Genotype by yield*trait biplot analysis to evaluate *Jatropha curcas* genotypes based on multiple traits

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Abstract. Jatropha hybridization conducted in ISFCRI has resulted in genotypes with various agronomic traits. The biplot analysis was used to evaluate the relationship between agronomic yield trait, the genotype by trait (GT), and genotype by yield*trait (GYT). Ten genotypes were planted in Pasirian, Lumajang, East Java from 2018 to 2019. Ten parameters were observed namely: plant height, harvest time, number of branches per plant (primary, secondary and tertiary branches), inflorescence number per plant, fruit cluster number per plant, fruit number per plant, 100 seed weight, and seed weight per plant. Based on GT biplot and Pearson Correlation, there was a strong positive correlation between yield and plant height, tertiary branch, fruit cluster, inflorescence number, and seed weight. The GYT biplot showed that genotype No. 6 had the best performance in combining yield and primary branch, secondary branch, and inflorescent number. The genotype No. 10 had the largest values in combining yield with the seven other traits. In this study, the GYT biplot approach can be used to identify the best genotypes in correlation between yield with other traits. Therefore, this approach can be applied to overcome the problem of genotypes selection based on several traits, in the Jatropha breeding program.

Keywords: correlation, yield, hybridization, identification

1. Introduction

*Jatropha curcas* is one of the family Euphorbiaceae and the most widespread species across different regions worldwide. Jatropha is famous as a multifunction plant. It has been used in traditional medicine for a long time and decrease soil degradation in dry land regions [1]. Jatropha leaves extract have potency in influenza virus protein inhibition; therefore, a broad spectrum of anti-influenza medicine can be developed from Jatropha leaves [2]. Various bioactive compounds that have potential for medical use were also found in several parts of a Jatropha plant, such as fruits, seeds, barks, branches, twigs, latex, and roots [3]. Furthermore, the Jatropha was widely used for soil and water conservation, for example, it had been utilized as a barrier to revitalizing gullies in Ethiopia [4].

In the last decades, the Jatropha has been more interesting as long as it produced oil as the main source of biodiesel production. The production of biodiesel from the Jatropha offers some profits in the countryside’s, economic, communal and ecological and can be solved the problem of the energy crisis in Indonesia [5]. In Egyptian, there are some advantages in developing the Jatropha: it does not compete for
land use, it is not an edible crop, and it produces more oil - in comparison to soy and rapeseed crops [6]. In addition, the biodiesel produced from Jatropha oil offers a similar or higher quality than fossil fuel when it was tried in diesel engines [5]. Moreover, the Jatropha seed cake is rich in Nitrogen and Phosphorus, which can be applied as a source of organic fertilizer [7]. The Jatropha seed cake can be processed into three different products, i.e., animal feed, fertilizers, and boiler fuel [6]. The study using the EWF Nexus approach also suggested that the Jatropha seed cake is useful for producing fertilizers directly [8].

Jatropha has been claimed as a promising renewable energy crop in arid and semi-arid regions and has good adaptation to different climatic conditions. Nevertheless, Jatropha cultivation might need irrigation for better seedling growth, especially in the dry season [9]. The experiment of Jatropha cultivation in pots indicated the best seed germination rate achieved when irrigation drainage water was applied [6]. The other experiments reported that in dry climate conditions, high seed and oil yields can be reached by maintaining the equilibrium between vegetative growth and reproductive capacity by applying both optimal irrigation and vegetative development induction [10].

Jatropha varieties that have been released in Indonesia still exhibited a limited yield. Therefore, hybridization between some Jatropha collected accessions was conducted to increase Jatropha productivity. Genotypes resulted from the hybridization were evaluated their relationship between agronomic traits and yield using biplot analysis. This method was used to identify the best genotype in producing seeds. The biplot method is a graphical display of multivariate data. It could be a powerful tool to visualize data because the data can be viewed as a multivariate extension of the scatterplot [11]. The genotype by trait (GT) and genotype by yield*trait (GYT) biplot has been used to study trait relationships and genotype evaluation in some crop species, including covered oat [12], sesame [13], and durum wheat [14]. A GYT biplot is proposed to overcome the obstacle of genotype assessment on multiple traits that have been reliant on setting a subjective weight for index selection of each trait [12]. This study aimed to conduct genotype assessment using analysis of genotype by trait and genotype by yield*trait of 10 Jatropha genotypes on multiple traits.

2. Materials and method

2.1. Plant materials and field experiment

The plant materials evaluated in this study consisted of 10 Jatropha genotypes (Table 1). The experiment was performed over two years (2018 and 2019) at Pasirian Experimental Station of ISFCRI, Lumajang, East Java. The experiment design used was RCBD (randomized complete block design), with three replications. Each genotype was arranged in a 10 m x 8 m plot size, the plant spacing used was 2 m x 2 m. The harvesting plot consisted of six plants in each plot.

| Genotype No. | Genotype Name       |
|--------------|---------------------|
| 1            | HS.49 x SP.103/24   |
| 2            | HS.49 x SP.65/32    |
| 3            | HS.49 x SP.65/31    |
| 4            | HS.49 x SP.10/20    |
| 5            | IP.3P x SP.65/18    |
| 6            | IP.3P x SP.7/5      |
| 7            | IP.3A x SP.89/4     |
| 8            | IP.3A x SP.65/11    |
| 9            | IP.3P/1x17/100      |
| 10           | Jet 1 Agribun       |
2.2. Data collection
The parameter observed consisted of plant height (PH), harvest time (HT), 100-seed weight, number of primary (PB), secondary (SB) and tertiary branches (TB) in a plant. The inflorescence number (IN), no. of fruit cluster (CN), fruit number (FN), and total seed weight (SW) were observed per plant, and yield was per hectare. Harvest time was measured as initial days for fruit harvesting. Plant height, number of primary, secondary and tertiary branches, inflorescence number, and fruit cluster number, were measured as final harvest time. Fruit number and seed weight were measured as whole fruit and seed weight from multiple harvesting each year. Yields were calculated as total seed yield from multiple harvesting for each year based on population (harvesting plot) and then conversed to the hectare. The fruits and seeds were harvested every two months in each year, starting from February to December.

2.3. Data analysis
The data of 10 genotypes over two years were subjected to analysis of variance, and means were separated using the least significant distance (LSD) test with significance at P< 0.05 and P<0.01 using PKBT-STAT 3.1 [15]

The genotype by yield*trait data was obtained by multiplying the yield value with the trait value for each genotype (e.g., yield*plant height). The data of genotype trait and genotype by yield*trait were standardized so that the mean for each trait or yield trait combination becomes 0 and the variance becomes the unit. The standardization was performed following [12] as:

\[ P_{ij} = \frac{T_{ij} - \bar{T}_j}{s_j} \]

Where \( P_{ij} \) is the standardized value of genotype \( i \) for trait or yield-trait combination \( j \) in the standardized table, \( T_{ij} \) is the original value of genotype \( i \) for the trait or yield trait-combination \( j \), \( \bar{T}_j \) is the mean across genotypes for trait or yield-trait combination \( j \), and \( s_j \) is the standardized deviation for the trait or yield trait combination \( j \).

2.4. Construction of GT (genotype by trait) and GY*T (genotype by yield*trait) biplot
The GT and GY*T biplot was based on the first two principal components (PC) using standardized data with model selection: singular partitioning method is column metric preserving; no centering and scaled divided by no scaling. The construction was done by the GGEBiplotGUI package [11) in R 3.6.3 [16]

3. Results and discussion
3.1. Genotype by trait biplot analysis
The combined analysis of variance for all traits studied, and trait means of 10 Jatropha genotypes were presented in Tables 2 and 3. The results showed significantly different for plant height, tertiary branch number, inflorescence number, fruit number, seed weight, and yield among the years. The interaction between the genotype and the year was significantly different only on three traits: inflorescence number, fruit number, and yield (Table 2.). For all traits, except harvest time and primary branch number were significantly different among the genotypes (Table 3.).
Table 1. Mean squares of agronomical and yield traits of J. curcas genotypes across years

| Source of variation | df | Year | Replication (Year) | Genotype | Genotype* |
|---------------------|----|------|---------------------|-----------|-----------|
|                     | 1  | 4    | 1                   | 1         | 1         |
|                     | 2  | 2    | 2                   | 1         | 2         |
|                     | 3  | 3    | 3                   | 1         | 2         |
|                     | 4  | 4    | 4                   | 1         | 2         |
|                     | 5  | 5    | 5                   | 1         | 2         |
|                     | 6  | 6    | 6                   | 1         | 2         |
|                     | 7  | 7    | 1                   | 1         | 1         |
|                     | 8  | 8    | 1                   | 1         | 2         |
|                     | 9  | 9    | 1                   | 1         | 2         |
|                     | 10 | 10   | 1                   | 1         | 2         |

| Mean square          | PH | HT  | PB  | SB  | TB  | IN  | CN  | FN  | 100SW | SW  | YIELD |
|----------------------|----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-------|
|                      |    |     |     |     |     |     |     |     |       |     |       |

Table 2. Genotype by trait data of 10 genotypes for agronomical and yield traits

| Genotype | aPH (cm) | bHT (days) | cPB | dSB | eTB | fIN | gCN | hFN | i100SW | jSW (gram) | kYIELD (kg ha⁻¹) |
|-----------|----------|------------|-----|-----|-----|-----|-----|-----|--------|------------|------------------|
| 1         | 120.583  | 98.889     | 2.750| 6.333| 5.556| 11.611| 4.639| 85.684| 0.633  | 0.184      | 294.548          |
| 2         | 115.278  | 102.000    | 2.639| 6.500| 6.239| 8.667| 4.778| 119.689| 0.623  | 0.254      | 304.015          |
| 3         | 114.056  | 101.733    | 2.750| 7.722| 8.589| 15.222| 4.594| 116.412| 0.609  | 0.244      | 304.065          |
| 4         | 126.389  | 100.711    | 2.556| 5.778| 6.194| 9.267| 3.028| 90.963| 0.654  | 0.190      | 260.631          |
| 5         | 127.889  | 100.311    | 2.250| 5.889| 6.722| 10.694| 5.056| 110.644| 0.651  | 0.234      | 306.050          |
| 6         | 119.333  | 100.311    | 4.028| 9.778| 11.861| 26.806| 7.428| 137.484| 0.635  | 0.316      | 440.543          |
| 7         | 116.222  | 99.422     | 2.639| 5.306| 5.486| 8.122| 4.717| 105.764| 0.651  | 0.213      | 290.667          |
| 8         | 121.111  | 99.333     | 2.111| 5.833| 6.350| 8.111| 4.583| 112.723| 0.644  | 0.231      | 279.545          |
| 9         | 108.889  | 100.222    | 2.444| 5.778| 6.250| 8.722| 4.044| 112.675| 0.632  | 0.221      | 284.130          |
| 10        | 170.861  | 101.200    | 2.806| 7.333| 10.611| 15.250| 7.289| 156.925| 0.676  | 0.342      | 543.669          |

| Mean       | 124.061 | 100.413 | 2.697| 6.625| 7.386| 12.247| 5.016| 114.896| 0.641  | 0.243      | 303.786          |
| SD         | 17.392  | 1.027   | 0.519| 1.337| 2.220| 5.782| 1.355| 20.654| 0.019  | 0.051      | 89.477           |
| LSD        | 14.64** | ns      | ns  | 1.19**| 1.94**| 4.50**| 2.18**| 25.75**| 3.60*  | *          | 66.44**         |
| CV (%)     | 0.108   | 0.174   | 0.150| 0.247| 0.310| 0.176| 0.216| 0.489  | 0.216  | 0.171      | 0.215           |

*Plant height; bHarvest time; cPrimary branch number; dSecondary branch number; eTertiary branch number; fInflorescence number; gFruit cluster number; hFruit number; i100 seed weight; jSeed weight
ns not=significant; *significant at P<0.05; ** significant at P<0.01
The mean plant height of genotypes across years varied between 115 to 170 cm, secondary and tertiary branch number between 5.3 to 9.8 and 5.5 to 11.8 respectively, inflorescence number between 8.1 to 26.8 per plant, fruit cluster number between 3.0 to 7.4, fruit number between 85.7 to 156.9 per plant, 100 seed weight between 0.61 to 0.67 g, seed weight between 0.18 to 0.34 kg per plant and yield between 279.54 to 543.67 kg ha\(^{-1}\). The harvest time was not significantly different across genotypes due to the days to first harvest in Jatropha genotypes in this study was similar between 98 to 103 days. Other researchers showed first harvesting time of \textit{J. curcas} varied between 90-91 days \[17\] and more than 90 to 120 days \[18\]. The similar days to first harvesting in the genotypes evaluated in this study were probably because the genotypes have been subjected to selection for early harvest time \[19\].

Genotype by trait (GT) biplot analysis can be applied to assess the superiority genotypes based on multiple traits, and identify the superior genotypes by recognizing the improvement of target traits in the breeding programs \[14\]. GT biplot of 10 Jatropha genotypes is presented in Figure 1. GT biplot is constructed from GT data in Table 3. The vectors of the GT biplot was drawn based on the original biplot data for every trait, to investigate the relationship between traits \[13\]. The cosine of the angle between the vectors of two traits describes the Pearson correlation between them. An angle smaller than 90° indicates a positive correlation, an angle greater than 90° indicates a negative correlation, and an angle of 90° indicates no correlation \[12\]. In Figure 1, the vectors of PH and Yield, and PH and 100-SW formed the angles smaller than 90°, indicating a positive correlation between those traits. The traits also showed a strong positive correlation when identified by the Pearson correlation (PC) coefficient (Table 4). Whereas, the vector of 100-SW trait and other traits (PB, SB, IN, and HT) formed the angles greater than 90°, it illustrates negative correlation between 100-SW trait and the other four traits. The negative correlation between those traits is also obtained in the PC coefficient (Table 4).

GT biplot could also be used to describe the relative level of the genotype for the trait. An acute angle between a genotype and trait indicates that the genotype is above-average for the trait, an obtuse angle indicates that the genotype is below-average for the trait, and a right angle indicates that the genotype is average of the trait \[12\]. The interpretation will make more meaningful if the goodness of the fit of the biplot is high. This is indicated by the percentage of variation that can be calculated by summing the two first coordinates (sum of PC1 and PC2) \[21,22\]. The goodness of the fit of the GT biplot in this study is 76.61 % and is categorized as high. Genotype no. 10 formed an acute angle with plant height and yield, it is indicating that the genotype had an above-average level for those two traits.

### 3.2. Genotype by yield*trait (GYT) biplot analysis

The GYT table (Table 5.) was derived from the original GT table (Table 3). Each column showed the combined level of yield trait with other agronomical traits. The GYT value for all agronomical traits were obtained by multiplying them with the yield, except for harvest time was obtained by dividing yield with harvest time value. The reason was caused the earlier first harvest time is more desirable. The GYT data then were standardized and used for constructing the GYT biplot.

The which-won-where view of the GYT biplot (Figure 2.) is used to highlight genotypes with the best performance in combining yield and other traits. The irregular polygon and the line were drawn starting from the original biplot data, and it illustrated the genotypes that have the larger values for the corresponding traits \[12\]. In Figure 2, genotype No. 10 had the largest values for Yield*PH, Yield/HT, Yield*TB, Yield*CN, Yield*FN, Yield*100SW, and Yield*SW. Genotype No. 6 had the largest value for Yield*SB, Yield*PB, and Yield*IN. The previous publications had reported the correlation between agronomical traits and yield of Jatropha. A positive correlation was obtained between plant height, the total number of branches per plant, number of primary branches per plant, number of fruits per plant, 100 seed weight, and seed yield \[22, 23\]. Those traits could be exploited as traits that wished to increase the yield of the Jatropha. The correlation between yield and other traits is a very important factor for the early selection
of high seed yield genotypes, because the seed yield character is influenced by genetic effects as well as genotype and environment interaction [22]. Some negative characters also can deliver the advantageous effect to yield in the particular environmental conditions. For example, reducing of vegetative growth could promote floral production and enhance reproductive capacity in arid conditions [10]. This GYT approach can be applied in Jatropha breeding to select the genotypes that can combine the yield with other desirable traits for improving the new varieties. Further research of GYT biplot should be conducted with more target traits that can be combined with yield, for example, oil content or chemical composition.

**Figure 1.** Genotype by trait (GT) biplot of 10 Jatropha genotypes and agronomical and yield traits. The number with green color showed Jatropha genotype No. 1 to 10 (Table 1). Trait codes are represented with blue color. The traits abbreviations are PH: plant height, HT: harvest time; PB: primary branching number; SB: secondary branching number; TB: tertiary branching number; IN: inflorescence number; CN: fruit cluster number; FN: fruit number; X100SW: 100 seed weight; SW: seed weight.
Table 4. Pearson correlations between traits across 10 Jatropha genotypes.

|           | PH  | HT  | PB  | SB  | TB  | IN  | CN  | FN  | YIELD | PH  | HT  | PB  | SB  | TB  | IN  | CN  | FN  | YIELD |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-------|-----|-----|-----|-----|-----|-----|-----|-----|-------|
| PH        | 1   |     |     |     |     |     |     |     |       |     |     |     |     |     |     |     |     |       |
| HT        | 0.184 | 1   |     |     |     |     |     |     |       |     |     |     |     |     |     |     |     |       |
| PB        | 0.032 | 0.123 | 1   |     |     |     |     |     |       |     |     |     |     |     |     |     |     |       |
| SB        | 0.144 | 0.330 | 0.885** | 1   |     |     |     |     |       |     |     |     |     |     |     |     |     |       |
| TB        | 0.472 | 0.369 | 0.753* | 0.905** | 1   |     |     |     |       |     |     |     |     |     |     |     |     |       |
| IN        | 0.178 | 0.161 | 0.915** | 0.967** | 0.903** | 1   |     |     |       |     |     |     |     |     |     |     |     |       |
| CN        | 0.549 | 0.123 | 0.665* | 0.742* | 0.851** | 0.767* | 1   |     |       |     |     |     |     |     |     |     |     |       |
| FN        | 0.601 | 0.471 | 0.420 | 0.602 | 0.823** | 0.552 | 0.843** | 1   |       |     |     |     |     |     |     |     |     |       |
| 100SW     | 0.791** | -0.225 | -0.169 | -0.217 | 0.142 | -0.077 | 0.296 | 0.299 | 1   |     |     |     |     |     |     |     |     |       |
| SW        | 0.607 | 0.452 | 0.551 | 0.718* | 0.895** | 0.678* | 0.906** | 0.980** | 0.283 | 1   |     |     |     |     |     |     |     |       |
| YIELD     | 0.785** | 0.265 | 0.557 | 0.643 | 0.853** | 0.658 | 0.914* | 0.883** | 0.485 | 0.923** | 1   |     |     |     |     |     |     |     |

*Plant height; **Harvest time; *Primary branch number; **Secondary branch number; **Tertiary branch number; *Inflorescence number; **Fruit cluster number; **Fruit number; *100 seed weight; **Seed weight

Table 5. Genotype by yield*trait data of 10 Jatropha genotypes for agronomical and yield traits

| Genotype | YIELD*PH | YIELD/HT | YIELD*PB | YIELD*SB | YIELD*TB | YIELD*IN | YIELD*CN | YIELD*FN | YIELD*100SW | YIELD*SWSW |
|----------|----------|----------|----------|----------|----------|----------|----------|----------|-------------|-------------|
| 1        | 35517.57  | 294.55   | 810.01   | 1865.47  | 1636.38  | 3420.03  | 1366.38  | 25238.15  | 186.52       | 54.21       |
| 2        | 35046.20  | 304.02   | 802.26   | 1976.10  | 1896.72  | 2634.80  | 1452.52  | 36387.38  | 189.40       | 77.19       |
| 3        | 34680.25  | 304.06   | 836.18   | 2348.05  | 2611.58  | 4628.54  | 1397.01  | 25238.15  | 185.31       | 74.34       |
| 4        | 32940.91  | 260.63   | 666.06   | 1505.87  | 1976.10  | 2634.80  | 1452.52  | 36387.38  | 170.36       | 49.52       |
| 5        | 39140.39  | 306.05   | 688.61   | 1802.29  | 2057.34  | 3273.03  | 1547.25  | 33862.54  | 199.25       | 71.53       |
| 6        | 52571.48  | 440.54   | 1774.41  | 4307.53  | 5225.33  | 60567.58 | 279.92   | 33862.54  | 139.27       | 57.39       |
| 7        | 33781.90  | 290.67   | 767.04   | 1542.15  | 1594.63  | 2360.86  | 1370.98  | 30742.07  | 189.04       | 71.79       |
| 8        | 31856.01  | 279.54   | 694.54   | 1641.64  | 1775.11  | 2267.42  | 1281.25  | 31511.20  | 180.10       | 64.49       |
| 9        | 30938.58  | 284.13   | 694.54   | 1641.64  | 1775.11  | 2267.42  | 1281.25  | 31511.20  | 179.61       | 62.85       |
| 10       | 92891.81  | 545.66   | 1525.29  | 3986.90  | 5768.93  | 8290.95  | 3962.74  | 85314.95  | 367.69       | 185.84      |

Mean 42136.51 330.78 915.45 2260.67 2595.63 4357.81 1758.87 39474.28 212.72 84.10

SD 18832.49 89.48 398.64 1026.89 1563.25 3192.91 1014.44 19004.40 62.55 43.61
Figure 2. The which-won-where of the genotype by yield*trait (GYT) biplot of 10 Jatropha curcas genotypes. The number with green color showed Jatropha genotype 1 to 10 (Table 1). Trait codes are represented with blue color. The traits abbreviations are PH: plant height, HT: harvest time; PB: primary branch number; SB: secondary branch number; TB: tertiary branch number; IN: inflorescence number; CN: fruit cluster number; FN: fruit number; X100SW: 100 seed weight; SW: seed weight.

4. Conclusions
GT and GYT biplot captured 76.61 and 99.08% of the total variation, respectively. Based on GT biplot and Pearson Correlation, there were strong positive correlations between yield and plant height, tertiary branching number, fruit cluster number, inflorescence number, and seed weight per plant. The which-won-where view of the GYT biplot showed that genotype No. 6 had the best performance in combining yield and primary, secondary branch, and inflorescent number. Genotype No. 10 had the best performance in combining yield with the other rest traits. The GYT biplot approach in this study can help visual identification of the best genotypes in combining yield with other traits and could be overcome the problem of subjectivity of genotype selection based on multiple traits in the Jatropha breeding program.

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References
[1] Abobatta W 2019 Journal of Advances in Agriculture 10 1650-1656
[2] Patil D, Roy S, Dahake R, Rajopadhye S, Kothari S, Deshmukh R and Chowdhary A 2013 Indian J Virrol 24 2 220-226
[3] Prasad D M R, Izam A and Khan Md M R 2012 Journal of Medicinal Plants Research 6 14 2691-2699
[4] Ehrensperger A, Bach S, Liniger H, Portner B and Ayele H 2015 Journal of Soil and Water Conservation 70 2 33A-38A
[5] Silitonga A S, Atabani A E, Mahlia T M I, Masjuki H H, Badruddin I A and Mekhilef S 2011 Renewable and Sustainable Energy Reviews 15 3733-3756
[6] Gamal-Fakhry, Azazz N A E, Abdel-Monem A and Mohamedin A 2016 *Minia J. of Agric. Res. & Develop.* 36 2 245-269

[7] Gudeta T B 2016 *American Journal of Agriculture and Forestry* 4 2 35-48

[8] Alherbawi M, McKay G, Mackey H R and Al-Ansari T 2021 *Renewable and Sustainable Energy Reviews* 135

[9] Ouattara B, Diedhiou I, Belko N and Cisse N 2018 *Agricultural Sciences* 9 639-654

[10] Vaknin Y, Yermiyahu U, Bar-Tal A and Samocha Y 2017 *CGB Bionergy* 10 382-392

[11] Frutos E, Galindo M P, Leiva V 2013 *Stoch Environ Res Risk Assess*

[12] Yan W and Fregeau-Reid J 2018 *Scientific Reports* 8 8242

[13] Boureima S and Y Abdoua 2019 *Turk J Field Crops* 24 2 237-244

[14] Kendall E 2019 *Chilean Journal of Agricultural Research* 79 4 512-522

[15] Center for Tropical Horticulture 2021 PKBT-STAT 3.1 [Internet] Bogor, Indonesia: Center for Tropical Horticulture Studies, IPB University Available from: https://www.pkbt-stat/index.php

[16] R Core Team 2020 R: A language and environment for statistical computing [Internet] Viena, Austria: R Foundation for Statistical Computing Available from: https://www.r-project.org

[17] Maftuchah, Zainudin A, Sudarmo H, and Reswari HA 2016 Proc. of 3rd International Conference on Agriculture and Forestry: Sustainable Agriculture and Forestry as Essential Response to The Challenge of Global Food Security and Environmental Stability (Manila/Philippines) pp 39-46

[18] Silip J J, Tambunan A H, Hambali H, Sutrisno and Surahman M 2010 *Journal of Sustainable Development* 3 2 291-295

[19] Purwati R D, Anggraeni T D A, Heliyanto B, Machfud M and Hartono J 2018 *International Journal of Agricultural and Biosystem Engineering* 12 10 412-417

[20] Grange A, Roux N and Gardner-Lubbe S 2009 *Journal of Statistical Software* 30 12

[21] Yousef E A A, Muller T, Borner A and Schmid K J 2018 *PlosONE* 13 2

[22] Shabanimofrad M, Rafii M Y, Wahab P E M, Biabani A R and Latif M A 2013 *Industrial Crops and Products* 42 543-551

[23] Gawali A S, Wagh R S and Sonawane CJ 2016 *Forest Res* 5 2