Caraka Tani Journal of Sustainable Agriculture
ISSN 2613-9456 (Print) 2599-2570 (Online)

Caraka Tani: Journal of Sustainable Agriculture, 40(3), 347-360, 2025
URL: https://jurnal.uns.ac.id/carakatani/article/view/94563
DOI: http://dx.doi.org/10.20961/carakatani.v40i3.94563

Assessment of F_5 Mungbean Genotypes from Intergeneric Hybridization with Common Bean for Agronomic Performance, Heritability, Variance Components, and Genetic Uniformity

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Abstract

Genetic improvement in mungbean (*Vigna radiata* L. [Wilczek]) is constrained by its narrow genetic base. Introducing genetic material from common bean (*Phaseolus vulgaris* L.) through intergeneric hybridization offers a promising strategy for enhancing yield potential and advancing sustainable agriculture. However, limited studies have evaluated the agronomic performance and genetic parameters of progenies derived from such crosses. This study aimed to assess agronomic performance, estimate genetic parameters, and evaluate genetic uniformity in mungbean progenies, to identify superior lines for breeding programs. The field experiment was conducted using a randomized complete block design with four replicates. Five selected F_5 genotypes (C419, B423, B1922, B119, and B1124), along with the mungbean progenitor PKHPL-1, were evaluated. Traits assessed included vegetative, generative, and yield-related characteristics. Significant variation was observed among genotypes for yield-related traits, while plant height, number of flowers, and phenological traits showed relative uniformity. Genotype C419 exhibited the highest agronomic performance, with superior values in 100-seed weight, number of seeds per pod, seed weight per plant, and number of pods per plant. High heritability was recorded for pod length and 100-seed weight (90.63% and 90.32%, respectively), indicating strong genetic control and potential for effective selection. Principal component analysis confirmed the major contribution of these traits to yield variation. Furthermore, molecular analysis using IRAP markers revealed high genetic uniformity in genotype C419. These findings demonstrate the potential of intergeneric hybridization for enhancing yield-related traits in mungbean and identify genotype C419 as a promising line for future breeding efforts.

Keywords: intergeneric hybridization; IRAP marker; seed yield improvement; selection of mungbean lines; yield-related traits

Cite this as: Aisah, B. N., Ikhwani, A. T., Setiawan, A. B., Purwantoro, A., Respatie, D. W., Ambarwati, E., Anggraeni, L., Teo, C. H., Setyawan, C., & Khamidah, A. (2025). Assessment of F_5 Mungbean Genotypes from Intergeneric Hybridization with Common Bean for Agronomic Performance, Heritability, Variance Components,

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[*] *Received for publication October 29, 2024*
Accepted after corrections May 19, 2025

and Genetic Uniformity. *Caraka Tani: Journal of Sustainable Agriculture*, *40*(3), 347-360. doi: http://dx.doi.org/10.20961/carakatani.v40i3.94563

INTRODUCTION

Mungbean (*Vigna radiata* L. [Wilczek]), widely cultivated across Asia and Africa, is a key pulse crop valued for its high protein content and bioactive compounds, including polyphenols and peptides, which support health benefits such as managing diabetes and cardiovascular disease (Hou et al., 2019; Lim et al., 2022; Ukwu et al., 2025). Beyond its nutritional importance, mungbean contributes significantly to food security and provides a stable income source for farmers in many developing countries (Sequeros et al., 2020). Despite these benefits, the long history of mungbean domestication and selective breeding has reduced its genetic diversity, compromising essential traits like yield potential and harvest timing (Burlyaeva et al., 2019). In Indonesia, low productivity is further impacted by the dependence on local landraces (Rahmianna et al., 2021; Afza et al., 2023), poor agricultural practices, diverse soil conditions, and the susceptibility of cultivars to various biotic and abiotic stresses, all of which led to yield instability (Kubota et al., 1998; Nair et al., 2019; Pratap et al., 2019). This narrow genetic base, combined with inadequate farming practices, limits mungbean's adaptability to changing environments, emphasizing the need to broaden its genetic diversity to improve resilience, adaptability, and productivity for sustainable agriculture.

Interspecific hybridization refers to the crossing of individuals from different species, resulting in progeny with recombinant or mixed genomic backgrounds (Runemark et al., 2019). It has been applied in mungbean breeding to enhance genetic diversity and nutritional value (Chen et al., 1983; Ujianto et al., 2018; Jain and Sharma, 2021). Several studies have demonstrated successful interspecific hybridization between mungbean and related *Vigna* species such as ricebean and urdbean, particularly when mungbean is used as the female parent. Success rates vary depending on genotype combinations, with crossability rates ranging from 44 to 65% and viable F_1 and backcross generations being obtained (Chen et al., 1983; Ujianto et al., 2018). However, limitations such as hybrid sterility, embryo abortion, and reciprocal cross failure remain significant challenges, often due to pre- and post-fertilization barriers and cytoplasmic-genetic incompatibilities. Despite these constraints, several nutritionally superior interspecific lines have been developed (Jain and Sharma, 2021), indicating the potential of this approach to broaden mungbean's genetic base.

Expanding mungbean's genetic base through intergeneric crosses to improve yield-related traits remains unexplored. Intergeneric hybridization introduces genetic material from distantly related species, promoting genetic and epigenetic diversity (Zhang et al., 2013). Fatmawati et al. (2021) successfully developed a mungbean hybrid from the cross of two species from different genera, producing an F_1 generation with distinctive seed size and color compared to the progenitor line. Hybrids from intergeneric hybridization often retain the female parent's physical traits and chromosome number while differing genetically, often due to loss of male parental material during embryo development, and further influenced by genomic rearrangements and diploidization (Faure et al., 2002; Madlung and Comai, 2004; Liu and Li, 2007).

Similar effects have been observed in coffee (Lashermes et al., 2000), sunflower (Faure et al., 2002), rapeseed (Zhang et al., 2013), and rice (Liu et al., 2004), leading to significant agronomic and genetic variations. While interspecific hybridization offers higher crossability and fertility, it is often constrained by limited genetic variation among closely related *Vigna* species. Intergeneric hybridization, despite its lower success rate due to deeper genomic divergence, can overcome these limitations by introducing novel alleles and broader genetic diversity from distantly related taxa. This approach facilitates the development of transgressive segregants with enhanced yield potential, stress tolerance, or seed quality, which are traits difficult to access through interspecific crosses alone.

This study evaluated five F_5 intergeneric mungbean genotypes derived from crosses with common bean. These genotypes inherited DNA fragments from common bean (Fatmawati et al., 2023) and exhibited larger seeds than the mungbean progenitor (Fatmawati et al., 2021), representing an opportunity to introduce beneficial traits for yield improvement. Researchers also used IRAP markers to assess the genetic uniformity of the selected genotypes. This molecular marker approach helps assess the genetic homogeneity of hybrids and enables analysis of associations between DNA markers and agronomic traits, providing insights into the genetic potential of mungbean genotypes (Sokolkova et al., 2020; Wu et al., 2020; Fatmawati et al., 2021; Sinha et al., 2023). This study aimed to assess agronomic performance, estimate genetic parameters, examine genetic uniformity, and identify high-yielding, superior mungbean genotypes. The findings highlight the potential of intergeneric hybridization in developing genetically uniform, high-yield mungbean cultivars, setting a foundation for breeding strategies to enhance mungbean productivity.

MATERIALS AND METHOD

Plant materials

This study was conducted from November 2023 to February 2024. The field experiment was conducted at Banguntapan Research Station, Faculty of Agriculture, Universitas Gadjah Mada (110°24’44” E, 7°48’16” S), and the molecular analysis was carried out at the Laboratory of Plant Breeding, Department of Agronomy, Faculty of Agriculture, Universitas Gadjah Mada. Five F_5 generation genotypes (C419, B423, B1922, B119, and B1124), along with their progenitor PKHPL-1, were used in this study. The genotypes were selected through the pedigree method and derived from an intergeneric cross between ‘PKHPL-1’ (*Vigna radiata* L. [Wilczek]), a mungbean landrace from Malang, East Java, Indonesia, and ‘Lebat-3’ (*Phaseolus vulgaris* L.). The field experiment was arranged in a randomized complete block design, with four blocks as replicates. Each experimental unit consisted of 25 plants, with a planting spacing of 30 cm × 20 cm.

Phenotypic data collection

Yield-related traits in mungbean were measured following the procedure described by Mbeyagala et al. (2023). The traits included plant height, number of flowers per plant, days to flowering, days to harvest, pod length, number of pods per plant, pod and seed weight, pod weight without seeds, number of seeds per pod, seed diameter, seed weight per plant, and 100-seed weight. Data were collected from 20 plants per experimental unit.

DNA isolation and PCR amplification

DNA was isolated from the leaves of 66 plants from the C419 genotype population, following the method described by Fatmawati et al. (2023). DNA concentration was quantified using a NanoDrop 2000c Spectrophotometer (Thermo Fisher Scientific, USA) and diluted into a 50 ng μl^{-1} working solution. The PCR reaction consisted of 6.25 µl of PowerPol 2x PCR Mix (ABclonal, USA), 0.25 µl each of forward and reverse V2, V3, and V5 IRAP primers (Fatmawati et al., 2021), 2.5 µl of DNA, and 2.75 µl of nuclease-free water. The PCR amplification was conducted using a T100™ Thermal cycler (Bio-Rad, USA) with the PCR conditions as described in Fatmawati et al. (2021).

Data analysis

Phenotypic data were analyzed using analysis of variance (ANOVA) in R software, followed by Tukey’s HSD test at α 5% significance level when differences were observed. Pearson correlation and principal component analysis (PCA) were analyzed using OriginLab. Path analysis was conducted to assess the direct and indirect effects of independent on the dependent variables through a matrix equation approach using Equation 1.

$$R_Y = R_X \cdot C \qquad (1)$$

Where, R_X is the correlation matrix of the independent variables, C is the vector of path coefficients (direct effects) for each independent variable, and R_Y is the column vector of correlations between the dependent variable Y and each independent variable.

The path coefficients were estimated by solving the Equation 2.

$$C = R_X^{-1} \cdot R_Y \qquad (2)$$

Where, R_X^{-1} is the inverse of the correlation matrix.

Indirect effects were calculated using Equation 3.

$$\text{Indirect effect} = p_{yj} \cdot r_{ji} \qquad (3)$$

Where p_{yj} is the path coefficient that represents the direct effect of the independent variable X_j on the dependent variable Y and r_{ji} is the correlation coefficient between two independent variables X_j and X_i.

The phenotypic and genotypic variances were estimated using Equations 4 and 5.

$$\sigma_G^2 = \frac{\text{MSg-MSe}}{\text{r}} \quad (4)$$

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2 \text{ ; } \sigma_E^2 = \text{MSe} \quad (5)$$

Where, MSg is the mean of square genotype, MSe is the mean of square error, r denotes the number of replications, σ_G^2 means the genotypic variance, σ_E^2 is the environmental variance, and σ_P^2 refers to the phenotypic variance.

The broad sense heritability was estimated using Equation 6.

$$h^2 = \frac{\sigma_G^2}{\sigma_P^2} \text{ x } 100\% \quad (6)$$

The genotypic and phenotypic coefficient of variance (GCV and PCV) and heritability were estimated and classified as described in Zaki and Radwan (2022).

RESULTS AND DISCUSSION

The agronomic and yield-related traits in six mungbean genotypes

The agronomic performance of six mungbean genotypes was evaluated across multiple traits, revealing significant differences in several key parameters. Plant height (p = 0.386661), number of flowers per plant (p = 0.289), days to flowering (p = 0.847), and days to harvest (p = 0.706) showed no statistically significant differences, indicating consistency in vegetative growth and reproductive timing among genotypes under the tested conditions (Figures 1a to 1d). In contrast, several yield-related traits exhibited significant variation. Pod length (p = 3.93e-08) differed significantly, with C419 producing the longest pods (12.96 cm) and B119 the shortest (8.8 cm) (Figure 1e). The number of pods per plant also varied significantly (p = 0.000114), with C419 showing the highest number of pods (Figure 1f), indicating its superior pod production capacity compared to the other genotypes.

Pod and seed weight parameters were notably different. Pod and seed weight (p = 0.004576) and pod weight without seeds (p = 0.00168) were highest in C419 and B1124 (19.41 and 16.32 g, respectively), whereas B119 and B1922 showed significantly lower weights (10.35 and 9.60 g, respectively) (Figures 1g and 1h). Similarly, the number of seeds per pod (p = 8.13e-05) was highest for C419 and B1124 (12.4 and 11.05, respectively), whereas B119 (9.10) and B1922 (9.50) produced fewer seeds per pod, potentially affecting overall yield (Figure 1i). Additionally, seed-specific traits, such as seed diameter (p = 0.01833) and seed weight per plant (p = 0.00205), revealed significant differences (Figures 1j and 1k), with C419 and B1124 demonstrating superior performance in terms of seed size and weight. The weight of 100 seeds (p = 1.04e-07) further highlighted the potential of these genotypes, with C419 (7.35 g) showing the highest 100-seed weight (Figure 1l).

These results suggest that genotype C419 consistently outperformed the other genotypes and the check variety PKHPL-1 across several key yield-related traits, including 100-seed weight, number of seeds per pod, seed weight per plant, and seed diameter. These traits were found to have significant positive correlations with overall yield potential (Figure 2b). This confirms previous studies that emphasize the importance of pod-related traits as key yield determinants in mungbean breeding (Priya and Babu, 2021; Parihar et al., 2022). This study advances the field by estimating genetic parameters and identifying pod length and 100-seed weight as highly heritable traits (heritability > 90%) (Table 3), suggesting strong genetic control and minimal environmental influence. The strong performance of C419 demonstrates the potential of introducing genetic material from *Phaseolus vulgaris*, aligning with findings in *Brassica napus*, where intergeneric hybridization improved yield and diversity (Zhang et al., 2013). These results offer valuable insights into the potential genetic gains achievable through selection and breeding.

PCA of various traits

A dataset is considered well-represented when its principal components (PCs) explain more than 80% of the variance (Wang et al., 2022). In this study, the first three components, with eigenvalues greater than 0.80, accounted for 66.90%, 19.31%, and 9.72% of the variance, respectively, capturing a total of 95.92% of the variation across 12 yield-related traits (Table 1). This indicates that these three components encapsulate most of the dataset's variability. The PCA biplot demonstrated that PC1 and PC2 alone explained 66.90% and 19.31% of the variation, highlighting substantial variability among the mungbean genotypes (Figure 2a). The first principal component had the highest positive loading for pod and seed weight (0.3498) and a negative loading for plant height (-0.15015). The second component had the highest positive loading for days to flowering (0.54854) and the highest negative loading for the number of pods

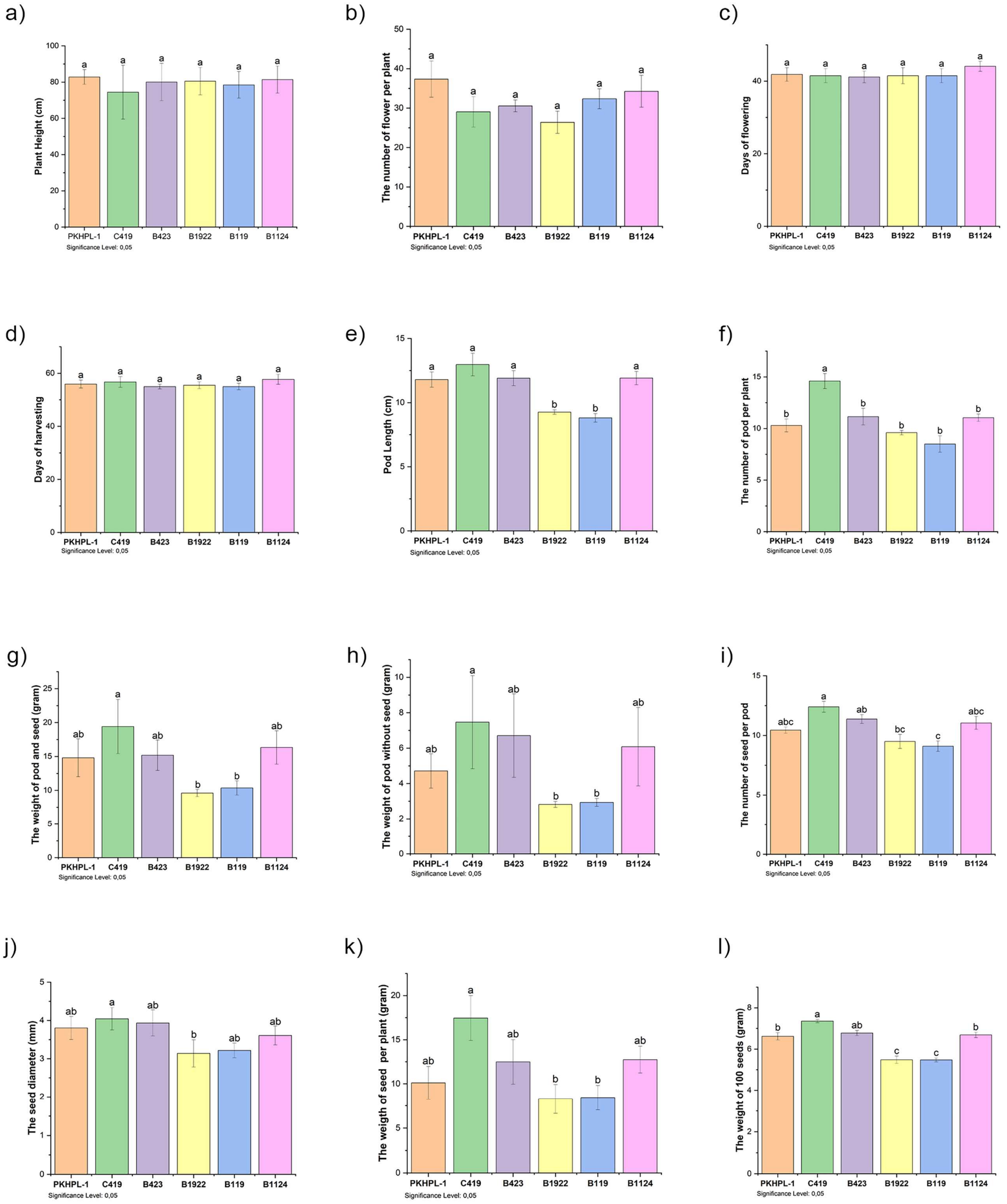

Figure 1. The agronomic and yield-related traits of six mungbean genotypes

Note: Bars followed by similar letters are not significantly different according to Tukey's HSD test with α = 0.05

per plant (-0.17462). The third component exhibited the highest positive loading for seed diameter (0.37545) and the highest negative loading for days to harvest (-0.51191) (Table 1).

Genotype B1124 is closely aligned with days to flowering and days to harvest, indicating strong performance in maturity-related traits. In contrast, genotype PKHPL-1 is more associated with plant height, suggesting greater vegetative growth. Genotype C419 stands out along the positive axis of principal component 1 (PC1), exhibiting distinct agronomic performance (Figure 2a). Its proximity to traits such as pod weight, seed weight per plant, pod length, pod and seed weight, 100-seed weight, seed diameter, number of seeds per pod, and number of pods per plant suggests strong seed and pod productivity. The separation from traits such as plant height, days of flowering, number of flowers per plant, and days of harvesting indicates that while C419 surpasses in yield traits, it does not exhibit superior vegetative growth or early maturity. These robust yield-related traits position C419 as a strong candidate for breeding programs aimed at improving mungbean productivity.

PCA is a statistical method for extracting essential information from high-dimensional data by reducing its dimensions into a few composite variables, grouping highly correlated data, visually representing relationships, and making analysis more intuitive (Ringnér, 2008; Barth et al., 2020). Eigenvalues are often used to

Table 1. Loadings, eigenvalues, percentage of variance, and cumulative percentage of variance of the top four PCs

Index	PC1	PC2	PC3	PC4
Pod length	0.34035	0.10197	0.16167	0.17135
Weight of pod and seed	0.34988	0.06213	0.02609	-0.14319
Weight of pod without seed	0.3421	-0.013	0.07676	0.17237
Weight of seed per plant	0.34095	-0.12251	-0.14673	-0.11745
Number of pods per plant	0.33096	-0.17462	-0.14329	0.02794
Number of seeds per pod	0.34831	-0.06719	0.0181	0.19711
Seed diameter	0.32237	-0.02076	0.37545	0.02727
Weight of 100 seeds	0.34701	0.04432	0.1541	0.0362
Days of flowering	0.06992	0.54854	-0.45338	0.05514
Number of flowers per plant	0.03491	0.51695	0.43142	-0.65042
Days of harvesting	0.21124	0.36829	-0.51191	-0.03907
Plant height	-0.15015	0.47895	0.3263	0.66131
Eigenvalue	8.02809	2.31681	1.16608	0.36377
Percentage of variance (%)	66.90	19.31	9.72	3.03
Cumulative percentage of variance (%)	66.90	86.21	95.92	98.96

identify the PCs that contribute most to total variability (Wang et al., 2022). This study utilized PCA as a fundamental approach to characterize and establish relationships between genotypes and yield-related traits, providing reliable differentiation among treatments. Several studies have used PCA to cluster genotypes based on morphological and yield-related traits in mungbean (Mwangi et al., 2021), Bambara groundnut (Esan et al., 2023), and strawberry (Verma et al., 2025). In this study, genotype C419 exhibited distinct agronomic performance, with its proximity to yield-related traits indicating strong seed and pod productivity.

Correlation and path analysis of traits influencing seed yield in mungbean

Pearson's correlation coefficient was used to evaluate the relationships between various trait parameters and their contributions to mungbean production (Figure 2b). Pod length exhibited a significant positive correlation with the weight of 100 seeds (r = 0.90***), indicating that longer pods are strongly associated with higher seed weight, a critical trait for yield improvement. Additionally, pod length was positively correlated with pod and seed weight (r = 0.70***), pod weight (r = 0.59**), seed weight per plant (r = 0.66***), number of pods per plant (r = 0.71***), number of seeds per pod (r = 0.78***), and seed diameter (r = 0.56**), further emphasizing its role in productivity. Seed-related traits were also strongly correlated. The number of seeds per pod had significant positive correlations with the weight of 100 seeds (r = 0.81***), the seed diameter (r = 0.57**), and the number of pods per plant (r = 0.63***), suggesting that genotypes with more seeds per pod tend to have larger seeds and produce more pods, contributing to overall yield. Notably, seed weight per plant was highly correlated with both the weight of pod and seed and the weight of pod without seed, as well as with the number of seeds per pod, demonstrating that these yield components are closely linked.

Conversely, traits like plant height and days to harvesting show negative correlations with several seed yield traits (Figure 2b). Plant height has a negative correlation with days of harvesting, with a correlation coefficient r = -0.58 (**), suggesting that taller plants may be associated with later maturity. This could have implications for breeding strategies focused on early-maturing varieties. The correlation analysis identifies key trait interactions that can inform breeding decisions. Traits such as pod length, number of seeds per pod, and seed weight per plant show significant positive relationships with yield components (weight of 100 seeds), making them priority traits for selection in mungbean breeding programs. Conversely, the negative correlation between plant height, maturity traits, and key yield traits such as pod length and seed weight may require careful consideration when selecting for both early maturity and optimal plant architecture. This finding is consistent with earlier reports by Rahmianna et al. (2021), which observed that taller mungbean plants were often associated with delayed maturity and reduced yield potential due to the allocation of resources to vegetative growth at the expense of reproductive output. In contrast, shorter genotypes tend to allocate energy toward reproductive structures, resulting in higher pod and seed production. This inverse relationship between plant height and yield traits has also been observed in cowpea, where breeders have selected for compact, high-yielding varieties with early maturity (Aliyu et al., 2022; Raina and Khan, 2023). Therefore, balancing plant architecture with yield traits should be a priority in future breeding efforts.

The correlation and path analysis of various factors affecting mungbean seed yield provide insights into the direct and indirect contributions of each trait. This analysis helps identify the most impactful traits and their interactions, facilitating more effective and targeted breeding strategies. The path analysis in Table 2 illustrates the direct and indirect effects of various traits on 100-seed weight in mungbean. The residual effect of 0.10 indicates that 90% of the total variability in 100-seed weight is explained by the traits included in the model, making the analysis highly reliable for identifying key contributors to 100-seed weight. Among the traits, pod length stands out, having the highest direct effect on 100-seed weight, with a coefficient of 0.821, a total indirect effect of 1.015, and a correlation coefficient of 0.90*** (Figure 2b). This suggests that pod length is a major determinant of seed weight, highlighting its importance in improving yield potential in breeding programs. Pod length also influences other yield-related traits, making it a key target for selection. Other traits affecting 100-seed weight include the number of seeds per pod, seed weight per plant, pod and seed weight, and seed diameter, with larger seed diameter leading to higher 100-seed weight.

The number of seeds per pod and seed diameter also make significant contributions to 100-seed weight. The number of seeds per pod utilizes a notable indirect effect on 100-seed weight through weight of seed per plant, weight of pod and seed, and pod weight (weight of pod without seed), indicating its crucial role in determining overall yield. Meanwhile, seed diameter has both direct and indirect effects, with a total indirect effect of 1.135 (Table 2), suggesting that larger seed size is associated with higher seed weight, making seed diameter another critical trait for enhancing yield. The path analysis results highlight pod length as the most significant determinant of seed yield, exhibiting the highest direct effect on 100-seed weight (path coefficient = 0.821). This finding aligns with the work of Sadras et al. (2019), Edematie et al. (2021), and Li et al. (2023), who similarly identified pod length as the most influential trait affecting seed yield in *Pisum sativum*, cowpea, and snap bean, emphasizing its importance in pulse crop

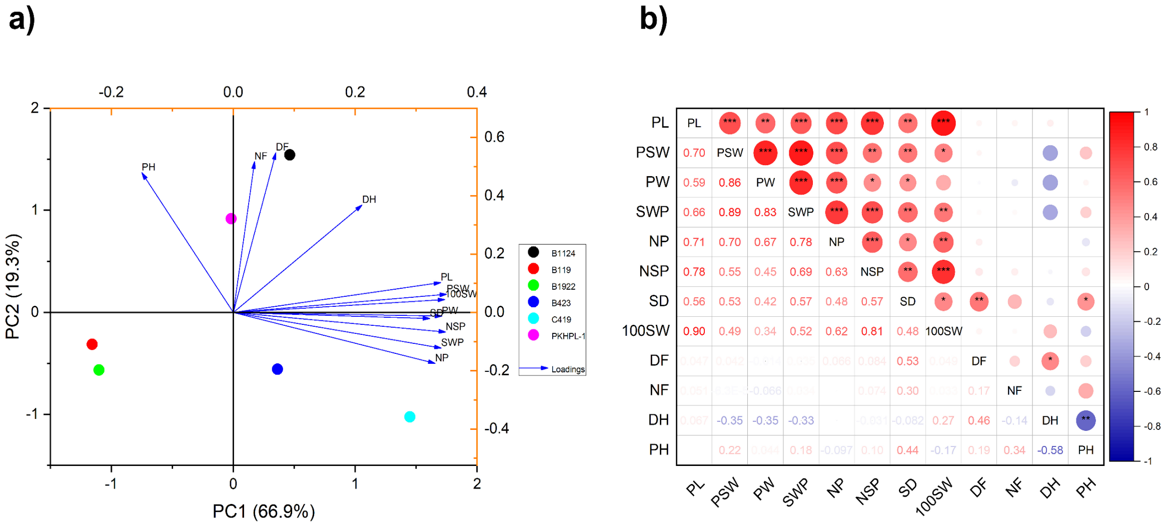

Figure 2. PCA biplot of six mungbean genotypes and 12 agronomic and yield-related traits along the first and two PCs; and Pearson correlation of agronomic and yield-related traits

Note: PL = Pod length, PSW = The weight of pod and seed, PW = The weight of pod without seed, SWP = The weight of seed per plant, NP = The number of pod per plant, NSP = The number of seed per pod, SD = The seed diameter, 100SW = The weight of 100 seeds, DF = Days of flowering, NF = The number of flower per plant, DH = Days of harvesting, and PH = Plant height. Single asterisk (*) depicts significantly correlated at $p \leq 0.05$, double asterisks (**) depict significantly correlated at $p \leq 0.01$, and triple asterisks (***) depict significantly correlated at $p \leq 0.001$

Table 2. Path analysis of 100 seed weight with its component traits

Traits	Indirect effect											Total of direct effects	Total indirect effects
	PH	DF	NF	DH	PL	NP	NSP	SD	PSW	PW	SWP		
PH	**-0.034**	-0.010	0.037	-0.080	-0.518	0.385	-0.394	-0.094	-0.076	0.222	-0.209	-0.034	-0.738
DF	-0.089	**0.004**	0.009	0.025	0.198	-0.006	0.028	-0.061	0.019	-0.064	0.027	0.004	0.084
NF	-0.100	-0.003	**0.012**	-0.022	0.525	0.103	0.010	0.066	0.023	-0.054	-0.011	0.012	0.536
DH	-0.104	0.004	0.011	**0.026**	0.628	-0.149	0.168	0.009	0.049	-0.156	0.087	0.026	0.546
PL	0.021	-0.001	0.008	-0.020	**0.821**	-0.180	0.251	0.143	0.039	-0.145	0.077	0.821	1.015
NP	0.066	0.000	-0.006	-0.019	0.745	**-0.198**	0.264	0.123	0.036	-0.123	0.085	-0.198	0.972
NSP	0.053	0.000	0.001	-0.017	0.826	-0.210	**0.249**	0.145	0.041	-0.168	0.090	0.249	1.009
SD	0.025	0.002	0.006	-0.002	0.923	-0.192	0.283	**0.127**	0.043	-0.167	0.086	0.127	1.135
PSW	0.070	-0.002	0.008	-0.034	0.868	-0.195	0.278	0.148	**0.037**	-0.139	0.078	0.037	1.117
PW	0.060	-0.002	0.005	-0.032	0.946	-0.194	0.334	0.169	0.040	**-0.126**	0.085	-0.126	1.286
SWP	0.087	-0.001	-0.002	-0.028	0.776	-0.205	0.275	0.133	0.035	-0.131	**0.082**	0.082	1.022
Residual effect = 0.10													

Note: PH = Plant height, DF = Days of flowering, NF = The number of flowers per plant, DH = Days of harvesting, PL = Pod length, NP = The number of pods per plant, NSP = The number of seed per pod, SD = The seed diameter, PSW = The weight of pod and seed, PW = The weight of pod without seed, and SWP = The weight of seed per plant. The bold numbers represent the direct effects (positive or negative) of each trait on 100-seed weight breeding. Additionally, the significant indirect effects of the number of seeds per pod and seed diameter on 100-seed weight suggest that selecting for these traits could also lead to overall yield improvements. The positive correlations between seed-related traits such as seed number, diameter, and weight are crucial, as genotypes that exhibit these correlations are likely to achieve higher yields. This is consistent with findings from wheat breeding programs (Pang et al., 2020), where grain number and size showed a positive correlation, contributing to increased yields.

Genetic parameter estimation of various traits and genetic similarity of mungbean population

Table 3 provides insights into the h^2, GCV, and PCV for several agronomic traits in mungbean, essential metrics for evaluating genetic improvement potential in breeding programs. Among the traits, pod length and 100-seed weight exhibit high heritability (h^2 = 90.63% and 90.32%, respectively) with moderate to high GCV values (pod length = 14.83%, 100-seed weight = 11.70%). This suggests that these traits are primarily controlled by genetic factors and can be effectively improved through selection. The close alignment between GCV and PCV for these traits indicates limited environmental influence, making them ideal for breeding programs focused on increased seed yield. This finding aligns with similar studies in rice by Awad-Allah et al. (2022), where high heritability and GCV in seed weight traits have indicated effective genetic gains through selection.

Traits such as seed weight per plant, pod weight, and pod and seed weight also show high GCV and PCV values with moderate heritability (seed weight per plant = 58%, pod and seed weight = 52%, pod weight = 30.82%) (Table 3). Their lower heritability compared to pod length and 100-seed weight may reflect greater environmental influence, as suggested by the wider gap between GCV and PCV values. Majidi et al. (2009) reported similar findings, where yield-related traits with moderate heritability often exhibit environmental sensitivity, potentially diluting genetic gains through direct selection. This highlights the need to consider genotype-by-environment interactions in breeding strategies.

Despite moderate heritability, seed weight per plant, pod weight, and pod and seed weight display substantial genetic variability, suggesting significant potential for yield improvement, especially if selection is paired with multi-environment trials. This approach aligns with Castiano et al. (2023), who emphasized that integrating yield traits with genotype-environment interactions is key to stabilizing gains under variable conditions. The study results highlight 100-seed weight and pod length as key traits for improving seed yield, given their high heritability and moderate GCV. Breeding programs aiming to enhance seed size and yield should prioritize traits such as pod length and 100-seed weight, as their genetic improvement is expected to result in significant gains in productivity.

Because of its superior agronomic performance, genotype C419 was selected for genetic uniformity assessment using IRAP markers. The dendrogram generated with the IRAP marker and Rohlf's simple matching coefficient provides insights into the genetic similarity within the C419 mungbean population. The clustering pattern reflects the genetic relationships among the evaluated genotypes, with the coefficient of similarity ranging from 0.80 to 1.00 (Figure 3).

Table 3. The h^2, GCV, and PCV of several agronomic traits

Traits	GCV (%)	Level	PCV (%)	Level	h^2 (%)	Level
PH	1.25	Low	7.02	Low	3.13	Low
NP	3.89	Low	18.97	Medium	4.10	Low
NSP	7.23	Low	12.33	Medium	34.00	Medium
PL	14.83	Medium	15.58	Medium	90.63	High
SD	8.93	Low	13.78	Medium	26.00	Medium
PSW	23.49	High	32.32	High	52.00	Medium
PW	30.61	High	55.14	High	30.82	Medium
SWP	27.44	High	36.02	High	58.00	Medium
100SW	11.70	Medium	12.37	Medium	90.32	High

Note: GCV = Genotypic coefficient of variance, PCV = Phenotypic coefficient of variance, h^2 = Broad-sense heritability, PH = Plant height, NP = The number of pods per plant, NSP = The number of seed per pod, PL = Pod length, SD = The seed diameter, PSW = The weight of pod and seed, PW = The weight of pod without seed, SWP = The weight of seed per plant, and 100SW = The weight of 100 seeds

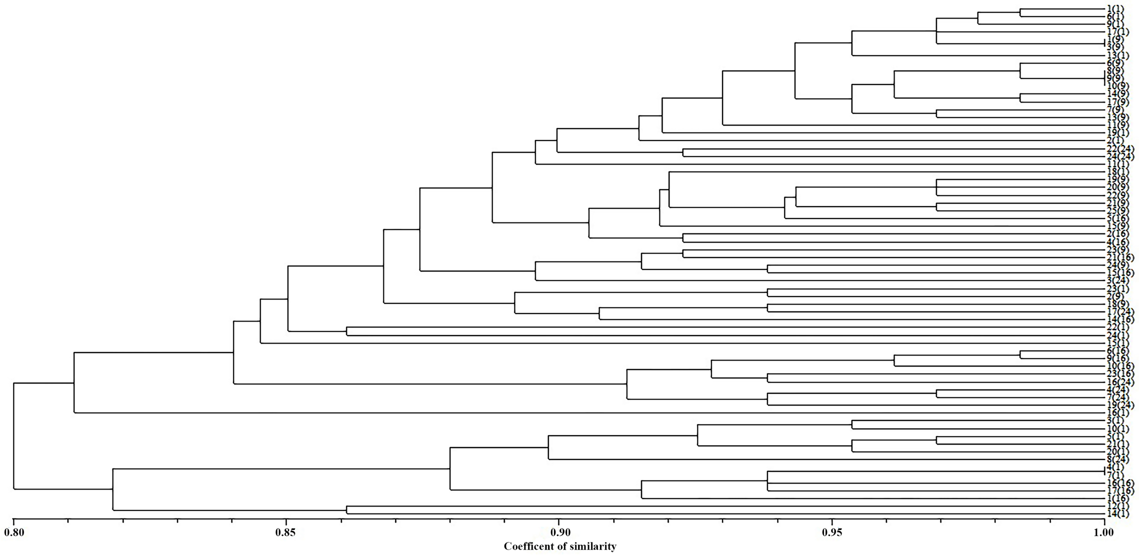

Figure 3. Genetic similarity of the C419 population based on the IRAP marker

Individuals of C419 are grouped into several clusters, with the majority showing a high degree of genetic similarity, as indicated by the large number of individuals clustering above the 0.90 similarity threshold. This result suggests a high level of homozygosity within the population, indicating that the individuals are genetically uniform. Genotype C419 forms a distinct subgroup with closely related individuals (Figure 3), suggesting high genetic similarity and likely shared agronomic traits, particularly in yield performance. The high degree of genetic similarity within this genotype suggests a high level of homozygosity, crucial for developing stable pure lines. Similar results were reported by Sokolkova et al. (2020) and Fatmawati et al. (2021) in their assessments of genetic diversity in mungbean, where molecular markers were employed to confirm genetic uniformity in high-performing genotypes. This result suggests that this genotype has undergone several generations of selfing through pedigree selection, leading to the fixation of desirable traits, such as yield performance.

By integrating both agronomic performance and molecular marker analysis, this study offers a more comprehensive approach to mungbean improvement. The genetic homogeneity observed in C419 is beneficial for the development of cultivars that are not only high-yielding but also stable across various environmental conditions. Such stability is critical for breeders aiming to release varieties that perform consistently across different agroecological zones. Similar approaches have been employed in soybean breeding (Boehm et al., 2019; Li et al., 2020; Zhang et al., 2020), where high genetic uniformity in elite lines has led to the successful release of commercial cultivars with stable yield traits.

This study demonstrates the potential of intergeneric hybridization to broaden the genetic base of mungbean by introducing beneficial traits from common bean (*Phaseolus vulgaris* L.), which enhance yield components, as reported in previous works (Fatmawati et al., 2021; 2023). In contrast to earlier studies that primarily focused on interspecific hybridization (Chen et al., 1983; Ujianto et al., 2018; Jain and Sharma, 2021), this research presents new opportunities for expanding the genetic diversity of mungbean through intergeneric crosses to improve yield-related traits. Similar approaches have been successfully applied in *Brassica napus* (Zhang et al., 2013), where intergeneric hybridization led to improvements in yield and increased genetic diversity.

Despite the promising results, the limitations of this study must be acknowledged. The field trials were conducted at a single location, which restricts the ability to fully assess genotype-by-environment interactions. Multi-environment trials are crucial for evaluating the stability of these genotypes across diverse agroecological conditions, especially given that environmental factors such as soil type, rainfall, and temperature can significantly influence mungbean performance (Nair et al., 2019). Furthermore, while this study focused primarily on yield-related traits, other critical factors, such as disease resistance, drought tolerance, and nutritional quality, were not assessed. Including these traits in future studies will provide a more comprehensive evaluation of these genotypes, further enhancing their suitability for commercial production.

CONCLUSIONS

Genotype C419 emerged as the most promising line because of its superior performance in yield-related traits, including 100-seed weight, number of seeds per pod, seed weight per plant, and number of pods per plant. Among these traits, 100-seed weight exhibited high heritability, indicating strong genetic control and suggesting its potential for effective selection in breeding programs. Furthermore, the high genetic uniformity observed in genotype C419, confirmed through molecular analysis, emphasizes its potential as a stable and high-performing cultivar suitable for commercial production. These findings highlight the value of intergeneric hybridization in developing high-yielding, genetically uniform mungbean cultivars, paving the way for future breeding strategies aimed at improving mungbean productivity across diverse environments. However, further multi-environment trials are recommended to assess the stability of these genotypes under various agroecological conditions.

ACKNOWLEDGEMENT

This research was funded by the National Research and Innovation Agency (BRIN) and the Indonesia Endowment Fund for Education (LPDP), Ministry of Finance, through the Research and Innovation for an Advanced Indonesia (RIIM) Scheme, Batch 4, under grant numbers 37/II.7/HK/2023 and 6815/UN1/DITLIT/Dit-Lit/KP.01.03/2023.

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