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Articles

Interaction of Genotype and Environment on the Productivity of 12 Genotypes of Rice (Oryza sativa L) using AMMI Analysis

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Abstract: Rice is the main food crop for most of the world's population. This research aims to obtain information on the influence of genotype interactions with the environment on potential grain yield characteristics and to obtain genotypes that have stability and adaptability to suboptimal environments. The research was carried out in March–July 2023 at Polinela Organic Farm. The experiment used a completely randomized group design (RKTS). Observations were made on the grain yield of 12 rice genotypes grown in three different environments. Statistical analysis using PBSTAT-GE software. There are three genotypes that have good stability based on eight stability analyses, namely Sertani 13 (G5), Inpari 30 (G12), and Trisakti (G6). Sertani 13 (G5) and Inpari 24 (G2) are genotypes with extensive adaptation. Genotypes based on specific environments are Baroma (G8), PTP 01 (G3), and Inpara 8 (G11), which adapt well to organic environments. Sertani 13 (G5) is adaptive to non-organic environments, and Mentik Susu (G4) is adaptive to aquaponic environments. The highest average production obtained based on the environment is non-organic, with an average yield of 5.95 tons/ha. Baroma (G8) is the genotype with the highest average, namely 6.85 tons/ha.

Keywords: Adaptation, AMMI, Genotype, Stability

1. Introduction

Rice yield is strongly influenced by genotype (G), environment (E), and genotype x environment interactions (GEI). The maximum yield potential of rice varieties will be obtained if they are planted in an environment that suits their needs. Multilocation testing, which is one of a series of plant breeding activities, is absolutely necessary. Multilocation testing aims to (1) map the consistency of genotype performance across environments and in specific environments, (2) estimate genotype x environment interactions, (3) select and determine adaptive environments for the tested genotypes, and (4) identify broadly adapted genotypes and specific (Yan & Kang, 2002) .

Stability analysis is used if the genotype x environment variations are significantly different. When interactions are real and there is a change in the performance ranking of genotypes, breeding is directed at site-specific genotypes. Stable genotypes have small variances, appear similar to the average genotype performance, and regression deviations have small mean squares (Bozo ğ lu & Gülümser, 2000) . The appearance of genotypes and environmental influences can be explained through the analysis of variance method.

Stability analysis is needed to estimate the performance of genotypes in various environments. This is to support the research objective, namely to determine the stability

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and adaptability of high-yielding and widely adaptable rice genotypes, as well as high-yielding genotypes in certain environments. The AMMI (Additive Main Effect and Multiplicative Interaction) method is a method used to see interactions between genotype and the environment. The AMMI model is reported to be effective in estimating GxE interactions (Suwarto & Nasrullah, 2011) because it can separate main effects and interaction effects, and provides multiple interpretations (Ebdon and Gauch 2002). AMMI and AMMI biplot graphs are able to provide more information about genotype x location interactions compared to the ANOVA method (Hadi & Sa'diyah, 2004)

GxE biplot is a model for visualization and interpretation of data from genotype testing results in different environments. Visualization of aspects of genotype (G) and environment (E), and their relationship (GxE) is depicted as a biplot. GxE Biplot analysis was carried out using PBSTAT-GE software (www.pbstat.com). PBSTAT-GE is variety testing data analysis software, which includes testing at one location, multi-location and multi-season.

2. Materials and Methods

The research was carried out in March–July 2023 at the Teaching Farm Polinela Organic Farm, Lampung State Polytechnic, Bandar Lampung, Indonesia. The research location is at an altitude of 100 meters above sea level (masl). 12 Genotypes of rice planted in three environments. The experiment in each environment was arranged using a Randomized Complete Block Design (RKTS) with three replications. Each rice genotype was planted in plots measuring 3 m x 2 m in 6 experimental plots with a spacing of 25 cm x 25 cm. Three samples were taken for each genotype so that the total samples observed were 216 plant samples.

Data were analyzed using PBSTAT-GE software (www.pbstat.com) to estimate several parametric and nonparametric stability parameters. Parametric stability parameters include: Coefficient of variability (CV_i) (Francis and Kannenberg, 1978), Regression coefficient of Finlay and Wilkinson (1963), Eberhart and Russell (1966), Wricke covalence (Wi^2), Hanson Genotype Stability (D_i) and Shukla Stability Variance (σ^2). Nonparametric stability parameters include the yield and stability indices of Kang (1988), Fox Stability (1990), and Thennarasu (1995). Stability analysis based on two main components was also carried out via AMMI biplot. PBTSTAT-GE was used to analyze the correlation between stability parameters.

3. Results and Discussion

The results of rice genotypes tested in 3 environments ranged from 2.60 – 6.85 tonnes/ha. The highest average yield was in a non-organic environment, namely 5.95 tonnes/ha. Based on the exploration of the yield response pattern using the boxplot method, there are indications that the yield power and genotype response to the testing environment have a high level of similarity (Figure 1).

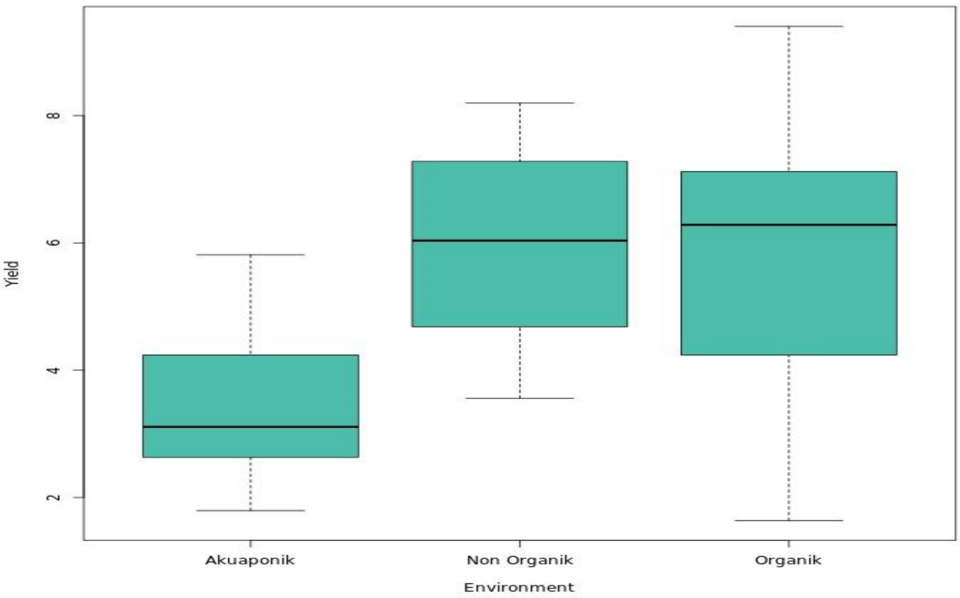


Figure 1: Distribution of grain yield data (t/ha) based on test location

Baroma has an average yield of 6.85 tonnes/ha. Five genotypes had higher yields than the comparison genotype, namely: Inpara 8, PTP 01, Sertani 13, Rajasa 01 and Baroma (table 1).

Table 1. Average results of 12 rice genotypes at 3 testing locations

Gen	Gen. Name	Aquaponics	Non-Organic	Organic	Mean
G1	Jeliteng	2.61	3.56	1.64	2.60
G10	Inpara 2	1.79	6.33	5.87	4.66
G11	Inpara 8	3.17	5.74	9.40	6.10
G12	Inpari 30	3.15	3.64	4.09	3.63
G2	Inpari 24	5.81	5.71	4.53	5.35
G3	PTP 01	3.07	7.82	6.85	5.91
G4	Drinking Milk	2.65	6.74	4.39	4.59
G5	Sertani 13	4.30	7.94	6.83	6.36
G6	Trisakti	2.54	5.24	3.48	3.76
G7	Rajasa 01	2.83	8.20	6.70	5.91
G8	Baroma	4.94	6.38	9.23	6.85
G9	Inpara 9	4.18	4.12	7.40	5.23
Mean		3.42	5.95	5.87	5.08
LSD 0.05		2.52	2.94	1.63	1.36
CV (%)		52.50	35.18	19.81	34.02
Rep p-value		0.60	0.12	0.01	0.05
G p-value		0.32	0.12	0.00	0.00

Parametric stability

1. Francis & Kannenberg Analysis

   According to Francis and Kannenberg (1978), a genotype is identified as stable if the grain yield (Y) is more than the average of all genotypes and the coefficient of diversity (CV) is less than the average. Average yield 5.08 tons/ha and CV 36.24%. Group I consists of genotypes that have grain yields higher than the average and CV lower than the average, namely Inpari 24, Sertani 13, Baroma, and Inpara 9. Group II consists of genotypes that have yields and CVs higher than the average is Inpara 8, PTP 01 and Rajasa 01. Group III consists of genotypes that have grain yield and CV lower than the average, namely Inpari 30, this group is stable but the grain yield is low. Group IV consists of genotypes that have grain yields lower than the average and CV higher than the average, namely Jaliteng, Inpara 2, Mentik Susu and Trisakti (Table 2). Genotypes in group I are considered more stable compared to other genotypes. The Inpari 24 genotype has a CV of 13.29% with a yield of 5.35 tonnes/ha, Sertani 13 has a CV of 29.33% with a yield of 6.36 tonnes/ha, Baroma has a CV of 31.81% with a yield of 6.86 tonnes/ha and Inpara 9 has a CV of 35.85% with a yield of 5.23 tonnes/ha. ha (image 2).

Table 2. Parametric stability analysis

No	Gen	Gen. Name	Y	EVar	CV	W^2	b	b_p	s^2d	s^2d_p	D^2	σ^2
1	G1	Jeliteng	2.60	0.92	36.89	5.87	0.01*	0.03	0.85ns	0.18	2.16	3.30
2	G10	Inpara 2	4.66	6.23	53.53	2.27	1.73ns	0.10	-0.95ns	0.82	16.56	1.14
3	G11	Inpara 8	6.10	9.82	51.34	9.47	1.73ns	0.10	6.27**	0.01	23.73	5.46
4	G12	Inpari 30	3.63	0.22	12.97	2.23	0.28ns	0.11	-0.89ns	0.74	1.36	1.11
5	G2	Inpari 24	5.35	0.51	13.29	7.34	-0.27**	0.01	-0.28ns	0.40	0.72	4.18
6	G3	PTP 01	5.91	6.29	42.41	2.49	1.72ns	0.10	-0.65ns	0.56	16.65	1.27
7	G4	Drinking Milk	4.59	4.21	44.66	2.68	1.19ns	0.65	1.52ns	0.12	11.32	1.38
8	G5	Sertani 13	6.36	3.48	29.33	0.77	1.25ns	0.57	-0.49ns	0.48	9.99	0.23
9	G6	Trisakti	3.76	1.88	36.53	1.70	0.75ns	0.56	0.44ns	0.23	5.70	0.79
10	G7	Rajasa 01	5.91	7.68	46.91	4.03	1.87ns	0.05	-0.11ns	0.35	19.76	2.19
11	G8	Baroma	6.85	4.75	31.81	4.38	1.12ns	0.78	3.33*	0.04	12.25	2.41
12	G9	Inpara 9	5.23	3.51	35.83	6.19	0.60ns	0.36	4.54*	0.02	8.64	3.49
Average			5.08									

Yi: average overall result, Evar: Environmental Variety, CV: Variability Coefficient (Francis and Kannenberg), b: Regression Coefficient (Finlay and Wilkinson; Eberhart and Russel), Stable (α = 0.05): 0.9 - 1.1, P_b: P-value for b with the null hypothesis b=1, s^2d : Regression Deviation (Eberhart and Russel), s^2d_P : P-value for s^2d with the null hypothesis s^2d=0, W^2 : Wricke Covalence, D^2 : Stability of Hanson parameters, (σ^2): Stability of Shukla variance

2. Finlay and Wilkinson's analysis

Finlay and Wilkinson (1963) stated that a genotype is declared stable with high adaptability to all environments if it has a Regression Coefficient (b) = 1 and the average yield is higher than the average of all genotypes. Regression coefficients that are significantly different with one indicating low average stability, where b < 1 indicates adaptation to an environment with low yields, this genotype has above average stability. The Jeliteng and Inpari 24 genotypes have a value of b < 1 and is significantly different from b = 1. This genotype has above average stability and is a genotype with static stability . The genotypes Inpara 2, Inpara 8, Mentik Susu and Baroma have b > 1 and are not significantly different from b = 1, which is a genotype with below average stability. This genotype is responsive to environmental changes and adapts well to favorable environments. This genotype is characterized by low yields in marginal conditions but its yield will increase as the environmental carrying capacity increases and has high yields in optimal environments (Rahayu *et al*. 2013; Pramadio *et al*. 2018). The Trisakti and Inpari 30 genotypes have b values that are not different from b=1 but the results are below average. Furthermore, this genotype is included in the category of stable genotype with low adaptability to all environments.

Genotypes **PTP 01 (G3), Sertani 13 (G5), Rajasa 01 (G7) and Inpara 9 (G9)** has a b value that is not significantly different from b=1 and the results are above average (figure 3). This genotype is classified as a stable genotype with high adaptability to all environments (Lestari *et al*. 2012). This genotype is categorized as a stable genotype with broad stability .

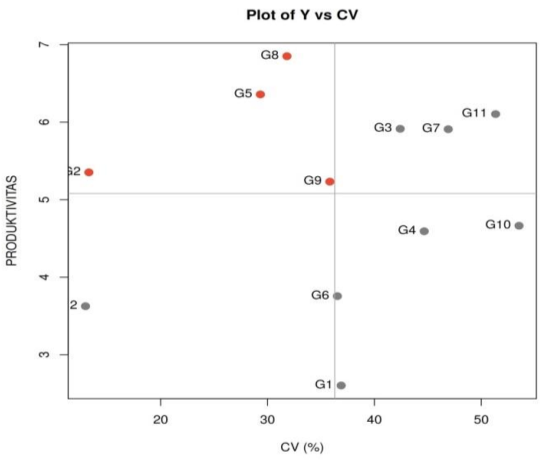
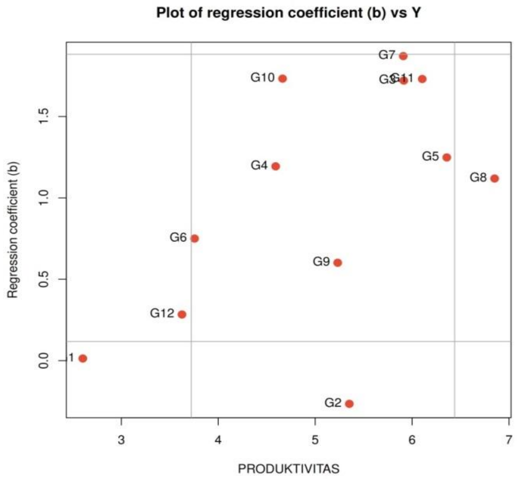


Figure 2: Plot of Y vs CV



FigFigure 3: Plot of regression coefficient (b) vs Y

3. Eberhart & Russell analysis

   Eberhart and Russell (1966) stated that a genotype is declared stable if it has a regression coefficient value (b) close to 1 and a regression deviation value (s^2d) close to 0. Inpara 2, Inpari 30, PTP 01 and Sertani 13 are genotypes that are considered stable. These four genotypes are considered stable according to Eberhart & Russell. Genotypes with b_i value close to 1 and S^2d_i not different from 0 indicate that the genotype has high stability in different environments (Sitaresmi *et al*., 2019) . If a genotype is planted in a different agronomic environment and has results that can fulfill its environmental potential, it is declared a genotype with high dynamic stability (Alwala *et al*., 2010).
4. Wricke's analysis

   A genotype is said to be stable if it has a low equivalence value (W_i^2). In this case, the stable genotypes are Inpara 2, Inpari 30, Sertani 13 and Trisakti (Table 2).
5. Hanson's analysis

   Hanson (1970) introduced a method for evaluating genotype stability when the number of genotypes and the environment is small, with the parameter D^2. Stable genotypes are indicated by small D^2 values. The stable genotypes are Inpari 24, Inpari 30, Jeliteng and Trisakti (Table 2).
6. Shukla Analysis

   Shukla stability variance ($\sigma 2$), an unbiased estimate using genotype stability variation was proposed by Shukla (1972) . These parameters indicate that stable genotypes have little variation across test environments. The stable genotypes according to Shukla are Sertani 13, Trisakti, Inpari 30 and Inpara 2 (Table 2).

Nonparametric stability

Several nonparametric stability methods were proposed based on the ratio of genotype ranks in each environment, with genotypes having the same rank in some environments as stable genotypes.

1. Kang Stability (YS)

   This statistic was introduced by Kang to select corn genotypes with high and stable yields in various environments. This method, named Kang's rank-sum (RK), uses yield stability variance and Shukla (σ^2) as the selection index. This parameter gives a weight of one to the yield and stability statistics to identify genotypes that have high and stable yields. The genotype with the highest yield and lower σ 2 is ranked first. The genotypes selected according to YSi are the genotypes with (+), namely Baroma, Sertani 13, PTP 01 and Rajasa 01 (Table 3)

Table 3. Nonparametric stability analysis

No	Gen	Gen. Name	YS	YS_sel	TOP	S1	Z1	S2	Z2	S3	S6	N1	N2	N3	N4
1	G1	Jeliteng	-5		0	6.67	2.25	25.00	2.03	1.60	1.60	3.33	0.28	0.36	0.59
2	G3	Inpara 2	10	+	1	4.00	0.00	9.33	0.08	1.04	0.56	2.00	0.50	0.53	0.86
3	G4	Inpara 8	3		0	4.67	0.15	13.00	0.01	2.94	1.18	2.33	0.26	0.40	0.64
4	G5	Inpari 30	12	+	2	2.00	1.21	2.33	1.09	0.48	0.34	1.00	0.33	0.37	0.60
5	G6	Inpari 24	2		0	3.33	0.13	7.00	0.29	1.00	1.00	1.67	0.15	0.21	0.32
6	G7	PTP 01	9	+	1	7.33	3.51	30.33	4.02	3.25	1.00	3.67	0.61	0.90	1.47
7	G8	Drinking Milk	12	+	2	6.00	1.28	20.33	0.84	0.60	0.40	3.00	1.50	1.23	2.00
8	G9	Sertani 13	3		1	6.00	1.28	24.33	1.83	3.91	1.18	3.00	0.75	0.71	1.06
9	G10	Trisakti	4		0	4.00	0.00	12.00	0.00	4.43	1.57	2.00	0.29	0.34	0.48
10	G11	Rajasa 01	3		1	6.67	2.25	30.33	4.02	2.15	0.77	3.33	0.67	1.04	1.54
11	G2	Baroma	4		1	6.67	2.25	26.33	2.46	4.45	1.27	3.33	0.42	0.74	1.18
12	G12	Inpara 9	0		0	4.00	0.00	10.33	0.03	3.50	1.50	2.00	0.20	0.29	0.44

YS: Kang Yield and Stability Index YS_sel: '+' The selected genotype has YS > mean of 4.75, TOP: Number of locations where the genotype is ranked in the top third (Fox, 1990), N1, N2, N3, N4: Nonparametric stability parameters Thennarasu, S1, S2, S3, S6: Nonparametric stability parameters Nassar and Huehn, SumZ1 : 14.40, SumZ2 : 16.69, Chi-sqtabelZ1,Zi2 : 8.2, Chi-sqtabelSumZ1,SumZ2: 21.03

2. Fox Stability (1990)

   The advantage of nonparametrics is for general adaptability using stratified genotype rankings. Based on Fox *et al*. (1990), genotypes found in the top three rankings of the test environment can be identified as well-adapted genotypes. In this study, Sertani 13 and Baroma were genotypes that adapted well.
3. Thennarasu (1995)

   Genotypes with small N1, N2, N3, and N4 values are considered more stable genotypes (Thennarasu, 1995). Based on the values of N1, N2, N3, and N4, the Sertani 13 and Trisakti genotypes are more stable genotypes than the other genotypes.

Correlation between stability parameters

Spearman correlation analysis between stability parameters shows that Y and YS have a positive correlation (Table 4). Selection to increase yield is expected to change the stability of grain yield by increasing TOP parameters. This can be directed at developing specific genotype locations by optimizing growing environmental conditions. This genotype will produce the lowest yield when planted in a suboptimal environment and will produce the highest yield when planted in an optimal environment. The regression coefficient b has no correlation with d in Y and all stability parameters are tested. YS is positively correlated with S (1), Si (2), Si (3), Si (6), TOP, NPi (2), and N1 If there is no strong and positive correlation (r = 0.93) between the average results mean and statistics of TOP parameters, indicating that TOP is a suitable stability parameter for identifying high-yield genotypes (Mut *et al*., 2010) .

PBSTAT-GE provides principal component analysis output that correlates genotype with yield and stability parameters (Figure 3). Genotypes that approach the stability parameters are considered “stable” or “good” based on the parameters. The Baroma (G8) and Sertani 13 (G5) genotypes had the highest and most stable yields based on TOP stability parameters. This is understandable because TOP is calculated based on the number of locations whose genotype has the highest yield ranking (figure 4).

Additive main effects and multiplicative interactions (AMMI)

The AMMI method separates main effects and interaction effects, and provides a lot of interpretation and information (Hadi & Sa'diyah, 2004) , and is quite effective in expecting G x E interactions (Suwarto & Nasrullah, 2011) . PBSTAT-GE revealed AMMI model anova, AMMI biplot (PC1 vs. PC2), and AMMI biplot (PC1 vs. Outcome). The interaction effects of location, genotype, and genotype x location were significant (Table 5). Decomposition of the interaction effect of genotype x location into 2 main components.

The AMMI biplot is presented by AMMI1 and AMMI2 biplot. The AMMI1 biplot is a plot of the main effect (yield) and the first principle component score (PC1), while the AMMI2 biplot is a plot of the first principle component score (PC1) and the second principle component score (PC2). The AMMI1 biplot shows genotype adaptation (Figure 5). The genotype that is best able to adapt to the environment is the genotype that has a high average yield and a unidirectional interaction score. The AMMI2 biplot depicts the interaction effect between genotype and environment (Figure 6). Biplots can be used to analyze genotype stability. A genotype is said to be location specific if it is able to adapt well to the environment. Location-specific genotypes are displayed via a plot between the PC1 score and the mean genotype. The Baroma genotype produced 6.85 tons/ha of grain, then Inpara 8 with a grain yield of 6.1 tons/ha and PTP 01 with a grain yield of 5.91 tons/ha, these genotypes were found to be close to Organic. It can be said that Baroma, Inpara 8 and PTP 01 can specifically adapt to an organic environment with grain yields above the average for all genotypes, namely 5.08 tonnes/ha (Figure 4). The Sertani 13 genotype can adapt specifically to non-organic environments and Milk Mentik adapts specifically to aquaponic environments.

The interaction between genotype and environment can also be shown through the AMMI2 biplot (Figure 5). Genotypes adjacent to the center of the plot (0, 0) and within the confidence interval of the ellipse have little contribution to the G x E interaction, and are broadly adapted genotypes. The genotypes Sertani 13 (G5) and Inpari 24 (G6) are broadly adaptive genotypes. The combination of genotype and environment has a positive interaction effect if the PC value is in the same direction and a negative interaction if the PC value is in the opposite direction. A genotype adjacent to a particular location means that the genotype is specific to that location. Inpara 8 (G11) is specifically adaptive in organic environments, the Mentik Susu genotype (G4) is adaptive in non-organic environments, and Inpari 24 (G2) is adaptive in aquaponic environments (Figure 5).

Table 4. Spearman correlation between stability parameters.

Param.	rY	rW2	Rb	rs2d	rD2	σ^2	rCV	rYS	rTOP	rS1	rS2	rS3	rN1	rN2	rN3
rW2	-0.16														
rb	-0.47	-0.20													
rs2d	-0.19	0.65*	-0.11												
rD2	-0.57	0.10	0.92**	0.17											
σ^2	-0.16	1.00**	-0.20	0.65**	0.10										
rCV	-0.02	0.15	0.75**	0.13	0.77**	0.15									
rYS	0.87**	0.12	-0.49	0.17	-0.47	0.12	0.00								
rTOP	0.93**	-0.22	-0.20	-0.23	-0.31	-0.22	0.25	0.80**							
rS1	-0.06	0.86**	-0.04	0.49	0.16	0.86**	0.24	0.11	-0.13						

rS2	-0.08	0.87**	0.02	0.50	0.20	0.87**	0.29	0.12	-0.11	0.98**					
rS3	0.37	0.38	-0.15	-0.20	-0.21	0.38	0.09	0.29	0.36	0.38	0.46				
rS6	0.83**	0.18	-0.43	-0.22	-0.50	0.18	0.05	0.70*	0.76**	0.24	0.26	0.72**			
rN1	-0.06	0.86**	-0.04	0.49	0.16	0.86**	0.24	0.11	-0.13	1.00**	0.98**	0.38			
rN2	-0.77**	0.61*	0.27	0.46	0.50	0.61*	0.10	-0.58*	-0.79**	0.49	0.50	-0.01	0.49		
rN3	-0.74**	0.71**	0.23	0.55	0.48	0.71**	0.12	-0.53	-0.73**	0.67*	0.66*	0.00	0.67**	0.90**	
rN4	-0.74**	0.71**	0.23	0.55	0.48	0.71**	0.12	-0.53	-0.73**	0.67*	0.66*	0.00	0.67**	0.90**	1.00**

Table 5. Analysis of various AMMI models

	Df	JK	Percent	KT	F-Count	P-value	Ket.
Environment (E)	2	148.8363		74.41814	11.11587	0.009599	**
Deuteronomy/E	6	40.16861		6.694769	2.241251	0.049834	*
Genotype (G)	11	159.4814		14.49831	2.152119	0.060678	.
GxE	22	148.2087		6.736759	2.255308	0.005914	**
PC1	12	85.74375	57.85	7.145312	2.392083	0.012401	*
PC2	10	62.46494	42.14	6.246494	2.091179	0.037487	*
Residuals	66	197.1465		2.987068			

DB = degrees of freedom, JK = Sum of Squares, KT = Middle Square* = significantly different at the 5% level of significance; ** = significantly different at the 1% level of significance; **.** = significantly different at the 10% level, tn = not significant, PC1 = Main Component 1, PC2 = Main Component 2, **.** = significantly different at the level of 10%.

Table 6. Genotype PC scores and Productivity in three testing environments

Genotype	Average Yield (tons/ha)	PC1	PC2
G1	2.60	-1,001	-0.335
G2	4.66	0.328	0.609
G3	6.10	1,311	-0.247
G4	3.63	-0.283	-0.629
G5	5.35	-0.983	-0.691
G6	5.91	0.199	0.707
G7	4.59	-0.429	0.609
G8	6.36	-0.104	0.394
G9	3.76	-0.542	0.166
G10	5.91	0.162	0.923
G11	6.85	0.767	-0.521
G12	5.23	0.574	-0.985

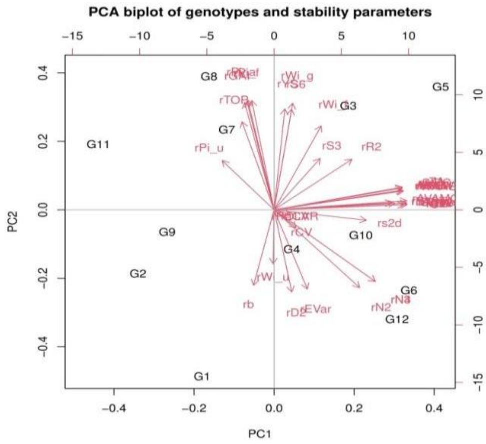


Figure 4. PCA biplot of genotype and stability parameters

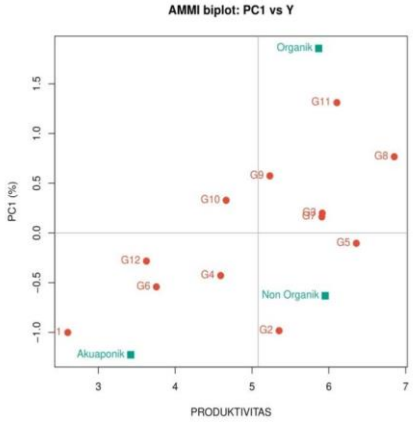


Figure 5. AMMI-1 biplot

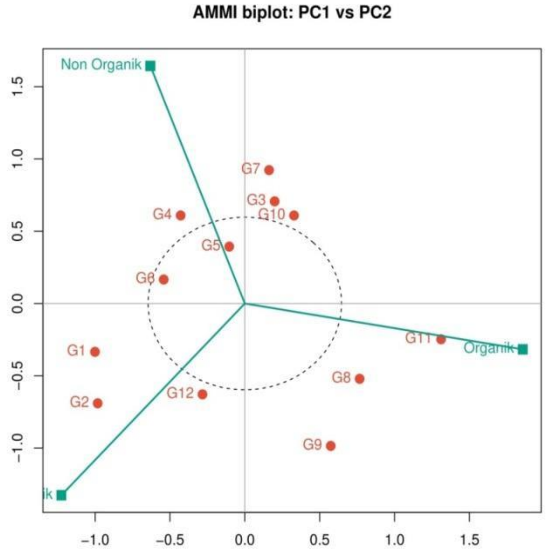


Figure 5. AMMI-2 biplot.

4. Conclusion

The highest average production obtained based on the environment is Non-Organic with an average yield of 5.95 tons/ha. Baroma (G8) is the genotype with the highest average of 6.85 tons/ha from the three environments.

Genotypes Sertani 13 (G5), Inpari 30 (G12) and Trisakti (G6). is a consistently stable and widely adapted genotype based on eight parametric and non-parametric stability analyses.

According to Biplot, the Sertani 13 (G5) and Inpari 24 (G2) genotypes are genotypes with extensive adaptation. Genotypes based on specific environments, namely Baroma (G8), PTP 01 (G3), and Inpara 8 (G11) can adapt well in organic environments, Sertani 13 (G5) is adaptive in non-organic environments and Mentik Susu (G4) is adaptive in aquaponic environments.

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