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HIGH YIELDING AND BLAST RESISTANT RICE CULTIVARS DEVELOPED FOR TROPICAL UPLAND AREA

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SUMMARY

The role of upland rice ecosystem to maintain sustainability of rice production in the future is expected to be more significant because the extension of irrigated areas would be more difficult. However, blast disease is the major biotic constraint of upland rice cultivation consequently identification high yielding and blast resistant rice cultivars are important to increase rice productivity in the upland. Yield trials of twelve advanced upland rice breeding lines and two check cultivars were conducted in eight sites representing tropical upland area to identify stable and high yielding rice genotypes. In addition, the blast disease resistance of these materials was studied in greenhouse using ten blast races. Average grain yield of upland rice genotypes across eight sites ranged from 4.95 to 6.65 t ha^{-1}. Stable and high yielding genotypes were identified including B12828E-TB-2-11-22 (6.65 t ha^{-1}), G37 UNSOED (6.19 t ha^{-1}), IPB159-F-7-1-1 (6.05 t ha^{-1}), and G8 UNSOED (6.00 t ha^{-1}). Investigation of blast disease resistance on these genotypes against ten blast races indicated that these lines had wide spectrum of blast resistance and different blast resistance mechanism apparently presented in each genotype. The identification of upland cultivars with different blast resistance for farmer's adoption has potential to increase rice productivity in tropical upland areas.

Key words: Upland rice, blast disease, AMMI, G × E interaction

Key findings: This study has identified stable, high yield and blast resistant rice genotypes which has potential to be adopted by farmers. The breeding materials are also important genetic resources for rice breeders in other tropical upland environments.

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INTRODUCTION

Rice is the staple food for almost half of world population. About 90% of rice was produced in Asia with three major rice producing countries are China, India and Indonesia (GRiSP, 2013). Rice is grown in diverse ecosystem including irrigated, rainfed lowland, flood prone and upland (Khush, 1997). About 75% of rice production in the world supplied from irrigated areas, while rainfed lowland and upland contributed for 19% and 4%, respectively (GRiSP, 2013).

In contrast to lowland rice ecosystem where rice cultivated in flooded condition, upland rice referred to rice cultivation system in non-flooded soil or in aerobic condition (Kato *et al.*, 2006; Saito *et al.*, 2018). Upland rice ecosystem ranged from humid to subhumid climates with diverse soil fertility and topography (GRiSP, 2013). Most of upland rice environments in Asia and Africa are characterized as marginal ecosystem, which are cultivated by poor farmers who grow rice for subsistence with little input and have low access to modern rice technology (Frei and Becker, 2004; Bernier *et al.*, 2008; Pandey, 2009). The global productivity of upland rice was lower than irrigated with the average yield less than 2 ton ha^{-1} (Saito *et al.*, 2018), however several studies indicated high yield potential of upland rice could be achieved in non-stress upland using improved rice cultivars (Dingkuhn *et al.*, 1998; Saito *et al.*, 2006; Atlin *et al.*, 2006; Kato *et al.*, 2009).

The contribution of upland rice ecosystem to maintain sustainability of rice production in the future is expected to be more significant, because the effort to expand irrigated areas would be more difficult due to water scarcity as the impact of climate change (Tuong and Bouman, 2003; Bouman *et al.*, 2005). In Indonesia, upland rice, cultivated once a year during wet season, it covers about 1 million hectares and contributes to about 5% of the rice production of the country (Hairmansis *et al.*, 2017; Saito *et al.*, 2018). It was estimated that an additional ~3.4 million ha of dry land in Indonesia has potential for upland rice cultivation (Sumarno and Hidayat, 2015). The areas included unutilized grass land and secondary forest (Partohardjono *et al.*, 2005; Purnomosidhi *et al.*, 2005; Sumarno and Hidayat, 2015).

Two main constraints of upland ecosystem for rice cultivation are biotic and abiotic stresses. Blast disease, caused by fungi *Pyricularia oryzae* Cavara, is a major biotic constraint of upland rice cultivation in the tropic (Khush and Jena, 2009).

Cultivation of blast resistance rice cultivars is the most effective way to control the disease. However, the disease showed high variability of races and therefore caused many blast resistant rice cultivars lost their resistance after few years of release (Valent and Chumley, 1991; Khush and Jena, 2009). Growing different rice cultivars with different resistance genes is important to minimize the production losses caused by the disease (Leung *et al.*, 2003; Suwarno *et al.*, 2009).

Availability of improved cultivars adapted to environmental stress in the upland is important to increase rice production and farmer's income in this vulnerable ecosystem. Evaluation of rice breeding lines having desirable characters for upland environment in multi environment is needed before the genotype is deployed to the farmers (Mandal *et al.*, 2010; Balestre *et al.*, 2010). Multi environment testing could give information for breeder in selecting the best genotype to be recommended in target environment (Braun *et al.*, 2010; Gauch, 2013). Several models have been used to study the interaction between genotype and environment in multi-location trials, such as joint regression model (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Becker and Leon, 1988) and the Additive Main Effects and Multiplicative Interaction (AMMI) model (Gauch, 2013). The AMMI model has been extensively used to analyse complex interaction of genotype and environment in rice breeding (Samonte *et al.*, 2005; Jiang *et al.*, 2010; Suwarto and Nasrullah, 2011; Kumar *et al.*, 2012; Shrestha *et al.*, 2012; Liang *et al.*, 2015).

This study was aimed to evaluate upland rice lines in different tropical upland environments in Indonesia. AMMI model was used to clarify complex interaction between rice genotype and the environment and to select the best cultivar for recommendation. In addition, variation of the response of breeding materials against different blast races were conducted in greenhouse to determine their resistance pattern as supporting data in recommendation of rice cultivars for blast endemic upland areas in the tropics.

MATERIALS AND METHODS

Plant material

Twelve advanced upland rice breeding lines (developed in four research centres) and two check cultivars were evaluated in multi-location trials. The lines were IPB158-F-16-1-1, IPB159-F-7-1-1 and IPB160-F-9-2-1 (IPB University), Bio199 (Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development), IR82571-581-1-2-3 and IR84047-24-3-3-3 (International Rice Research Institute), B12828E-TB-2-11-22, B11592F-MR-16-1-5-1, B12498F-MR-1-9, and B12154D-MR-10 (Indonesian Centre for Rice Research) and G8 and G37 (Jenderal Soedirman University). Inpago 6 and Limboto cultivars were used as checks.

Multi-location yield trials

Field trials were conducted in two sites during wet season (WS) 2013-2014 and in six sites during the WS 2014-2015 (Table 1). At all sites, the experiments were designed in randomized complete block design with four replications. Each genotype

Table 1. Description of upland rice multi-location yield trials sites.

Code	Growing season	Sites	Location	Soil type
A	WS 2013/2014	Pekalongan sub district, Lampung Timur	5°04'S 105°20'E	Podsolik
B	WS 2013/2014	Batanghari Nuban sub district, Lampung Timur	5°02'S 105.43'E	Podsolik
C	WS 2014/2015	Pekalongan sub district, Lampung Timur	5°04'S 105°20'E	Podsolik
D	WS 2014/2015	Batanghari Nuban sub district, Lampung Timur	5°02'S 105.43'E	Podsolik
E	WS 2014/2015	Purbolinggo sub dictrict, Lampung Timur	5°00'S 105.48'E	Podsolik
F	WS 2014/2015	Bogor Selatan sub district, Bogor	6°64'S 106.77'E	Latosol
G	WS 2014/2015	Pacet sub district, Cianjur	6°69'S 107.03'E	Andosol
H	WS 2014/2015	Cikembar sub district, Sukabumi	6°96'S 106.82'E	Latosol

was grown in 4.2 m x 4.5 m plot. Rice seeds were directly sown in soil at 30 cm x 15 cm spacing. Inorganic NPK (15:15:15) fertilizers were applied two times (200 kg ha^{-1} at 10 days after sowing (das) and 100 kg ha^{-1}at 35 das) and 100 kg ha^{-1} urea (at the booting stage). Data were recorded for important agronomic traits such as: number of productive tillers, plant height, flowering times, maturity, number of filled grains per panicle, grain weight, and grain yield (moisture content of 14%). Stability analysis was performed using AMMI model by using web based statistical tool PBSTAT-GE 2.3 (www.pbstat.com).

Evaluation of rice blast disease resistance

Blast disease resistance evaluation carried out in the greenhouse at the seedling stage (21 das). Blast susceptible rice cultivar Kencana Bali was used as check. The rice genotypes were evaluated using ten rice blast races, namely 033, 073, 133, 173, 001, 013, 041, 023, 051, and 101. The upland rice genotypes were grown in a plastic box of 20 cm × 35 cm × 10 cm containing soil mixed with fertilizers (10 kg soil was mixed with 5 g urea, 1.3 g phosphate (SP36) and 1.2 g potassium (KCl)). Ten seeds of each genotype were planted in a row and the rice plants were maintained under normal condition. Rice blast inoculums were prepared on potato dextrose agar (PDA) for 5 to 7 d and then transferred to sporulation media using oatmeal agar for 12 d. Rice blast disease was inoculated on 21 d old plants by spraying rice blast spore suspension with 2×10^5 ml^{-1} concentration and incubated in a humid room for 24 h. The seedlings were then transferred to greenhouse with humidity over 90%. Rice blast infection was scored at 7 d after inoculation following IRRI (2014). Based on the scale, the genotypes were classified as resistant (score 0, 1, 2), moderately resistant (score 3), moderately susceptible (score 4), and susceptible (score 5, 6, 7, 8, 9).

RESULTS AND DISCUSSION

Performance of rice genotype across environments

Field trials of rice lines were conducted in eight locations representing tropical upland rice area. AMMI analysis was used to clarify complex interaction of upland rice genotype (G) and environment (E) on grain yield

Table 2. Analysis of variance for AMMI model for grain yield of upland rice across eight environments in the 2013 to 2015 wet seasons.

Source	DF	SS	MS	F value	P value	G x E SS explained (%)	Cumulative (%)
Environment (E)	7	624.60	89.23	69.96	<0.0001	-	-
Replication within environment	24	30.61	1.28	2.27	<0.0001	-	-
Genotype (G)	13	112.53	8.66	15.42	<0.0001	-	-
G x E	91	376.51	4.14	7.37	<0.0001	-	-
IPCA1	19	182.77	9.62	17.13	<0.0001	48.5	48.5
IPCA2	17	85.09	5.01	8.92	<0.0001	22.6	71.1
IPCA3	15	55.10	3.67	6.54	<0.0001	14.6	85.8
IPCA4	13	30.08	2.31	4.12	<0.0001	8.0	93.8
IPCA5	11	11.90	1.08	1.93	0.0351	3.2	96.9
IPCA6	9	6.45	0.72	1.28	0.2468	1.7	98.6
IPCA7	7	5.13	0.73	1.30	0.2497	1.4	100
Residuals	312	175.16	0.56	-	-	-	-

character. The sum of squares (SS) for G, G × E signal (GE_S), and G × E noise (GE_N) were used as indicators (Gauch, 2013). The SS for G was 112.53 (Table 2), while the SS for GE_N was estimated by multiplying the error mean square by the degrees of freedom (df) for GE (0.56 × 91 = 50.96). The SS for GE_S was obtained by subtracting GE_N from GE (376.51 - 50.96 = 325.55). The SS for GE_S of 325.55 was larger than SS for G (112.53), therefore AMMI analysis was suitable for this dataset.

Analysis of variance on grain yield across the environments indicated that the rice grain yield was significantly affected by environment (E), genotype (G), and G × E interaction which explained 56.1%, 10.1%, and 33.8% of the total variation respectively (Table 2). The partitioning of G×E interaction trough AMMI model analysis showed the first five interaction principal components (IPCs) were significant. These five IPCs explained 96.9% of G × E sum squares (Table 2).

Average grain yield of upland rice genotypes across eight sites ranged from 4.95 to 6.65 t ha^{-1} (Table 3). The overall mean yield of 14 genotypes tested in all sites was 5.83 t ha^{-1}. The two highest productivity average data comes from location Purbolinggo (E) with 7.58 t ha^{-1} and Cikembar (H) at 7.52 t ha^{-1} respectively. The highest mean yield (6.65 t ha^{-1}) was shown by the genotype G7 (B12828E-TB-2-11-22).Based on the results of this study, the tested lines have very high yield potential, compared to the average global upland rice, which is in the range less than 2 ton ha^{-1} (Saito *et al.*, 2018). A high yielding upland rice cultivar of about 4 t ha^{-1} has been reported in productive and fertile upland areas in China and Philippines (Atlin *et al.*, 2006). Moreover, an average grain yield of 9.4 t ha^{-1} has been achieved in aerobic rice production in Japan (Kato *et al.*, 2009).

The presence of the interaction between genotypes and environments was indicated by the differential yield ranking of rice genotype across sites (Table 3). Different genotypes achieved the highest grain yields at

Table 3. Mean grain yield (t ha^{-1}) for 14 rice genotypes across eight environments in the 2013 to 2015 wet seasons.

Code	Genotypes	Environments								Means ± SD
		WS 2013-2014			WS 2014-2015					
		A	B	C	D	E	F	G	H	
G1	IPB158-F-16-1-1	4.09	5.68	4.05	4.34	6.70	3.80	5.67	5.24	4.95±1.03
G2	IPB159-F-7-1-1	5.00	6.24	6.06	4.47	7.93	3.71	5.90	9.09	6.05±1.77
G3	IPB160-F-9-2-1	5.25	5.13	5.52	4.87	6.47	4.61	6.59	5.43	5.49±0.71
G4	Bio199	5.31	6.08	4.20	5.26	6.59	3.78	6.03	5.35	5.33±0.95
G5	IR82571-581-1-2-3	4.37	5.81	5.71	5.21	6.76	3.88	4.75	7.17	5.46±1.14
G6	IR84047-24-3-3-3	6.09	4.65	6.46	4.80	6.85	2.84	3.58	6.04	5.16±1.43
G7	B12828E-TB-2-11-22	5.75	6.35	6.24	5.84	9.00	3.86	5.98	10.20	6.65±2.00
G8	B11592F-MR-16-1-5-1	4.58	6.54	4.39	4.91	8.88	5.40	3.48	9.03	5.90±2.08
G9	B12498F-MR-1-9	5.54	4.87	6.47	5.73	8.64	5.34	3.54	10.61	6.34±2.25
G10	B12154D-MR-11	6.10	5.44	4.92	5.36	8.32	3.77	4.24	5.49	5.46±1.37
G11	G8 UNSOED	5.89	6.46	4.72	5.63	7.79	6.34	3.96	7.21	6.00±1.25
G12	G37 UNSOED	4.92	5.69	6.10	5.33	7.01	5.02	6.08	9.40	6.19±1.46
G13	Inpago 6	6.51	6.79	6.54	4.77	7.96	3.57	5.05	9.22	6.30±1.81
G14	Limboto	6.33	7.14	4.85	6.10	8.75	5.12	2.96	9.53	6.35±2.13
	Means	5.24	5.74	5.40	5.15	7.58	4.36	4.98	7.52	5.83
	CV (%)	14.99	8.48	14.38	12.51	9.73	14.12	14.73	13.47	12.85
	LSD (5%)	1.16	0.72	1.12	0.93	1.07	0.88	1.02	1.5	0.37

different environments. The check cultivar G13 (Inpago 6) was the best performing genotype from location Pekalongan at planting season 2013/2014 and also 2014/2015, while Limboto as another check was the best performing in environment Batanghari Nuban at wet season 2013/2014 and 2014/2015. Some of the best genotype performances were obtained at site: genotype G7 at Purbolinggo (WS 2014/2015), G11 at Bogor Selatan (WS 2014/2015), G3 at Pacet (WS 2014/2015), and G9 at Cikembar (WS 2014/2015) respectively.

Variations were also observed in some important agronomic traits, including plant height, tiller number, flowering times, maturity, grain filling and grain weight (Table 4). Plant height ranged from 79.4 cm (G8) to 125.7 cm (G9) with an average of 103 cm. The tiller number varied from 10 to 14 tillers per hill. These features represented the characteristics of improved indica upland rice adapted to high fertile soil, which were having intermediate plant height and tillering (Atlin *et al.*, 2006). The genotypes showed different maturity from 108 d to 120 d. The lowest number of fertile grains was 83 (G1) and the highest 139 grains per panicle (G14) while the grain weight of upland rice genotypes ranged from 25.5 (G5) to 27.7 g (G9).

The difference on rice genotype responses to different environments was shown in the AMMI biplot of main and IPCA1 effects of both genotype and environments on grain yield (Figure 1). The AMMI biplot explained 82.60% of the total G + E + GE SS (1113.65), including 56.1% due to environment SS (624.60), 10.1% due to genotype SS (112.53) and 16.4% due to IPCA1 SS (182.77) (Table 2). Rice genotypes, which had IPCA1 scores >0, responded positively (adaptable) to environments, which had IPCA1 scores >0, but responded negatively to environments which had IPCA1 scores <0 (Samonte *et al.*, 2005). Therefore, rice genotypes G1, G3, G4, G5, G6, G10 and G11 were adapted to environments A, B, C, D, F, and G. In contrast, rice genotype,

Table 4. Mean and standard deviation of agronomic characters of upland rice genotypes in the multi-location yield trials in eight environments in 2013 to 2015 wet seasons.

Code	Genotypes	Plant height (cm)	Tiller number	Flowering times (d)	Maturity (d)	Filled grain per panicle	Empty grain per panicle	1000 grain weight (g)
G1	IPB158-F-16-1-1	96.4±5.9	11.9±3.9	90.1±6.8	115.5±11.6	83.2±33.8	66.2±29.2	26.2±1.6
G2	IPB159-F-7-1-1	98.2±6.9	11.1±1.9	88.1±3.2	112. 8±8.4	129.2±21.8	46.2±20.7	26.7±1.7
G3	IPB160-F-9-2-1	89.8±8.2	11.0±1.2	86.4±5.8	110.8±8.3	101.0±23.0	37.9±12.0	26.1±2.9
G4	Bio199	112.6±12.8	13.3±3.0	93.9±5.4	120.7±10.4	91.0±10.3	29.6±10.6	25.6±2.2
G5	IR82571-581-1-2-3	88.4±9.5	12.8±2.1	87.7±2.7	113.8±8.3	94.4±15.0	26.6±8.3	25.5±1.5
G6	IR84047-24-3-3-3	93.0±10.9	10.9±2.3	88.2±3.8	117.1±12.0	98.3±12.9	31.7±10.2	25.8±2.5
G7	B12828E-TB-2-11-22	106.9±8.2	10.5±1.1	83.5±4.1	111.0±8.6	128.2±20.0	30.6±18.7	26.1±1.0
G8	B11592F-MR-16-1-5-1	118.8±11.3	9.7±1.6	87.2±3.4	113.5±8.8	127.5±16.4	57.0±17.3	27.1±2.2
G9	B12498F-MR-1-9	125.7±7.9	11.5±3.7	87.3±4.5	113.9±12.1	114.5±28.2	51.1±19.5	27.7±3.1
G10	B12154D-MR-11	124.9±6.9	10.5±2.3	88.5±7.2	113.7±12.4	115.6±25.8	44.4±12.3	26.4±2.9
G11	G8 UNSOED	79.4±4.5	14.0±2.3	86.3±5.4	111.1±9.9	109.6±11.5	36.7±14.9	25.3±0.7
G12	G37 UNSOED	90.4±4.2	11.1±1.4	84.6±4.4	111.2±8.7	107.6±13.6	34.2±12.2	26.3±2.4
G13	Inpago 6	107.5±10.1	10.9±1.6	80.7±4.2	108.2±8.8	117.4±11.9	29.2±11.4	26.3±0.8
G14	Limboto	106.5±5.6	10.0±1.1	84.4±2.8	111.2±7.2	138.6±21.4	35.4±12.8	26.8±1.6
	CV (%)	6.1	13.9	1.4	1.3	19.0	32.0	3.2
	$\text{LSD}_{0.05}$	3.08	0.99	0.58	0.71	10.4	6.26	0.41

which had IPCA scores <0 responded positively to environments, which had IPCA1 scores <0 and responded negatively to environment, which had IPCA scores >0. Therefore, genotypes G2, G7, G8, G9, G12, G13, and G14 were adapted to environment E and H.

The direction and magnitude of rice genotypes along the *x* axis (grain yield) and *y* axis (IPCA1) indicated the stability of rice genotype across environments (Samonte *et al.*, 2005). The rice genotypes, which had lower absolute IPCA1 scores compared to other genotypes had more stable yield across environments. Therefore, the genotypes G2, G11, G12, G13, G5, G6, and G7 were more stable compared to others. The genotype G2, G11, G12, G13 and G7 were also identified as high yielding genotypes.

Response of rice genotypes against rice blast disease

Rice genotypes showed different responses against 10 blast races (Table 5). The susceptible check cultivar Kencana Bali showed compatible response to all blast races indicating the virulence of all blast isolates. Only one of twelve rice genotype (G8) showed moderate or high resistance to all blast races, while other lines were susceptible to one or more blast race(s). Majority of rice genotypes were susceptible to blast race 133 and 173. Genotypes showing incompatible response to blast race 133 were G1, G7, G8, G12 and G13, while genotypes showing incompatible response against blast race 173 were G1, G8, G10, and G11. More than 60

Table 5. Reaction of upland rice genotypes against ten blast races in seedling stage.

Code	Genotypes	Blast (*Pyricularia oryzae* Cavara) races									
		033	073	133	173	001	013	041	023	051	101
G1	IPB158-F-16-1-1	R	R	R	MR	MR	S	S	S	S	S
G2	IPB159-F-7-1-1	MR	R	S	S	MR	S	S	S	MR	S
G3	IPB160-F-9-2-1	S	S	S	S	MR	MR	MR	MR	MR	MR
G4	Bio199	S	MR	S	S	MR	MR	MR	MR	MR	MR
G5	IR82571-581-1-2-3	R	R	S	R	MR	MR	MR	MR	MR	MR
G6	IR84047-24-3-3-3	MR	MR	S	S	MR	S	MR	MR	MR	MR
G7	B12828E-TB-2-11-22	R	R	MR	S	MR	MR	S	MR	MR	MR
G8	B11592F-MR-16-1-5-1	R	R	MR	R	MR	MR	MR	MR	MR	MR
G9	B12498F-MR-1-9	MR	S	S	S	R	R	MR	MR	R	MR
G10	B12154D-MR-11	R	R	S	MR	R	MR	R	S	S	R
G11	G8 UNSOED	R	R	S	MR	MR	R	R	S	S	S
G12	G37 UNSOED	S	R	MR	S	MR	R	MR	MR	S	R
G13	Limboto	MR	R	MR	S	R	R	R	R	MR	na
G14	Inpago 6	MR	R	S	S	R	R	R	R	R	na
Kencana Bali (susceptible check)		S	S	S	S	S	S	S	S	S	S

Abbreviations: R= resistant, MR= moderately resistant, S= susceptible, na= not available

blast resistant genes have been identified in rice through conventional genetic analysis and molecular techniques (Khush and Jena, 2009; Ashkani *et al.*, 2015). The upland rice genotypes, tested in this experiment, showed wide spectrum of blast resistance pattern. Possibly, they harbour multiple resistance genes. Efforts to combine multiple blast resistance genes are common objective in breeding for blast resistant cultivars (Khush and Jena, 2009; Ashkani *et al.*, 2015). Several studies indicated that many improved rice cultivars possess more than one blast resistance genes (Ebron *et al.*, 2004; Cho *et al.*, 2007; Suwarno *et al.*, 2009; Zhang *et al.*, 2015).The reaction pattern of upland rice genotypes against blast race 133 and 173 suggested that these two blast races were more virulent to upland rice compared to others and therefore, it is important to improve the resistance of upland rice against these two blast races.

Recommendation for the adoption of improved upland rice lines

Selection of best genotypes to be recommended for target areas is the major objective of multi-location yield trials (Gauch, 2013). In this study, stable genotypes having high yield potential have been identified, including B12828E-TB-2-11-22 (G7), Inpago 6 (G13), G37 UNSOED (G12), IPB159-F-7-1-1 (G2) and G8 UNSOED (G11) with average yielded 6.65; 6.30; 6.19; 6.05; and 6.00 t ha^{-1}, respectively. These genotypes have potential to be adopted by farmers in tropical upland areas, specifically in Indonesia. In addition, these genotypes showed wide spectrum of blast resistance, and each genotype showed different response pattern against 10 blast races, indicating the differences in blast resistance mechanism in each genotype. Deployment of several new upland rice cultivars with different blast resistance could be an option to reduce the crop failure due to blast disease (Leung *et* *al.*, 2003; Suwarno *et al.*, 2009). Recently, the genotypes IPB159-F-7-1-1 (G2), B12828E-TB-2-11-22 (G7), and G37 UNSOED (G12) were registered as new rice cultivars in Indonesia as IPB 9G, Inpago 12 Agritan, and Unsoed Parimas, respectively. Adoption of these genotypes provides opportunity to increase the rice production as well as farmers income in upland areas.

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