

Agronomical traits performance and variability of the SSD F₄ mungbean population

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Abstract. Genetic variability is critical in order to create candidates for new superior varieties. This research objective was to evaluate the performance and variability of agronomical traits on the mungbean SSD F₄ V422H/129 population. The research was conducted at IPB University, Bogor, from March to June 2021. The SSD F₄ VR422H/129 population (378 genotypes with single plant as a representative of one genotype) and five check varieties were evaluated. The treatments were arranged in augmented design for RCBD in three replications. For agronomical traits, every F₄ plant and 10 sample plants for each check variety were observed. Statistical analysis includes mean, frequency-distribution, heritability, genetic variability, correlation. The days to flowering, days to harvesting, generative periods, plant height on F₄ V422H/129 were not significantly different from Vima 5, while total pod number, total pod weight, total seed weight, pod length were significantly higher. The agronomical traits were affected by genetic factors (heritability 0.71-0.99%), except for days to harvest. Based on the high genetic variability (CGV 0.62-0.64%), it was possible to select of total pod weight, total seed weight, or pod length in the next generation V422H/129. The total seed weight had a significant positive correlation with total pod weight and pod length.

Keywords: augmented design, correlation, genotype, heritability

INTRODUCTION

Mungbean (*Vigna radiata* L. Wilczek) is a functional pulses crop, as a raw material or a sprouts vegetable, a source of protein and antioxidants [1,2]. Mungbean is easy to get, inexpensive, and almost 97% of Indonesia's provinces cultivated it [3]. Indonesia's agro-climatological suitability should make Indonesia self-sufficient for mungbean. However, in reality, it is not. Based on national mungbean production statistics, mungbean productivity in 2014-2016, from 0.63 to 0.61 t ha⁻¹ and grew by 1.63% in 2018 until productivity reached 0.64 t ha⁻¹ [3]. In the last few years, Indonesia has shown success in exporting mungbean amidst the mungbean imports issue [4], and the main cause of low mungbean productivity needs to be resolved.

The inappropriate technology in mungbean cultivation such as superior varieties [5] contribute to low mungbean production. Mungbean breeding should be done without stopping. Maybe few are interested in breeding mungbean or maybe a lot of development has not yet been completed to produce varieties. The fact is that the number of mungbean varieties has been recorded 27 varieties between 1945 to 2021 or 0.35% growth varieties per year [6,7,8].

Genetic variability in the selection population will create superior varieties. Genetic variability can be assessed from early generations, including detecting superior genotypes named transgressive segregants [9]. This superior genotype is the target of selection in the breeding of self-pollinated crops such as mungbean, as well as other self-pollinated plants such as mungbean [9], soybean [10], and wheat [11]. This research aims to assess one of the mungbean breeding populations, namely the SSD F₄ V422H/129 population for the performance and variability on agronomical traits. Single seed descent (SSD) is a plant breeding method applied to targeted traits

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selection with less genetic control on self-pollinated crops.

METHODOLOGY

Research Time and Location

The research was conducted in Leuwikopo experimental station (275 m asl), Department of Agronomy and Horticulture, IPB University, Bogor, from March to June 2021.

Plant Material Genetic

The research material was mungbean genotypes consists of a population of F₄ V422H/129 and check varieties. A total of 378 F₄ genotypes were derived from crossing V422H (P1) and No.129 (P2) in single seed descent (SSD) method selection. The check variety consisted of one local cultivar VR422H and four national varieties No.129, Vima 1, Vima 2, Vima 5, with each check variety consisting of 54 plants.

Experimental Design

The genotype treatments were placed in an augmented design with three-replication randomized complete block design (RCBD) for check varieties. Five check varieties were planted in each replication. In contrast, 126 genotypes F₄ V422H/129 were planted in each block, so the total was 378 genotypes. Single F₄ plant (one seed) is represented one genotype derived from F₃ single plant.

Research Procedures

Dolomite (1 t ha⁻¹) was applied one week before planting. Seeds were planted one seed per planting hole with a distance of 40 cm x 10 cm. The insecticide carbofuran 3G was applied at the planting time. Fertilization was carried out one week after planting time and doses of fertilizer, namely 50 kg ha⁻¹ Urea, 100 kg ha⁻¹, SP-36, 50 kg ha⁻¹ KCl. Weeding was carried out at 3 weeks after planting/wap (vegetative phase) and 6 wap (generative phase). Pest control was carried out based on field monitoring, especially pod-sucking pests using insecticides (profenofos 500 g L⁻¹). Harvesting pods is only once when ± 90% of the pods per plant have matured or 3 weeks since the first pods ripen. Harvested pods were dried in an electric oven (30°C, 24 hours) before data collecting and post-harvest process.

Trait Observations

Observations were done on each F₄ single plant and 10 sample on every check variety. Observational traits included days to flowering (DF), days to harvesting (DH), generative phase period (DH-DF), plant height (at the last harvest), total pod number, total pod weight,

total seed weight, and pod length. Technical observations refer to the descriptors for mungbeans [13].

Statistical Analysis

Data analysis includes the estimation of mean, adjustment. The F₄ mean data was justified first prior to statistical analysis [12]. The effect of a block on the phenotypic F₄ population was estimated according to the justification $a_j = x_j - \bar{x}$ [12], with a_j : block adjustment value in j-th block (j = 1, 2, 3), x_j : mean of all checks in the j-th block, $\bar{x}$: grand mean of all checks. Heritability, coefficient of genetic variance, and correlations are parameter genetics measurements [14]. Duncan's tests are significantly different between check varieties, while t-test for the F₄ population with one of the best checks. The statistical software supporting were Microsoft Excel, Minitab v.16, SAS v.9.0, and PBSTAT online software.

RESULTS AND DISCUSSION

General Research Condition

The environmental conditions of the study were quite suitable for mungbean with the average rainfall during the study was 252 mm month⁻¹ and temperature was 25°C [15]. Mungbean plants grow well in the lowlands with rainfall of 50-200 mm month⁻¹, temperature 25-27 °C, and 50-80% humidity [16].

Up to 85% of quantitative F₄ data from healthy plants can be analyzed and generated as F₅ seeds. The loss of the F₄ genotype in the single seed descent (SSD) selection method is common due to natural selection. The death of one plant is the same as the loss of one mungbean genotype. The same incident was described as natural selection by [17], which caused a reduction in the population of the SSD method on soybeans.

The variation among experimental blocks can be measured and excluded from experimental error. Experimental error in the augmented

Table 1. Adjustment value as the effect of the blocks on each agronomical trait of mungbean

Traits	a ₁	a ₂	a ₃
Days to flowering (dap)	1.71	-0.71	-1.00
Plant height (cm)	-1.06	2.03	-0.97
Days to harvesting (dap)	1.36	-0.65	-0.71
Generative period (dap)	-0.35	0.06	0.29
Pod length (cm)	0.03	-0.05	0.02
Total pods number	-0.59	0.73	-0.13
Total pods weight (g)	-1.34	1.20	0.14
Total seed weight (g)	-0.61	0.72	-0.11

dap: days after planting, a_j: adjustment value in the j-th block check variety (j = 1, 2, 3).

Table 2. Mean value of agronomical traits on five mungbean varieties

Traits	No.129	V422H	Vima 1	Vima 2	Vima 5
Days to flowering (dap)	48.35a	39.54b	34.67c	33.67c	35.67c
Plant height (cm)	89.06a	75.28b	74.98b	75.96b	76.89b
Days to harvesting (dap)	40.71a	35.74b	40.31a	42.29a	41.22a
Generative period (dap)	89.06a	75.28b	67.86b	77.90b	74.14b
Pod length (cm)	11.76c	16.26a	13.76bc	15.64ab	15.14ab
Total pod number	13.18c	16.90a	13.15c	15.97ab	13.97bc
Total pod weight	9.11b	11.84a	9.08b	11.86a	9.30b
Total seed weight (g)	10.10c	9.67bc	10.70ab	10.55ab	10.83a

Numbers followed by the same letter in the same row were not significantly different based on Duncan's test at 5% level.
dap: days after planting.

design was measured from the check varieties (pure lines), which was planted repeatedly [12]. The uncontrollable microenvironment influences the plant phenotype. Individual phenotypic values of F₄ plants were justified based on adjustment values in Table 1.

Performance of Agronomic Traits on Population Evaluated

Vima 1, Vima 2, and Vima 5 have early flowering and harvesting times (Table 2). They are national varieties released following No.129. Improvement of mungbean varieties is directed to early maturity to reduce yield loss due to environmental stress [18]. Plant growth was shorter in Vima 1, Vima 2, and Vima 5 than No.129 and V422H. Mungbean cultivars should have a determinate growth type with a short habitus to support simultaneous harvesting [19]. On the yield component traits, such as total pod number, total pod weight, total seed weight, and pod length, V422H showed superior yield component traits that are not significantly different from Vima 2. Vima 2 shows superior on all the traits measured in this study.

Mean value of total pod number, total pod weight, total seed weight, and pod length in F₄ V422H/129 were significantly higher than Vima 5, except for days to flowering, days to

harvest, and generative phase times (Table 3). Although days to flowering and harvesting traits in F₄ V422H/129 were not significant to Vima 3; several genotypes had less and more days than Vima 5.

The frequency distribution of F₄ is more clearly shown in Figures 1, 2, and 3. Many genotypes were identified in the minimum and maximum value areas for the traits evaluated. Breeding self-pollinating crops such as mungbean purposes to derive transgressive segregants. Transgressive segregants are marked with a higher mean value than the best parent and have a low variance, so marked as potential superior varieties. The segregant transgressive can be selected in these minimum and maximum areas depending on trait selected [9,10].

A total of 167 genotypes F₄ V422H/129 had early flowering less than 36 days after planting (Vima 2 = 36 dap, Table 3) in Figure 1a. Selection of the days to flowering trait has a higher chance than the days to harvesting trait which centered at 76 and 80 days after planting (Figure 1b). The early of the days of harvesting trait is 56-60 dap [18]. Several genotypes on the left side of the distribution curve can be selected as early genotypes at flowering and harvesting traits compared to Vima 2.

Table 3. Phenotypic value of F₄ V422H/129 mungbean population

Traits	F ₄ V422H/129 population			Vima 5
	Minimum	Maximum	Mean	Mean
Days to flowering (dap)	27.10	53.29	36.27tn	35.67
Days to harvesting (dap)	51.71	80.64	77.02tn	76.89
Generative period (d)	15.32	50.70	40.70tn	41.22
Plant height (cm)	18.46	107.46	74.05tn	74.14
Total pod number	2.10	79.32	17.58*	15.14
Total pod weight (g)	0.50	75.68	19.39*	13.97
Total seed weight (g)	0.51	44.47	13.34*	9.30
pod length (cm)	4.57	12.12	9.93*	10.83

*: significant different based on t-test at 5%, tn = tidak berbeda nyata berdasarkan uji t dua populasi, dap: days after planting, d: days

The range value of the generative period of F4 V422H/129 is quite wide (Table 3 and Figure 2a). Length of the generative period is related to pods times formed. Perhaps the long generative period will be followed the high number of pods formed, which is may also not true. A short generative period with high yield is more favorable. This performance stated as short harvest periode or simoultaneously harvesting [20]. Selection of generative period trait has a negative direction with the left-side of the distribution curve as targetted. A total of 147 genotypes had a generative period trait less than 41 days.

Most of the F4 V422H/129 has a plant height of 85 cm (high category). Compared to Vima 2 (Table 3), 83 F4 genotypes were identified, less than 74 cm (Figure 2b). The height of the national variety of mungbean ranges from 50-60 cm. Breeding mungbean for forage yield require a high canopy [19,21].

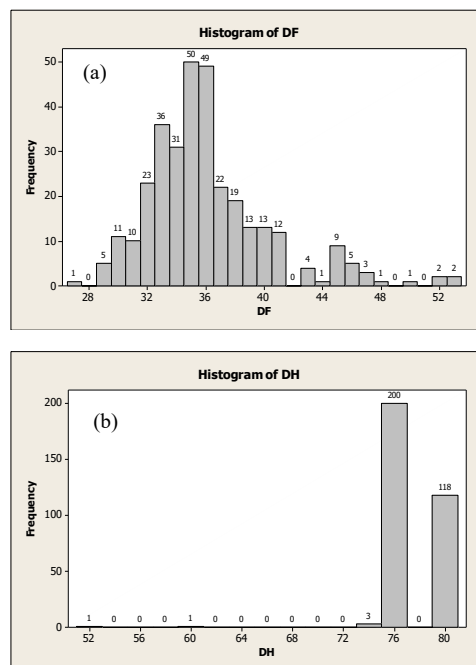


Figure 1. Frequency distribution of F4 V422H/129 mungbean: a. days to flowering (DF), b. days to harvesting (DH)

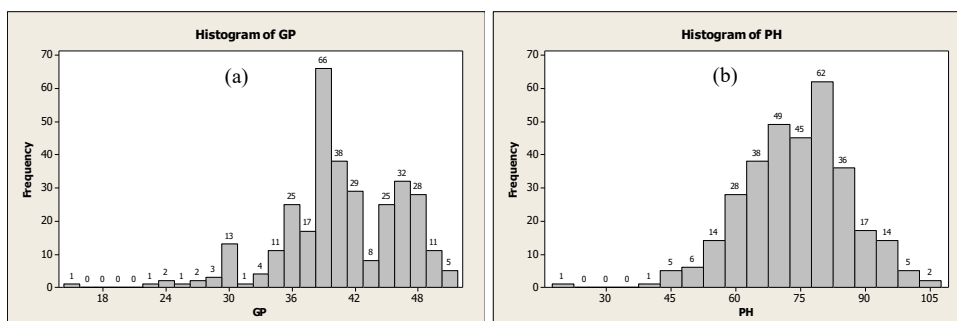


Figure 2. Frequency distribution of F4 V22H/129 mungbean: (a) generative period (GP), (b) plant height (PH)

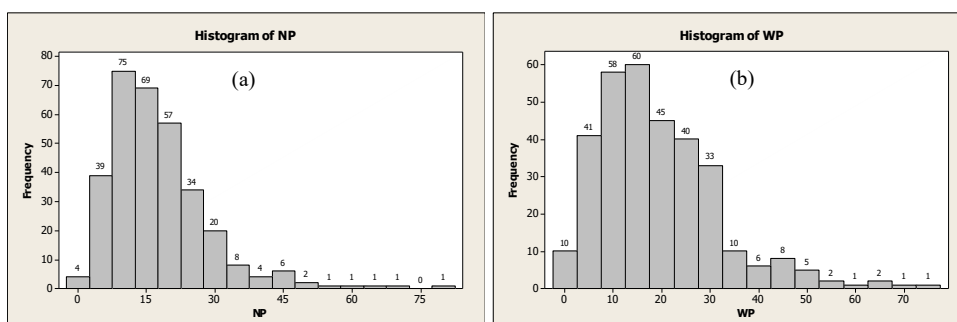


Figure 3. Frequency distribution of F4 V22H/129 mungbean: (a) total pod number (NP), (b) total pod weight pods (WP)

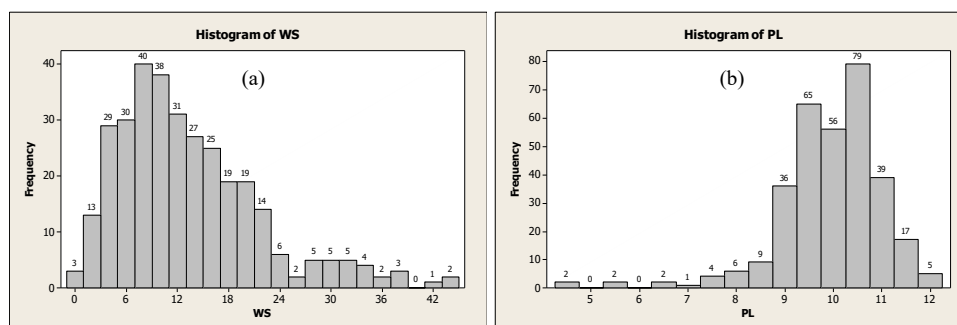


Figure 4. Frequency distribution of F4 V22H/129 mungbean: (a) total seed weight, (b) pods length.

Single seed descent method has a selection provision starting on the F5 generation [22]. Selection will be successful if genetic factor play a major role in traits. The magnitude of genetic factor is reflected in heritability value, while genetic variability is in coefficient of genetic variance (CGV). Heritability and genetic factor are guidelines for decision breeding in selection [14]. Table 4 shows that all observed traits are high heritability values or affected by genetic factor so that potential to be selected in the F4 V422H/129 population, except for days to harvesting trait.

The frequency distribution curve of F4 V422H/129 shows the skewness, indicating the affecting of non-additive genes. The epistasis genes (non-additive genes) were affected on yield components of F2 V422H/129 population (early generation) and suggested to delaying selection [23]. With indications of non-additive (skewness) on this study, that delaying selection

on F5 generations, are suggested for F4 V422H/129 population.

The genetic variability of total pod weight, total seed weight, and pod length traits were wide categories. This is very favorable to selection. Actually, variance of genetic factor consists of additive (inherited) and epistatic or dominant (non-inherited). It takes two generations of selection to ensure genetic control by additive or non-additive factors and separate genotypes for different selection methods.

Selection can be done directly or indirectly using other traits with a high and significant correlation with the target trait. Seed weight is a targeted selection trait. It was significantly positively correlated with days to harvesting, total pod number, generative periods were high correlation (r close to 1) with total pod number and total pod weight. There is a very significant negative correlation with days to flowering (Table 5). Those traits can be an indirect selection trait for seed weight (yield), while pod weight is recommended based on heritability, coefficient of genetic variance, and correlation values.

Table 4. Genetic parameter values of the agronomical trait in F4 V422H/129 mungbean

Traits	h^2_{bs}	CGV	Criteria
Days to flowering (dap)	0.71	0.10	Narrow
Days to harvesting (dap)	0.01	0.00	Narrow
Plant height (cm)	0.95	0.14	Moderate
Total pod number	0.80	0.15	Moderate
Total pod weight (g)	0.99	0.62	High
Total seed weight (g)	0.98	0.64	High
Pod lenght (cm)	0.98	0.63	High

h^2_{bs} : broad-sense heritability, CGV: coefficient of genetic variance.

Table 5. Correlations among the agronomical trait in F4 V422H/129 mungbean

	DF	DH	GP	PH	PN	PW	SW
DH	-0.301**						
GP	-0.89**	0.702**					
PH	-0.074	0.197**	0.151**				
PN	-0.31**	0.318**	0.392**	0.333**			
PW	-0.332**	0.346**	0.423**	0.379**	0.929**		
SW	-0.335**	0.342**	0.423**	0.381**	0.881**	0.97**	
PL	-0.252**	0.124*	0.248**	0.363**	0.277**	0.476**	0.494**

*, **: significance in 0.05 and 0.01 probably levels, respectively. DF: days to flowering, DH: days to harvesting, GP: generative phase, PH: plant height, PN: number of pods, PW: total pod weight, SW: total seed weight, PL: pod length.

CONCLUSION

The total pod number, total pod weight, total seed weight, and pod length were significantly higher than the best check variety. The agronomical traits of the F4 V422H/129 mung bean were highly affected by genetic factors ($h^2_{bs} > 71\%$). There is wide genetic variation in

total pod weight, total seed weight, and pod length. Direct selection based on yield component traits such as total pods weight, total seeds weight, or pod length could be suggested in the next generation of the V422H/129 population.

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