Lawal et al. 2019). This positive correlation indicates that genotypes allocating substantial resources to pod development simultaneously enhance individual seed size, suggesting common physiological control or favorable genetic linkage between reproductive biomass accumulation and seed filling efficiency (Sriwichai et al. 2021). From a breeding perspective, this correlation is highly favorable: selection for heavier pods (PWG) will concurrently improve seed quality (HSW), eliminating a typical selection bottleneck (Mohanty et al. 2020).

The strong positive correlation between flowering time and pod maturity (FLA-FPHA, $r=0.74$) confirms biological expectations and indicates stable trait inheritance across the F4 generation (Mishra et al. 2019). Flowering time's strong positive correlation with seed weight (FLA-HSW, $r=0.73$) further suggests that later-flowering families extend their resource-accumulation period, enabling development of larger seeds (Lawal et al. 2019). However, these positive correlations with later flowering present a fundamental constraint for early maturity breeding: later-flowering genotypes generally have heavier pods and seeds, creating an apparent trade-off between the breeding objectives of early maturity and high yield (Sriwichai et al. 2021).

Nevertheless, several critical findings provide pathways to break this maturity-yield trade-off. Most notably, pod number per plant (NPP) showed moderate negative correlations with fresh pod weight per plant (FPWP-NPP, $r=-0.47$) and seed weight (HSW-NPP, $r=-0.43$), and weak negative correlations with flowering time (FLA-NPP, $r=-0.17$) and pod weight (PWG-NPP, $r=-0.31$) (Figure 1). This reveals a clear yield component trade-off: genotypes with many pods tend to have lower fresh pod weight and smaller seeds, while those with fewer pods allocate more resources to pod and seed size. This trade-off indicates that breeders can develop high-yielding cultivars through two distinct mechanisms: (i) by increasing individual pod and seed weight in families with moderate pod numbers, or (ii) by increasing pod number in families with acceptable pod and seed size (Bhadmus et al. 2023). This dual pathway dramatically expands selection possibilities and allows early-maturing families to achieve high yields through

diverse physiological strategies. The relationship between pod number and yield components has been reported in other legumes, suggesting that breeders must carefully balance these traits (Mohanty et al. 2020).

The moderate positive correlations between pod dimensions and seeds per pod (PDL-SPP, $r=0.57$; PDW-SPP, $r=0.57$) and between pod dimensions and fresh pod weight (PDL-FPWP, $r=0.36$; PDW-FPWP, $r=0.39$) reveal an important relationship: larger pods accommodate more seeds and contribute to higher yield. Interestingly, negative correlations between fresh pod harvest age (FPHA) and pod width (PDW, $r=-0.31$) and between flowering time (FLA) and pod width ($r=-0.15$) reveal a manageable trade-off: earlier-maturing families tend to produce slightly narrower pods, but the correlations are moderate and non-deterministic, permitting selection of early-maturing families with acceptable pod width (Mackay et al. 2021). In practical breeding terms, pod diameter is less critical for market acceptance than pod weight and seed quality, making this trade-off acceptable (Sriwichai et al. 2021; Chankaew et al. 2022)

The correlation analysis provides crucial insights for strategic selection: breeders should prioritize high pod weight (PWG) and seed weight (HSW) in early-generation selection, as these traits are strongly intercorrelated and positively associated with yield (FPWP). Pod number (NPP) should be balanced against pod and seed size, with the optimal strategy depending on whether the breeding objective favors many smaller pods or fewer larger pods.

Genotype-by-Trait clustering and identification of elite phenotypes

The Genotype-by-Trait (G×T) analysis based on principal components, which together explain 84.0% of the total phenotypic variation (PC1=64.9%, PC2=19.1%) (Table 4), provides an integrated view of the associations between genotypes and traits, allowing objective classification of families into distinct phenotypic groups (Sriwichai et al. 2021). The PCA biplot reveals clear clustering patterns among the F4 families based on their trait profiles, which reflect distinct yield formation strategies relevant to winged bean improvement (Mohanty et al. 2020).

The trait loadings (Table 4) indicate that PC1 is strongly associated with production-related traits, showing high positive loadings for Fresh Pod Weight per Plant (FPWP: 0.40), Pod Weight (PWG: 0.39), and Flowering Age (FLA: 0.35). This suggests PC1 represents a "Yield and Biomass Accumulation" axis. In contrast, PC2 is most strongly associated with Number of Pods per Plant (NPP: 0.64) and shows negative loadings for Hundred Seed Weight (HSW: -0.49) and Pod Length (PDL: -0.45), indicating PC2 represents a "Pod Number vs. Seed Size" trade-off axis.

Genotypes MDM (PC1: 2.85, PC2: -1.92) and PM 126.126 (PC1: 1.42, PC2: 0.28) (Table 5) cluster in the high PC1 region, indicating they achieve yield primarily through high fresh pod weight, heavy pods, and larger seeds - a strategy associated with later maturity (higher FLA and FPHA) that allows greater biomass accumulation

for pod and seed development (Bhadmus et al. 2023). Similarly, PM 118.118 (PC1: 1.08) falls within this high-yield cluster. However, PM 118.118 shows near-zero PC2 score (-0.02), indicating it achieves this yield through a balanced approach rather than extreme values in either pod number or seed size.

In contrast, PLB (PC1: -2.74, PC2: 1.68) occupies the opposite quadrant, characterized by higher pod numbers (positive PC2) but lower overall yield (negative PC1). The genotype PM 99.99 (PC1: -0.02, PC2: 0.95) follows a similar strategy with moderate PC2 but near-zero PC1, indicating it achieves yield primarily through prolific pod production rather than heavy individual pods (Sriwichai et al. 2021). The performance of PM 99.99 demonstrates that genotypes can achieve competitive yields without relying on large pod size, making it valuable for breeding programs (Singh et al. 2016).

A third group, including PM 57.57 (PC1: 0.92, PC2: -0.15) and PM 100.100 (PC1: 0.41, PC2: -0.88), shows intermediate to high PC1 scores with negative PC2 scores, indicating they achieve yield through moderate pod numbers combined with good pod and seed size. This group represents a balanced phenotypic strategy that maintains yield potential while favoring seed quality over pod number (Sriwichai et al. 2021).

The largest cluster (Group C) contains genotypes with moderate PC1 and varying PC2 scores, including PM 2.2, PM 8.8, PM 10.10, PM 19.19, and others. These represent intermediate phenotypes that do not specialize in either high yield through biomass accumulation or high pod numbers, but rather show balanced trait expression (Yan 2024).

Overall, the PCA visualization highlights the inherent yield-component relationships in winged bean, where genotypes cluster along a primary axis of yield potential (PC1) and a secondary axis representing the pod number vs. seed size trade-off (PC2). The spatial distribution reveals that high yield can be achieved through multiple strategies: either through fewer but larger pods and seeds (high PC1, negative PC2) or through more numerous pods (moderate PC1, positive PC2), providing considerable breeding flexibility (Mohanty et al. 2020).

Selection of elite families for early-maturing, high-yielding cultivar development

Based on integrated analysis of phenotypic variation (Table 2), correlation patterns (Figure 1), and Genotype-by-Trait clustering (Tables 4 and 5), three F4 families represent exceptional genetic resources that successfully break the conventional early maturity-yield trade-off and warrant immediate advancement to subsequent breeding generations and multi-environment testing (Kindie et al. 2022):

PM 99.99: Early maturity and high pod production. PM 99.99 (Table 2) achieves the earliest pod harvest age (FPHA=80.50±0.55 days; CV=0.68%) combined with competitive fresh pod weight (FPWP=775.7 g/plant). This genotype's yield strategy emphasizes high pod number (PPP=40.87 pods/plant) rather than heavy seeds (HSW=35.00 g), demonstrating that early maturity can be

successfully combined with reproductive capacity. The near-zero correlation between pod number and flowering traits (Figure 1) indicates genetic independence between these characteristics, allowing simultaneous selection for earliness and productivity (Akeem et al. 2019; Bhadmus et al. 2023; Olawuyi et al. 2025). PM 99.99's position in PCA Group C with positive PC2 loading (0.95) (Table 5) confirms its specialization in pod number rather than seed size, making it particularly valuable for short-season environments where rapid crop cycle completion is essential.

PM 1.1: Early maturity with high yield potential.

PM 1.1 combines early flowering (FLA=64.57±0.54 days; CV=0.83%) with exceptional fresh pod weight (FPWP=825.9 g/plant) (Table 2), matching the yield of the high-yielding parent MDM while maturing significantly earlier. This family achieves this through balanced expression of pod length (PDL=21.03 cm) and pod weight (PWG=17.75 g), demonstrating that early-maturing families need not sacrifice yield potential when pod dimensions remain favorable. In PCA analysis (Table 5), PM 1.1 clusters in Group B with high PC1 (1.23) and negative PC2 (-1.05), indicating strong yield component expression with emphasis on pod/seed size rather than pod number. This reflects successful genetic recombination of early maturity alleles from PLB with yield component alleles from MDM, exemplifying transgressive segregation for earliness and yield (Mackay et al. 2021; Bhadmus et al. 2023; Kaur et al. 2025)

PM 131.131: Early uniformity with consistent yield.

PM 131.131 offers the most uniform early flowering (FLA=64.29±0.49 days; CV=0.76%, lowest among early families) combined with stable fresh pod weight (FPWP=743.6 g/plant) (Table 2). This genotype's strength lies in its phenotypic stability across replications, particularly for flowering time a critical trait for cultivar certification and farmer adoption (Falconer and Mackay 1996; Singh et al. 2019). With moderate pod number (PPP=32.93) and medium seed weight (HSW=38.37 g), PM 131.131 demonstrates that competitive yields in early-maturing lines can be achieved through balanced trait expression rather than extreme values in any single component. Its PCA position (PC1=-0.71, PC2=-0.51) in Group C/B (Table 5) indicates moderate yield with slight emphasis on seed characteristics, suggesting a stable genetic background suitable for cultivar development (Lande and Thompson 1990; Akinyosoye et al. 2025)

In conclusion, this study demonstrates that selection in F4 winged bean families successfully identified elite germplasm that breaks the conventional early maturity-yield trade-off through favorable genetic recombination. PM 99.99, PM 1.1, and PM 131.131 represent valuable genetic resources for developing competitive, early-maturing winged bean cultivars suited to short-season tropical environments. The demonstrated independence between pod number and maturity traits, combined with strong yield expression in early families, provides a scientifically sound foundation for advancing these genotypes toward cultivar development programs targeting early maturity without yield penalty (Kindie et al. 2022;

Chinnadurai and Devi 2025; Gomathi et al. 2025; Rakshitha et al. 2026)

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