

GENOTYPE × ENVIRONMENT INTERACTION AND STABILITY ANALYSIS FOR HIGH YIELDING DOUBLED HAPLOID LINES OF LOWLAND RICE

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ABSTRACT

This study was aimed at obtaining information on the effects of G × E interaction on yield among doubled haploid lines (DH) of lowland rice and to obtain stable and high yielding lines. The experiment was conducted in 9 environments (E), namely Indramayu (2018), Subang (2018), Malang I (2018), Malang II (2019), Blitar (2019), Cianjur (2019), Lombok (2019), Bali (2019), and Madiun (2019). A randomized complete block design with 3 replications was used in each location. The genotypes evaluated were fourteen doubled haploid rice lines and two check varieties namely Ciherang and Inpari 18. The results of the combined analysis of variance indicated significant effects of genotype (G), environment (E), and genotype × environment (G × E) interactions on grain yield. G1, G4, G9, G10, G11, G12, G13, and G14 DH lines had higher genotype mean yield than the average. Among those genotypes, the DH line of G9 was classified as high yielding, stable, and widely adapted in all locations based on Francis and Kannenberg, Finlay-Wilkinson, Eberhart-Russell, Kang, and AMMI analyses.

Keywords: Advanced lines, anther culture, G × E interaction, yield stability

INTRODUCTION

The world population is predicted to increase in the future so that efforts to maintain food availability are very important. Rice (*Oryza sativa* L) has the largest production after wheat as a staple food for more than one-third of the world's population (Ajmera et al., 2017). The largest production of rice comes from Asia (Sharifi et al., 2017). In Indonesia, rice becomes the most important crop with a production of 81.4 million tons and an average yield of 5.2 tons ha⁻¹ (FAO, 2017). Ministry of Agriculture Republic of Indonesia (2018) estimated that the lowland area for rice production is ± 8.16 million hectares, however, only 4.74 million hectares can be cultivated optimally because the remaining area is categorized as a rainfed area which is prone to drought. Therefore, the development of new lowland rice varieties which is suitable for different conditions in lowland area is very important. Rice breeding programs through the use of anther culture can accelerate the effort to obtain varieties (Dewi and Purwoko, 2012). From previous research 14 doubled haploid (DH) advanced lines of lowland rice have been selected through preliminary and

advanced yield trials (Akbar et al., 2019; Akbar et al., 2021). These DH lines were obtained from anther culture of crosses between varieties with good agronomic characters and drought tolerant and rainfed rice elite lines (Akbar et al., 2018; Gunarsih et al., 2016). Those advanced DH lines need to be evaluated further in multilocation yield trials to obtain superior lowland rice variety. Indonesia has various agro-ecological environments due to the influence of water availability, soil conditions, and climate factors. This condition complicates breeding and evaluation for high-yielding and stable variety. Thus, the development of high and stable yield performance varieties under various environments becomes a challenge for breeders.

The expression of phenotype is a combination of genotype (G), environment (E), and the interaction between genotype and environment (G × E). G × E interactions may cause inconsistency of the responses of genotypes to different conditions of environments. The G × E interactions may also cause bias in the selection process. The study of G × E interactions in plants is very important as a decision tool to obtain information on yield

stability and genotype adaptability to different environmental conditions (Yan and Kang, 2003; Goksoy et al., 2019). Several $G \times E$ interaction studies on rice have been carried out by scientists, such as Bose et al. (2014) and Sharifi et al. (2017).

Statistical methods for describing $G \times E$ interactions have been developed by several researchers. The stability method is classified as univariate and multivariate stability methods. The common univariate methods, i.e., Francis and Kannenberg (1978) with the coefficient of variation (CV_i), Finlay and Wilkinson (1963) with linear regression parameter (b_i), Eberhart and Russell (1966) with linear regression (b_i) and deviation from regression (S^2_{di}), and Kang (1993) with yield stability parameter (YS_i). The YS_i is obtained from Shukla's stability variance (σ_i^2) (Shukla, 1972), which is classified as type 2 stability (Lin et al., 1986). The problem with the univariate stability method is that the model used is less able to accurately describe $G \times E$'s interaction because the response of genotypes varies in different environments (Lin et al., 1986). $G \times E$ interaction can be explained more using multivariate analysis (Crossa, 1990). One of the popular multivariate

methods used is the additive main effects and multiplicative interaction (AMMI) (Gauch, 1988). AMMI analysis is a combination of variance analysis (ANOVA) between additive parameters of genotype and environment with the principal component of $G \times E$ interactions (Zobel et al., 1988; Erdemci, 2018). This study was aimed at obtaining information on the effects of $G \times E$ interaction on yield among doubled haploid lines (DH) of lowland rice and to obtain stable and high-yielding lines.

MATERIALS AND METHODS

The genetic materials evaluated were 14 doubled haploid lines and two check varieties of lowland rice, namely Ciherang and Inpari 18 (Table 1). The DH lines derived from anther culture of F_1 namely CG-8: Inpago 8/ IR8770514-11-B-SKI-12; CG-9: Inpago 8/ IR83140-B-11-B; and CG-12: B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN/ IR83140-B-11-B. Inpago 8 is a high-yielding upland rice variety, while IR8770514-11-B-SKI-12, IR83140-B-11-B, B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN are rainfed rice elite lines. These genotypes had good agronomic and drought tolerance traits.

Table 1. List of DH lines used in multilocation yield trials

Code	Lines/Varieties*	Code	Lines/Varieties*
G1	CG-8-18-1-1	G9	CG-9-81-1-2
G2	CG-8-18-1-2	G10	CG-12-30-1-2
G3	CG-8-92-1-2	G11	CG-12-30-1-3
G4	CG-9-2-1-5	G12	CG-12-58-1-1
G5	CG-9-53-1-1	G13	CG-12-85-1-2
G6	CG-9-53-1-3	G14	CG-12-85-1-3
G7	CG-9-62-1-1	G15**	Ciherang
G8	CG-9-81-1-1	G16**	Inpari 18

*CG-8: Inpago 8 x IR8770514-11-B-SKI-12; CG-9: Inpago 8 x IR83140-B-11-B; CG-12: B1111430D-MR-1-1-PN-3-MR-2-Si-3-PN x IR83140-B-11-B; ** Check Varieties.

Experimental procedures

The study was conducted during the years 2018 and 2019 at 9 locations. They were Terisi-Indramayu (2018), Sukamandi-Subang (2018), Pakisaji-Malang (2018), Kepanjen-Malang (2019), Wlingi-Blitar (2019), Bojongpicung-Cianjur (2019), Sikur-East Lombok (2019), Singaraja-Bali (2019), and Mojarayung-Madiun (2019). Environments' main characteristics were given in Table 2. The experimental design for each location was a randomized complete block design with three replications. Each location had a plot size 4 m x 5 m. Seedlings from the nursery were planted 21 days after sowing with a plant spacing of 25 cm x 25 cm. In each location, plant maintenance was carried out according to the optimum standard practice of rice cultivation. Each location was

given fertilizer at a dose of 90 kg ha⁻¹ N, 54 kg ha⁻¹ P₂O₅, and 60 kg ha⁻¹ K₂O. Fertilizers were given in three stages: (1). The first fertilization was given one week after planting (WAP), i.e. 30 kg ha⁻¹ N, 54 kg ha⁻¹ P₂O₅, and 60 kg ha⁻¹ K₂O; (2). The second fertilization was given at four WAP (30 kg ha⁻¹ N); (3). The third fertilization was given at 7 WAP (30 kg ha⁻¹ N).

Rice grains were harvested when 80% of rice panicles in one plot turned yellow. The grains were dried to reach $\pm 14\%$ moisture content and later converted to dry grain yield per hectare (tons ha⁻¹). The data of grain yield were collected from all environments in the form of dry grain weight per hectare by the conversion of dry grain weight per plot.

Table 2. Environments used in the study and their main characteristics

Code	Environment	Year	Latitude (S)	Longitude (E)	Altitude (m)	Sum of precipitation (mm)	Mean of temperature (°C)
E1	Terisi-Indramayu	2018	6°33'20"	117°57'46"	46	483	27.4
E2	Sukamandi-Subang	2018	6°21'15"	107°38'52"	13	484	27.6
E3	Pakisaji-Malang	2018	8°05'07"	112°35'58"	377	830	23.6
E4	Kepanjen-Malang	2019	8°06'01.7"	112°35'55.1"	361	962	24.1
E5	Wlingi-Blitar	2019	8°04'32.1"	112°18'53.1"	298	967	24.2
E6	Bojongpicung-Cianjur	2019	8°04'33.4"	112°18'48.2"	465	452	21.5
E7	Sikur-East Lombok	2019	8°37'53.6"	116°25'15.7"	318	1010	26.5
E8	Singaraja-Bali	2019	8°06'32.0"	115°05'51.0"	18	305	23.5
E9	Majorayung-Madiun	2019	7°37'46.4"	111°34'33.6"	85	423	27.8

Data analysis

The grain yield data was performed to a combined analysis of variance and stability analysis using STAR IRRRI (bbi.irri.org) and PBSTAT-GE (www.pbstat.com). If $G \times E$ interaction was significant, then stability analysis was performed. Stability analysis was performed for grain yield using the stability parameters based on the coefficient of variation (CV_i) as described by Francis and Kannenberg (1978), yield stability parameter (YS_i) as described by Kang (1993), linear regression coefficients (b_i) as described by Finlay and Wilkinson (1963), regression coefficients (b_i) and mean squares of deviations from regressions (S^2_{di}) as described by Eberhart and Russell (1966). In addition, the Additive Main Effect Multiplicative Interaction (AMMI) analysis was also carried out to determine specific areas where rice genotypes would be most adapted (Gauch, 2013).

Regression coefficient (b_i) and mean squares of deviations from regression (S^2_{di}) were formulated as follow:

$$b_i = 1 + \frac{\sum_j (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})(\bar{X}_{.j} - \bar{X}_{..})}{\sum_j (\bar{X}_{.j} - \bar{X}_{..})^2}$$

$$S^2_{di} = \frac{1}{E-2} \left[\sum_i (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..}) - (b_i - 1)^2 \sum_i (\bar{X}_{.j} - \bar{X}_{..})^2 \right]$$

where X_{ij} = grain yield of genotype- i in environment- j , $\bar{X}_{i.}$ = mean yield of genotype- i , $\bar{X}_{.j}$

= mean yield of environment- j , $\bar{X}_{..}$ = grand mean, E = number of environments, genotypes with $b_i = 1.0$ had average stability.

The yield stability index (YS_i) is based on Shukla's stability variance (σ^2_i) following the formula:

$$\sigma^2_i = [1/(s - 1)(t - 1)(t - 2)] \times [t(t - 1)\sum_j (u_{ij} - \bar{u}_{i.})^2 - \sum_i \sum_j (u_{ij} - \bar{u}_{i.})^2]$$

where s is the number of environments, t is number of genotypes, u_{ij} is $X_{ij} - \bar{X}_{.j}$, X_{ij} is grain yield for the genotype- i in environment- j , $\bar{X}_{.j}$ is mean yield of environment- j , and $\bar{u}_{i.}$ is $\sum_j \mu_{ij}/s$.

The AMMI formula according to Gauch (2013) was used for $G \times E$ interaction and yield stability analyses based on the principal component analysis (PCA):

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge}$$

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 δ_{en} are the genotype and environmental PCA scores for the n^{th}

PCA axis, and ρ_{ge} is the residual.

RESULTS AND DISCUSSION

Yield performance of lowland rice lines

The combined analysis of variance on grain yield of 16 genotypes in nine environments indicated that genotype, environment, and $G \times E$ interaction effects were significant ($p < 0.01$) (Table 3). The environmental effects explained 63.98% of the total sum of squares, while $G \times E$ interaction and genotype explained 18.52% and 5.94%, respectively (Table 3). The significance of $G \times E$ interaction of tested genotypes indicated the complexity of $G \times E$ interaction, thus it was needed to be studied further using stability analysis (Farshadfar and Sutka, 2006; Bose et al., 2014). This finding of the relative proportion of $G \times E$ interaction was similar with previous studies in wheat (Karimizadeh et al., 2016; Mohammadi et al., 2012). In the present study, the doubled haploid lines mean yield across all environments ranged from 5.82 to 7.30 tons ha⁻¹ (Table 4). Eight DH lines showed genotype mean yield higher than the average, i.e., G1, G4, G9, G10, G11, G12,

G13, and G14, and significantly higher from Inpari 18 (6.26 tons ha⁻¹). It is shown in Table 4 that the G12 line had the highest yield potential (10.73 tons ha⁻¹), followed by G14 (10.13 tons ha⁻¹) among the tested DH lines.

It was shown that the genotypes had different rankings in different environments (Table 4). Environmental mean yield for all of the genotypes ranged from 4.73 to 8.72 tons ha⁻¹. The environmental mean yield of E1 (Terisi-

Indramayu 2018) was the lowest, indicating a low-yielding environment. On the other hand, the environmental mean yield of E3 (Pakisaji-Malang 2018) was the highest, implying a high-yielding environment. In addition, E4, E5, and E6 were also categorized as high-yielding environments in which the lowest genotype yield was 6 tons ha⁻¹ and the highest genotype yield was 9-10 tons ha⁻¹. Tariku et al. (2013) reported that genotypes might have different responses in different environments.

Table 3. Combined analysis of variance for grain yield in nine environments

Source of variation	d.f.	Sum of squares (SS)	Mean of squares	F-value	(%) SS proportion
Treatments	161	1308.71	8.13		
Genotypes (G)	15	86.94	5.80	2.57**	5.94
Environments (E)	8	936.24	117.03	145.69**	63.98
Replication (E)	18	14.46	0.80	1.40	0.99
G × E	120	271.08	2.26	3.94**	18.52
Error	270	154.70	0.57		
Total	431	1463.41	3.40		

* significant at the level <0.05; ** significant at the level <0.01; df= degrees of freedom

Table 4. The grain yield (tons ha⁻¹) of doubled haploid lines in nine environments

Genotypes	E1	E2	E3	E4	E5	E6	E7	E8	E9	Genotypes mean yield
G1	5.01	5.34	9.27b	9.25b	8.93b	6.67	7.28ab	6.62ab	4.90	7.03b
G2	4.72	4.53	9.00	8.59b	8.07b	8.33	6.03a	5.69b	4.92	6.65b
G3	2.58	5.32	8.47	8.27b	7.94b	6.00	4.40	4.77	4.63	5.82
G4	4.74	5.05	8.67	7.37	7.48	9.33	6.16a	6.56ab	7.02ab	6.93b
G5	5.06	4.71	6.60	8.10b	6.05	7.33	6.43a	5.37b	5.22b	6.10
G6	4.65	5.34	6.80	6.83	6.62	7.83	5.89a	5.46b	5.31b	6.08
G7	4.07	5.11	8.13	8.08b	6.43	9.67	6.12a	5.73b	6.56b	6.66b
G8	3.77	4.38	8.40	8.29b	8.34b	9.67	6.21a	6.94ab	4.02	6.67b
G9	4.87	5.22	8.87	7.90b	8.63b	9.50	6.29a	6.81ab	6.64b	7.19b
G10	4.83	5.46	9.60	9.95b	9.15b	8.83	6.40a	6.83ab	3.89	7.21b
G11	6.10ab	5.29	7.60	8.79b	8.23b	8.83	6.11a	5.91ab	8.09b	7.22b
G12	6.32ab	4.82	10.73ab	7.66b	8.32b	7.17	5.88	5.89ab	5.97b	6.97b
G13	4.85	4.39	9.57b	8.57b	8.91b	7.50	5.25	6.83ab	6.97ab	6.98b
G14	3.96	4.24	10.13b	8.51b	8.33b	8.17	6.21a	7.36ab	6.19b	7.01b
Ciherang	4.63	5.15	9.67b	10.04b	8.89b	10.33b	5.34	5.71b	5.96b	7.30b
Inpari 18	5.47a	5.61	8.00	6.67	7.04	7.83	6.14a	5.19	4.38	6.26
Environmental mean yield	4.73	5.00	8.72	8.30	7.96	8.31	6.01	6.10	5.67	6.76
LSD (0.05)	0.58	0.88	0.97	0.86	0.53	2.43	0.50	0.10	0.82	0.34
CV (%)	8.92	12.73	7.99	7.47	4.85	21.09	5.96	1.16	10.42	11.20

E1: Terisi-Indramayu 2018, E2: Sukamandi-Subang 2018, E3: Pakisaji-Malang 2018, E4: Kepanjen-Malang 2019, E5: Wlingi-Blitar 2019, E6: Bojongpicung-Cianjur 2019, E7: Sikur-East Lombok 2019, E8: Singaraja-Bali 2019, E9: Mojorayung-Madiun 2019. Numbers within the same column followed by letter "a" indicate yield significantly higher than Ciherang, while the one followed by letter "b" indicate yield significantly higher than Inpari 18 according to LSD test at α 5%.

Yield stability and adaptability of lowland rice lines

In this study, stability methods for elucidating G × E interaction effects were categorized as type 2 and type 3 concepts of stability according to Lin et al. (1986). In Francis and Kannenberg (1978), a genotype was classified as high-yielding and stable if its yield was higher than average and CV_i was less than average. According to this, five genotypes were identified as stable, namely G1, G4, G9, G11, and G12 (Table 5).

In Finlay and Wilkinson model, b_i -values ranged from 0.59 to 1.47 (Table 5). The variation of b_i -value indicated that genotypes had different responses due to the environmental changes (Sayar et al., 2013; Goksoy et al., 2019). According to Finlay and Wilkinson's model, five DH lines with b_i -values not significantly different from 1, i.e., G1, G7, G9, G12, and G13, showed as stable genotypes with wide adaptability to all environments (Table 5). There were six genotypes, i.e., G2, G3, G8, G10, G14, and Ciherang ($b_i > 1$), classified as genotypes

suitable for optimal environments. Meanwhile, G4, G5, G6, G11 lines ($b_i < 1$) were categorized as suitable for sub-optimal environments conditions.

In the Eberhart and Russell's model, high-yielding and stable genotypes were determined by high mean yield

across all environments, regression coefficient approximating unity 1.0 ($b_i = 1$), and the sum of squares of regression deviation was close to zero ($S^2_{di} = 0$). According to this model, there was only G9 identified as stable (Table 5). This line had yield above environmental mean yield and can be adapted to all environments.

Table 5. Mean grain yield and estimates of stability parameters for yield of doubled haploid lines in nine environments

Genotypes	Yi (ton ha ⁻¹)	CVi (Francis and Kannenberg, 1978)	b _i (Finlay and Wilkinson, 1963)	S ² _{di} (Eberhart and Russell, 1966)	YSi (Kang, 1993)
G1	7.03	25.36	0.98ns	0.79**	5+
G2	6.65	27.43	1.16*	-0.11ns	4+
G3	5.82	34.79	1.14*	0.85**	-10
G4	6.93	21.87	0.87*	0.33**	1
G5	6.10	18.54	0.60**	0.27*	-7
G6	6.08	16.48	0.59**	-0.02ns	-8
G7	6.66	25.78	0.95ns	0.64**	-3
G8	6.67	32.85	1.31**	0.51**	-2
G9	7.19	22.66	0.99ns	0.08ns	15+
G10	7.21	31.07	1.34**	0.53**	8+
G11	7.22	18.93	0.68**	0.64**	9+
G12	6.97	25.29	0.93ns	0.97**	2+
G13	6.98	26.54	1.07ns	0.52**	3+
G14	7.01	29.17	1.24**	0.32*	4+
Ciherang	7.30	32.38	1.47**	0.18ns	10+
Inpari 18	6.26	19.58	0.67**	0.28*	-6
Average	6.76	25.55			

Yi: Yield mean over all environments; CVi: coefficient of variance, b_i : coefficient of regression; S^2_{di} : sum of squares deviation from regression; ns= non-significant. *significantly different from 1 at $p < 0.05$, **significantly different from 1 at $p < 0.01$; YSi: Kang's yield and stability index. '+': selected genotypes having YSi > mean of 3.44

Kang's yield-stability index (YS_i) is a combined measure of yield and stability of a genotype (Kang, 1993). This method helped to identify high-yielding and stable genotypes. Selection of genotypes should not only be based on a single stability parameter (Mohammadi and Amri, 2008) but rather consider both mean yield and stability in a single index (Kang, 1993; Farshadfar, 2008; Babarmanzoor et al., 2009). According to Kang's stability method, eight lines, namely G1, G2, G9, G10, G11, G12, G13, and G14, were categorized as stable and high-yielding genotypes (Table 5). An ideal genotype is defined as one that achieves the highest yielding across test environments and is stable in performance (Yan and Kang, 2003).

Conventional statistical methods are unable to sufficiently explain $G \times E$ interaction from multi environments yield trials. For better understanding, a multivariate method such as AMMI may be used for elucidating $G \times E$. AMMI analysis combines ANOVA

and PCA into a single model to make a simple visual interpretation of the $G \times E$ interaction (Ilker et al., 2011). AMMI model consists of the first two (or more) IPCA axes. The understanding of $G \times E$ interaction is very important to determine an optimum breeding strategy for releasing genotypes in specific environments (Fox et al., 1997).

The result of the AMMI analysis of variance showed that the first three principal components were significant and contributed to 73.71% of the $G \times E$ interaction variance (Table 6). The first principal component (IPC 1) contributed 34.09% of the variation due to the interaction, while IPC 2 and IPC 3 contributed 21.15% and 18.47%, respectively (Table 6). The stability of the tested genotypes can be evaluated using a biplot (Figure 1). Biplot of the interaction between PC1 and PC2 could indicate which lines were stable across all locations or adapted to a specific location. The closer a genotype is to the center point, the higher the level of stability.

Table 6. AMMI analysis of variance for grain yield

Source of variance	df	SS	MS	F-value	% variance explained
Genotype (G)	15	86.94	5.80	2.57**	
Environment (E)	8	936.24	117.03	145.69**	
Replications (E)	18	14.46	0.80	1.40	
G × E	120	271.08	2.26	3.94**	
IPC1	22	92.42	4.20	7.33**	34.09
IPC2	20	57.32	2.87	5.00**	21.15
IPC3	18	50.07	2.78	4.85**	18.47
IPC4	16	27.36	1.71	2.98**	10.09
IPC5	14	19.54	1.40	2.44**	7.21
IPC6	12	13.98	1.16	2.03**	5.16
Error	270	154.70	0.57		
Total	431	1463.41	3.40		

E: Environment; IPC= interaction principal component analysis; **= significant in a α level of < 0.01; *= significant in a α level of < 0.05; df= degrees of freedom; SS= Sum of squares; MS= Mean squares

Figure 1 showed that G2 and G9 were located around the center point (0,0) of the biplot. This indicated that these two genotypes can be classified as stable and widely adapted to different environmental conditions. Genotypes that were far from the center point of coordinate indicated

that they have relatively better adaptability at locations adjacent to. The relationship between genotype and environment where the genotypes had specific adaptation has been shown between G10 to E4 and G11 to E9 (Figure 1).

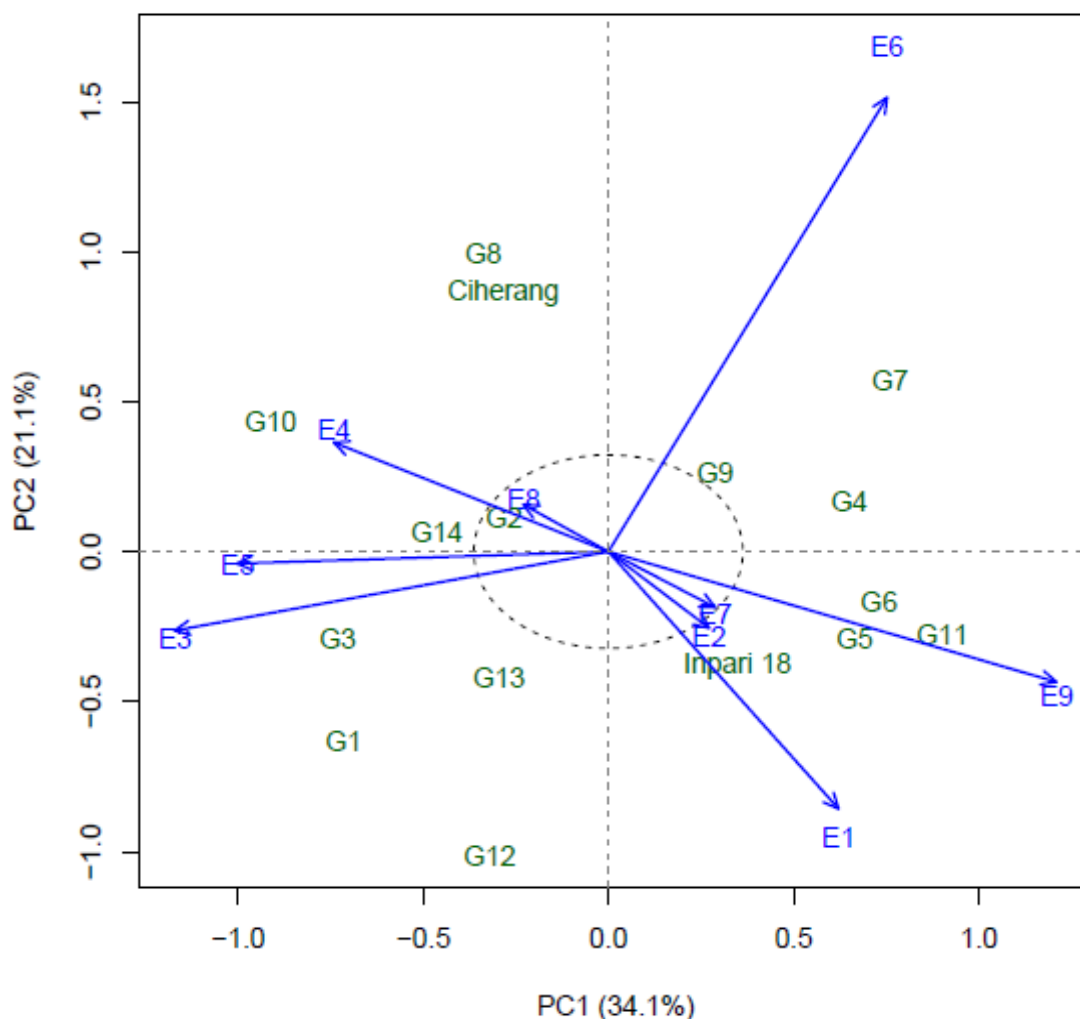


Figure 1. AMMI-2 biplot where abscissa is PC1 and ordinate is PC2 showing interaction between specific doubled haploid lines and environment. E1: Terisi-Indramayu 2018, E2: Sukamandi-Subang 2018, E3: Pakisaji-Malang 2018, E4: Kepanjen-Malang 2019, E5: Wlingi-Blitar 2019, E6: Bojongpicung-Cianjur 2019, E7: Sikur-East Lombok 2019, E8: Singaraja-Bali 2019, E9: Mojorayung-Madiun 2019

Stability analysis of DH lines using five stability analyses is presented in Table 7. According to stability analysis, some genotypes were indicated as stable: five genotypes based on Francis and Kannenberg, five genotypes based on Finlay-Wilkinson, one genotype based on Eberhart-Russell, nine genotypes based on Kang, and two genotypes based on AMMI. We obtained that G9 was classified as stable according to all stability analyses. This DH line had a higher mean yield over environments (7.19 tons ha⁻¹) than the average (6.76 tons ha⁻¹) and was

classified as stable and widely adapted genotypes. In addition, there were some potential DH lines, i.e., G1 and G12 which had high yields and were classified as stable according to Francis and Kannenberg, Finlay-Wilkinson, and Kang. On the other hand, another DH line namely G10 had narrow adaptability. This line only showed optimum performance in a specific area (Malang) for two years, and therefore may be cultivated in such environments.

Table 7. Genotype stability of DH lines across 9 environments

Genotype	Yi (ton ha ⁻¹)	Francis and Kannenberg	Finlay-Wilkinson	Eberhart-Russell	Kang	AMMI
G1	7.03	Stable	Stable	-	Stable	-
G2	6.65	-	-	-	Stable	Stable
G3	5.82	-	-	-	-	-
G4	6.93	Stable	-	-	-	-
G5	6.10	-	-	-	-	-
G6	6.08	-	-	-	-	-
G7	6.66	-	Stable	-	-	-
G8	6.67	-	-	-	-	-
G9	7.19	Stable	Stable	Stable	Stable	Stable
G10	7.21	-	-	-	Stable	-
G11	7.22	Stable	-	-	Stable	-
G12	6.97	Stable	Stable	-	Stable	-
G13	6.98	-	Stable	-	Stable	-
G14	7.01	-	-	-	Stable	-
Ciherang	7.30	-	-	-	Stable	-
Inpari 18	6.26	-	-	-	-	-

Yi= Yield mean over all environments; - = unstable

CONCLUSIONS

Significant G × E interaction effects indicated that the genotypes had different responses across test environments and changed in rankings of grain yield of DH lines from location to location. G1, G4, G9, G10, G11, G12, G13, and G14 DH lines had higher genotype mean yield than the average. Among those high-yielding DH lines, G9 (7.19 tons ha⁻¹) was classified as stable DH lines and widely adapted in all locations according to Francis and Kannenberg, Finlay-Wilkinson, Eberhart-Russell, Kang, and AMMI stability analysis. G1 and G12 were categorized as stable genotypes according to Francis and Kannenberg, Finlay-Wilkinson, and Kang.

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