



GENOTYPE BY ENVIRONMENT INTERACTION AND YIELD STABILITY ANALYSIS OF DOUBLED HAPLOID LINES OF UPLAND RICE

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SUMMARY

The aims of this research was to determine the effect of genotype-by-environment (G x E) interaction on grain yield among upland rice doubled haploid lines (DH) of upland rice in order to obtain stable and high yielding lines through multilocation yield trials. Fourteen DH lines and two upland varieties i.e. Inpago 10 and Limboto were planted at 6 different locations in Indonesia, i.e. Bogor, Indramayu and Sukabumi (West Java Province), Malang and Blitar (East Java Province), and East Lampung (Lampung Province). In each location, the experimental design was randomized complete block design with three replications nested in locations. Stability was analyzed using linear regression model. Combined analysis of variance showed that the effects of location, genotype and interaction of genotype × location were highly significant ($p < 0.01$) for grain yield. There was considerable variation for grain mean yield among both genotypes (DH lines) and environments (locations) which made it difficult to select stable lines in response to environmental change. DH lines of ST6 and ST9 were classified as stable and widely adapted in all locations based on Finlay-Wilkinson, Eberhart-Russel and AMMI stability analysis. ST13 was classified as stable only by Finlay and Wilkinson's analysis, but achieved the highest average yield of six locations ($5.00 \text{ tons ha}^{-1}$), higher than check variety Inpago 10 ($4.03 \text{ tons ha}^{-1}$), and similar to Limboto ($4.98 \text{ tons ha}^{-1}$). ST6, ST9, and ST13 DH lines also had high yield potential, i.e. 6.26 , 6.28 , and $7.18 \text{ tons ha}^{-1}$, respectively. In addition, AMMI analysis also showed that ST1 was DH lines specifically adapted to Malang, while ST7 was specifically adapted to Blitar.

Key words: Multilocation yield trials, stability, adaptability, upland rice

Key findings: The multilocation yield trials enabled us to identify stable and high yielding upland rice DH lines obtained from anther culture. Those lines i.e., ST6, ST9 and ST13, have the potential to be released as new upland rice varieties in Indonesia.

Manuscript received: January 29, 2019; Decision on manuscript: May 04, 2019; Accepted: May 16, 2019.

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Communicating Editor: Dr. C.N. Neeraja

INTRODUCTION

The increase in demand for rice (*Oryza sativa* L.) must be met with production increase in many parts of Asia, Africa and Latin America (Devi *et al.*, 2011) because rice is the second most important cereal crop and staple food for more than one third of the world's population (Ajmeera *et al.*, 2017). In Asia, Indonesia has been a major rice producing as well as the rice consuming country. However, national rice production is still dominated by contributions from lowland rice. The upland rice production contributed only 5.28% to the national rice production. According to Ministry of Agriculture, Republic of Indonesia (2017) estimated potential dryland area for food crops \pm 5,1 million hectares, but only 1,05 million hectares has been planted with upland rice. Therefore, optimization of dryland utilization is one of the strategies to increase national rice production through the development of new upland rice varieties (Purwoko, 2017). From previous research 14 doubled haploid (DH) advanced lines of upland rice have been selected through preliminary and advanced yield trials (Akhmadiet *al.*, 2017). These DH lines obtained from anther culture of crosses between varieties and high yielding elite lines with tolerance to abiotic stresses (drought, Al toxicity, shade) and resistance to

pest and diseases (blast disease, bacterial leaf blight and brown plant hopper) (Dewi and Purwoko, 2012; Dewi *et al.*, 2014). In order to select potential lines suitable for variety release purpose, the DH advanced lines need to be tested further in multilocation yield trials.

In Indonesia rice is grown in various land ecologies with different biophysical conditions and various biotic pressures (Sitaresmi *et al.*, 2012). The ability of some crop varieties to perform well over such a wide range of environmental conditions has long been appreciated by the agronomists and plant breeders to develop stable genotypes with maximum economic yield per unit area and consistent performance for productivity across environments (Singh *et al.*, 2014). While national rice breeding program focuses towards developing not only high yielding varieties but varieties with ability to adapt to various environments, thus evaluation of rice lines in various agro-ecological zones and seasons or multilocation yield trials must be done prior to release new varieties. Multilocation yield trials are commonly conducted to allow for estimating line's genotypic value and its consistency with the corresponding phenotypic value across environments (Kharimizadeh *et al.*, 2012). As stated by Finlay and Wilkinson (1963) even in a uniform edaphic environment a

considerable degree of general adaptability will be important because of the marked fluctuation of climatic conditions from season to season.

Estimation of line's adaptability and stability in multilocation yield trials are important steps to demonstrate the influence of genotype by environment (G x E) interaction on yield (Lakshmi *et al.*, 2014; Horn *et al.*, 2018). Several methods of stability analysis to explain and interpret response of genotypes to various environment have been developed based on regression analysis by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). In stability analysis, Finlay and Wilkinson (1963) considered linear regression as a measure of stability, whereas Eberhart and Russell (1966) emphasized that with linear (b_i) and non-linear (S^2_{di}) components of genotype by environment interaction be considered while judging the phenotypic stability of a genotype. Recently, Additive Main Effect Multiplicative Interaction

(AMMI) analysis reported to be the most effective tool in estimating G x E interaction for identifying high yielding and stable genotypes adapted to diverse production environments, and for determining the areas where rice genotypes would be adapted and produce economically competitive yields (Islam *et al.*, 2014). Therefore, the aim of this research was to determine the effects of G x E interaction on yield among doubled haploid lines (DH) of upland rice in order to obtain stable and high yielding lines through multilocation yield trials.

MATERIALS AND METHODS

Experimental materials

The materials consisted of 14 upland rice DH lines derived from anther culture of F_1 and two upland rice varieties as check, i.e. Inpago 10 and Limboto (Table 1).

Table 1. Upland rice DH lines used in multilocation yield trials.

Code	Lines / Varieties*	Code	Lines / Varieties*
ST1	HR-1-12-1-1	ST9	HR-5-7-1-1
ST2	HR-1-32-1-1	ST10	HR-5-9-1-1
ST3	HR-2-22-2-1	ST11	HR-5-9-4-1
ST4	HR-2-27-2-7	ST12	HR-7-15-2-1
ST5	HR-2-34-1-3	ST13	B3-2
ST6	HR-3-6-2-1	ST14	B6-4
ST7	HR-5-11-1-1	ST15**	Inpago 10
ST8	HR-5-13-2-2	ST16**	Limboto

*HR1: IR83821-99-2-2-2/ I5-10-1-1; HR2:IR85640-114-2-1-3 /I5-10-11-1; HR3: IR83821-99-2-2-2/ O18-b-1; HR5: BIO R81/I5-10-1-1; HR7: BIO R81 /O18-B1. ** Check Varieties.

Experimental procedures

Planting and harvesting

The research was conducted during rainy season of 2017 at 6 locations in Indonesia, i.e. Bogor, Sukabumi, Indramayu (West Java Province), Malang, Blitar (East Java Province) and East Lampung (Lampung Province). In each location, each genotype was planted in a plot of 4 m x 5 m with plant spacing of 30 cm x 15 cm, so there were 13 rows and 33 planting hills each plot (population per plot was 429 hills). In each location, plant maintenance was carried out according to the appropriate standard practice of rice production. The seeds were planted directly with a depth of 3-5 cm by 3-5 seeds per hill. Fertilizers used were manure as much as 10 tons ha⁻¹ and NPK sources, i.e. urea with a dose of 200 kg ha⁻¹, SP-36 100 kg ha⁻¹, and KCl 100 kg ha⁻¹. Fertilizers were given in three stages: (1). The first fertilization was given one week after planting (WAP), i.e. 40 kg ha⁻¹ urea, 100 kg ha⁻¹ SP-36, and 100 kg ha⁻¹ KCl; (2). The second fertilization was given at four WAP (80 kg ha⁻¹ urea); (3). The third fertilization was given at 7 WAP (80 kg ha⁻¹ urea).

Harvesting was carried out when 80% of rice panicles in one plot turned yellow. Seeds were harvested to estimate grain yield per plot. The grain were dried to reach \pm 14% moisture content and later converted to dry grain yield per hectare (ton ha⁻¹). The outer rows were not used for

yield estimation in order to control border effects and to minimize experimental error.

Experimental design and data collection

The experimental design was randomized complete block design with three replications nested in locations. Data of yield was collected from 6 locations in the form of dry grain weight per hectare by the conversion of dry grain weight per plot.

Data Analysis

Grain yield data was subjected to a combined analysis of variance and also to stability analysis using SAS 9.0, STAR, and PBSTAT-GE. If there was a significant difference, an LSD test was performed at the level of 5% significance. If the G x E interaction was significant, then stability analysis was performed. Stability analysis was applied for yield trait using the stability parameters based on linear regression model as proposed by Finlay and Wilkinson (1963) and Eberhart and Russell (1966). These parameters were regression coefficients (b_i) of the genotype means over environments on the environmental indices (environmental means in the study) and mean squares of deviations from regressions (S^2_{di}). In addition Additive Main Effect Multiplicative Interaction (AMMI) was also used to determine specific areas where rice genotypes would be most adapted (Gauch, 2013).

1. Finlay and Wilkinson (1963).

Coefficient of regression (b_i) for the genotype i was calculated by the following formula:

$$b_i = \frac{\sum_{j=1}^m Y_{ij} X_j - \frac{(Y_i)(X)}{m}}{\sum_{j=1}^m X_j^2 - \frac{X^2}{m}}$$

In this equation of regression coefficient, i and j indices explain genotype ($i = 1 \dots 14$) and environment ($j = 1 \dots 6$), respectively. In addition m was the number of environments.

2. Eberhart and Russell (1966).

Mean squares of deviations from regression (S_{di}^2) were calculated by subtracting the regression SS from total SS of genotype or dependent variable with following formula:

$$S_{di}^2 = \frac{1}{(m-2)} \left[\left(\sum_{j=1}^m Y_{ij}^2 - \frac{Y_i^2}{m} \right) - b_i^2 \left(\sum_{j=1}^m X_j^2 - \frac{X^2}{m} \right) \right]$$

where b_i^2 was square of regression coefficient for the i^{th} genotype.

Mean regression coefficient (b) calculated over single regression coefficients (b_i) of genotypes was considered as equal to 1 ($b=1$) because the environment means were used as environmental indices in the study.

3. Additive main effect multiplicative interaction (AMMI)

In statistical analysis using AMMI analysis and biplot facility, the rice yield data were analyzed to determine the nature and magnitude of G x E interaction effects on grain yield in diverse production environments. The following AMMI model according to Gauch (2013) was used for G x E interaction and yield stability analyses based on the principal component analysis (PCA):

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \eta_{en} + \theta_{ge}$$

where Y_{ge} is the yield of genotype g in environment e , μ is the grand mean, α_g is the genotype mean deviation, β_e is the environment mean deviation, λ_n is the eigenvalue of the n^{th} principal component (PCA) axis, γ_{gn} and η_{en} are the genotype and environmental PCA scores for the n^{th} PCA axis, and θ_{ge} is the residual.

RESULTS AND DISCUSSION

Yield performance of upland rice lines

Analysis of variance of multilocation yield trials is useful for estimating variance components related to different sources of variation, including genotypes and G x E interaction. Combined analysis of variance on grain yield of DH lines showed that location (environment), genotype and G x E interaction had very significant effect (Table 2).

Table 2. Combined analysis of variance for yield of upland rice DH lines at six locations.

Source of variance	d.f.	SS	MS	F-value	SS proportion (%)
Environment (E)	5	371.76	74.35	25.47**	55.87
Reps (Environment)	12	35.03	2.92	5.91**	5.26
Genotype (G)	15	37.37	2.49	5.05**	5.62
G x E	75	132.37	1.77	3.57**	19.89
Error	180	88.89	0.49	-	-
Total	287	665.43	-	-	-

Note: ** highly significant at the level <0.01; E= Environment or locations; df= degrees of freedom; SS= Sum of squares; MS= Mean squares

Table 3. The grain yield (tons ha⁻¹) of upland rice DH lines in multilocation trials.

Genotype	Bogor	Lampung	Sukabumi	Indramayu	Malang	Blitar	Genotype mean yield
ST1	2.88	4.31	3.56	3.58a	6.62a	4.81	4.29
ST2	3.01	5.20	2.70	3.11	5.10	4.70	3.97
ST3	3.28	5.07	3.35	2.92	6.17	4.21	4.17
ST4	3.99	5.45	4.07	2.58	6.31	3.26	4.28
ST5	2.55	5.74	2.07	2.90	6.07	5.55ab	4.15
ST6	4.40a	5.64	3.23	2.65	6.26	5.90ab	4.68a
ST7	3.08	5.58	2.35	2.82	6.06	5.35b	4.20
ST8	2.95	5.24	2.70	2.04	5.44	4.94	3.89
ST9	3.93	5.60	2.70	3.19	6.28	5.06b	4.46
ST10	3.84	5.14	3.18	2.27	5.31	5.9ab	4.27
ST11	3.50	5.28	2.44	3.44a	5.18	5.70ab	4.26
ST12	5.88a	5.57	3.52	2.70	3.07	3.68	4.07
ST13	3.53	4.87	3.96	4.02a	7.18a	6.42ab	5.00a
ST14	2.70	4.06	2.46	2.01	7.3ab	2.94	3.58
Inpago 10	3.13	5.34	2.80	2.17	5.33	5.38	4.03
Limboto	5.18	5.86	4.02	3.62	6.21	4.97	4.98
Environments mean yield	3.62	5.25	3.07	2.88	5.87	4.92	4.18
CV (%)	8.9	13.5	12.2	12.06	10.72	14.11	15.95
LSD _{0.05}	1.26	1.18	1.31	1.05	1.05	0.00	0.50

Note: Numbers within the same column followed by letter 'a' indicate yield significantly higher than Inpago 10, while letter 'b' indicate yield significantly higher than Limboto according to LSD test at a 5%.

Proportion of variance component indicated that environment (location) provided the largest contribution (55.87%) followed by G x E interaction (19.89%), while genotype gave the smallest contribution to variance (5.62%). Therefore, rice grain yield obtained will depend heavily on the environmental conditions where the rice planted. However, because of G x E interaction is also significant to yield, thus it is necessary to study further about the pattern of G x E interaction in order to be able to identify high yielding and stable lines (Palanog *et al.*, 2015; Sitaresmi *et al.*, 2016; Ajmeera *et al.*, 2017; Bose *et al.*, 2012).

In this study, the DH line's mean yield over all environments ranged from 3.58 to 5.00 tons ha⁻¹ (Table 3).

There were eight DH lines that showed genotype mean yield higher than environment mean yield, i.e. ST1, ST4, ST6, ST7, ST9, ST10, ST11 and ST13. However, only two DH lines, i.e. ST6 and ST13, showed genotype mean yield higher than and significantly different from check variety Inpago 10, and similar to Limboto. It is shown in Table 3 that ST13 DH line achieved for both the highest genotype mean yield (5.00 tons ha⁻¹) and yield potential (7.18 tons ha⁻¹).

It is appeared that there is a great array of change in rankings of genotypes (DH lines) from location to other location (Table 3). Location (environment) mean yield for all of the genotypes ranged from 2.88 to 5.87 tons ha⁻¹. Distribution of rice yield showed that the environmental means yield of Indramayu was very low (less than 3 tons ha⁻¹) which indicated a low-yielding environment. On the other hand Malang was a high-yielding

environment, as shown by the very high environmental means yield (more than 5.5 tons ha⁻¹). According to Mut *et al.* (2010) changes in response of each genotype to each environment (location) indicated the dynamic response of lines to different environments.

Yield stability and adaptability of DH lines

This different response of each DH line to its environment made it difficult to select stable lines in response to environmental change (Table 3). However, a successfully developed new cultivar should have stable performance and broad adaptation over a wide range of environments, in addition to high yield potential. According to Romagosa and Fox (1993), the concept of stability is divided into two terms, namely static and dynamic stability or in terms of plant breeding better known as biological and agronomic stability. Static or biological stability revealed the performance of a relatively similar genotypes from one location to another (homeostasis), while dynamic stability or agronomic stability revealed genotype performance with fluctuating values from one location to another to develop stability response. All stability procedures based on quantifying G x E interaction effects belong to the dynamic concept., i.e. Finlay and Wilkinson model, Eberhart and Russell model, and AMMI (Becker and Leon, 1988; Jambormias and Riry, 2008).

Finlay and Wilkinson (1963) stability analysis is a stability model based on the slope of regression line or regression coefficient (b_i) between the yield average of a genotype and the general average of all genotypes

in all test environments. In general, genotypes with b_i -values; (1) <1.00 were considered unresponsive to different environments or had above average stability, (2) $= 1.00$ were considered to have average stability, and (3) >1.00 were considered responsive to good environments or had below average stability. Genotype that has a regression coefficient (b_i) equal to unity or $= 1$ expressed as a stable genotype. Therefore, stability below or above average basically shows the pattern of adaptability of the genotypes.

In this study, b_i -values ranged from 0.13 to 1.40 for grain yield. This variation in b_i -value indicated that genotypes had different responses to environmental changes as mentioned by Akçura *et al.* (2006). According to Finlay and Wilkinson model, eight DH

lines with b_i -values not significantly different from 1, i.e. ST1, ST3, ST4, ST6, ST9, ST10, ST11, and ST13 showed as stable genotypes that have wide adaptability to all environments because their average yield was higher than environment mean yield (Table 4). Those genotypes have no deviations from the general response to environments and thus permits a predictable response to environments. There were two lines i.e., ST12 and Limboto, classified as genotypes with above average stability and adapted in marginal environments, while ST5, ST7, and ST14 were DH lines that have below average stability. Those DH lines with below average stability were sensitive to environmental changes and should be recommended for cultivation under favorable environments only. Those three DH

Table 4. Mean grain yields and estimates of stability parameters for yield of upland rice DH lines in multi location trials.

Genotypes	Y_i (ton ha ⁻¹)	b_i (Finlay and Wilkinson, 1963)	S^2_{di} (Eberhart and Russell, 1966)
ST1	4.29	0.89 ^{ns}	0.50**
ST2	3.97	0.88 ^{ns}	-0.02 ^{ns}
ST3	4.17	0.96 ^{ns}	0.02 ^{ns}
ST4	4.28	0.84 ^{ns}	0.85**
ST5	4.15	1.40*	0.21 ^{ns}
ST6	4.68	1.16 ^{ns}	0.02 ^{ns}
ST7	4.20	1.28*	-0.04 ^{ns}
ST8	3.89	1.18 ^{ns}	-0.08 ^{ns}
ST9	4.46	1.12 ^{ns}	-0.09 ^{ns}
ST10	4.27	1.03 ^{ns}	0.26**
ST11	4.26	0.93 ^{ns}	0.28**
ST12	4.07	0.13*	2.01**
ST13	5.00	1.01 ^{ns}	0.59**
ST14	3.58	1.30*	1.28**
Inpago10	4.03	1.15 ^{ns}	0.03 ^{ns}
Limboto	4.98	0.74*	0.05 ^{ns}
Environment			
Mean yield	4.18		

Y_i : Yield means over all environments; b_i : coefficient of regression; S^2_{di} : sum of squares deviation from regression; ns= non-significant.* significantly different from 1,** significantly different from 0.

lines can produce more than 6 tons ha^{-1} in a high-yielding environment such as Malang (Table 3).

Stability analysis by Eberhart and Russell (1966) is the method to describe the third type of stability as described by Lin *et al.* (1986) and Becker and Léon (1988). In Eberhart and Russell model, the regression coefficient (b_i) is used together with the sum of squares deviation from regression (S^2_{di}) parameters to determine the stability of a genotype. The genotype is considered to be stable if the residual mean square from the regression model on the environmental index is small. In this stability model, genotypes having b_i approximating unity (1.0) coupled with S^2_{di} of zero (0.0) indicated an average stability and expressed as a stable genotypes. When this is associated with the high mean yield, genotypes have wide adaptability and when associated with low mean yield, genotypes are poorly adapted to all environments (Akçura *et al.*, 2006). Therefore, according to Eberhart and Russell model, ST2, ST3, ST6, ST8, and ST9 DH lines and also check variety, Inpago 10, were classified as stable genotypes, but only ST6 and ST9 DH lines that have wide adaptability (Table 4).

Significant $G \times E$ interaction effects on yield observed in the present study indicate that the genotypes do not show consistent performance across test environments (Table 2). This allows for an investigation of the nature and magnitude of $G \times E$ interaction effects on grain yield in diverse production environments, which can not be achieved by a standard analysis of variance. The additive main effects and multiplicative interactions (AMMI) model, which combines standard

analysis of variance with principal component analysis (PCA) and biplot facility, can be used to investigate $G \times E$ interaction. AMMI analysis is an experimental data analysis technique of two treatment factors with the main effect of the treatment and environment being additive while the interaction effect is modeled with the bilinear model (Mattjik dan Sumertajaya, 2006). Unlike other $G \times E$ statistical analysis, AMMI analysis is reported to be effective in estimating $G \times E$ interaction, because it is capable of separating genotype, environment, and $G \times E$ interaction components which is important in most agricultural research (Suwanto and Nasrullah, 2011; Lal, 2012).

The result of the AMMI analysis of variance showed that the interaction between major components 1 and 2 (PC1 and PC2) was highly significant (Table 5). The contribution of $G \times E$ interaction effects of variance could be explained by the five components 50.3, 31.8, 8.7, 6.0, and 3.1%, respectively. Based on the value of the variance contribution of the biplot interaction effect, PC1 and PC2 contributed 82.1% information from the various distribution patterns of interaction between the genotype \times environment (Figure 1). It means that the variance that could not be explained by the model was 17.9%. Therefore, the presumption response to genotype interaction with the environment is quite high. Biplot interaction between PC1 and PC2 could explain which lines were stable at all locations or specific location. The closer a genotype is to the center point, the higher the level of stability. In addition, the proximity of the genotype point with the location line showed the relationship between the genotype and the location which

means that the location is specifically supported for growth and development of the genotype (Ganefianti *et al.*, 2009; Rasyad and Idwar, 2010).

Figure 1 showed that ST2, ST6, ST8, and ST9 approach the center point (coordinate 0,0), which is the axis meeting point that divides the biplot field into 4 quadrants. This indicates that the four genotypes can be classified as stable and widely adapted genotypes to diverse environmental conditions. Genotypes that are far from center point (0,0) indicate that they have relatively better adaptability at locations adjacent to certain imaginary axes. The relationship between genotype and environment where the genotypes well adapted has been shown between ST1 to Malang and ST 7 to Blitar (Figure 1).

Stability analysis of DH lines using three stability analysis is presented in Table 6. Based on Finlay-Wilkinson, Eberhart-Russell, and AMMI, it can be stated that ST2, ST6, ST8, and ST9 are classified as stable DH lines in all locations. In this study, only ST6 and ST9 are selected as the most stable DH lines, because both of them had high mean yield over

environment ($Y_i > 4.5 \text{ ton ha}^{-1}$) and classified as stable and widely adapted genotypes by all those three stability analysis used. Those two DH lines can be recommended for variety release. However, ST13 which is classified as high and stable in yield and also widely adapted DH line according to Finlay and Wilkinson's but not stable according to Eberhart and Russell's, can also be considered for variety release, because when sum of squares deviation from regression (S^2_{di}) is significantly different from 0, the conclusion may be drawn by the joint consideration of high mean yield and regression coefficient (b_i) values given (Mohammadi *et al.*, 2014). Therefore, ST13 can be recommended as the selected DH lines because it has a high grain mean yield over six environment (5.00 ton ha^{-1}) and coefficient of regression equal to unity ($bi = 1.01$) and also its deviation from regression is as small as possible ($S^2_{di} = 0.59$) (Table 4). Another DH lines such as ST1 and ST7 have narrow adaptability. They showed good performance in specific area like in Malang (ST1) and Blitar (ST7) thus those genotypes may be cultivated in these environments.

Table 5. AMMI analysis of variance for yield.

Source of variance	d.f.	SS	MS	F-value	% variance explained
Environment (E)	5	371.76	74.35	25.47**	-
Reps (Environment)	12	35.03	2.92	5.91**	-
Genotype (G)	15	37.38	2.49	5.05**	-
G x E	75	32.46	1.77	3.58**	-
IPC1	21	66.65	3.51	7.11**	50.3
IPC2	19	42.13	2.48	5.02**	31.8
IPC3	17	11.59	0.77	1.56ns	8.7
IPC4	15	7.94	0.61	1.24ns	6.0
IPC5	3	4.15	0.38	0.76ns	3.1
Error	180	88.87	0.49	-	-

E: Location (Environment); IPC = Interaction Principal Component Analysis; ** = significant in a α level of < 0.01 ; ns = non significant; d.f. = degrees of freedom.

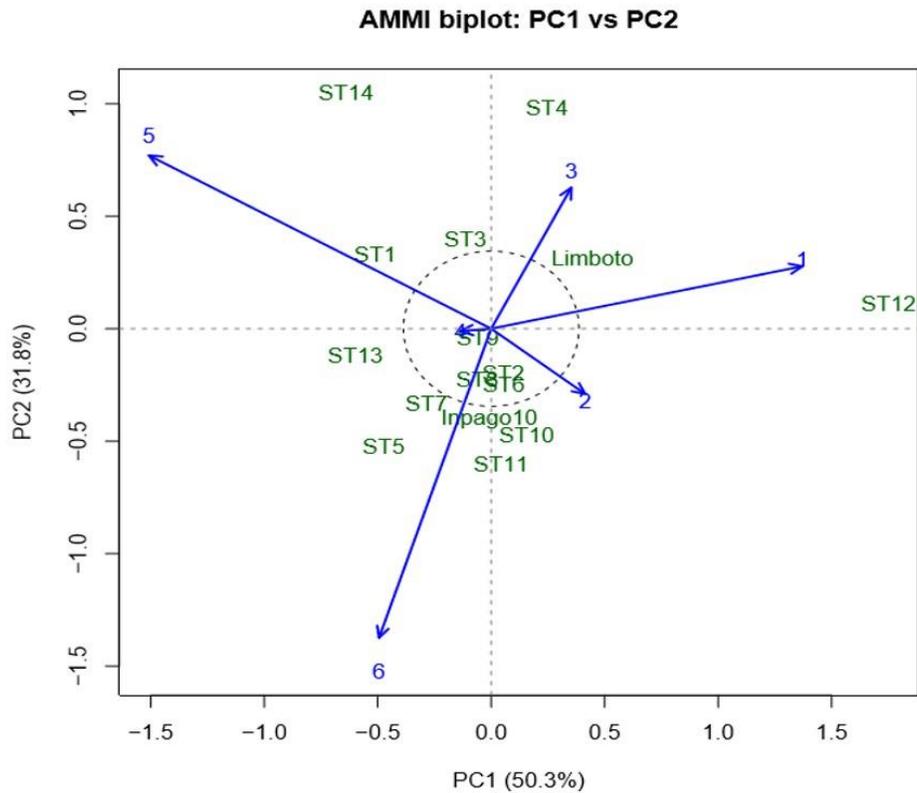


Figure 1. AMMI-2 biplot where ordinate is PC2 and abscissa is PC1 showing interaction between specific DH lines of upland rice and environment. Locations 1-6: Bogor, Lampung, Sukabumi, Indramayu, Malang and Blitar.

Table 6. Genotype stability of upland rice DH lines across six locations.

Genotype	Y_i	Finlay-Wilkinson	Eberhart-Russell	AMMI
ST1	4.29	Stable	-	-
ST2	3.97	Stable	Stable	Stable
ST3	4.17	Stable	Stable	-
ST4	4.28	Stable	-	-
ST5	4.15	-	-	-
ST6	4.68	Stable	Stable	Stable
ST7	4.20	-	-	-
ST8	3.89	Stable	Stable	Stable
ST9	4.46	Stable	Stable	Stable
ST10	4.27	Stable	-	-
ST11	4.26	Stable	-	-
ST12	4.07	-	-	-
ST13	5.00	Stable	-	-
ST14	3.58	-	-	-
Inpago10	4.03	Stable	Stable	-
Limboto	4.98	-	Stable	-

Y_i = Yield means over all environments; - = unstable

CONCLUSIONS

Significant G × E interaction effects indicated that the genotypes showed inconsistent performance across test environments and caused changing in rankings of grain yield of DH lines from location to other location. ST1, ST4, ST6, ST7, ST9, ST10, ST11, and ST13 DH lines exhibited higher genotype mean yield than environmental mean yield. Among those high-yielding DH lines, only ST6 (4.68 tons ha⁻¹) and ST9 (4.46 tons ha⁻¹) were classified as stable DH lines and widely adapted in all locations based on Finlay-Wilkinson, Eberhart-Russell and AMMI analysis, while ST13 was classified as stable by Finlay and Wilkinson's stability analysis. However, ST13 revealed the highest productivity at six location (5.00 tons ha⁻¹). The productivity of ST13 was higher than check variety Inpago 10 (4.03 tons ha⁻¹), but similar to Limboto (4.98 tons ha⁻¹). Therefore, those three genotypes have potential to be released as new upland rice varieties. Based on AMMI stability analysis, ST1 and ST7 are recommended as DH lines which specifically adapted in Malang and Blitar, respectively.

ACKNOWLEDGEMENTS

The authors wish to thank Ministry of Research, Technology, and Higher Education, Republic of Indonesia for funding the research through "STRANAS" Research Scheme.

REFERENCES

Ajmeera S, Sudheer S, Kumar, Ravindrababu (2017). Studies on stability analysis for grain yield and its attributes in rice (*Oryza sativa*

- L.) genotypes. *Int. J. Pure App. Biosci.* 5(4): 892-908.
- Akçura M, Kaya Y, Taner S, Ayranci R (2006). Parametric stability analyses for grain yield of durum wheat. *Plant Soil Environ.* 52 (6): 254-261.
- Akhmadi G, Purwoko BS, Dewi IS, Wirnas D (2017). Pemilihan karakter agronomi untuk seleksi pada galur-galur padi dihaploid hasil kultur antera. *J. Agron. Indonesia* 45(1): 1-8.
- Ministry of Agriculture Republic of Indonesia (2017). Agricultural Statistics 2017. Center for Agricultural Data and Information System, Ministry of Agriculture Republic of Indonesia.
- Becker HC, Léon J (1988) Stability analysis in plant breeding. *Plant Breed.* 101: 1-23.
- Bose LK, Nagaraju M, Singh ON (2012). Genotype × environment interaction and stability of lowland rice genotypes. *J. Agric. Sci.* 57: 1-8.
- Dewi IS, Purwoko BS (2012). Kultur antera untuk percepatan perakitan varietas padi di Indonesia. *J. Agro-Biogen.* 8(2): 78-88.
- Devi SA, Krishnasamy V, Raveendran M, Senthil N, Manonmani S (2011). Molecular and genetic dissection of peduncle elongation in rice. *Electr. J. Plant Breed.* 2(1): 1-7.
- Dewi IS, Putri NH, Purwoko BS (2014). Dihaploid rice line production through anther culture to accelerate the development of new rice varieties. *Proceedings of 8th Asian Crop Science Association Conference.* Agricultural University Press, pp. 122-126.
- Eberhart SA, Russell WA (1966). Stability parameters for comparing varieties. *Crop Sci.* 6: 36-40.
- Finlay KW, Wilkinson GN (1963). The analysis of adaptation in a plant-breeding programme. *Aust. J. Agric. Res.* 14: 742-754.
- Ganefianti DW, Suryati D, Hasannudin (2009). Analisis stabilitas hasil

- enam genotipe cabai menggunakan metode additive main effect multiplicative interaction (AMMI). *Akta Agrosia*. 12: 147-154.
- Gauch HG (2013). A simple protocol for AMMI analysis of yield trials. *Crop Sci*. 53: 1860-1869.
- Horn L, Shimelis H, Sarsu F, Mwadzingeni L, Laing MD (2018). Genotype-by-environment interaction for grain yield among novel cowpea (*Vigna unguiculata* L.) selections derived by gamma irradiation. *The Crop J*. 6: 306-313.
- Islam MR, Anisuzzama M, Khatun H, Sharma N, Islam MZ, Akter A, Biswas PS (2014). AMMI analysis of yield performance and stability of rice genotypes across different haor areas. *Eco-friendly Agric. J*. 7(02): 20-24.
- Jambormias E, Riry J (2008). Aplikasi GGE biplot untuk evaluasi stabilitas dan adaptasi genotipa-genotipa dengan data percobaan lingkungan ganda. *J. Budidaya Pertanian* 4(2): 84-93.
- Karimizadeh R, Mohammadi M, Shefazadeh MK, Mahmoodi AA, Rostami B, Karimpour F (2012). Relationship among and repeatability of ten stability indices for grain yield of food lentil genotypes in Iran. *Turk. J. Field Crops* 17(1): 51-61.
- Lakshmi BV, Veni BK, Chamundeswari N, Ramana JV (2014). Stability analysis of grain yield and its components in rice (*Oryza sativa* L.) genotypes. *J. Rice Res*. 7(1&2): 10-15.
- Lal RK (2012). Stability for oil yield and variety recommendations using AMMI (Additive Main Effects and Multiplicative Interactions) model in Lemongrass (*Cymbopogon* Sp). *Ind. Crops Prod*. 40: 296-301.
- Lin CS, Binns MR, Lefkovitch LP(1986). Stability analysis: where do we stand? *Crop Sci*. 26: 894-900.
- Mattjik AA, Sumertajaya IM (2006). *Perancangan Percobaan dengan Aplikasi SAS dan Minitab* (Edisi Kedua.). IPB Press. Bogor, Indonesia.
- Mohammadi M, Sharifi P, Karimizadeh R (2014). Stability analysis of durum wheat genotypes by regression parameteres in dryland conditions. *ACTA Univ. Agriculturae Et Silviculturae Mendelianae Brunensis* 6: 1049-1056.
- Mut Z, Gülümser A, Sirat A(2010). Comparison of stability statistics for yield in barley (*Hordeum vulgare* L.). *Afr. J. Biotechnol*. 9: 1610-1618.
- Palanog AD, Cherry A, Tayson E, Giocon IMG, Leo T, Ines STA, Tizon BU, Bibar JEA, Seville CU, Palanog MO, Donayre DKM, Suner ACS, Libetario EM (2015). Grain yield performance and stability analysis of rice varieties under rainfed lowland conditions of Western Visayas, Philippines. *Asia Life Sci*. 24(1): 399-408.
- Purwoko, BS (2017). Pengembangan teknik kultur antera dan aplikasinya pada percepatan pemuliaan tanaman padi di Indonesia. In: Sudarsono, B.S. Purwoko (Eds.). *Landasan Teoritis dan Penerapan Genetika serta Rekayasa Lingkungan untuk Peningkatan Produksi Tanaman*. IPB Press, Pp. 135-182.
- Rasyad A, Idwar(2010). Interaksi genetik x lingkungan dan stabilitas komponen hasil berbagai genotipe kedelai di Provinsi Riau. *J. Agron. Indonesia* 38:25-2.
- Romagosa I, Fox PN (1993). Genotype x environment interaction and adaptation. in: Hayward MD, Bosemark, Romagosa I, editor. *Plant Breeding. Principle and Prospects*. London: Chapman & Hall. 373-390.
- Sitaesmi T, Nafisah, Gunarsih C, Daradjat AA (2012). Analisis stabilitas hasil gabah galur-galur padi melalui pendekatan parametrik dan nonparametrik. *J. Penelitian Pertanian Tanaman Pangan*. 31(2): 79-86.

- Sitairesmi T, Gunarsih C, Nafisah, Nugraha Y, Abdullah B, Hanarida I, Aswidinnoor H, Muliarta IGP, Daradjat AA, Suprihatno B (2016). Interaksi genotipe x lingkungan untuk hasil gabah padi sawah. *J. Penelitian Pertanian Tanaman Pangan.* 35 (2): 89-97.
- Singh S, Singh VV, Choudhary AD (2014). Genotype × environment interaction and yield atability analysis in multienvironment. *Trop. Subtrop. Agroecosys.* 17: 477-482.
- Suwarto, Nasrullah (2011). Genotype x environment interaction for iron concentration of rice in Central Java of Indonesia. *Rice Sci.* 18 (1): 75-78.