

## Yield stability and agronomical performance of inland swamp rice lines developed using molecular breeding

D W Utami<sup>1\*</sup>, I Rosdianti<sup>1,2</sup>, I Khairullah<sup>3</sup>, P Sinaga<sup>4</sup>, Subardi<sup>5</sup> and A Muarepey<sup>6</sup>

<sup>1</sup> Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD), Indonesian Agency for Agricultural Research and Development, Ministry of Agriculture, Jalan Tentara Pelajar No. 3A, Bogor 16111, West Java, Indonesia

<sup>2</sup> IPADS, Graduate School for Agriculture and Life Sciences, University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113-8657, Japan

<sup>3</sup> Indonesian Wetland Research Institute, Jalan Kebun Karet, Banjarbaru 70712, South Kalimantan, Indonesia

<sup>4</sup> Riau Assessment Institute for Agricultural Technology, Jalan Kaharuddin Nst No. 15000, Bukit Raya, Pekanbaru 28284, Riau, Indonesia

<sup>5</sup> Indonesian Soil Research Institute, Taman Bogo Experimental Station, Purbolinggo, East Lampung 34192, Lampung, Indonesia

<sup>6</sup> Faculty of Agriculture, Padjadjaran University, Jalan Raya Bandung Sumedang Km 21, Jatinangor, Sumedang 45363, West Java, Indonesia

\*E-mail: dnitawu@windowslive.com

**Abstract.** Yield stability of rice varieties in diverse locations is an important aspect in a varietal recommendation to ensure better economic benefits for farmers. Multi-location trials in different locations or seasons will identify consistently high-performing varieties. This study aimed to test the yield stability of selected promising lines previously developed by means of Marker-assisted Breeding. Field trials were conducted in three different types of swampland locations: Lampung, South Kalimantan and Riau. The experiments were carried out in a randomized complete block design with three replications. A total of 15 selected rice lines were evaluated. Seedlings were transplanted to 2 m × 5 m plots with 20 cm × 20 cm planting distance. Yield stability was estimated using various analyses that measure coefficient of variability (Cvi), coefficient of regression (bi), deviation parameter ( $\delta_2$ ), coefficient determination (Ri<sup>2</sup>) and AMMI biplot. Combined analysis of variance showed that line effect (G), environmental effect (E), and G × E interaction were statistically significant different. Using CVi25% and bi<1 threshold followed by AMMI biplot analyses, four lines (line number 1, 4, 6 and 11) were classified as having broad stability. Five lines (line number 5, 12, 13, 14 and 15) showed less yield stability but had better adaptation in tidal swamp environment. The other two lines (line number 3 and 7) showed a greater yield in the coastal swamp area, suggesting their potential as adapted lines suitable to this swampy environment.

Keywords: inland swamp rice lines, molecular breeding, yield stability.



## 1. Introduction

Indonesia has vast arable lands, especially outside of Java Island, which could play major roles in supporting food crops production. There are around 33.4 million hectares of swampy areas distributed in Sumatra, Kalimantan, Papua and Sulawesi Islands. However, only 1.3 million hectares have been reclaimed by the government and they are mostly located in Sumatra and Kalimantan. Swampy areas also have various rice production constraints, including flash flooding, stagnant flooding, acid sulfate soils, pests, diseases and weeds. Droughts also often occur in the upper portion of swamps. Swamplands are rich in acidic soils that contain a high concentration of iron that can cause iron toxicity. In Indonesia, 2.27 million ha of rice are cultivated in peatlands, tidal swampy lands, red-yellow podzolic soils, permanently flooded lowlands, poor drainage lowlands and new wetland fields, which are characterized by high iron content [1,2]. These type of lands spread throughout the Indonesian archipelago [1,2].

One of the approaches to get promising lines is testing the performance of selected lines in widely different agro-ecological conditions to evaluate their adaptability. Selected rice lines which show low variation in diverse conditions are likely to have broad adaptability. On the other hand, lines with varied responses to diverse environmental conditions may have specific adaptation to specific environments, which can be optimized to obtain maximum yield potential and yield component [3].

Genotypes tested in different locations and different years may have significant fluctuations in yield due to variations in soil fertility, unpredictable rainfall and the presence of other biotic and abiotic stresses. Differential responses of genotypes to different environmental conditions are termed as Genotype by Environment Interaction (GEI). It reduces progress in plant breeding programs since it obfuscates the association between phenotype and genotype value [4,5]. However, GEI can be exploited by selecting superior genotypes for each specific target environment, or avoided by selecting widely adapted and stable genotypes across a wide range of environments [6].

GEI can be quantified using several procedures that are based on evaluation of genotypes under multiple environments. These methods are classified into univariate and multivariate stability statistics [7]. The most widely used ones are univariate methods, which are based on regression of the mean value of each genotype on the environmental index or marginal means of environments [8,9]. Multivariate analysis is an alternative and complementary method for evaluating genotype stability. Additive Main Effects and Multiplicative Interaction (AMMI) model is also widely used for studying GEI [10].

To support national rice production and food security, extensification strategy at sub-optimal marginal land (swampland) is one of the approaches that can be attempted. Tolerance to Fe toxicity and adaptability in swampy environment is one of the keys to successful expansion to such land to increase rice production. Through molecular breeding approach, ICABIOGRAD has developed promising rice lines for swampy area. These lines were selected using molecular markers based on targeted genes which are known to contribute to Fe toxicity tolerance, such as *IRT1* (iron regulation transporter) gene that plays a role in strategy I of the Fe tolerance mechanisms [11–13], *NAS* (nicotianamine synthase) gene, which is active in long-distance transport of iron [12,14] and *FRO* (Fe<sup>3+</sup> chelate reductase) gene, which converts insoluble Fe<sup>3+</sup> to soluble Fe<sup>2+</sup> [12,15,16].

The phenotypic stability of a variety is influenced by its ability to respond to diverse environments. Thus, it is important to perform yield stability test of rice lines to select the ones which have the most stable yield in different locations. The objective of this study was to determine the stability of yield traits of promising inland swamp rice lines across three different locations and planting seasons. The output of this research is selected rice lines with wide adaptation and/or specific adaptation to swampy environment.

## 2. Materials and methods

### 2.1. Planting materials, experimental design and test locations

A total of 15 selected rice lines and two check varieties (Table 1) were evaluated from 2015 to 2017 at three locations consisting of three environments: swampy coastal land (Taman Bogo, Lampung), type

B tidal swampy land (KP Belandean, South Kalimantan) and type C tidal swampy land (KP Siak, Riau).

**Table 1.** List of genotypes used in the study.

Lines	Pedigree	Code
B14301E-KA-17-a	Kao Daok Mali-105-9/B13143-8-MR-3-KA-14//Inpara 5	B1-17a
B14308E-KA-38	Setail/Inpara 2//Code	B2-38
B14315E-KA-1	B11844-MR-29-7-1/Inpara 3//Cisantana	B3-1
B14316E-KA-4	B11844-MR-29-7-1/Inpara 5//Code	B4-4
B14339E-KA-14	IR42/Ciherang	B5-14
B14354E-KA-4	Banyuasin/Ketankutuk	B6-4
B14357E-KA-4-b	Siakraya/B13132-7-MR-1-KA-6	B7-4-b
B13925E-KA-1-a	Swarna Sub-1/Mekongga	B8-1-a
B13926E-KA-29-a	Swarna Sub-1/Ciherang	B9-29-a
B13957E-KA-50	Batanghari/Conde	B10-50
B13983E-KA-44	Inpari 9/Swarna Sub1	B11-44
B13988E-KA-40	Cimelati/Inpara 3//Inpari 9/FR13A	B12-40
IR70213-10-CPA-2-UBN-B-1-1-3	Mekongga/Inpara 3//Mekongga/Inpara 3	I13-3
B13522E-KA-5-B	Kebo/BR11 Sub-1	B14-5-B
B13545E-KA-1-B	Ciherang/Swarna Sub-1//Ciherang///Inpara 3	B-15-1-B
IR64	Sensitive Control	IR64
Mahsuri	Tolerant Control	Mhs

The locations where the trials were conducted differ in soil type, altitude, temperature and rainfall received per annum (Table 2). At each location, the trial was laid out in a randomized complete block design (RCBD) with three replications. Each plot had six rows that were 5 m long with 0.2 m spacing between rows. Fertilizer (urea and DAP) was applied as per the recommendation for each respective location. All of the DAP was applied at planting time while one-third of urea was applied at planting, one-third at tillering and the remaining one-third at panicle initiation. A seed rate of 60 kg/ha was used, and seeds were directly drilled in a row. Plantings were done in the main rainy season following the optimal dates in each respective location.

**Table 2.** Description of the experimental locations.

Location	Elevation (m asl)	Latitude	Longitude	Annual rainfall (mm)	Average temperature (°C)	Swampy type
Taman Bogo, Lampung	30	50°58'01 <sup>11</sup> S	105°30'44 <sup>11</sup> E	2,143	26.9	Coastal
KP Siak, Riau	10	100°03'1 N	104° 0' E	2,000	25.9	Tidal, type C
KP Belandean, South Kalimantan	31	4°10'14 <sup>11</sup> S	57°19'13 <sup>11</sup> E	1,796.9	27	Tidal, type B

## 2.2. Data collection and statistical analysis

Data were collected for the following traits: days to heading, days to maturity, panicle length, plant height, filled grains/panicle, fertile tillers/plant, grain yield and 1,000-seed weight. Grain yield (t/ha)

was estimated based on extrapolation at 14% moisture level on the basis of four central harvestable rows. The grain yield and other agronomic parameters were subjected to analysis of variance using the SAS version 8.1 software. The stability of grain yield data was also analyzed using several methods described by Finlay and Wilkinson [8], Eberhart and Russell [9], Francis and Kannenberg [17] as well as AMMI analysis.

### 3. Results and discussion

#### 3.1. Soil chemical compositions of the field experiments

The results of soil analysis (Table 3) showed that among the three locations, the swampland in South Kalimantan had the highest soil acidity (pH 3.8). The other areas in Lampung and Riau had lower soil acidity: pH 4.0 and 4.6, respectively. Taman Bogo swampland (Lampung) also suffered from iron toxicity. As a comparison, normal upland soil in a nearby area had pH 5.4.

**Table 3.** Soil chemical status in three locations of swampy lowland area at dry season (DS) and wet season (WS) in 2015–2017.

Description	Taman Bogo, Lampung 2015 (DS and WS)		KP Belandean, South Kalimantan 2016 (WS)	KP Siak, Riau 2017 (DS)
	Normal site	Iron toxicity site	Iron toxicity site	Iron toxicity site
pH (H <sub>2</sub> O)	5.4	4.0	3.8	4.6
C organic (%)	1.14	1.1	5.1	2.3
N total (%)	0.09	0.09	0.25	0.13
C/N	12.7	11	-	17
P <sub>2</sub> PO <sub>5</sub> Bray 1 (ppm)	10.5	6.8	12.8	12.47
K <sub>2</sub> O Morgan (ppm)	30	27.7	8.0	77.67
Exchangeable base (me/100 g)				
P	0.32	0.31	-	0.22
K	0.02	0.02	0.034	0.57
Ca	0.03	0.01	1.50	0.05
Mg	0.04	0.02	1.37	0.28
Na	0.01	0.01	0.62	0.03
Fe (ppm)	765	2,030	631	334.38
Pyrite as total Fe & S (%)	0.01	0.02	4.37	0.02
Texture (%)				
Clay	29	18	69	-
Silt	33	38	31	-
Sand	39	44	0	-

#### 3.2. Analysis of variance and agronomic performance

The variance analysis for plant height, fertile tillers/plant, days to flowering, number of filled grain and grain yield (t/ha) showed significant differences ( $P \leq 0.01$ ) attributed to the effects of genotypes and locations (Table 4). The  $G \times E$  interaction effect was also significant ( $P \leq 0.01$ ) in all characters except for plant height. Significant effect of  $G \times E$  interaction indicates that the influence of location on traits observed on each genotype in different environments is different. In particular, the number of fertile tillers per plant, days to flowering, number of filled grain and the average of grain yield (t/ha, converted from 4 m  $\times$  5 m plots) were the characters that were significantly influenced by different environments ( $P \leq 5\%$ ).

**Table 4.** ANOVA for plant height, fertile tillers/plant, days to flowering, number of filled grain, and grain yield of 15 genotypes of promising rice lines evaluated at three locations of swampland in Taman Bogo (Lampung), KP Belandean (South Kalimantan) and KP Siak (Riau) in 2015–2017.

Source	df	F value	df	F value	df	F value	df	F value	df	F value
L	2	181.44**	2	12.27**	2	224.5**	2	101.9**	2	1.021**
Rep*L	6	0.78ns	6	11.6**	6	1.39ns	6	2.41*	6	1.05ns
G	16	3.49**	16	1.65**	16	4.68**	16	1.62**	16	1.18**
G*L	32	5.68	32	1.90**	32	2.89**	32	1.93**	32	3.80**
cv		8.04%		10.42%		4.23%		13.51%		14.70%

L = location, Rep = replicate, G = genotype.

The yield performance of the tested lines varied from 4.16 (B6-4 line) to 5.7 (B12-40 line) t/ha. There are six lines with the average grain yield of more than 5 t/ha (Table 5).

**Table 5.** Combined observations of trait performance of 15 genotypes of promising rice lines evaluated at three locations of swampland in 2015–2017<sup>a</sup>.

Genotype	PH <sup>b</sup>	FT/P <sup>c</sup>	DtF <sup>d</sup>	FG <sup>e</sup>	AvrGY (t/ha) <sup>f</sup>
B1-17a	103.22a-e	13.89a	89.78bc	91.23ab	4.33ab
B2-38	97.86b-e	11.93ab	83.33cd	101.64a	4.22bc
B3-1	108.58abc	12.93ab	81.89d	85.18ab	4.64ac
B4-4	99.02a-e	15.24a	89.11bc	83.53ab	5.40abc
B5-14	88.16de	9.98b	83.11cd	99.23a	5.51abc
B6-4	97.96b-e	12.6ab	88.44bcd	85.93ab	4.16bc
B7-4-b	94.13b-e	12.42ab	88.22bcd	89.89ab	5.07abc
B8-1-a	94.42b-e	12.47ab	93.44b	105.33a	4.72ac
B9-29-a	108.27abc	14.22a	93.56b	105.06a	4.44ab
B10-50	109.52abc	14.91a	91.06b	94.88a	4.52ac
B11-44	101.9a-e	12.38ab	93.89b	83.84ab	4.59ac
B12-40	106.26a-d	11.93ab	88.67bcd	109.66a	5.7abc
I13-3	111.14ab	14.36a	94.67ab	100.32a	5.32abc
B14-5-B	108.77abc	11.6ab	95.11ab	84.02ab	4.87ac
B-15-1-B	92.26cde	13.16ab	90.89b	87.96ab	5.07abc

<sup>a</sup> Location and planting seasons (PS): Taman Bogo (Lampung) at PS II 2015 until PS I 2016, KP Belandean (South Kalimantan) at PS II 2016–2017 and KP Siak (Riau) at PS II 2016–2017.

<sup>b</sup> PH = plant height.

<sup>c</sup> FT/P = number of fertile tillers per plant.

<sup>d</sup> DtF = days to flowering.

<sup>e</sup> FG = number of filled grain.

<sup>f</sup> AvrGY = average grain yield (t/ha, converted from 4 m × 5 m plots).

### 3.3. Stability analysis of grain yield performance

Stability parameter tests from the three locations were presented in Table 6. Analyses were done based on Lin et al. [18] concept, who stated that a genotype is classified as stable if: (1) its variance between environments is small; (2) its response to the environment is proportional to the mean of all tested

genotype's responses; (3) the residual mean square from the regression model for environmental index is small. The parameters were quantified using various approaches described in the following sub-sub-sections.

**3.3.1. Finlay and Wilkinson analysis.** In this method, stability was analyzed based on the regression coefficient ( $b_i$ ) between the mean of a genotype compared to the general mean of all genotypes tested in all environments. This method can explain the stability and adaptability of each genotype. Finlay and Wilkinson [8] used the  $b_i$  values to classify stability standards into three groups: (1) if  $b_i > 1$ , stability is lower than the mean; (2) if  $b_i = 1$ , stability is the same with the mean; (3) if  $b_i < 1$ , stability is higher than the mean.

**3.3.2. Francis and Kannenberg analysis.** Stability analysis based on this method used the diversity coefficient (CVi) of each tested genotype as a standard [17]. The smaller the value of CVi coefficient, the more stable the genotype. The value of CVi can be divided into four groups: (1) low (CVi < 25%), (2) slightly low (CVi = 25–50%), (3) slightly high (CVi = 50–70%) and (4) high (CVi = 75–100%). Based on those categories, there were eight lines that had CVi < 25%, namely: B1-17-a, B2-38, B3-1, B4-4, B6-4, B7-4-b, B10-50, and B11-44.

**Table 6.** Yield stability parameters of promising swampland rice lines.

Genotype	Taman Bogo, Lampung	KP Belandean, South Kalimantan	KP Siak, Riau	Yi <sup>a</sup>	CVi <sup>b</sup>	$b_i$ <sup>c</sup>	$\delta^2$ <sup>d</sup>	Ri <sup>e</sup>
B1-17-a	3.89	3.89	5.20	4.32	17.52 (S)	0.60 (S)	0.209	0.535
B2-38	3.87	4.20	4.60	4.22	8.62 (S)	0.32 (S)	0.037 (S)	0.999 (S)
B3-1	4.81	3.71	5.40	4.64	18.52 (S)	0.31 (S)	0.033	0.150
B4-4	4.59	5.62	6.00	5.4	13.54 (S)	0.61 (S)	0.224	0.665
B5-14	3.73	6.07	6.73	5.51	28.63	1.30	0.341	0.289
B6-4	3.81	3.59	5.07	4.15	19.2 (S)	0.58 (S)	0.189	0.406
B7-4-b	4.80	5.22	5.20	5.07	4.68 (S)	0.17 (S)	0.012 (S)	0.796 (S)
B8-1-a	2.48	4.68	7.00	4.72	47.88	2.00	0.003 (S)	0.841 (S)
B9-29-a	2.91	4.09	6.33	4.44	39.17	1.53	0.097	0.722
B10-50	3.31	5.46	4.80	4.52	24.36 (S)	0.61 (S)	0.224	0.117
B11-44	3.95	4.02	5.80	4.59	22.83 (S)	0.85 (S)	0.622	0.424
B12-40	2.99	6.71	7.40	5.7	41.62	1.90	0.007	0.064
I13-3	3.65	5.44	6.87	5.32	30.31	1.42	0.190	0.704
B14-5-B	3.05	5.04	6.53	4.87	35.86	1.53	0.097	0.639
B15-1-B	3.37	5.30	6.53	5.07	31.45	1.39	0.223	0.579

<sup>a</sup> Yi = yield predicted based on Finlay-Wilkinson stability.

<sup>b</sup> CVi = genetic diversity coefficient [17].

<sup>c</sup> S = yield is stable (<25%).

<sup>d</sup>  $b_i$  = genotype regression coefficient [8], scored as S if  $b_i < 1$ .

<sup>e</sup>  $\delta^2$  = deviation parameters.

<sup>f</sup> Ri = determination coefficient, scored as S if  $\delta^2$  small and R1 approaching 1.

**3.3.3. Eberhart and Russell analysis.** In this method, the analysis was based on the deviation from regression of the average of each genotype on different environment index [9]. A genotype is stable if the residual of mean squares from their line regression is small. Stability parameters were determined

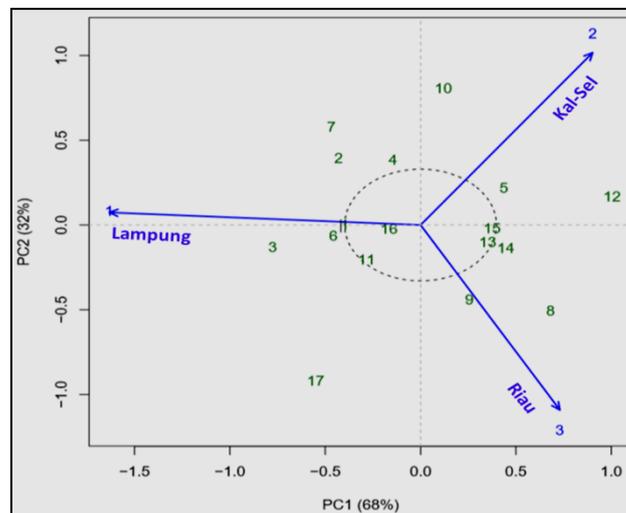
based on the value of the deviation ( $\delta_2$ ) and the coefficients determination ( $R_1$ ) of each genotype. The stability of a genotype is verified if it has small  $\delta_2$  value and high  $R_1$  value (approaching 1).

3.3.4. *Stability analysis using AMMI model.* Combined analysis of variance for grain yield (GY) showed that the effects of genotype, environments and their interaction ( $G \times E$ ) were significant (Table 7). Significant effect of  $G \times E$  interactions could be further analyzed with biplot analysis to figure out the interaction patterns between genotypes and environments using AMMI model.

**Table 7.** Combined ANOVA of grain yield in three environments.

Source	Df	Sum Sq	Mean Sq	F value	Pr (>F)
Environment	2	129.93	64.96	12.28	0.008
Rep(Env)	6	31.74561563	5.291	3.006	0.0098
Genotype	16	41.46792582	2.592	1.473	0.00126
$G \times E$	32	71.00774979	2.22	1.261	0.00194
PC1	17	48.290547	2.841	1.61	0.0076
PC2	15	22.717203	1.514	0.86	0.0061
Residuals	96	168.96	1.760		

AMMI method is a popular extension of ANOVA for studying  $G \times E$  interaction [10]. This method extracts genotype and environment main effects and uses interaction of principal components to explain patterns in  $G \times E$  or residual matrix, which provides a multiplicative model [19]. The AMMI model is a two-factor data analysis with genotype as the main factor and environments as the additive factor, while the effect of  $G \times E$  interaction are modeled as a bilinear model [20].



**Figure 1.** AMMI biplot for grain yield (kg/ha) of 15 upland rice genotypes (G) and three environments (E) using genotypic and environmental scores. 1 = Taman Bogo, Lampung (2015), 2 = KP Belandean, South Kalimantan (2016), 3 = KP Siak, Riau (2017).

**3.3.5. AMMI biplot stability.** The best way to visualize the interaction patterns between genotypes and environments is provided in the biplot analysis of  $G \times E$  [21]. This can be used to predict the possible existence of different environment which will enable the genotype to grow well [22]. Genotype and environment additive main effect against their respective first multiplicative term PC1 dan PC2 was charted in AMMI biplot (Figure 1).

The AMMI biplot in Figure 1 explained which genotypes were stable on all three environments tested or flourished in specific locations. Mattjik and Sumertajaya [20] stated that if a genotype is stable, it will be plotted close to the zero point (0.0), which means that it shows general adaptation to all environments used in the test. Genotypes plotted far from the zero point and closer to a specific location line means that it has a better adaptation to that specific location [23]. Based on those criteria, genotypes number 1, 4, 6 and 11 were indicated as the stable genotypes, while genotypes number 5, 12, 13, 14 and 15 were optimum in tidal swamp environments. Genotype number 3 and 7 were shown to be optimum in coastal swamp area.

Yield stability concepts proposed by Francis and Kannenberg [17] and Eberhart and Russel [9] are statistical analyses of yield stability, but can only indicate if one genotype is classified as a stable genotype or not. On the other hand, the concept from Finlay and Wilkinson [8] was a dynamic method that can also show the adaptability pattern of a genotype. By using AMMI method, the  $G \times E$  pattern which affects yield stability can be visualized using biplot analysis.

#### **4. Conclusions**

Yield stability of rice is important in a varietal recommendation to indicate whether the variety could be planted in a broad range of environments or not. The  $G \times E$  interaction is a key factor in yield and yield component performance.  $G \times E$  interaction is an important source of rice yield variation and its visualization in a biplot is a powerful tool for depicting the response of genotypes in different environments. Five lines (line number 5, 12, 13, 14 and 15) showed less yield stability, but optimum growth in a tidal swamp environment. Two lines (line number 3 and 7) showed optimum yield in the coastal swamp area.

#### **5. Acknowledgement**

This study was funded by the 2015–2019 Indonesian National Budget for the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD.

#### **6. Authors contribution**

DWU: main contributor, designed the experiment, analyzed and interpreted data, and wrote the manuscript. IR: analyzed the data. IK, PS and S: conducted the field experiment.

#### **7. References**

- [1] Ismunadji M 1990 Alleviating iron toxicity in lowland rice *Indones. Agric. Res. Dev. J.* **12** 67–72
- [2] Haryono 2013 Lahan rawa: lumbung pangan masa depan Indonesia *Badan Penelitian dan Pengembangan Pertanian, Kementerian Pertanian* (Jakarta: IAARD Press)
- [3] Allard R and Bradshaw A 1964 Implications of genotype-environmental interactions in applied plant breeding *Crop Sci.* **4** 503
- [4] Pan C, Ye L, Qin L, Liu X, He Y, Wang J, Chen L and Lu G 2016 CRISPR/Cas9-mediated efficient and heritable targeted mutagenesis in tomato plants in the first and later generations *Sci. Rep.* **6** 1–9
- [5] Lakew T, Dessie A, Tariku S and Abebe D 2017 Evaluation of performance and yield stability analysis based on AMMI and GGE models in introduced upland rice genotypes tested across Northwest Ethiopia *Int. J. Res. Stud. Agric. Sci.* **3** 17–24

- [6] Ceccarelli S 1996 Positive interpretation of genotype by environment interactions in relation to sustainability and biodiversity *Plant Adaptation and Crop Improvement* ed M Cooper and G Hammer (Wallingford: CAB International) pp 467–486
- [7] Sharifi P, Aminpanah H, Erfani R, Mohaddesi A and Abbasian A 2017 Evaluation of genotype  $\times$  environment interaction in rice based on AMMI model in Iran *Rice Sci.* **24** 173–80
- [8] Finlay K and Wilkinson G 1963 The analysis of adaptation in plant breeding programme *Aust. J. Agric. Res.* **4** 742–54
- [9] Eberhart S and Russell W 1966 Stability parameters for comparing varieties *Crop Sci.* **6** 36
- [10] Gauch H and Zobel R 1996 AMMI analysis of yield trials *Genotype by Environment Interaction* ed M Kang and H Gaugh-Jr (Boca Raton, FL, USA: CRC Press) pp 85–122
- [11] Bennett S, Hansman R, Sessions A, Nakamura K and Edwards K 2011 Tracing iron-fueled microbial carbon production within the hydrothermal plume at the Loihi seamount *Geochim. Cosmochim. Acta* **75** 5526–39
- [12] Utami D W and Hanarida I 2014 Evaluasi lapang dan identifikasi molekuler plasma nutfah padi terhadap keracunan Fe *J. AgroBiogen* **10** 9–17
- [13] Rout G and Sahoo S 2015 Role of iron in plant growth and metabolism *Rev. Agric. Sci.* **3** 1–24
- [14] Inoue H, Higuchi K, Takahashi M, Nakanishi H, Mori S and Nishizawa N K 2003 Three rice nicotianamine synthase genes, *OsNAS1*, *OsNAS2*, and *OsNAS3* are expressed in cells involved in long-distance transport of iron and differentially regulated by iron *Plant J.* **36** 366–81
- [15] Eide D, Broderius M, Fett J and Guerinot M 1996 Sk-interfaces: exploding borders - creating membranes in art, technology and society *Proc. Natl. Acad. Sci. U. S. A.* **93** 5624–8
- [16] Robinson N, Procter C, Connolly E and Guerinot M 1999 A ferric-chelate reductase for iron uptake from soils *Nature* **397** 694–7
- [17] Francis T and Kannenberg L 1978 Yield stability studies in short-season maize, a descriptive methods for grouping genotype *Can. J. Plant Sci.* **58** 1029–34
- [18] Lin C, Binns M and Levkovitch L 1986 Stability analysis: where do we stand *Crop Sci.* **26** 894–900
- [19] Romagosa I, Fox P, García del Moral L, Ramos J, García del Moral B, Roca de Togores F and Molina-Cano J 1993 Integration of statistical and physiological analyses of adaptation of near-isogenic barley lines *Theor. Appl. Genet.* **86** 822–6
- [20] Mattjik A and Sumertajaya I 2006 *Perancangan Percobaan dengan Aplikasi SAS dan Minitab* (Bogor: IPB Press)
- [21] Yan W, Hunt L A, Sheng Q and Szlavnic Z 2000 Cultivar evaluation and mega-environment investigation based on the GGE biplot *Crop Sci.* **40** 597–605
- [22] Yan W and Kang M S 2002 *GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists, and Agronomists* (Boca Raton, FL, USA: CRC Press)
- [23] Zali H, Sofalian O, Hasanloo T and Asghari A 2016 AMMI and GGE biplot analysis of yield stability and drought tolerance in AMMI and GGE biplot analysis of yield stability and drought tolerance in *Brassica napus* L. *Agric. Commun.* **4** 1–8