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YIELD PERFORMANCE AND ADAPTATION OF PROMISING AMPHIBIOUS RED RICE LINES ON SIX GROWING ENVIRONMENTS IN LOMBOK, INDONESIA

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ABSTRACT

The objectives of this study were to examine yield performance of promising amphibious red rice lines, and to evaluate their adaptability to six growing environments in Lombok, Indonesia. Ten promising amphibious red rice lines were tested together with their three parents and one national cultivar (Aek Sibundong), during the rainy extended to dry season 2014 (January-June 2014). The ten promising lines were obtained from two population sources, while the three parents were AKBC52, AKBC86, and a local cultivar, i.e. Kala Isi Tolo (KIT). The testing environments were lowland in Mambalan village (West Lombok), medium highland in Mantang village (Central Lombok), and highland in East Sembalun village (East Lombok), and each location consisted of two systems, i.e. flooded and dry (upland) systems. The experiment in each environment was designed according to Randomized Complete Block Design, with three replications and 14 genotypes as the treatments. Adaptation analysis was based on ANOVA using AMMI and Biplot. The results indicated that among the 14 genotypes, G10(F2BC4A52-42) showed the highest yield, with an average of 7.8 t ha⁻¹ dry seeds. There was a significant Genotype x Environment interaction on the dry seed yield. Biplot analysis indicated that G2(F2BC4A52-44) and G8(F2BC4A52-37) were stable genotypes across locations.

Keywords: adaptation; amphibious; G x E interaction; red rice; yield performance

INTRODUCTION

In Indonesia, rice (*Oryza sativa* L.) is the most important food crop, because most Indonesian people use husked rice seeds as the

daily staple food source. In terms of the color, white rice is the most common in the market. However, there are also brown, red and black rice in the community in certain regions including Lombok Island. The red color in the red rice seed is due to the presence of anthocyanins in the seeds (Abdel-Aal *et al.*, 2006), which are members of phenolic compounds (Fasahat *et al.*, 2012). In Malaysia, among the colored rice examined, i.e. Thailand red rice (red), G37 (red), G33 (red), and MR219 (brown), the total phenolic contents were Thailand red rice > G37 > G33 > MR219, which content ranged from an average of 0.32 to 1.58 mg GAE/g, and they all showed antioxidant properties (Fasahat *et al.*, 2012). Anggraini *et al.* (2015) also reported that among some red, black and white rice cultivar from West Sumatra, Indonesia, the red rice cultivar from South Solok was the best, with antioxidant activity of 54.2% at concentration 0.25 mg/ml. Thus, since they have antioxidant properties, red rice products would be good for human health.

In Indonesia, the improvement of red rice has not received adequate attention yet from the Government, as indicated by the fact that from approximately 233 rice varieties released by the Ministry of Agriculture, there has been only one cultivar of red rice released as a flooded (or paddy) rice, i.e. Aek Sibundong, and one red rice cultivar released as upland (dry) rice, i.e. Inpago Unram 1. Nevertheless, the opportunities to form amphibious red rice cultivars, which perform well both under irrigated and upland (dry) environments, have been initiated by Muliarta and Permatasari (2012) by utilizing local red rice germplasms from West Nusa Tenggara (NTB) Province. The development of a number of promising amphibious red rice lines was started by crossing "Kenya" cultivar with "Angka" cultivar. Kenya is a local white rice

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cultivar (drought tolerant) from Japonica sub-species, whereas Angka is a local irrigated (paddy) red rice cultivar from Indica sub-species. The selected lines from the F1 generation obtained from those crossings were then back-crossed four times with "Kala Isi Tolo" (KIT), a local red rice cultivar used as the donor parent. After selfing and selections for yield potential and drought tolerance, 10 promising amphibious red rice lines were obtained (Muliarta and Permatasari, 2012).

Since these promising lines were developed from many donor parents consisting of cultivars having good traits, such as high yield and/or drought tolerance, then ideally it may be expected that they show those potentials in varied locations where they were cultivated. This means that their yield potential might be stable across diverse growing environments, and this also means that they might be highly adaptive across environments. According to Akter *et al.* (2014), in countries of increasing population consuming rice, high yielding stable cultivars with high adaptation capabilities to diverse environments need to be developed. Or otherwise, as stated by Anputhas *et al.* (2011), it is required to find out "which won where", by conducting multi-location trials in different locations or seasons.

Subandi *et al.* (1979) asserted that in the development of high-yielding varieties, breeders need to consider yield stability systematically and continuously, from the formation of the base population until finishing the variety tests. In this case, seed yields are important criteria in evaluating the adaptability and yield stability of a genotype. Measurement of the relative stability of a genotype in a wide range of regions is important to determine the efficiency of breeding process. Plant genotype with a broad adaptability has a stable yield (Tollenaar and Lee, 2002; De Vita *et al.*, 2010), which indicates that the genotype has a high adaptability to different conditions of growing environment (Tollenaar and Lee, 2002). A genotype that has adaptability with the same productivity in a variety of growing environments shows a static stability, whereas adaptability that follows environmental index shows a dynamic stability (Tollenaar and Lee, 2002; Mohammadi *et al.*, 2010).

Testing variety candidates on various environments needs to be done because in Indonesia, rice growing environments are highly

variable either in types of land use, types of soil, techniques of cultivation, cropping patterns, or growing seasons. The variability of growing environments will affect yield per unit area. With the phenomenon of genotype by environment interactions due to the different responses of the genotypes tested in every environment, yield of a genotype is often inconsistent from one environment to another. It is then difficult for breeders in selecting the best genotypes. The magnitude of the genotype by environment interactions needs to be considered to avoid loss of superior genotypes. Stable genotypes with high yields are needed by farmers having small plots of land to reduce the risk of crop failure due to changes in environmental factors that cannot be predicted (Mut *et al.*, 2010; Akter *et al.*, 2014).

Information on adaptability, yield potentials and stability of candidates of rice varieties is one of the requirements to release a variety, as well as in making variety recommendation to achieve better economic benefits for farmers (Anputhas *et al.*, 2011). Adaptability and yield stability of a plant genotype can be determined through multi-location trials (Tollenaar and Lee, 2002; Anputhas *et al.*, 2011; Akter *et al.*, 2014). The objectives of this study were to examine yield performance of promising amphibious red rice lines grown on 6 different growing environments either in upland or irrigated rice systems, and to determine the adaptability and yield stability of the lines on the island of Lombok.

MATERIALS AND METHODS

The experiments were conducted on six different growing environments, which are located in three sites, i.e. on lowland areas of 10 m above sea level (asl) in Mambalan village West Lombok (L1), on medium highland areas (550 m asl) in Mantang village Central Lombok (L2), and on upper highland areas (1200 m asl) in Sembalun village East Lombok (L3). In each site, there were two types of environment for the systems of growing the red rice lines and cultivars, i.e. irrigated (flooded) and dry (or upland) systems, which were practiced from the mid rainy season of 2013/2014 (planting in January 2014) to the dry season I of 2014 (the crops were harvested in June 2014). Therefore, there were 6 combinations of different growing

environments to test the 10 promising amphibious red rice lines together with their three parents, and a national red rice cultivar (Aek Sibundong).

In each testing environment, the experiment was designed using Randomized Complete Block Design (RCBD) with 14 treatments of red rice genotypes, each with three replications. The 14 genotypes tested consisted of five promising amphibious red rice lines, i.e. F2BC4A86-1, F2BC4A86-3, F2BC4A86-32, F2BC4A86-36, F2BC4A86-GS1, derived from back-crossing S-F2BC4AKBC52-16-22-18 with "Kala Isi Tolo" (KIT); five promising amphibious red rice lines, i.e. F2BC4-A52-12, F2BC4A52-44, F2BC4A52-36, F2BC4-A52-37, F2BC4A52-42, derived from back-crossing SF2BC4AKBC86 - 47-43-23 with KIT; the three parents (AKBC52, AKBC86, and KIT), and one national red rice cultivar (Aek Sibundong).

Each treatment genotype was grown with plant spacing of 25 cm x 25 cm, on a plot of 4 m x 5 m, built on a piece of land after tilling of twice plowing and harrowing. In the irrigated growing environments, the rice plants were grown from transplanting seedlings of three weeks old (one seedling per hill), and flooded irrigated using the technical irrigation water. In the upland environments, seeds of the genotypes were direct-dibbled in January 2014, 3-5 seeds per hill, but then tinned to maintain one young plant per hill, and irrigation was based on the rain during the mid to end of the rainy season 2013/2014, but during the dry season 2014, additional irrigation was done using technical irrigation water as necessary. For the upland rice system in Mambalan (L4), the additional irrigation was done at 50 days after seeding (DAS), soon after the 2nd N fertilization, 70 DAS (flowering) and 80 (seed-filling); for the location in Mantang (L5), the additional irrigation was done at 50 DAS (after the 2nd N fertilization), 80 DAS (flowering), and 90 DAS (seed-filling), while for the location in Sembalun (L6), the additional irrigation was

done at 50 DAS (after the 2nd N fertilization), 90 DAS (flowering), and 105 DAS (seed-filling).

The crops were fertilized with Phonska (15-15-15) fertilizer 7 days after seeding or transplanting at a dose of 300 kg ha⁻¹, followed with Urea fertilizer (46% N) 30 and 50 days after seeding or transplanting at a dose 100 kg/ha each. The crops were harvested after they reached physiological maturity by harvesting one sample quadrat of 1 m x 1 m per plot. After drying the seeds to reach water content of 14%, the dry seeds were weighed for each plot, and then converted into kg ha⁻¹ dry seed yield.

The data, i.e. dry seed yield, were analyzed using analysis of variance (ANOVA), followed by Additive Main Effect and Multiplicative Interactions (AMMI) analysis for the interaction between genotypes and environments, and to select an adaptive and stable genotype, Biplot analysis was done on dry seed yield data, as described by other researchers previously (Yan *et al.*, 2006; Akter *et al.*, 2014; Bose *et al.*, 2014).

RESULTS AND DISCUSSION

The results of the combined analysis of variance for dry seed yield per hectare shows that the influence of genotype (G), environment (E) and genotype x environment (GxE) interactions were significant. The contribution of environmental factors, genotypes and genotype x environment interactions to the diversity of dry seed yield was 59.54%, 5.34% and 13.72%, respectively (Table 1). This means that the ratings of superiority of the genotypes tested will not be the same in all growing environments. This is due to the different response of the genotype on one or more variables of the physical environment (Akter *et al.*, 2014). Sujiprihati *et al.*, (2006) also indicates that level of crop yield potential is highly dependent on the conditions of the environment where the genotypes were grown, as well as the types of the genotypes cultivated.

Table 1. Combined analysis of variance for the effects of genotypes, environments and genotype x environment interactions for dry seed yield of the promising amphibious red rice lines (kg ha⁻¹)

Sources of variation	Df	SS	MS	F-calc	Contribution to the variance (%)
Environments (E)	5	380.00	76.00	62.4035*	59.54
Replication (Environments)	12	14.61	1.22		
Genotype (G)	13	34.08	2.62	1.9453*	5.34
G x E interactions	65	87.60	1.35	1.7249*	13.72
Combined Error	156	121.89	0.78		
Total	251	638.19	2.54		
CV (%)			10.95		

Remarks: *) significant (p-value < 0.05)

Table 2. Averages of dry seed yield (t ha⁻¹) of the 14 genotypes of red rice grown in six different growing environments or locations

Genotypes	Environments or locations **)						Average
	Irrigated (or "paddy") system			Upland (or dry) system			
	L1	L2	L3	L4	L5	L6	
G1 (F2BC4A52-12)	6.5 ab(A) *)	6.0 a(A) *)	3.9 b(BC) *)	5.5 ab(AB) *)	5.1 ab(AB) *)	2.6 ab(C) *)	4.9 abc *)
G2 (F2BC4A52-44)	7.2 ab(A)	5.6 a(BC)	3.8 b(BC)	6.3 ab(AB)	5.3 ab(BC)	2.8 a(CD)	5.2 abc
G3 (F2BC4A86-1)	6.8 ab(A)	4.7 a(B)	4.1 b(B)	6.6 a(A)	6.4 a(A)	3.1 a(B)	5.3 ab
G4 (F2BC4A86-3)	6.9 ab(A)	6.0 a(AB)	5.1 ab(BC)	6.5 ab(AB)	5.4 ab(B)	4.0 a(BC)	5.6 a
G5 (F2BC4A86-32)	7.4 ab(A)	4.8 a(BC)	4.6 ab(BC)	6.4 ab(AB)	6.2 a(AB)	3.4 a(CD)	5.5 ab
G6 (F2BC4A86-36)	5.8 bc(A)	4.8 a(AB)	4.8 ab(AB)	5.5 ab(AB)	5.1 ab(AB)	3.8 a(BC)	4.8 abc
G7 (F2BC4A52-36)	7.1 ab(A)	5.8 a(BC)	4.2 b(BC)	5.0 b(BC)	4.3 b(BC)	3.1 a(CD)	4.9 bc
G8 (F2BC4A52-37)	6.5 ab(A)	4.9 a(BC)	3.0 bc(CD)	5.3 ab(AB)	5.1 ab(AB)	2.0 b(D)	4.5 c
G9 (F2BC4A86-GS1)	7.3 ab(A)	5.2 a(BC)	3.9 b(CD)	6.7 ab(AB)	6.5 a(AB)	3.7 a(CD)	5.5 ab
G10 (F2BC4A52-42)	7.8 a(A)	4.7 a(CD)	4.4 b(CD)	5.3 ab(BC)	5.2 ab(BC)	3.5 a(CD)	5.1 abc
G11 (AKBC52)	7.3 ab(A)	4.8 a(BC)	2.3 c(DE)	6.0 ab(AB)	5.0 ab(BC)	1.3 b(DE)	4.4 c
G12 (AKBC86)	6.6 ab(A)	4.6 a(BC)	4.3 b(BC)	6.6 a(A)	6.5 a(AB)	2.3 b(CD)	5.1 abc
G13 (Kala Isi Tolo)	6.3 b(A)	5.3 a(AB)	6.0 a(AB)	5.4 ab(AB)	5.1 ab(AB)	4.2 a(BC)	5.4 ab
G14 (Aek Sibundong)	7.0 ab(A)	4.6 a(BC)	3.1 bc(CD)	5.5 ab(B)	5.5 ab(B)	2.3 b(DE)	4.7 bc
Average	6.8 A	5.1 C	4.1 D	5.9 B	5.5 BC	3.0 E	5.1

Remarks: *) Means in each column followed by the same lowercase letters, or in each row followed by the same uppercase letters, are not significantly different based on HSD test at 1% level of significance **) Growing environments or locations: L1 = irrigated system on lowland, L2 = irrigated system on medium highland, L3 = irrigated system on highland, L4 = upland (or dry) system on lowland, L5 = upland system on medium highland, and L6 = upland system on highland areas

Based on the average dry seed yield of each genotype in each environment (Table 2), it can be seen that in the irrigated system on the lowland environment (L1), the genotype G10 (F2BC4A52-42) shows the highest dry seed yield, with an average of 7.8 t ha⁻¹. Dry seed yield of this genotype in this environment was higher than those achieved by the three parents, i.e. G11 (AKBC52), G12 (AKBC86), G13 (Kala Isi Tolo), and the national red rice cultivar, i.e. G14 (Aek Sibundong), with an average dry seed yield of 7.3, 6.6, 6.3, and 7.0 t ha⁻¹, respectively. Unfortunately, dry seed yields of the promising line G10 (F2BC4A52-42) were different between growing environments, especially between

irrigated system on the lowland (L1) and other environments. However, one of the parents, i.e. G13 (Kala Isi Tolo), showed non-significantly different dry seed yields between almost all environments (L1 to L5), except in L6 (upland system on the upper highland area) (Table 2).

Due to the significant interaction between genotype and environment (G x E interaction), it was possible to do AMMI analysis and plotting the patterns of the G x E interactions using Biplot. Through the AMMI analysis, yield stability of the genotypes can be seen on the Biplot (Anputhas *et al.*, 2011; Akter *et al.*, 2014). Based on the results of AMMI analysis, it can be seen that the genotype x environment interaction effects produced 4

components of IPCA (Inter-action Principle Component Analysis), i.e. IPCA1, IPCA2, IPCA3 and IPCA4, which in general show significant different. Contributions to the variances of the interactions that can be explained by those four IPCA components are 56.6%, 26.7%, 11.1% and

3.7%, respectively (Table 3). Based on the values of the contribution, it appears that IPCA1 and IPCA2 resulted from the analysis of interaction between the main components are able to explain the G x E interaction for dry seed yields up to 83.3%.

Table 3. Analysis of variance with AMMI model for dry seed yield of the promising amphibious red rice lines

Source of variation	df	SS	MS	Fcalc	Contribution to G x E (%)
Environment (E)	5	380.00	76.00	62.4035 *	
Replication (Environment)	12	14.61	1.22		
Genotype (G)	13	34.08	2.62	1.9453 *	
G x E interactions	65	87.60	1.35	1.7249 *	
IPCA 1	17	49.60	2.92	3.6851 *	56.6
IPCA2	15	23.39	1.56	3.5208 *	26.7
IPCA3	13	9.71	0.75	3.0475 *	11.1
IPCA4	11	3.26	0.30	1.6234 *	3.7
Combined Error	156	121.89	0.78		
Total	251	638.19	2.54		
CV (%)			10.95		

Remarks: *) = significant (p-value < 0.05)

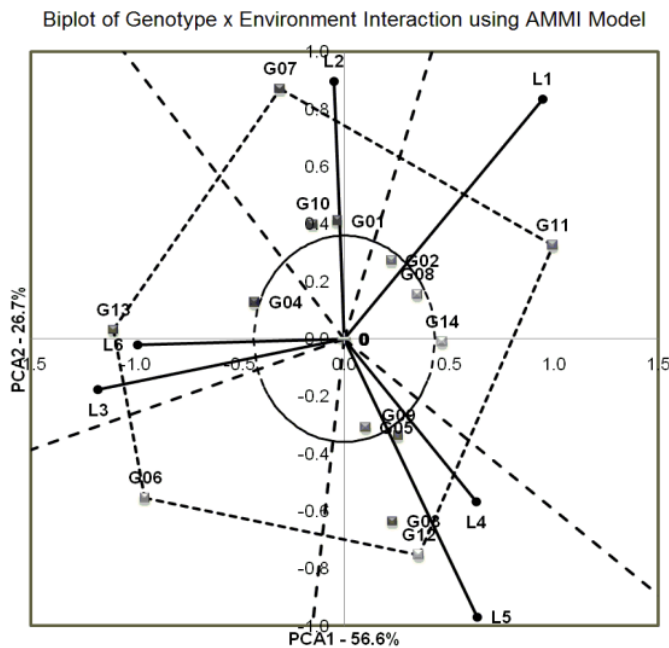


Figure 1. Biplot of AMMI-2 for the average data of dry seed yields

To categorize the genotypes into stable or environment specific, it is visualized in the AMMI-2 biplot, i.e. biplot between IPCA1 and IPCA2 scores against the averages of dry seed yield. From the AMMI-2 biplot (Figure 1), it can be seen that there are three stable genotypes, and are widely adapted to the six growing environments. Those genotypes are G2 (F2BC4A52-44), G8 (F2BC4A52-37), and G9 (F2BC4A86-GS1), with an average dry seed yield across the six locations is 5.2, 4.5, and 5.5 t ha⁻¹, respectively. This is consistent with the statement of Gauch (1992) that a genotype that grows well across diverse testing environments and shows IPCA values approaching zero, gives an indication that the genotype is stable. Bose *et al.* (2014) also categorized these types of genotypes as stable, while Akter *et al.* (2014) categorized these types of genotypes as non-sensitive to environmental interactive forces. However, if IPCA value of a genotype is very far from the zero point, it indicates that the genotype has a specific adaptability.

However, not all stable genotypes showed their dry seed yield above its average across locations. Based on Table 2 and Figure 1, it can be seen that stable genotypes having dry seed yield over its average values are G2 (F2BC4A52-44) and G9 (F2BC4A86-GS1), with an average dry seed yield across locations is 5.2 and 5.5 t ha⁻¹, respectively (Table 2). The stable genotypes will give equally good yields across growing environments both as paddy (irrigated) and upland (dry) rice, either on lowland, medium highland or upper highland areas. Therefore, these genotypes may be recommended for use as breeding materials to develop high-yielding varieties of red rice under upland and/or irrigated conditions (amphibious varieties).

The closeness of a genotype point to the environment line shows the closeness of the relationship between the genotype to the environment. It means that the environment highly supports the genotypes for dry seed yield. In other words the genotype is environment or location specific in nature, or it is not a stable genotype (Ganefianti *et al.*, 2009).

Based on this view, as can be seen from Figure 1, the genotype G11 (AKBC52) is categorized as having specific adaptation to only one environment, i.e. paddy system on lowland (L1) with dry seed yield above its average. The genotypes G1 (F2BC4A52-12), G7 (F2BC4A52-36),

and G10 (F2BC4A52-42) are specifically adapted to medium highland environment under irrigated (paddy) system (L2). In the location L2, the genotypes G1 (F2BC4A52-12) and G7 (F2BC4A52-36) yielded above its average, with dry seed yield of 6.0 and 5.8 t ha⁻¹, respectively. The promising lines G5 (F2BC4A86-32) and G8 (F2BC4A52-37) as well as the parent G12 (AKBC86) are genotypes having location specific for cultivation on medium highland as upland rice (L5). The promising lines G5 (F2BC4A86-32) and G12 (AKBC86) also yielded above its average with a dry seed yield of 6.2 and 6.5 t ha⁻¹, respectively. The promising red rice lines G4 (F2BC4A86-3) with a dry seed yield of 4.0 t ha⁻¹ as well as the parent G13 (Kala Isi Tolo) with a dry seed yield of 4.2 t ha⁻¹, which yielded above its average, are categorized as specific genotypes for cultivation on highland areas as upland rice (L6).

The genotypes adapted to two environments are G14 (Aek Sibundong), which is specially adapted to both lowland areas as irrigated rice (L1) and lowland areas as upland rice (L4), while G6 (F2BC4A86-36), a promising line that is specially adapted to highland areas as irrigated rice (L3), is also suitable for medium highland as upland rice (L5).

CONCLUSION

It is concluded that among the 14 genotypes, G10 (F2BC4A52-42) showed the highest yield, with an average of 7.8 ton ha⁻¹ dry seeds. There was a significant Genotype x Environment interaction on the dry seed yield. However, Biplot analysis reveal that G2 (F2BC4A52-44) and G8 (F2BC4A52-37) were stable genotypes with an average dry seed yield of 5.2 and 5.5 ton ha⁻¹, while G6 (F2BC4A86-36) was specifically adapted to L3 and L5, and G14 (Aek Sibundong) was specifically adapted to L1 and L4 environments.

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