



TRANSGRESSIVE SEGREGATION ANALYSIS OF MULTIPLE TRAITS IN MUNGBEAN (*Vigna radiata* L. Wilczek)

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SUMMARY

The success of selection in self-pollinated crops depends on the extent to which breeders can fix transgressive segregation in early generations. The objectives of this research were to predict the heritabilities of quantitative traits and the mixing variance, and to detect the multiple traits transgressive segregant families of the early generation of mungbean. Material genetics were the F₃ generation progeny of a cross *Gelatik* × *Mamasa Lere Butsiw* variety. The experiment design used 1-stage nested-augmented randomized incomplete block design. Recovery of the phenotypes and the breeding values use a transformed linear mixed model with logarithm natural transformation. Analysis of heritabilities is expressed by the proportion of additive variance to the phenotypic variance, and mixing variance by the value of the within-control variance minus the within-check variance. Furthermore, analysis of transgressive segregation used BLUPWFT and BLUPFT biplot. The results showed that the mixed models produce BLUP with an accuracy of the breeding values of quantitative traits ranged from moderate to high (0.36-0.95); the narrow sense heritability is low to high (0.13-0.91), and the presence of the mixing variance. There were at least 18.90% families of multiple traits transgressive segregant for selection characters with seed weight and simultaneous harvest index ranged between 11-18 g and 0.56-0.65, respectively. Most of these families were better or at least equal to the superior variety *Gelatik* as the best varieties.

Key words: Biplot analysis, multiple traits, transgressive segregation, genetic value, mungbean

Key findings: Transgressive segregation analysis can identify desirable breeding lines at the F₃ generation. Early generation selection can save considerable resources required for breeding.

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INTRODUCTION

Mungbean is one of the food crops which are an important source of protein for humans. Genetic improvement of this crop is still required for yields to exceed 2 t per ha and simultaneously

harvest on the range 55-65 days (Chadha, 2010; Fernandez and Shanmugasundaram, 1988). In Indonesia, productivity of mungbean at the farmers level in 5 year last is 1.07-1.16 t per ha (BPS, 2014), while the average productivity for recommended varieties ranges between 1.4 – 1.7

t per ha (Suhartina, 2005). This fact indicates that increase of yield and trend of simultaneous harvest remains a major problem in the breeding program.

Selection plays an important role in the plant breeding program, specifically in producing new superior genotypes. A selection program on self-pollinated crops such as mungbean ended when a large number of transgressive segregant in transgressive population has been fixed. Transgressive segregant can be predicted and observed within progenies of an early segregating generation. Expected transgressive segregant can be predicted at the F₁ generation while observed transgressive segregant can be obtained at F₂, F₃ and F₄ generation (Chahota *et al.*, 2007). Yadav *et al.* (1998) predicted transgressive segregant using generation mean approach and variance test at the F₂ and F₃ progenies, and showed that variance tests at the F₃ generation was more accurate in comparing to that of the generation mean approach. Statistically, the families in the F₃ and further generations with a high phenotypic performance and lower variance in comparison to superior varieties (as a lines) are the transgressive segregant (Jambormias and Riry, 2009).

An augmented design (Federer, 1956, 1961; Federer and Ragharvarao, 1975) is recommended for use in the analysis of transgressive segregation in the early generations due to the influence of dominance or over-dominance gene action (Jambormias *et al.*, 2011). Its analysis is more effective when using breeding values. The best linear unbiased predictions (BLUP) of an additive factor of a mating design is a breeding values (Satoh, 1998; Bauer *et al.*, 2006). BLUP was originally developed in the livestock breeding to predict breeding values (Mrode and Thompson, 2005) and is now widely used in various fields of research. BLUP for phenotypic selection can also be used in plant breeding and variety testing (Piepho *et al.*, 2008). Development of BLUP to allow for comparison of genetic material from different populations evaluated in different environments. This ability comes from the ability of mixed linear models (Searle *et al.*, 1992; McCulloch and Searle, 2001; Galwey, 2006; Myers *et al.*, 2010) utilize information

from relatives of pedigree breeding system even without the use of mating design (Piepho *et al.*, 2008). Mixed linear models is suitable for improve the inference of breeding program using augmented block design (Santos *et al.*, 2002). In addition, because BLUP produced from mixed linear models, then it can also be used to recover the lost information of phenotypic values due to systemic influences such as the block effect on the augmented design (Lin and Poushinsky, 1983; Schaalje, 1987; Federer, 1994; Wolfinger *et al.*, 1997; Bhagyalakshmi and Somarajan, 1999).

Breeding populations in augmented design produces many restricts like unbalance data with heterogeneous variance and not normal distribution. Similarly, the planting in the row of crops such as pedigree selection method can produce the mixing effect (Jambormias *et al.*, 2013b). McCullagh and Nelder (1987) developed generalized linear models to solve like this problem. Extension of this models and linear mixed models configure generalized linear mixed models (McCulloch dan Searle, 2001; Myers *et al.*, 2010, Gbur *et al.*, 2012). Its models can be used to produce most accurate BLUP on many restricted conditions as above. On the other hand, Cordeiro dan de Andrade (2009) developed transformed generalized linear models to solve the restriction with box-cox transformation. Simplification of its approach into transformed linear mixed models can also produce sufficient accurate BLUP.

The above concept can be designed for the development of an early generation selection method of multiple traits at F₃ or F₄ generations. The biplot analysis can be used to analysis of multiple traits. It is a multivariate analysis method that is able to explore sampling units and variables simultaneously (Johnson and Wichern, 2002). In the breeding populations, the genetic materials and quantitative traits are the sampling units and the variables, respectively; so that the analysis approach called genotype-by-traits biplots (GT biplot) (Yan and Fregeau-Reid, 2008). If quantitative traits are its BLUP, then the approach called BLUP of genotype-by-traits biplot. Biplot analysis with BLUP as variables has been carried out in the AMMI (*additive main effect and multiplicative interaction*) analysis (Mattjik *et al.* 2011). Therefore, the GT biplot

analysis can use BLUP as multiple traits. In this analysis, the multiple homogeneous families can be seen from the biplot analysis based on information from BLUP value of within-family (BLUP of within-family-by-traits biplot, BLUPWFT Biplot). On the other hand, the best performance of multiple families can be seen from the biplot analysis based on information from BLUP between-family (BLUP of family-by-traits biplot, BLUPFT Biplot).

The objectives of this research are to predict the broad and narrow sense heritability and mixing variance of quantitative traits, to select the families that are multiple homogeneous and best performances as the families that are transgressive segregation to seed weight and harvest index simultaneously in the early generation of mungbean. The results of this research will be used to support the development of an early generation selection of multiple traits in self-pollinated crops.

MATERIALS AND METHODS

Place and time

The experiment was conducted at the "Leuwikopo" experimental station, Department of Agronomy and Horticulture, Faculty of Agriculture, Bogor Agricultural Institute, Indonesia, from June to October, 2010.

Genetic materials

Genetic materials used in this experiment were 217 F₃ families segregating generation of mungbean. Genetic materials were developed from a cross of a national superior variety *Gelatik* and a local variety *Lasafu Lere Butsiw*. Both varieties have a high general combining ability based on the results of the analysis of diallel cross (Jambormias *et al.*, 2013a). Two of this variety, and 2 other national varieties, i.e. Kutilang and Perkutut also planted for the goal of evaluating the yield potential, uniformity and mixing variance of the families in early generations of mungbean.

Experimental design

The experiment design used a nested-augmented incomplete block design. 217 Families of crossing progenies F₃ and 4 varieties (as lines) were planted as rows in 8 experimental blocks. Progeny rows of each family were present only once in a block and didn't present in other blocks, while rows of each variety were randomized complete in every block. Sample size of each row is 20 sample units in each families and varieties. Moreover, one check plot as the same size of a previous block was prepared to plant the 4 varieties in plots. Varieties planted in each block and neighbored with families of cross progenies were called control genotypes and in the check plots were called check genotypes. The observed values of check genotypes were used to evaluate the presence of mixing variation in control genotype and family rows within each block. Mixing variation is the variation that occurs in the uniform family emerged as a result of competition between homogeneous crop in the rows with its heterogeneous neighbors in obtaining the input of light and nutrients in the same microenvironment (Jambormias *et al.*, 2013b).

Linear model

Linear model of the experiment was (Jambormias *et al.*, 2013b):

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

for $i' = 1, 2, \dots, f$ families, $i'' = i''' = 1, 2, 3, \dots, c$ varieties; $j = 1, 2, \dots, s_i$ sample and $k = 1, 2, \dots, r$ blok; where: μ = general means, β_k = effects of k^{th} block, $\varphi_{i'(k)}$ = effects of i^{th} families, $\chi_{i''}$ = effects of i'^{th} controls, $\eta_{i'''}$ = effects of i''^{th} checks, $\omega_{j(i'(k))}$ = effects of j^{th} individual plants nested in within i^{th} family in k^{th} block, $\varpi_{j(i'')}$ = effects of j^{th} individual plants nested in within i'^{th} controls, $\gamma_{j(i'''')}$ = effects of j^{th} individual plants nested in within i''^{th} checks, and ε_{ijk} = experimental errors.

Observed variables

Variables were observed per plant individual (*per se*) within each families and varieties. Quantitative traits observed were plant height (cm), number of branch plant⁻¹, number of viable pods, number of viable seeds, 100-seed weight (g), days to flowering, days to harvest, seed weight (g), harvest time (days), and simultaneous harvest index. Two last variables are used to measure the tendency of simultaneous harvest in mungbean. Harvest time (days) is the number of days required for harvesting, i.e. from the first until the last day of harvest. On the other hand, simultaneous harvest index is a measure of the relative simultaneity harvest centered on a specific day of the whole harvest. Simultaneous harvest index (SHI) is calculated according to the equation:

$$SHI_i = \sum_{j=1}^k \left(y_{ij} / [|Q_i - DH_{ij}| + 1] \right) / \sum_{j=1}^k y_{ij}$$

for $i = 1, 2, \dots, f$, $j = 1, 2, \dots, k$; where $f =$ number of families, $k =$ number of harvests, $y_{ij} =$ seed weight of i^{th} family for j^{th} harvest, $Q_i =$ days to harvest that produced the highest seed weight in i^{th} family, and $DH_{ij} =$ days to harvest of i^{th} family for j^{th} harvest.

Both quantitative traits i.e. seed weight and simultaneous harvest index were the selection character, i.e. the quantitative traits that were the goal of improvement in the selection.

Data analysis

The BLUPs, Analysis of genetic variances component, and heritabilities

BLUPs values required in the analysis of transgressive segregation are the breeding values and genetic deviations of SAS PROC MIXED. Because of non-normality of the quantitative traits in segregating population, then the natural logarithm transformation it uses in the mixed linear models analysis. The breeding values (A) and the genetic deviation (\bar{A}) were obtained from the equation:

$$A = BLUPFT = \varphi_i,$$

$$\bar{A} = BLUPWFT = \omega_{j(i)}$$

where: $\varphi_i =$ the predicted value of random effect of the i^{th} family, $\omega_{j(i)} =$ the predicted value of random effect of the j^{th} (i^{th}) within-family. BLUPWFT is non-additive gene action deviation alone or include mixing variances.

Components of variance and evaluation of mixing variance

Output of the variance components of PROC MIXED SAS consists of variance of between-family (S_{BF}^2), between-control (S_{BC}^2), between-check (S_{BH}^2), within-family (S_{WF}^2), within-control (S_{WC}^2) and within-check (S_{WH}^2). Both components of variance (S_{WC}^2 and S_{WH}^2) are used to determine the mixing variance. If $S_{WC}^2 > S_{WH}^2$, then there are indications of mixing variance. Mixing variance (S_{Mixing}^2) is estimated according to this equation:

$$S_{Mixing}^2 = S_{WC}^2 - S_{WH}^2$$

On the other hand, variance of additive (S_A^2) and non-additive ($S_{\bar{A}}^2$) is calculated using decomposition of variance components of F_3 (Bos and Caligari, 2008) and is rounded to

$$S_A^2 = 2s_{BF}^2 \text{ and } S_{\bar{A}}^2 = 2S_{WF(adj.)}^2,$$

and variance of genotypic (S_G^2) and phenotypic (S_P^2) were $S_G^2 = S_A^2 + S_{\bar{A}}^2$ and $S_P^2 = S_G^2 + S_E^2$, respectively, where

$$S_E^2 = 1 / \bar{s}_f (S_{Mixing}^2 + S_e^2) \text{ and } S_{WF(adj.)}^2 = S_{WF}^2 - S_{Mixing}^2,$$

in terms $S_E^2 =$ environmental variance, $\bar{s}_f =$ coefficient of variance component of between-family variance in type 3 sum of square of the analysis of variance, and $S_{WF(adj.)}^2 =$ within-family variances adjusted to the mixing variance.

Heritability estimation and accuracy of predicting genetic value from the BLUP model

Estimation of broad- and narrow-sense heritability was done using the following equation:

$$H = S_G^2/S_P^2 \text{ and } h^2 = S_A^2/S_P^2$$

The accuracy of additive genetic value of a trait based on this method was determined by the correlation between BLUP and the observed value according to the equation:

$$r_{A\hat{A}} = \sqrt{1 - (\text{PEV}/S_A^2)}$$

Where S_A^2 = additive variance based on the restricted maximum likelihood (REML) prediction and PEV = prediction error variance = $S_A^2(1 - h^2)$ (Korsgaard *et al.*, 2002).

The BLUP of each trait was used in the GT biplot analysis. BLUPFT was used to analyze the GT biplot of between-family (BLUP of family-by-trait biplot, BLUPFT biplot) and BLUPFWFT was used to analyze the GT biplot of within-family (BLUP of within-family-by-trait biplot, BLUPWFT biplot). Both analyses were used to carry out the selection of transgressive segregant families.

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Analysis of multiple traits transgressive segregation

Analysis of transgressive segregation of the multiple traits carried out by taking into account the results of GT Biplot analysis on the BLUPWFT and BLUPFT genetic values. Biplot analysis used macro SAS procedure by Friendly (2008). Variation of the selected principal's components (PC's) of the biplot could explain at least 70-90% of the total variation (Jolliffe, 2002). A family was categorized as a transgressive segregant if its family tends to be

homogenous and has the best phenotypic performance.

A family tends to have multiple homogenous when interquartile ranges (IQR) of the performance index (PI) of BLUPWFT biplot (PI-IQR of BLUPFT biplot) less than PI-IQR of check or control genotypes. Calculation of PI-IQR was according to the equation (Mattjik *et al.*, 2011):

$$PI = \sqrt{\sum_{i=1}^m \left(\left[\lambda_i^{1/2} / \sum_{i=1}^m \lambda_i^{1/2} \right] c_i \right)^2}$$

where: λ_i = singular values of i^{th} PC, c_i = PC_{*i*} scores (SPC_{*i*}), $i = 1, 2, \dots, m$ for $i = \text{SPC}_1, \text{SPC}_2, \dots, \text{SPC}_m$ of BLUPWFT Biplot.

A family was selected as a high-performance when the value of its family is outside of the vertex hull of check or control genotypes in BLUPFT biplot. The superiority of each family are interpreted based on the relative distance to the axis of the seed weight, simultaneous harvest index and other yield components.

RESULTS AND DISCUSSION

Variance components of within genotypes, heritability and the accuracy of BLUP on mungbean in early generation

The results of genetic analysis showed that there is variation within the family and the mixing of the quantitative traits in early generations of mungbean. However, the within-family variance dependent of the mixing variance, i.e. variance arising as a result of competition between neighboring rows of plants and can cause genotypic variation of within-varieties (lines) and the families that have homogeneous (Table 1). Within-lines variation of the varieties evaluated as control and check genotypes. It can be seen that the within-control variance is greater than the within-check variance. This situation indicates that there was a mixing variance is positive on all quantitative traits. These results indicate that the families also happen mixing. Therefore, the within-family variance can be adjusted with the mixing variance. The adjustment shows that the within-

family variance of all quantitative traits still be positive. Within-family variance that was positive value indicates that the persistence of the influence of non-additive gene action on the quantitative traits of mungbean in the early generations.

The narrow sense and the broad sense heritability of quantitative traits showed a large difference, where the broad sense heritability was high while the narrow sense was low to high. The narrow sense and the broad sense heritability each ranging between 0.13-0.91 and 0.93-0.98 (Table 1). Khatkhat *et al.* (2002) showed the same situation, i.e. narrow sense heritability was smaller than the broad sense, but is still relatively high for all traits, except for seed yield per plant. Quantitative traits related to plant growth such as plant height and number of branches each have a broad sense heritability of 0.97 and 0.95, whereas narrow sense of 0.91 and 12.33. The heritability of number of branches of mungbean was low and plant height was high also reported by Zubair *et al.* (2007). Other trait related to the age of the plant i.e. days to flowering and days to harvest, each with the same broad sense heritability i.e. 0.98. Broad sense heritability were high similar to reports Siddique *et al.* (2006) and Zubair *et al.* (2007) that shows the heritability of the days to flowering and days to mature pods was high, which is between 0.5-0.9. By contrast the narrow sense heritability of both traits in this study was only 0.36 and 0.24, which is still relatively low. The next quantitative trait related to the yield and yield components i.e. number of viable pods, number of viable seeds, 100-seed weight and seed weight. Broad sense heritability of these traits are also quite high, i.e. 0.94, 0.94, 0.98 and 0.93, respectively. High heritability of yield and yield components was also reported by Siddique *et al.* (2006). By contrast the narrow sense heritability of yield and yield components only reaches 0.55, 0.49, 0.38 and 0.45. Results such as these, i.e. heritability of yield component was low to moderate were also reported by Zubair *et al.* (2007). Last quantitative traits related to the tendency to simultaneously harvest is harvest time and simultaneous harvest index. Broad sense heritability of both traits was high,

i.e. 0.78 and 0.81, but the narrow sense heritability was reduced to 0.19 and 0.13.

Broad sense heritability which very high but the low narrow sense indicates that the influence of non-additive gene action was great. This situation has implications for the implementation of selection. Selection of individuals tend to continue the non-additive gene effect, otherwise the family selection tend to continue the effect of additive gene but with a slow response to selection (Falconer and Mackay, 1996, Bos and Caligari 2008, Hallauer *et al.* 2010). The low of the narrow sense heritability of the harvest time and simultaneous harvest index indicates the difficulty to maintaining trends of harvesting simultaneously.

Prediction accuracy of BLUP breeding value of quantitative traits ranged from was low to high. High accuracy seen in the plant height, number of viable pods, number of viable seeds, seed weight, 100 seed weight, days to flowering, and number of branches. Accuracy of each trait was 0.95, 0.74, 0.70, 0.67, 0.62, respectively (Table 1). Only days to harvest, harvest time and simultaneous harvest index which has low accuracy, each only 0.49, 0.43 and 0.36. These results also show that the selection based on BLUP breeding values tend to be more successful in improving of yield and yield components when compared with improving days to harvest and trends of simultaneously harvesting.

The families of homogeneous multiple traits in early generations of mungbean

Analysis of BLUPWFT Biplot showed that the number of principal components required to cover at least 4 of the first PCs to be able to explain 70% variance of the original data, i.e. reached 75.9% of total of variation. These results indicate that there were the multiple homogenous and heterogeneous families. The influence of mixing on most quantitative traits, indicating also that the evaluation of homogeneous families made only by comparing the PI-IQR of control and the families. It families is considered as a homogenous family but not stable against mixing.

Table 1. Variance components of within genotypes, heritability and the accuracy of BLUP model in early generation of mungbean.

Quantitative Traits ¹⁾	Variance Component of Within-genotypes ($\times 10^{-2}$)			Variance of ($\times 10^{-2}$)		Heritability		Accuracy of BLUP
	Family	Control	Check	Mixing	Within-Family (adjusted)	Broad Sense	Narrow Sense	
DF	0.80	0.74	0.31	0.43	0.37	0.98	0.36	0.60
PH	2.54	4.51	2.13	2.38	0.16	0.97	0.91	0.95
NB	23.55	8.48	0.00	8.48	15.07	0.95	0.33	0.58
DH	1.50	0.76	0.00	0.76	0.74	0.98	0.24	0.49
NVP	26.24	19.56	0.00	19.56	6.68	0.94	0.55	0.74
NVS	32.15	23.15	0.00	23.15	9.00	0.94	0.49	0.70
HT	116.18	51.81	0.00	51.81	64.37	0.97	0.19	0.43
100SW	4.06	2.38	1.05	1.33	2.73	0.98	0.38	0.62
SW	34.00	24.49	0.00	24.49	9.51	0.93	0.45	0.67
SHI	2.68	1.37	0.00	1.37	1.31	0.94	0.13	0.36

¹⁾DF = days to flowering, PH = plant height (cm), NB = number of branch, DH = days to harvest, NVP = number of viable pods, NVS = number of viable seeds, HT = harvest time (days), 100SW = 100 seed weight (g), SW = seed weight (g), and SHI = simultaneous harvest index

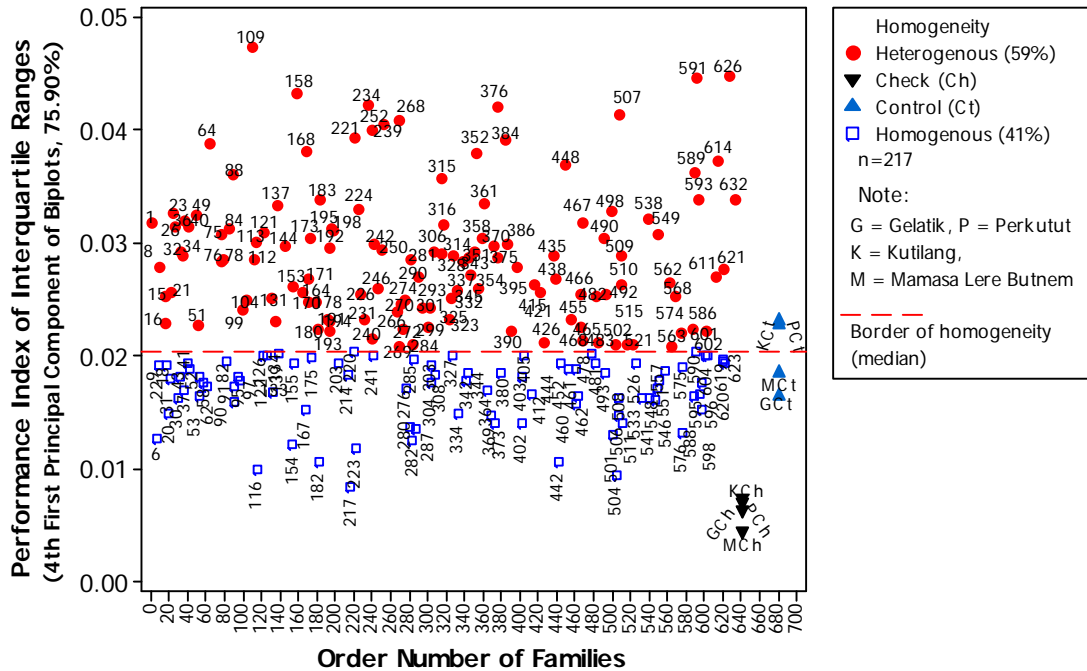


Figure 1. PI-IQR of the families of 4 of the First Principal Component BLUPWFT Biplot of quantitative traits in early generations on mungbean.

Graph of IP-IQR BLUPWFT Biplot shows that the families of multiple homogenous include \pm 41% of the total 217 families (Figure 1). The families with smaller IP-IQR and be around 0.02 detected as the families of multiple homogenous. If the families have high performance for seed weight and/or simultaneous harvest index then it can be considered as transgressive families.

The best of multiple homogenous families on early generation of mungbean

Singular value analysis of BLUPFT Biplot on early generations of mungbean showed that the contribution of the variation of 2 of the first PCs can only explain the total variation of 58.47%, and 3 of the first PCs reach 70.22%. Nevertheless, these first of 3 PCs is sufficient to be able to explain the variation of the total breeding value.

The Analysis of BLUPFT Biplot of PC1 vs PC2 showed that the yield component, especially seed weight, number of viable seeds and number of viable pods occupy a relatively small sector. However, this sector is relatively not different from the sectors where there is the trait of plant height and days to flowering, so as to form a joint sector with both traits, i.e. sector 4 (Figure 2).

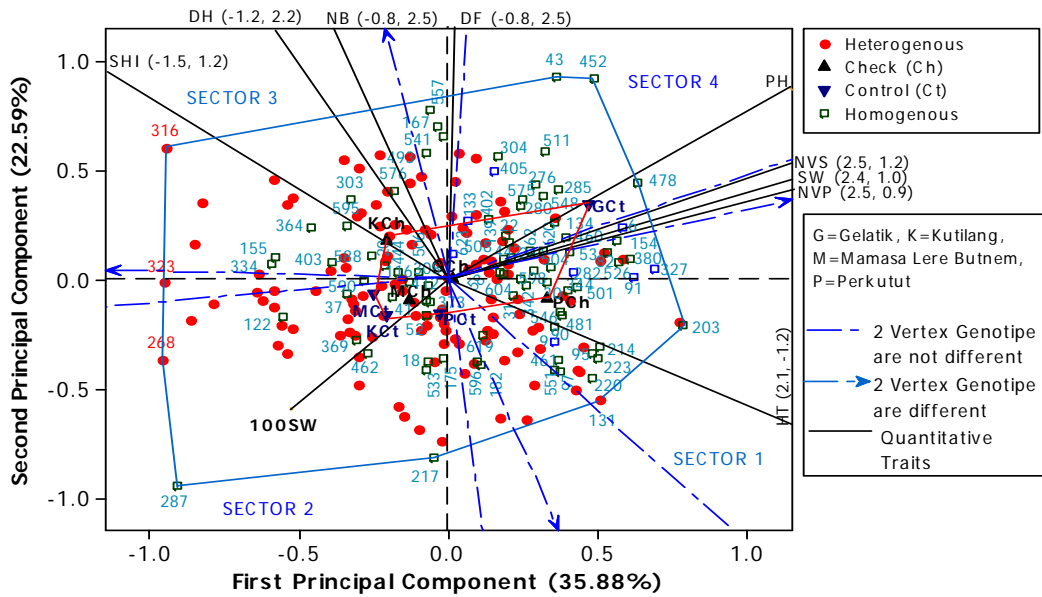
Almost all of the families that multiple homogenous which were in Sector 4 of PC1 vs PC2 can be considered as the best families. The families which multiple homogenous with high breeding value of seed weight and simultaneously harvest index but are in the vertex hull layer of check and control genotypes can also be sustained as the best family. In addition, yield components in Sector 4 is also shown to be positively correlated with harvest time in Sector 1, so that the families in this sector, which is along the vectors of the character of yield components to the outer layer of this sector, i.e. GS-203, is the best families. However, the selection character of simultaneously harvest index tend not correlated with seed weight.

Expectation to obtaining the families of multiple homogenous with high yield only from sector of the days to flowering that same with the plant height, where days to flowering slightly correlated with simultaneous harvest index.

Other expectation comes from the layer in the family at Sector 4 if it has a high seed weight and simultaneous harvest index. Some of the best family of the KU2 vs KU1 were GS-478, GS-43, GS-452, GS-203, GS-327, GS-380, GS-154, GS-66, GS-91, GS-501, GS-526, GS-282, GS-53, GS-62, GS-460, GS-511, GS-304, GS-405, GS-276, GS-285, GS-548, GS-575, GS - 280, GS-133, GS-402, GS-557, GS-167, GS-541 and GS-493. Four last families are expected to the best for simultaneous harvest index.

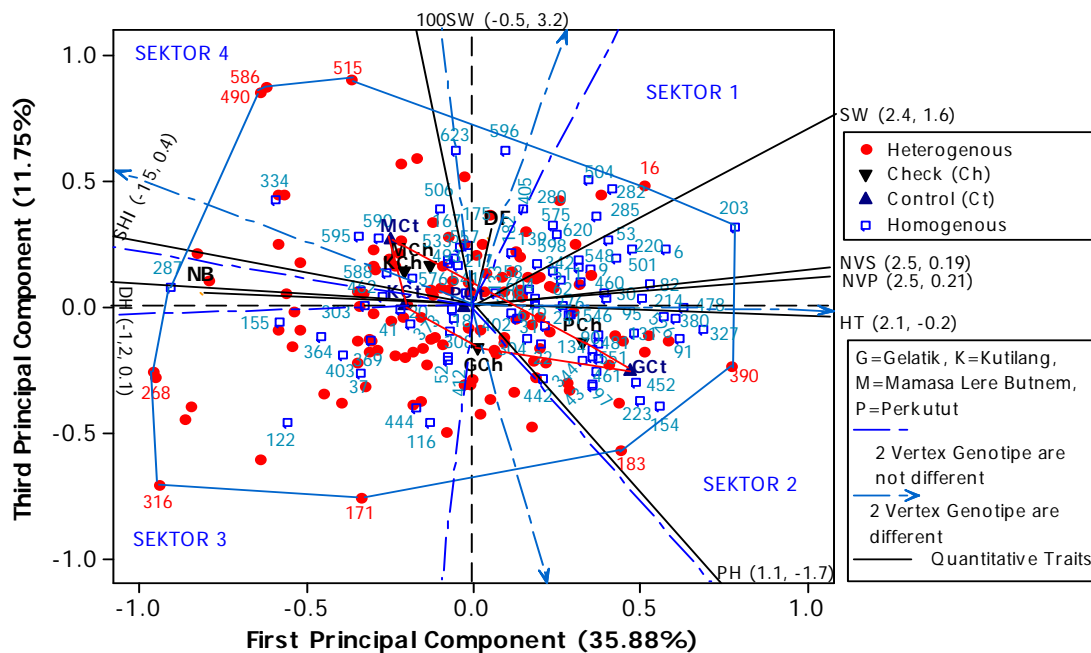
The analysis of BLUPFT Biplot of PC1 vs. PC3 shows selection character of seed weight does not show a high correlation with the other yield components such as on the PC1 vs. PC2. Nevertheless, number of viable seed and number of viable pods still form one sector with the seed weight in Sector 1 (Figure 3). The trait plant height and other yield components i.e. 100-seed weight were positively correlated with seed weight. Instead days to harvest and selection character of simultaneous harvest index tend to correlate negatively.

BLUPFT Biplot of PC1 vs PC3 explain large enough of the total variation, i.e. 47.63%. The proportion of PC1 vs PC3 quite enough to evaluate the best of other new homogenous families, whereas joint accumulation with PC2 biplot can evaluate multiple homogenous families of PC1 vs PC2 biplot with higher precision. All families in Sector 1 is a best multiple homogenous families, followed by the families in Sector 2 and Sector 4 which has a close relative with the selection character of seed weight. The families who approach the origin of the biplot in Sector 1 and 4 are expected to have a fairly high harvest index simultaneously, although the possibility of it yield was lower than control genotype Gelatik.



Note: DF = days to flowering, PH = plant height (cm), NB = number of branch, DH = days to harvest, NVP = number of viable pods, NVS = number of viable seeds, HT = harvest time (days), 100SW = 100 seed weight (g), SW = seed weight (g), and SHI = simultaneous harvest index

Figure 2. BLUPFT biplot of PC1 vs PC2 and multiple homogenous families in early generation of mungbean.



Note: DF = days to flowering, PH = plant height (cm), NB = number of branch, DH = days to harvest, NVP = number of viable pods, NVS = number of viable seeds, HT = harvest time (days), 100SW = 100 seed weight (g), SW = seed weight (g), and SHI = simultaneous harvest index

Figure 3. BLUPFT biplot of PC1 vs PC3 and multiple homogenous families in early generation of mungbean.

Most of the best families in PC1 vs. PC3 include the best families in PC1 vs. PC2. Total variation of the multiple breeding values that was explained with the addition of the PC2 is 70.22%. The best multiple homogenous families include correlation between traits in PC1 vs. PC2 and PC1 vs. PC3. The families that include GS-43, GS-53, GS-62, GS-91, GS-133, GS-154, GS-167, GS-203, GS-276, GS-280, GS-282, GS-285, GS-327, GS-380, GS-402, GS-405, GS-452, GS-460, GS-478, GS-501, GS-511, GS-526, GS-548, GS- 557 and GS-575.

The extreme selection methods (Walsh, 2010) that were carried out with only regard to the selection character of the seed weight and simultaneous harvest index, and with involves only the best families of multiple homogenous were shows that most of the families that have higher seed weight of the varieties check/control, except the varieties Gelatik as control (Figure 4). There were ± 18.90% families who still have seed weight better than varieties Gelatik, with simultaneous harvest

index was equal to or better than other varieties, except the varieties Kutilang. Seed weight of the multiple transgressive segregant of the families ranges between 11-18 g with simultaneous harvest index between 0.56-0.65. When using the independent culling levels method, then there were only 3.23% family of the total of the multiple segregant transgressive families were high of seed yield and simultaneous harvest index. The families are GS-405, GS-285, GS-501, GS-575, GS-280, GS-511 and GS-526. Most of the families were tall and long age. There was only one family with days to flowering and harvesting early maturing, i.e. GS-511.

The families of transgressive segregant with the superiority of high seed weight but low simultaneous harvest index reaches 5.53%. The families with category like this are a GS-82, GS-452, GS-504, GS-282, GS-327, GS-478, GS-548, GS-380, GS-91, GS-6, GS-53 and GS-203. Most of the families were early maturing i.e. GS-82, GS-282, GS-327, GS-91, GS-203, GS-504, GS-380 and GS-6.

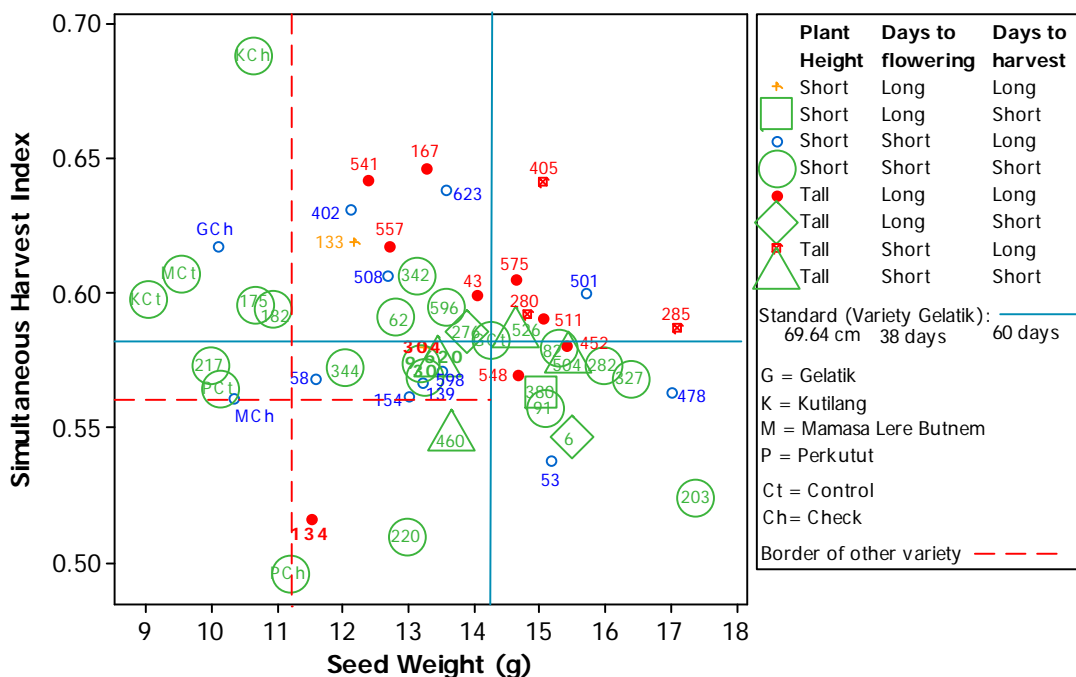


Figure 4. The best of multiple homogenous families based extreme selection methods to the BLUPFT Biplot of PC1 vs PC2 and PC1 vs PC3 of early generation in mungbean

Five of the first families also are ideal posture i.e. short and early flowering. Instead there were last 3 families, each tall but flowering is early, short posture but flowering is late, and tall posture and flowering is late.

The families with the superiority high simultaneous harvest index, but the weight of seed around variety Gelatik reaches 10.14%. The families of which this is GS-167, GS-402, GS-402, GS-541, GS-623, GS-133, GS-557, GS-508, GS-342, GS-43, GS-598, GS-276, GS-62, GS-304, GS-9, GS-20, GS-30, GS-598, GS-620, GS-344, GS-154 and GS-139. Four families from this group were short posture and has an early flowering and maturing, i.e. GS-342, GS-62, GS-596, GS-9 and GS-30, respectively. In addition, GS-620, although tall, but also has early flowering and maturing.

The presence of multiple transgressive segregates at the F₃ generation will enables a simultaneous early generation selection to be carried out for several multiple traits on self-pollinated crops such as mungbean. These results also indicate the use of information from relatives in selection can eliminate the effect of dominant gene action (Jambormias *et al.*, 2011). Selection without detection of the transgressive segregant families, still possess the risk of obtaining selected heterozygous individuals which will segregate in the next generation.

CONCLUSION AND RECOMMENDATION

Conclusion

(1) The transformed-mixed linear model can be produce BLUP for breeding value of quantitative traits in mungbean, with accuracy ranged from 0.36-0.95; (2) There were mixing variance that contribute to the phenotype values of all quantitative traits of mungbean; (3) The broad sense heritability of quantitative traits in early generation of mungbean categorized high, ranging between 0.93-0.98. However, the narrow sense heritability is low to high, ranging from 0.13-0.91; (4) Analysis of BLUPWFT biplot with 4 of the first principal components produces about 41% of the homogenous families in the early-generation of mungbean; (5) Analysis of BLUPFT of PC1 vs. PC2 and PC1

vs. PC3 showed that there were the best performance of multiple transgressive segregant families in early generation of mungbean; (6) The extreme selection methods produced at least 18.90% of the transgressive segregant families of selection characters for seed weight and/or simultaneous harvest index with weights of seed ranging between 11-18 g and simultaneous harvest index between 0.56-0.65.

Recommendation

This transgressive segregation analysis methods should be adjusted through planting the families of self-pollinated crops with a number of viable seeds in the plots that can be used to eliminate mixing variation and the precision of BLUP; (2) There is a need to develop a BLUP selection method based on a selection indeces method and combined of between- and within families according to biplot or principal component analysis (eigenanalysis), to be able to optimally make use of the results of this transgressive segregation analysis.

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