Stability Analysis of Genotype the Local Red Union Palu to determine the Cultivation Location using Additive Main Effect and Multiplicative Interaction (AMMI)

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Abstract. Additive Main Effect and Multiplicative Interaction (AMMI) is a method used to learn the interaction between genotype and location. The objective of this research is to apply the AMMI model in verifying stability of several genotypes of the local red union Palu towards the growth of genotype location based on biplot and stability value AMMI (SVA). This research used seven genotypes red union. Four genotypes namely, Sumenep, Sanren F1, Tuk-Tuk and Kawak are not from Palu while the three genotypes are the native palu plant (Batu, Kertas and Palasa). These are planted in different five experiment locations, Wombo, Guntarano, Bolupounto, Okoboju and Soulove with three replications. The Interaction Principle Component AMMI (IPCA) which is significant is included into the model based on analysis of variance of AMMI. These are IPCA1 and IPCA2 with the total of variance interaction equals 88,02%. Biplot picture shows that the Batu genotype can only be able to adapt in Oloboju while Kawak, Sumenep and Kertas genotypes location are far away from the main line. This indicates that the three genotypes tend to unstable or in another word those genotypes could not adapt well in the five plantation locations. Furthermore, Biplot picture shows the genotype which is stable in all location is Palasa, Sanren F1 and TukTuk due to nearby the main line. The SVA based on the index stability denotes that the first ranking is Palasa followed by Sanren F1 and TukTuk. This indicates that from the three genotypes of the red union Palu, it can be concluded that Palasa is the best genotype.

Keywords: AMMI, Biplot, SVA, Red Union

1. Introduction
This research is conducted because of superiority the fried union from Palu. The product is a highly competitive horticulture commodity. Palu fried union is a favored specific Palu culinary. It is very popular in Indonesia due to very tasty and crispy.

The decreasing productivity of the red union is a problem that faces because of environmental factor that does not able to support its growth. [1] The incompatibility between the red union seed which will be planted with the growth location is the main problem faced. This means that both the seed and location cannot adapt well. [2] As a result, conducting stability analysis for genotype of the red union in several locations need to be carried out.

The increasing productivity and quality of the red union can be conducted by plantation innovation program. In the plantation innovation, stability of genotype in several locations is the main
purpose to increase productivity. The response of specific plant for the different location can impact an interaction between genotype and location [3].

AMMI is a method used to the plantation innovation program in design experiment. In this method, interaction between genotype and location (GEI) will be examined. If genotype and location have been assumed as factors, then the properly treatment design used is the two factor design so that in analysis of variance the interaction can be considered [3].

In the estimation of interaction factor, replication should be carried out. The replication can be a regular repetition, Completely Randomized Design or Randomize Block Design. The further examined which is used in analysis of variance is multiple comparison tests if there is any interaction. However, the multiple comparisons are not sufficient to detect the stability of genotype. In consequence, another method such as Additive Main Effect and Multiplicative Interaction (AMMI) is needed to measure the stability [2].

The interaction of genotype with location (GEI) is variance from two or more genotypes in several different locations [1]. The stability analysis of AMMI can be analyzed using AMMI biplot and Stability Value AMMI (SVA).

This research used the data from seven red union genotypes. Three of genotypes are native Palu plant (Batu, Kertas and Palasa) while others not from Palu (Sumenep, Sanren F1, TukTuk and Kawak). These are planted in five locations with three replications. The objective of this research is to determine the stability of seven the red union genotypes based on AMMI biplot and SVA.

2. Methodology

2.1 Data

Data used in this research is observed data which is obtained by cultivation of seven the red union genotypes in five locations. The obtained data is from the production of red union genotype with 35 treatments and three replications. Table 1 and Table 2 are the genotype code and the location of experiment code, respectively.

| Genotype   | Code |
|------------|------|
| Batu       | G1   |
| Kertas     | G2   |
| Kawak      | G3   |
| Sanren F1  | G4   |
| Tuk-Tuk    | G5   |
| Sumenep    | G6   |
| Palasa     | G7   |

| Location    | Code |
|-------------|------|
| Desa Wombo  | E1   |
| Desa Guntarano | E2  |
| Desa Bolupountu | E3  |
| Desa Oloboju | E4   |
| Desa Soulove | E5   |

2.2 Procedure of Analysis

Procedure of analysis in this research are as follow: (1) Analyzing data using classical analysis of variance two factor experiments of Completely Randomized Block Design, (2) Creating of 7 x 5 matrix with its element is the mean of the production of seven the red union genotypes in five different locations, (3) Exploring the Singular Value Decomposition (SVD) based on Principle
Component Analysis (PCA), (4) Analysis of variance of AMMI, (5) Calculating the contribution each of Interaction Principle Component AMMI (IPCA), (6) Calculating the Stability Value AMMI (SVA), (7) Interpreting the stability of genotype based on AMMI biplot and Stability Value AMMI (SVA).

3. Result

3.1 Analysis of Variance

Examining the analysis of variance is conducted to determine the effect of genotype interaction with location. Table 3 shows the results of the analysis of variance.

| Source          | df | SS     | MS   | F      | p        |
|-----------------|----|--------|------|--------|----------|
| Genotype        | 6  | 2537.47| 422.91| 73.061*| 2.2x10^{-16} |
| Location        | 4  | 131.34 | 32.84| 5.673* | 0.000    |
| Block           | 4  | 26.43  | 6.61 | 1.142  | 0.339    |
| Genotype*Location | 24 | 307.72 | 15.74| 2.215* | 0.002    |
| Error           | 136| 787.22 | 5.89 |        |          |
| Total           | 199| 3310.66|      |        |          |

*) Significant

The results of the analysis of variance for the interaction of the red union productivity from seven red union genotypes in five locations indicate that the main effect (genotype and location) and interaction effect between genotype with location have real impact due to $p$-value < $\alpha$.

3.2 Exploring of Singular Value

By exploring the singular value, we obtained five nonzero singular values. These are 6.072913; 4.243517; 1.971931; 1.892480; 5.216328x10^{-15}. The IPC that can be considered for the AMMI model, based on the singular value, is the first to the fifth component with its eigenvalue $\lambda_1 = 36.88028$; $\lambda_2 = 18.00743$; $\lambda_3 = 3.888512$; $\lambda_4 = 3.581479$; $\lambda_5 = 2.721007$x10^{-29}, respectively.

3.3 Analysis of Variance AMMI

The eigenvalue which was obtained from exploring the singular value furthermore is used to calculate the analysis of variance AMMI. The analysis of Variance AMMI determines the IPC score. Furthermore, the IPC score which is significant can be included in the model.

Table 4. Analysis of variance AMMI

| Source          | df | SS     | MS   | F      | p        |
|-----------------|----|--------|------|--------|----------|
| Genotype        | 6  | 2537.47| 422.91| 73.061*| 2.2x10^{-16} |
| Location        | 4  | 131.34 | 32.84| 5.673* | 0.000    |
| Block           | 4  | 26.43  | 6.61 | 1.142  | 0.339    |
| Genotype*Location | 24 | 307.72 | 15.74| 2.215* | 0.002    |
| IPCA1           | 9  | 184.64 | 20.52| 3.54*  | 0.000    |
| IPCA2           | 7  | 92.15  | 13.16| 2.27*  | 0.032    |
| IPCA3           | 5  | 19.42  | 3.88 | 0.71   | 0.646    |
| IPCA4           | 3  | 11.49  | 3.83 | 0.662  | 0.576    |
| IPCA5           | 1  | 5x10^{-31} | 5x10^{-31} | 9x10^{-32} | 1.000    |
| Error           | 136| 787.22 | 5.89 |        |          |
| Total           | 199| 3310.66|      |        |          |

*) Significant

By comparing $p$-value and significant level (in Table 4) the $p$-value of IPCA1 and IPCA2 are smaller than the significant level ($\alpha = 0.05$) As a result, $H$ is rejected meaning that IPCA1 and IPCA2
have impact to the red union productivity. In concluding the productivity can be determined using AMMI2 model.

3.4 Contribution Value of Interaction Principle Component

The value of IPC that can be included in the model can be conducted by calculating the contribution value each of IPC. The contribution of IPC is IPC1 (59.14%); IPC2 (28.88%); IPC3 (6.23%); IPC4 (5.74%); and IPC5 (4.36x10^{-29}%). Based on analysis of variance AMMI model and contribution of IPC, the IPC that can be included in the model is IPC1 and IPC2. The two main components give the total variability of productivity the red union, 59.14% + 28.88% = 88.02%. In consequence, the stability of genotype is determined using IPC1 and IPC2 scores. The two IPCs indicate that the variability of contribution is sufficiently high because of more than 50%. It means that the stability of genotype is already high.

3.5 Biplot of Confidence Interval

Biplot AMMI2 from AMMI analysis can be used to determine genotype which is stable in all location of experiment. In order to determine genotype which is stable, the ellipse interval confidence is used with the central point (0,0). The Stability of genotype is determined using the two value of IPC with the first and the second highest variability. The contribution of variability which is used from the two value of IPC is high (88.02%).

**Figure 1.** Biplot of AMMI$_1$ (Plot IPC1 for the mean of red union productivity)

Biplot between IPC1 and mean of the result considered as AMMI$_1$ biplot is graphic which provides summary effect of information the main genotype and location at mean line and the effect of genotype interaction and location at IPC1 line. Genotype which is laid at one point with the horizontal line indicating that it has the same main effect. Furthermore, genotype which is laid at one point with the vertical line indicating that it has the same interaction effect [3].

AMMI$_1$ biplot in Figure 1 shows that G4 is the lowest of the mean productivity while G3 is the highest. The G2, G5 and G6 have the same of mean productivity, however their interaction are different at E (environment/location).
Figure 2. AMMI2 biplot (KUI1 plot to KUI2)

Figure 2 shows the interaction of variance is 88.02% with the value of IPC1 and IPC2 are 59.14% and 28.88%, respectively. The contour which indicates the confident interval is ellipse.

The Stability concept is also indicated by SVA which determines the relative position of genotype to the central point of AMMI2 biplot. Table 5 gives the SVA calculation. The SVA is then ordered based on ranking of genotype with the lowest to the highest index.

| Genotype | SVA | Ranking |
|----------|-----|---------|
| G1       | 1.17| 4       |
| G2       | 2.52| 7       |
| G3       | 1.65| 6       |
| G4       | 0.80| 3       |
| G5       | 0.28| 2       |
| G6       | 1.29| 5       |
| G7       | 0.27| 1*      |

Based on AMMI2 biplot and SVA, we can estimate that the genotype which is stable for all location of experiment is the genotype which is in the contour area and has the distance close to the central point (0,0). Genotype that includes in stable categorized in all location of experiment is G2 based on AMMI2 biplot and SVA with the distance is 0.02. This is at the first ranking followed by G3 with the distance is 0.04.

In the meantime, for the unstable genotype or genotype that can only adapt at finite location is genotype which is laid in the outside of contour and has the distance far away from the central point (0,0). These genotypes are G4, G6, G5 and G1 with the distance to the central point (0,0) is 0.93; 1.34; 1.53; 1.63, respectively.

Genotype which can adapt at finite location can be seen based on the correlation among of variables. If the angle between two variable vectors is small, then their correlations tend to high. Genotype that can adapt at finite location can be seen in Table 6.
4. Conclusion
The AMMI model which uses the data of productivity from seven genotypes red union planted in five locations with three replications provides two IPCs score that are significant with the total of variance is 88.02%. The stability of genotype is determined using AMMI biplot and SVA. The variance interaction obtained is 88.02 and genotypes which are categorized can provide good result at all location of experiment is Palasa, Sanren F1 and TukTuk. The Batu genotype can only adapt at finite location as Oloboju. The other genotypes (Kawak, Sumenep and Kertas) which are far away from the main point tend to unstable or cannot adapt well in the five plantation locations. Researchers who interest with this topic can add physic factors in experiment of red union with multi locations.

References

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