



## BREEDING VALUE ESTIMATION OF FIFTEEN RELATED CASSAVA GENOTYPES USING BLUP

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### ABSTRACT

The cassava tuber yield is strongly influenced by environmental conditions, clones, harvest time and harvest age. Because of the existence of genotype x environment interaction, the cassava plant must be planted in a suitable environment for maximum yield potential. Therefore, genotype testing in various environments will help to identify both specific and wide adaptation of varieties. The yield stability of 15 cassava genotypes was estimated using Best Linear Unbiased Prediction (BLUP) across five locations. In this study, locations are treated as fixed factor while genotypes as random factor. The BLUP procedure was used to estimate random effects. Both matrix A contains coefficient of coancestry and matrix A is assumed not to be related, the result indicate that the lowest expected yield is in Ponorogo and the highest in Kediri. The use of coefficient of coancestry causes lower  $\hat{\beta}$  value of fixed factors, but enhance  $\hat{u}$  value of random factors. In general, breeding values that are achieved using coefficients of coancestry are higher than breeding values that are achieved if matrix A is equal to identity matrix (assumed genotypes are not related). Among the cassava promising clones, CMM 03038-7 had the highest breeding value and higher than control clones UJ 5, Malang 6, Adira 4, but slightly lower than Malang 4.

**Keywords:** cassava, yield stability, GE interaction, BLUP, mixed models.

### INTRODUCTION

In Indonesia, cassava is the second foodstuff after rice and maize. Cassava has an important role in the diversification program and supports the food security program. Cassava is grown almost all over Indonesia, but most are in Java and Southern Sumatera. Cassava planting area has different physical environments both soil and climate. Although cassava is able to adapt to diverse environmental conditions, but in general, its adaptability is narrow and large, and it showed genotype x environment interaction (Tan and Mak, 1995; Dixon *et al.*, 1994 and Dixon and Nukenine, 1997; cit Dixon *et al.*, 2002).

The cassava tuber yield is strongly influenced by environmental conditions and types of clones in addition to time and harvest age. Because of the existence of genotype x environment interaction, the cassava plant must be planted in a suitable environment for maximum yield potential. Therefore, genotype evaluation in various environments will help to identify varieties adaptation both specific and wide environments (Baafi and Sappho-Kantanka, 2008). Genotype x environment interaction is also important to know the adaptability and stability of a genotype in a particular environment (Sneller *et al.*, 1997); as well as to quantify the role of environmental factors on the genetic potential of a genotype (Rao *et al.*, 2002).

Crossa *et al.* (2006) explained that traditional statistical analysis of multi environment trial has assumed that in each sites individual field plot errors are spatially independent and that genotypes are unrelated. This assumption are not realistic because sites in close geographic locations can be expected to be alike, related genotypes, such as full-sibs, half-sibs, sister lines tend to be more alike than unrelated genotypes, and observations

made in field plots in close proximity tend to be correlated.

Analysis of genotype x environment interactions can also be done using Best Linear Unbiased Prediction technique (BLUP). BLUP technique is originally developed in dairy cattle breeding and used to estimate the random effects (Robinson, 1991; Bernardo, 2002; Piepho *et al.*, 2007), but now it is applied in various research fields including studying genotype x environment interactions in plants. Mixed linear models allow an accurate prediction of genotypic performance by using covariate structures that consider correlations between sites, years, and plots in the field, as well as genetic associations between relatives (Crossa *et al.*, 2006). Further, Benardo (2002) explained that the BLUP procedure is useful due to (1) the BLUP procedure allows the analysis of unbalanced data, and (2) the BLUP procedure exploits information from relatives. The use of genetic relationships among individuals provides a significant advantage to plant breeder since observation of related individuals contribute to predictions of each other (Panther and Allen, 1995).

In multilocation trials, genotypes are usually considered to have a fixed effect. When the genotypes are large, holding genotypes effects as random (Stroup and Multize, 1991; cit Bajpai and Kumar, 2005). Random genotypes also imply random genotype-environment interaction. Panther and Allen (1995) also explained that with mixed models, genotypic effects can be considered random and, if narrow inference space is acceptable, other effects, such as years and locations, can be considered fixed. The prediction of the outcome of random variables is commonly done by BLUP (Bajpai and Kumar, 2005).



The purpose of this study is to compare the BLUP procedure with and without information of the coefficient of coancestry among the genotypes.

## MATERIALS AND METHODS

### Experimental design

Eleven cassava promising clones (CMM 03025-43, CMM 03036-7, CMM 03036-5, CMM 03038-7, CMM 03094-12, CMM 03094-4, CMM 03095-5, CMM 02040-1, CMM 02033-1, CMM 02035-3, CMM 02048-6) with four control varieties i.e., UJ5 (Kasetsart 50), Malang 6, Malang 4, and Adira 4 were evaluated in five locations using randomized complete block design with three replications. The experiment was done from November 2010 until August 2011. The five locations were Kediri (Entisol soils), Ponorogo (Alfisol soils), Probolinggo (Alfisol soils), Malang (Associated Alfisol and Inceptisol soils), and Mojokerto (Entisol soils). All of the locations are in West Java Province, Indonesia. Harvest was done at ten months old after planting. Variable that observed was fresh tuber yield.

### Statistical analysis

The basic statistical model in multi environment trial is  $Y_{ijk} = \mu + e_j + r(e_j) + g_i + ge_{ij} + \varepsilon_{ijk}$ , where  $y_{ijk}$  is the observed response of the experimental unit in the  $k^{\text{th}}$  replicate within the  $j^{\text{th}}$  location planted to the  $i^{\text{th}}$  genotype;  $\mu$  is general mean;  $e_j$  is the main effect of the  $j^{\text{th}}$  location;  $r(e_j)$  is the effect of  $k^{\text{th}}$  replicate within location  $j$ ;  $g_i$  is the main effect of the  $i^{\text{th}}$  genotypes;  $ge_{ij}$  is the genotype x location interaction effect; and  $\varepsilon_{ijk}$  is the random error associated with  $ijk^{\text{th}}$  observation.

The linear mixed model can be written in matrix notation as:

$$y = X\beta + Zu + \varepsilon$$

where  $y$  is a vector of observations,  $X$  is a matrix of known constants,  $\beta$  is a vector of fixed effects,  $Z$  is a known constants matrix,  $u$  is a vector of random effects, and  $\varepsilon$  is a vector of residuals. The random effect ( $u$ ) and residuals ( $\varepsilon$ ) are assumed to be random and normally distributed with zero mean vectors and variance-covariance matrices.

$$E \begin{bmatrix} u \\ \varepsilon \end{bmatrix} = \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G & 0 \\ 0 & R \end{bmatrix} \right)$$

The solution for  $\hat{\beta}$  and  $\hat{u}$  are obtained using mixed model equation (MMEQ) according to Henderson (1985) as follow:

$$\begin{bmatrix} \beta \\ u \end{bmatrix} = \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & X'R^{-1}Z + G^{-1} \end{bmatrix} \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \end{bmatrix}$$

If the genotypes used are related, the genetic relationships matrix ( $A$ ), can be used to adjust the matrix  $G$ . Covariance matrix for genetic effects are generally written as  $G = \sigma^2_G A$ , which the elements of  $A$  describes genetic relationship between the two genotypes, and expressed as genetic variance. If  $A = I$  means that the genotype was not related. If some genotypes are related, so matrix  $A$  becomes =

|   |     |     |     |     |     |     |     |     |     |     |   |     |     |     |
|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|---|-----|-----|-----|
| 1 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0 | 0   | 0   | 0   |
| 0 | 1   | 0   | 0   | 1/2 | 0   | 0   | 0   | 0   | 0   | 0   | 0 | 0   | 1/2 | 0   |
| 0 | 0   | 1   | 1/2 | 0   | 1/2 | 1/2 | 1/2 | 1/2 | 1/2 | 0   | 0 | 1/4 | 0   | 0   |
| 0 | 0   | 1/2 | 1   | 0   | 1/8 | 1/4 | 1/4 | 1/4 | 1/4 | 0   | 0 | 1/2 | 0   | 0   |
| 0 | 1/2 | 0   | 0   | 1   | 1/8 | 1/4 | 0   | 0   | 1/4 | 1/4 | 0 | 0   | 1/4 | 0   |
| 0 | 0   | 1/2 | 1/8 | 1/8 | 1   | 1/2 | 1/4 | 1/4 | 1/2 | 1/4 | 0 | 1/8 | 0   | 0   |
| 0 | 0   | 1/2 | 1/8 | 1/8 | 1/2 | 1   | 1/4 | 1/4 | 1/2 | 1/4 | 0 | 1/8 | 0   | 0   |
| 0 | 0   | 1/2 | 1/8 | 0   | 1/8 | 1/4 | 1   | 1/4 | 1/4 | 0   | 0 | 1/8 | 0   | 0   |
| 0 | 0   | 1/2 | 1/8 | 0   | 1/8 | 1/4 | 1/4 | 1   | 1/2 | 0   | 0 | 1/8 | 0   | 0   |
| 0 | 0   | 1/2 | 1/8 | 1/8 | 1/2 | 1/2 | 1/2 | 1/2 | 1   | 1/4 | 0 | 1/8 | 0   | 0   |
| 0 | 0   | 0   | 0   | 1/8 | 1/8 | 1/4 | 0   | 0   | 1/4 | 1   | 0 | 1/4 | 0   | 1/8 |
| 0 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 1 | 0   | 0   | 0   |
| 0 | 0   | 1/8 | 1/2 | 0   | 1/8 | 1/4 | 1/8 | 1/8 | 1/8 | 1/4 | 0 | 1   | 0   | 1/8 |
| 0 | 1/2 | 0   | 0   | 1/8 | 0   | 0   | 0   | 0   | 0   | 0   | 0 | 0   | 1   | 0   |
| 0 | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 0   | 1/8 | 0 | 1/8 | 0   | 1   |



## RESULTS

**Table-1.** Analysis of variance of fresh tuber yield.

| Source                 | Df  | Sum square | Mean square | F value | ProbF   |
|------------------------|-----|------------|-------------|---------|---------|
| Location               | 4   | 49843.52   | 12460.88    | 263.46  | <0.0001 |
| Replication (location) | 10  | 2495.11    | 249.51      | 5.28    | <0.0001 |
| Genotype               | 14  | 3806.41    | 271.89      | 5.75    | <0.0001 |
| Location x genotype    | 56  | 5029.75    | 89.82       | 1.90    | 0.0014  |
| Plant population       | 1   | 134.29     | 134.29      | 2.84    | 0.0943  |
| Error                  | 134 | 6337.89    | 47.30       |         |         |
| Corrected total        | 219 | 77050.72   |             |         |         |

**Table-2.** Fresh tuber yield (t ha<sup>-1</sup>) of fifteen genotypes across location.

| Klon                     | Kediri | Ponorogo | Probolinggo | Malang | Mojokerto | Average |
|--------------------------|--------|----------|-------------|--------|-----------|---------|
| CMM 03025-43             | 53.35  | 6.09     | 24.79       | 30.51  | 19.13     | 26.91   |
| CMM 03036-7              | 67.53  | 10.14    | 26.96       | 33.03  | 20.79     | 31.52   |
| CMM 03036-5              | 52.14  | 9.78     | 37.90       | 22.53  | 24.09     | 29.93   |
| CMM 03038-7              | 65.13  | 11.11    | 42.02       | 44.10  | 21.83     | 37.52   |
| CMM 03094-12             | 46.56  | 5.77     | 26.20       | 38.40  | 10.49     | 24.40   |
| CMM 03094-4              | 58.20  | 8.94     | 29.41       | 51.34  | 23.16     | 34.55   |
| CMM 03095-5              | 44.23  | 3.46     | 27.54       | 27.79  | 14.34     | 23.95   |
| CMM 02040-1              | 48.52  | 9.00     | 25.07       | 37.19  | 18.22     | 28.13   |
| CMM 02033-1              | 53.14  | 5.63     | 30.95       | 39.86  | 14.09     | 29.49   |
| CMM 02035-3              | 58.52  | 7.82     | 26.59       | 26.68  | 11.24     | 24.16   |
| CMM 02048-6              | 41.67  | 10.78    | 24.14       | 30.51  | 23.87     | 26.69   |
| <b>Control varieties</b> |        |          |             |        |           |         |
| UJ5 (Kasetsart 50)       | 43.96  | 7.43     | 28.62       | 33.45  | 14.20     | 25.22   |
| Malang 6                 | 62.77  | 9.39     | 37.65       | 37.15  | 15.40     | 32.58   |
| Malang 4                 | 67.70  | 8.39     | 36.79       | 51.73  | 25.50     | 37.79   |
| Adira 4                  | 56.07  | 7.99     | 43.68       | 28.62  | 19.70     | 31.51   |
| Average                  | 54.63  | 8.11     | 31.22       | 35.53  | 18.40     | 29.59   |
| Genotype (G)             | **     | *        | **          | ns     | **        | **      |
| Location (E)             | -      | -        | -           | -      | -         | **      |
| G x E                    | -      | -        | -           | -      | -         | **      |
| CV (%)                   | 12.88  | 30.65    | 14.26       | 33.93  | 25.20     | 23.23   |

\*\* : significant (p < 0.01) \* : significant (p < 0.05) ns : not significant

**Table-3.** BLUP analysis of fresh tuber yield.

| No. | Treatment        | Effects         | BLUP values<br>(If matrix A using coefficient of<br>coancestry) | BLUP values<br>(If matrix A not using<br>coefficient of coancestry) |
|-----|------------------|-----------------|---|---|
|     | <b>Locations</b> |                 |   |   |
| 1   | Kediri           | $\hat{\beta}_1$ | 53.05   | 54.56   |
| 2   | Ponorogo         | $\hat{\beta}_2$ | 6.60  | 8.11  |
| 3   | Probolinggo      | $\hat{\beta}_3$ | 29.71   | 31.22   |
| 4   | Malang           | $\hat{\beta}_4$ | 34.02   | 35.52   |
| 5   | Mojokerto        | $\hat{\beta}_5$ | 16.89   | 18.40   |
|     | <b>Genotypes</b> |                 |   |   |
| 1   | UJ 5             | $\hat{u}_1$     | -2.10   | -3.36   |
| 2   | Malang 6         | $\hat{u}_2$     | 3.12  | 2.42  |
| 3   | Malang 4         | $\hat{u}_3$     | 8.23  | 7.05  |
| 4   | Adira 4          | $\hat{u}_4$     | 3.37  | 1.37  |
| 5   | CMM 03025-43     | $\hat{u}_5$     | -0.66   | -2.33   |
| 6   | CMM 03036-7      | $\hat{u}_6$     | 3.58  | 1.77  |
| 7   | CMM 03036-5      | $\hat{u}_7$     | 1.86  | -0.23   |
| 8   | CMM 03038-7      | $\hat{u}_8$     | 7.96  | 6.23  |
| 9   | CMM 03094-12     | $\hat{u}_9$     | -1.10   | -3.74   |
| 10  | CMM 03094-4      | $\hat{u}_{10}$  | 4.71  | 3.87  |
| 11  | CMM 03095-5      | $\hat{u}_{11}$  | -3.78   | -5.08   |
| 12  | CMM 02040-1      | $\hat{u}_{12}$  | -0.38   | -1.64   |
| 13  | CMM 02033-1      | $\hat{u}_{13}$  | 0.65  | -0.69   |
| 14  | CMM 02035-3      | $\hat{u}_{14}$  | -1.16   | -2.83   |
| 15  | CMM 02048-6      | $\hat{u}_{15}$  | -1.63   | -2.81   |

## DISCUSSIONS

The analysis of variance showed that location and genotype main effect as well as genotype x location interaction were highly significant ( $p < 0.01$ ). The location and genotype main effect explained most of the total variation (69.82%). The contribution of genotype main effect as well as genotype x location interaction was very small (which is about 5 to 7%). Location main effect by itself explained 64.69% of the total variations, so that locations were the most important source of yield variability (Table-1). The presence of genotype x location interaction indicates that genotype responded differently to different locations.

Among the five locations, Kediri provided the highest tuber yield (54, 63 t ha<sup>-1</sup>), while the lowest was Ponorogo (8.11 t ha<sup>-1</sup>) (Table-2). Kediri probably had soil with high sand content (about 80%) compared to other locations allowing the optimal tuber development. Other locations had soil with dominant clay therefore in the dry season the soil becomes hard and inhibit tuber development. The altitude is also another factor that may cause low tuber yield. Cassava is an important crop in

lowland tropical areas, which can grow until 1500 meters above sea level (Suharno *et al.* 1999), even up to 2300 meters (Norman *et al.*, 1995), however, the higher altitude tends to reduce tuber yield (Onwueme, 1978). In this study, Ponorogo is situated at altitude of about 900 meters above sea level or the highest location than the other locations and has the lowest tuber yield.

The average tuber yield of 15 genotypes in five environments was 29.59 t ha<sup>-1</sup>. There were three clones that had tuber yield above the average i.e., CMM 03036-7, CMM 03038-7, and CMM 03094-4. The CMM 03038-7 had the highest tuber yield among other clones, but not significantly different with Malang 4 (control clone). Tuber yield of CMM 03038-7 was higher than other control clones such as UJ 5, Malang 6, and Adira 4 (Table-2).

The BLUP analysis result indicates that the lowest expected yield is in Ponorogo, whereas the highest is in Kediri. The use of coefficient of coancestry causes lower  $\hat{\beta}$  value of fixed effects, but enhances  $\hat{u}$  value of random effects. In general, breeding values that are



achieved using coefficients of coancestry is higher than breeding values that achieved if matrix A is equal to identity matrix (assumed that genotypes are not related). Among the cassava promising clones, CMM 03038-7 had the highest breeding value and higher than control clones UJ 5, Malang 6, Adira 4, but slightly lower than Malang 4 (Table-3). CMM 03038-7 had the highest tuber yield among others promising clones but it was not significantly different with Malang 4. Bernardo (2002) explained that superior breeding value reflects the progress from selection. The BLUP values are useful not only for selecting the best genotypes, but also for selecting the best genotypes to form new breeding population. In this study, CMM 03038-7 clone can be proposed as a new candidate variety.

### CONCLUSIONS

- a) The use of coefficient of coancestry causes lower  $\hat{\beta}$  value of fixed effects, but enhances  $\hat{u}$  value of random effects.
- b) CMM 03038-7 clone had the highest breeding value among the other clones and high tuber yield which is higher than control clones UJ 5, Malang 6, Adira 4, but slightly lower than Malang 4.

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