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Extension of the Eeigenvalue-Based Selection Index Method for Fixation of Multiple Trait-Transgressive Segregates in Mungbeans (*Vigna radiata* L. Wilczek)

Edizon Jambormias[1,*], Surjono Hadi Sutjahjo[2], Ahmad Ansori Mattjik[3], Yudiwanti Wahyu[2], Desta Wirnas[2], Jacob Richard Patty[4]

[1]Plant Breeding Study Program, Faculty of Agriculture, Pattimura University, Ambon
[2]Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural Institute
[3]Department of Statistics, Faculty of Mathematics and Natural Sciences, Bogor Agricultural Institute
[4]Agrotechnology Study Program, Faculty of Agriculture, Pattimura University, Ambon
[*] Corresponding author e-mail: edy_jambormias@yahoo.com; edizon.jambormias@lecturer.unpatti.ac.id

ABSTRACT

The early generation selection is a viable strategy for rapidly developing new plant varieties. The selection process in mungbeans (*Vigna radiata* L. Wilczek) is carried out to obtain high seed yield, early maturity, and sufficiently large seed size. To enhance this process, the extension of the combined-eigenanalysis selection index method (CESIM) with transgressive segregation variables can be used to fix multiple-trait transgressive segregates. Therefore, this research aimed to (1) develop an eigenvalue-based selection index method in information from relatives analysis capable of fixing multiple-trait transgressive segregates in the early generation, (2) predict expected and realized multiple-trait selection responses, and (3) verify the presence of multiple-trait transgressive segregates in the early generation of mungbeans. The material used consisted of the F3 generation population and its selection outcomes in F4, originating from the crossbreeding of mungbean varieties Gelatik × Lasafu Lere Butsiw. The empirical breeding values (EBV) between and within families were obtained using the BLUP values of the F3 generation from the generalized linear mixed model with a nested-augmented design and log-normal distribution. The EBV values between families and dummy variables of transgressive segregate families were used in the selection process with CESIM. Furthermore, analysis of variance in EBV values within families in the F4 generation was applied to verify the presence of multiple-trait transgressive segregates. The results showed that the selection from the best CESIM equation yielded index scores with a determination coefficient $R^2 = 97.76\%$ and an expected selection response of 136.62. The verification process confirmed the presence of 9 families as multiple-trait transgressive segregate families in the early generation.

Keywords: *eigenvalue, empirical breeding value, selection index, transgressive segregation, true breeding value.*

INTRODUCTION

The development of new mungbean (*Vigna radiata* L. Wilczek) varieties is carried out to increase yields beyond 2 tons ha^{-1} and achieve harvest within the age range of 55-65 days with seed sizes of 5-6 g (100 seeds)$^{-1}$ (Fernandez & Shanmugasundaram, 1988; Chadha, 2010). An essential component of this process is selection, which is crucial in developing new plant varieties, particularly when it successfully fixes transgressive segregates during early generation (Jambormias & Riry, 2009). The early generation population, starting from F3, is suitable for genetic analysis (Bos and Caligari, 2008), providing information from relatives between and within families (Jambormias *et al*., 2011).

A selection process is generally performed to enhance the chances of selecting breeding values. During this process, the combined selection index is used as a procedure for the phenotype values that maximize breeding values (Smith, 1936; Hazel, 1943; Kempthorne & Nordskog, 1959; Cerón-Rojas *et al*., 2006; Cerón-Rojas *et al*., 2008). Maximizing the selection index using eigenanalysis enhances effectiveness (Cerón-Rojas *et al*., 2006; Cerón-Rojas *et al*., 2008), particularly using multiple principal components (Mattjik *et al*., 2011). The Combined-Eigenanalysis Index Selection Method (CESIM) is the extension of the Combined Selection Index Method (CISM), incorporating information between and within families (Falconer & Mackay, 1996) as well as the Eigenanalysis Index Selection Method (ESIM) (Cerón-Rojas *et al*., 2006) with several principal components (Mattjik *et al*., 2011).

Breeding values and genetic deviations are generated from the information between and within families (Falconer & Mackay, 1996) using Best Linear Unbiased Predictions (BLUP) (Satoh, 1998; Bauer *et al*., 2006; Viana *et al*., 2011). The CESIM can be applied to the BLUP breeding values of several important traits, assuming that these values represent empirical breeding values (EBV) (Muir, 2007) to maximize the true breeding values (TBV). Specifically, CESIM focuses on important traits, including selection characters and indicators, those with high heritability, and categorical variables of transgressive segregate families. These indicators are used to support indirect character selection and construct a selection index capable of simultaneously fixing multiple traits (Wirnas *et al*., 2006; Jambormias *et al*., 2011). Previous research has shown the potential of transgressive segregated families to be fixed in the early generation (Jambormias *et al*., 2015).

Based on the background above, this research aimed to (1) develop an eigenvalue-based selection index method in information from relatives analysis capable of fixing multiple-trait transgressive segregates in the early generation, (2) predict expected and realized multiple-trait selection responses, and (3) verify the presence of multiple-trait transgressive segregates in the early generation of mungbeans.

MATERIALS AND METHODS

Research Place and Time

This research comprised two field experiments conducted from June to October 2010 and July to November 2013 at the Leuwikopo Experimental Garden, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural Institute.

Genetic Material

In the first experiment, the genetic material consisted of 143 early-generation families derived from crossbreeding the local strains Mamasa Lere Butnem × Lasafu Lere Butnem. Furthermore, it included four varieties: Gelatik, Perkutut, and Kutilang, considered superior, and one local strain, Mamasa Lere Butnem, as a tester. In the second experiment, the genetic material comprised transgressive and some non-transgressive segregate families selected from the first experiment. In addition to the previous four varieties, this experiment included Vima 1 and two local strains, Lasafu Lere Butsiw 1 and Lasafu Lere Butsiw 2. Gelatik and Vima 1 are high-yielding superior varieties, whereas Vima 1 is also characterized by early maturity and simultaneous harvest. All local strains were obtained from West Southeast Maluku Regency, Maluku Province, Indonesia.

Experimental Design

In this research, the two experiments were conducted using a pedigree selection method, where the individual family was planted in rows. In the first experiment, each row of families represented a single experimental unit with no replications, except for the four completely randomized varieties within each block. The design used was a one-stage nested-augmented incomplete block design. The crossbreeding families and the four varieties were planted in rows of 20 plants within eight experimental blocks. Additionally, a check plot of the same size as one block was prepared to plant the four varieties in the form of plots. The varieties planted in each block served as control genotypes, which were used to evaluate the presence of genetic diversity and recover genetic value information. Meanwhile, the varieties in the check plot were termed check genotypes, which were used to estimate random variance,

The second experiment followed the procedure of the first experiment, with the only difference being the replication of check genotype plots in each block. The planting was conducted in three blocks, and the varieties used as checks and controls included Gelatik, Perkutut, Kutilang, Vima 1, Mamasa Lere Butnem, Lasafu Lere Butsiw 1, and Lasafu Lere Butsiw 2.

Linear Model

The general linear model for the first and second experiments is (Equation 1):

$$y_{ijk} = \mu + \beta_k + \varphi_{i'(k)} + \chi_{i''} + \eta_{i'''} + \varphi_{i'(k)\chi i'')} + \omega_{j(i'(k))} + \varpi_{j(i'')} + \gamma_{j(i''')} + \varepsilon_{ijk} \quad \ldots (1)$$

for i' = 1, 2, ..., f families, i'' = 1, 2, 3, ..., c varieties as control; i''' = c varieties as check; j = 1, 2, …, s_i samples and k = 1, 2, ..., r block; where: μ = overall mean, β_k = effect of the k^{th} block, $\varphi_{i'(k)}$ = effect between i'^{th} families, $\chi_{i''}$ = effect between i''^{th} controls, $\eta_{i'''}$ = effect between i'''^{th} checks, $\omega_{j(i'(k))}$ = effect within $j(i'(k))^{th}$ family, $\varpi_{j(i'')}$ = effect within $j(i'')^{th}$ control, $\gamma j_{(i''')}$ = effect within $j(i''')^{th}$ tester, and ε_{ijk} = experimental error.

Observed Quantitative Traits

The observed traits in this research included plant height at harvest (cm), number of branches, days to flowering, days to harvest, harvest time (days), number of viable pods, number of viable seeds, 100-seed weight, seed weight plant^{-1}, and simultaneous harvest index. The data used were the Best Linear Unbiased Predictions (BLUP) between families (BLUPFT) as family Estimated Breeding Values (EBV), BLUP within families (BLUPFT) as EBV within families, and dummy variables for transgressive segregate families. Furthermore, BLUP values were obtained from information recovery using a Generalized Linear Mixed Model (GLMM) with a log-normal distribution (Jambormias, 2014), and dummy variables for transgressive segregate families were derived from transgressive segregation analysis (Jambormias *et al*., 2015).

Data Analysis

CESIM. The multiple-trait selection was carried out using CESIM with a 20% percentage, followed by an extreme selection of the best families, according to Walsh (2010). Subsequently, the thresholds used were seed weight and simultaneous harvest index of the F3 generation.

The CESIM index and weight **b** that maximize the BLUP breeding values are:

$$I = \mathbf{b}_f z_f + \mathbf{b}_w z_w \text{ and } \mathbf{b} = \mathbf{G}_{CE}^{-1}\mathbf{A}_{CE}\mathbf{a} \quad \ldots (2)$$

where $\mathbf{b}' = (\mathbf{b}_f \quad \mathbf{b}_w)$ and $\mathbf{a}' = (\mathbf{a}_f \quad \mathbf{a}_w)$,

$$\mathbf{G}_{CE} = \begin{pmatrix} \mathbf{G}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w \end{pmatrix} \text{ and } \mathbf{A}_{CE} = \begin{pmatrix} \mathbf{A}_f & \mathbf{0} \\ \mathbf{0} & \mathbf{A}_w \end{pmatrix}$$

for $\mathbf{b}_f$ = the weight vector of EBV between families ,$\mathbf{b}_w$ = the weight vector EBV within families, $\mathbf{G}_f = t\hat{\mathbf{G}}$= covariance matrices of EBV families, $\mathbf{G}_w = (1-t)\hat{\mathbf{G}}$= covariance matrices of EBV within families, $\mathbf{A}_f = r\hat{\mathbf{A}}$= covariance matrices of TBV families, $\mathbf{A}_w = (1-r)\hat{\mathbf{A}}$= covariance matrices of TBV within families, each of dimension ($p\times p$); with r = the resemblance between relatives of 2 individuals from the same parent = $\frac{2f}{\sqrt{(1+F_{F3})^2}}$, in the case of $f = 0.5$ (Falconer and Mackay, 1996) and $F_{F3} = 0.5$ (Bos and Caligari, 2008; Hallauer *et al.*, 2010); and $t = \frac{trace\hat{\mathbf{A}}}{trace\hat{\mathbf{G}}}$ in the case of $\hat{\mathbf{G}}$ and $\hat{\mathbf{A}}$ are full rank matrices; $\mathbf{a}_f$ = the weight vector of TBV between families and $\mathbf{a}_w$ = the weight vector of TBV within families.

In CESIM $\hat{\mathbf{G}}$ is the EBV covariance matrix and $\hat{\mathbf{A}}$ is the TBV covariance matrix obtained from the eigenanalysis with characteristic Equation 3 (Cerón-Rojas *et al.*, 2008):

$$\mathbf{Gk} = \lambda\mathbf{k} = (\mathbf{G} - \lambda\mathbf{I})\mathbf{k} = 0 \quad \ldots (3)$$

where **G** = the covariance matrix of BLUP breeding values, a correlation matrix due to different units of observation for breeding values, and $\lambda = (\lambda_1 \ \lambda_2 \ \ldots \ \lambda_j \ \ldots \ \lambda_p)'$ the characteristic root, **k** = the characteristic vector, consisting of $\mathbf{k}_1 \ \mathbf{k}_2 \ldots \mathbf{k}_j \ldots \mathbf{k}_p$, and **I** = the identity matrix. The analysis is conducted to select q principal components (PC) from p PC with optimum variance. Ideally, the number of selected q PC should be able to explain 70-90% of the total variance cut-off (Jolliffe, 2002). The EBV and TBV additive covariance matrices are obtained from the characteristic root according to the Equation 4

$$\hat{\mathbf{A}} = \sigma_q^{2'}\mathbf{I}_p \text{ and } \hat{\mathbf{G}} = \sigma_p^{2'}\mathbf{I}_p \quad \ldots (4)$$

where $\boldsymbol{\sigma}_q^2 = (\boldsymbol{\sigma}_{(a)1}^2 \ \boldsymbol{\sigma}_{(a)2}^2 \ \ldots \ \boldsymbol{\sigma}_{(a)i}^2 \ldots \ \boldsymbol{\sigma}_{(a)p}^2)'$ = the variance vector of TBV quantitative traits up to q PC and $\boldsymbol{\sigma}_p^2 = (\boldsymbol{\sigma}_{(g)1}^2 \ \boldsymbol{\sigma}_{(g)2}^2 \ \ldots \ \boldsymbol{\sigma}_{(g)i}^2 \ldots \ \boldsymbol{\sigma}_{(g)p}^2)'$= the variance vector of EBV quantitative traits up to p PC, for $\boldsymbol{\sigma}_{(a)i}^2 = \sum_{j=1}^{q}\left(k_{ij}^2 \Big/ \sum_{j=1}^{q}\sum_{i=1}^{p}k_{ij}^2\right)\lambda_j$ and $\boldsymbol{\sigma}_{(g)i}^2 = \sum_{j=1}^{p}\left(k_{ij}^2 \Big/ \sum_{j=1}^{p}\sum_{i=1}^{p}k_{ij}^2\right)\lambda_j$ which are the elements of the quantitative trait z_i in the vectors $\boldsymbol{\sigma}_q^2$ dan $\boldsymbol{\sigma}_p^2$. Because **G** = the EBV correlation matrix, then $\hat{\mathbf{G}} = \mathbf{I}_p$.

Best Selection Index Simulation. The best-combined selection index was obtained by simulating economic values that yielded the determination coefficient for the best index (Moeljopawiro, 2002). The determination coefficient for the index was calculated using the Equation 5 (Walsh, 2010).

$$\rho_{HI}^2 = \left(\mathbf{b}'\mathbf{G}_{CE}\mathbf{b} / \mathbf{a}'\mathbf{A}_{CE}\mathbf{a}\right)100\% \quad \ldots (5)$$

Expected Selection Response. The expected selection response index (R_{HI}) (Equation 6) and the vector response of index components ($\underline{R}_c$) (Equation 7) were calculated according to the following equations:

$$R_{HI} = i\sqrt{\mathbf{b}'\mathbf{G}_{CE}\mathbf{b}} \quad \ldots (6)$$

$$\underline{R}_c = i\left(\mathbf{A}_{CE}\mathbf{b}\right) \Big/ \left(\sqrt{\mathbf{b}'\mathbf{P}_{CE}\mathbf{b}}\right) = i\left(\mathbf{A}_{CE}\mathbf{b}\right) \Big/ \left(\sqrt{\mathbf{a}'\mathbf{A}_{CE}\mathbf{b}}\right) \quad \ldots (7)$$

The predicted F4 means ($\bar{x}_{F4(P)}$) and the selected F3 means ($\bar{x}_{F3}$) for each trait are the results of a reverse transformation according to the Equation 8 and 9.

$$\bar{x}_{F4(Pi)} = e^{[R_{ci}][s_{\text{BLUP}F(i)}]+\text{BLUP}\beta_0(i)} \quad \ldots (8)$$

$$\bar{x}_{F3(i)} = \sum_{i=1}^{f}\left(s_f \Big/ \sum_{i=1}^{f} s_f\right)e^{[\text{BLUP}F(i)+\text{BLUP}\beta_0(i)]} \quad \ldots. (9)$$

where R_{ci} = element vector of the ith trait component response, $s_{\text{BLUP}F(i)}$ = the EBV standard deviation of the ith trait, BLUP$F_{(i)}$ = EBV family of the ith trait, BLUP$\beta_{0(i)}$ = the overall mean of the ith trait, f = the frequency of selected families, s_f = the frequency of selected individuals within families.

Realized Selection Response or Genetic Gain. The BLUP values from the transformed one-stage nested-augmented incomplete block design mixed linear model of the F4 generation data or the $S_{1:3}$ selection generation were used to obtain the mean of the $S_{1:3}\,(\overline{x}_{F4})$ selection generation and the breeding values of each family ($\overline{x}_{F(i)}$). Subsequently, the realized selection response was calculated according to the following Equation 10.

$$R_{realized} = \overline{x}_{F4} - \overline{x}_{F3(adj)} \qquad \ldots (10)$$

where $\overline{x}_{F3(adj)} = \overline{x}_{F4} - [\overline{x}_{GP(F4)} - \overline{x}_{GP(F3)}]$ for $\overline{x}_{GP(F4)}$ and $\overline{x}_{GP(F3)}$ are the means of the check genotypes in the F3 and F4 generations, respectively.

Verification of Homogeneous Families. The verification of multiple homogeneous families was done by examining the PROC MIXED SAS analysis results of the F4 generation experiment data with natural logarithm transformation. Families were considered homogeneous when the variance within the adjusted family was equal to zero. This variance was calculated using the following Equation 11.

$$\hat{\sigma}^2_{WF(adj.)} = \tilde{\sigma}^2_{WF} - \hat{\sigma}^2_{Mixed} \qquad \ldots (11)$$

where $\tilde{\sigma}^2_{WF}$ = variance within families, and $\tilde{\sigma}^2_{WC} - \tilde{\sigma}^2_{WH} = \hat{\sigma}^2_{Mixed}$, for $\tilde{\sigma}^2_{WC}$ = variance within controls, and $\tilde{\sigma}^2_{WH}$ = variance within checks.

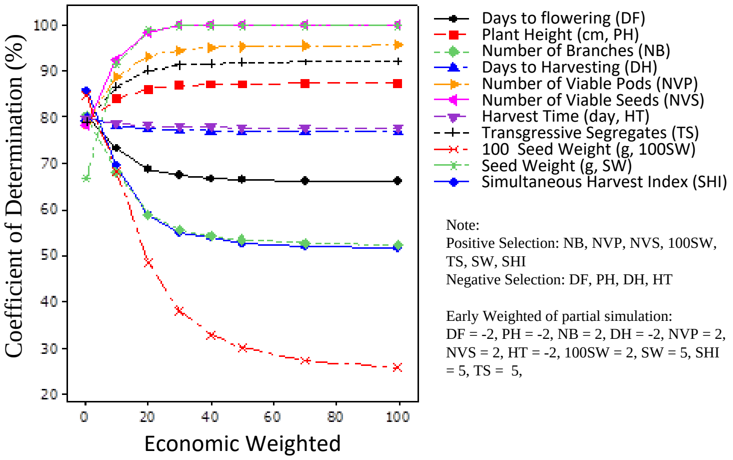
Verification of Transgressive Segregates. When the variance within families of the selection characters in the F4 generation was equal to zero, families with a high and positive realized selection response could be recommended as new expected strains. However, when the variance within families was greater than zero, transgressive segregation analysis for multiple traits was conducted, similar to the F3 generation, to detect multiple homogeneous and heterogeneous families.

RESULTS AND DISCUSSION

Best CESIM Simulation, Extreme Selection, and Their Selection Responses

The selection of economic weights in the CESIM simulation plays a crucial role in determining the accuracy of the index. As presented in Figure 1, the partial selection index simulation results for each trait showed an increase in index weights and determination coefficients. The simulation focusing on increasing the economic weights of important selection characters and indicators yielded a determination coefficient of 97.76% and an expected selection response of 136.62, as illustrated in Table 1. The index weights between and within families were significantly high for traits such as the number of viable pods, seeds, 100-seed weight, seed weight, and simultaneous harvest index. However, the component response was only high for seed weight as an important selection character, followed by the number of viable seeds and pods.

Extreme selection based on CESIM results, using seed weight and simultaneous harvest index thresholds above the F3 generation mean and around the Gelatik variety, showed promising potential in yielding the best families. As presented in Figure 2, the performance of individuals from the best families included a seed weight of 12-20 g and a simultaneous harvest index of 0.5-0.80. The frequency of selected individuals within families also varies. The frequency of selected individuals within these families varied significantly, with MN69 having the highest number at 8, followed by MN15 with 5. Furthermore, MN17 and MN58 consisted of 4 individuals each, MN11, MN18, MN31, and MN113 had 3 individuals, MN-100 and MN176 with 2 individuals, and the remaining families, namely MN47, MN64, MN67, MN82, MN114, and MN149 comprised 1 individual, respectively.



Note:
Positive Selection: NB, NVP, NVS, 100SW, TS, SW, SHI
Negative Selection: DF, PH, DH, HT

Early Weighted of partial simulation:
DF = -2, PH = -2, NB = 2, DH = -2, NVP = 2, NVS = 2, HT = -2, 100SW = 2, SW = 5, SHI = 5, TS = 5,

Figure 1. Economic weighting of partial selection index for quantitative traits in the initial filial generation of mungbeans from a cross between Mamasa Lere Butnem × Lasa Lere Butnem varieties

Realized Selection Response

The realized selection response was slightly lower compared to the expected response. This response was significantly effective for traits with positive selection, such as the number of viable seeds at 51.17, the number of viable pods at 6.49, seed weight at 3.44 grams, and a simultaneous harvest index of 0.06, as presented in Table 2. However, traits with negative selection showed the opposite response in the direction of selection, except for the harvest time at -6.87 days, which remained significantly different from the actual response at -13.63 days.

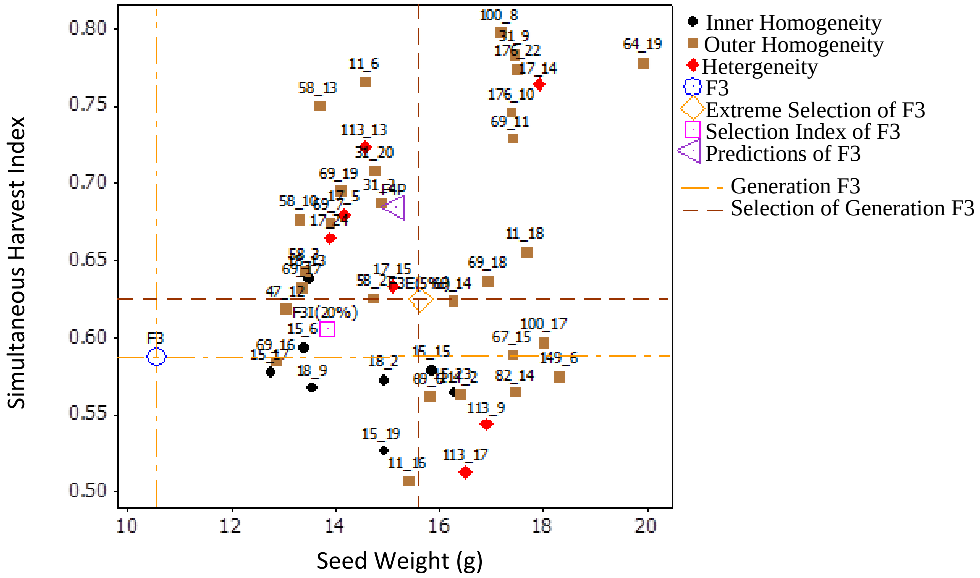


Figure 2. Performance of individuals from families resulting from CESIM-based selection and extreme selection in the initial generation of offspring crosses of mungbean varieties Mamasa Lere Butnem × Lasa Lere Butnem

The improvement in the realized selection response for yield components and simultaneous harvest index increased seed weight from 10.74 g in the F3 generation to 14.18 g in the F4. Furthermore, there was an increase in a simultaneous harvest index from 0.58 to 0.65 and a decrease in days to harvest from 22.13 days to 15.25 days. As illustrated in Table 2, the plant height also increased from 58.57 cm to 66.25 cm, and the days to harvest increased from 59.23 days to 72.54 days. These results showed the advantage of improving yield potential and harvest synchronization but with the potential drawback of increased days to harvest and plant growth.

Table 1. Some estimates of genetic parameters of the best partial index from the results of economic weighting simulations for each trait in offspring crosses of mungbeans Mamasa Lere Butnem × Mamasa Lere Butsiw varieties

Quantitative Traits	Economic Weighted	Indeces Weighted		Response of Component	
		Between Families	Within Families	Between Families	Within Families
Days to flowering	-2	-1.09	-1.79	-0.012	-0.006
Plant Height (cm)	-10	-7.20	-11.85	-0.078	-0.039
Number of Branches	2	0.85	1.41	0.009	0.005
Days to Harvesting	-10	-6.33	-10.42	-0.068	-0.034
Number of Viable Pods	25	19.72	32.46	0.212	0.106
Number of Viable Seeds	30	25.10	41.31	0.270	0.135
Harvest Time (day)	-2	-1.28	-2.11	-0.014	-0.007
100 Seed Weight (g)	10	7.59	12.50	0.082	0.041
Seed Weight (g)	90	75.81	124.78	0.816	0.408
Simultaneous Harvest Index	30	12.62	20.78	0.136	0.068
Transgressive Segregates	30	5.93	9.77	0.064	0.032
R_I^2 = 97.76% and R_{HI} = 139.62					

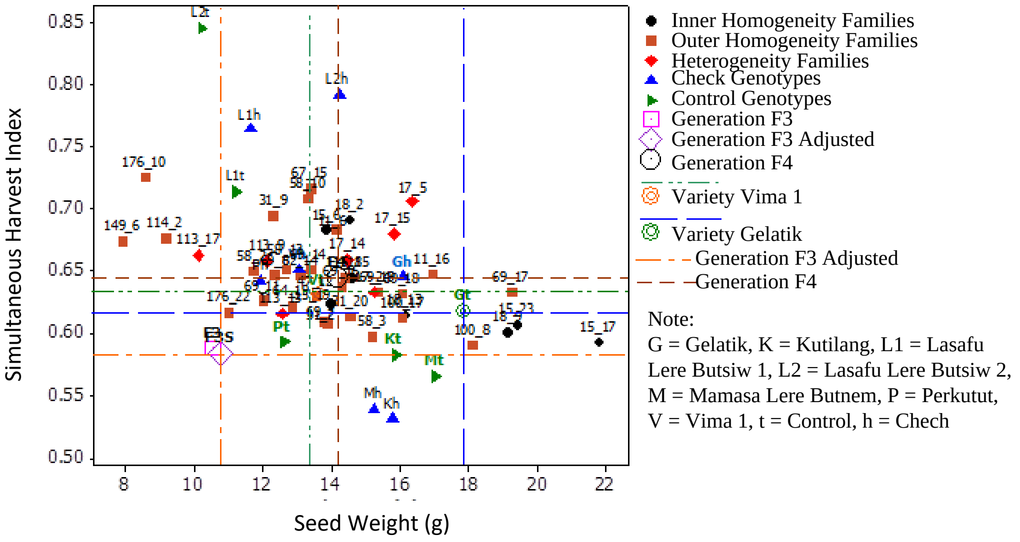
Note: R_I^2 = Coefficient of determination index; R_{HI} = expected selection response of merit index

The next families in the F3 generation with a better simultaneous harvest index than the superior varieties were MN11, MN18, and MN17. The first two families were transgressively segregated in the F3, while the three families in the F4 showed a simultaneous harvest index of 0.65-0.70 with a seed weight of 14-18 grams. The simultaneous harvest index of these families in the F3 ranged from 0.60-0.65, with a seed weight of 14-16 grams. Therefore, MN-11-16, MN18-2, MN17-5, MN17-15, and MN17-14 can also be maintained as families with the best performance.

Generally, there was an improvement in the performance of selection characters from the F3 to the F4 generation. Seed weight and simultaneous harvest index in the F4 ranged from 8-22 grams and 0.60-0.75, which was relatively better than the F3 randing from 8-18 grams and 0.5-0.70, as shown in Figure 3. Multiple-trait transgressive segregate families, namely MN15-17, MN15-23, MN69-17, MN18-9, and MN100-8, produced a seed weight of 18-22 grams per plant, higher than their parent generation in F3 with a seed weight of 16-18 grams. These families also outperformed the superior varieties Gelatik and Vima 1. The simultaneous harvest index of these families in the F4 ranged from 0.60-0.65, relatively similar to F3, except for MN100-8, which approached 0.70 (MN100) in the F3 but reached 0.60 in the F4. Consequently, these families can be maintained as those with the best seed weight.

Table 2. Realized selection response, performance of quantitative traits of early generation in Generation F3 and F4, and variance information between families and within families in mungbeans Generation F4 of Mamasa Lere Butnem × Lasa Lere Butnem varieties cross

Quantitative Traits	Realized Selection response of Component	Performance		Variance of Generation F4		
		Generation F3 (Adjusted)	Generation F4	Between Families	Within Families	Error
Days to flowering	10.37	37.07	47.44	0.0082	0.0017	0.0084
Plant Height (cm)	7.67	58.57	66.25	0.0316	0.0001	0.0278
Number of Branches	0.90	1.06	1.96	0.0628	0.0000	0.2620
Days to Harvesting	13.32	59.23	72.54	0.0043	0.0007	0.0062
Number of Viable Pods	6.49	22.49	28.99	0.0675	0.0000	0.1827
Number of Viable Seeds	51.17	188.23	239.40	0.0942	0.0000	0.1990
Harvest Time (day)	-6.87	22.13	15.25	0.0000	0.0000	0.3829
100 Seed Weight (g)	0.04	5.75	5.79	0.0071	0.0000	0.0223
Seed Weight (g)	3.44	10.74	14.18	0.0641	0.0000	0.1980
Simultaneous Harvest Index	0.06	0.58	0.65	0.0022	0.0000	0.0179



Note:
G = Gelatik, K = Kutilang, L1 = Lasafu Lere Butsiw 1, L2 = Lasafu Lere Butsiw 2, M = Mamasa Lere Butnem, P = Perkutut, V = Vima 1, t = Control, h = Chech

Figure 3. Seed weight and simultaneous harvest index of mungbeans of offspring families from a cross between Mamasa Lere Butnem × Lasa Lere Butnem varieties resulting from CESIM-based selection and extreme selection in the F4 Generation

Verification of Transgressive Segregates

The analysis showed that variance between and within families differed significantly, which tended to be close to zero, as illustrated in Table 2. However, days to flowering, plant height, and days to harvest traits still showed genetic diversity within families. These results indicated that MN15-17, MN15-23, MN69-17, MN18-9, MN100-8, MN-11-16, and MN18-2 originating from multiple-trait transgressive segregate families in the F3 generation were verified as transgressive segregates. Although not categorized as multiple-trait transgressive segregates, CESIM-based selection maintained MN17, resulting in MN17-5, MN17-15, and MN17-14 with the best performance in the F4 generation. These three families were associated with traits containing genotype variance within families, such as days to flowering, plant height, and days to harvest. Beyond these three traits, the verification showed that all three families were transgressive segregates for important traits such as simultaneous harvest index, seed weight, 100-seed weight, harvest time, and number of viable seeds, pods, and branches.

CONCLUSION

The CESIM simulation and extreme selection from the best CESIM equation resulted in index scores with a determination coefficient R2 = 97.76% and an expected selection response of 136.62. The component response was positive for almost all traits except for days to flowering, plant height, and harvest time. Based on the results, the best component response was observed for seed weight at 1.22 g and the number of viable seeds and pod at 0.41 and 0.32, respectively. The realized selection response was positive for all traits except harvest time. The best-realized response showed an increase in seed weight of 3.44 g, the number of viable pods at 6.49, the number of viable seeds at 51.17, a simultaneous harvest index of 0.06, and a decrease in harvest time at 6.87 days. Meanwhile, the realized selection response for plant height, days to flowering, and days to harvest increased by 7.67 cm, 10.37 days, and 13.32 days, respectively. The verification results showed that nine families were multiple-trait transgressive segregates. However, there was still a possibility that three families might have genetic diversity for the traits of days to flowering, plant height, and days to harvest.

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