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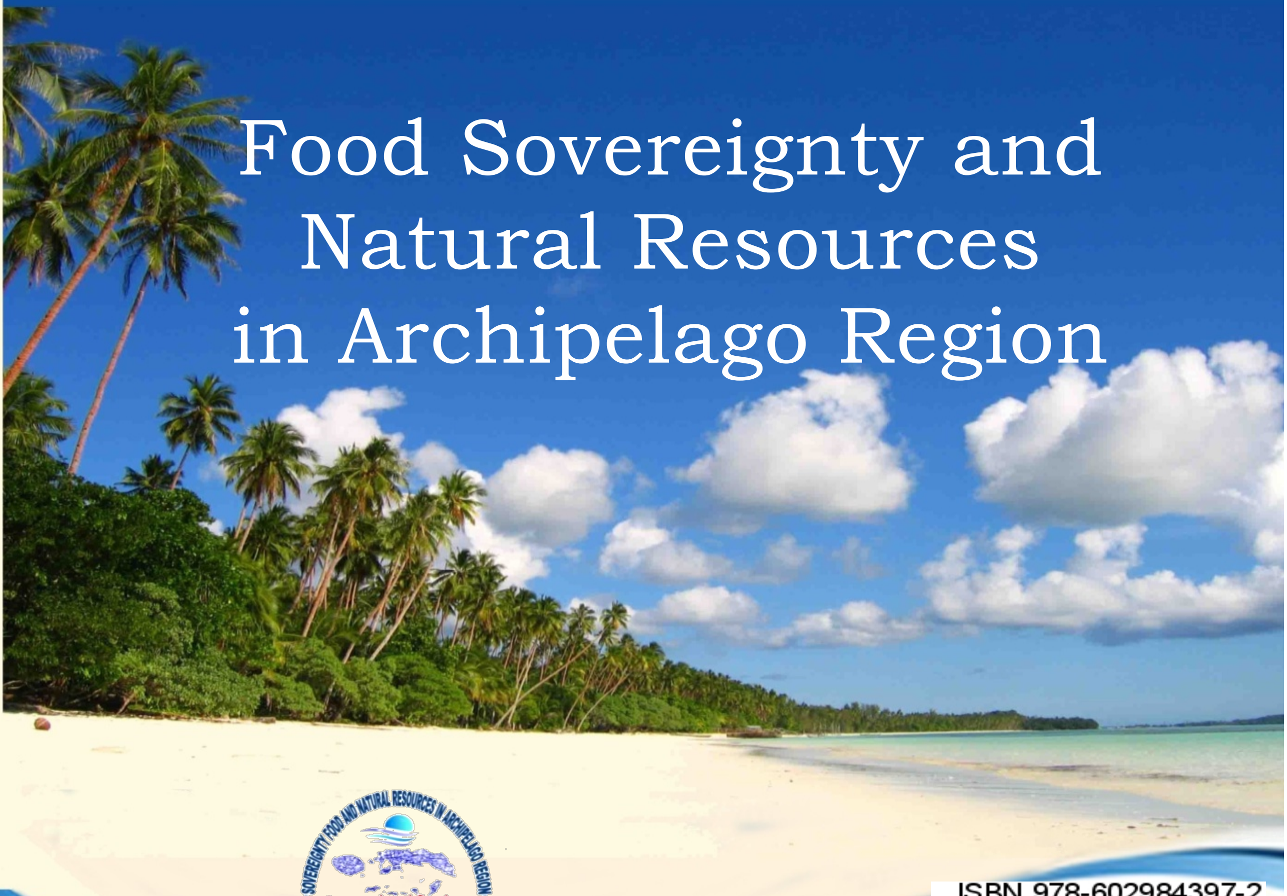

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MULTILOCATION TEST OF UPLAND RICE LINES OBTAINED FROM CROSSBREEDING BETWEEN LANDRACE UPLAND RICE FROM BURU ISLAND AND NEW PLANT TYPE OF LOWLAND RICE

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Abstract

The objectives of the research were to obtain information of genotype x environment interaction, yield potential, adaptability and stability of up land rice lines obtained from crossbreeding between landrace upland rice from Buru Island and new plant type of lowland rice. Ten lines and two cultivars were planted at seven different locations in November 2010 – March 2011, used randomized complete block design with four replications. Observation was done on grains weight per hectare. Estimation stability used two yield stabilities analysis, Finlay and Wilkinson, and Additive Main Effect Multiplicative Interaction (AMMI). The results showed that genotype x environment interaction factors contributed to yield variance by 16.6%. The highest productivity was achieved by FM1R-1-3-1 (4.52 tons ha^{-1}). Genotypes FG1R-30-1-5, FG1-65-1-2, FG1R-30-1-3 and FG1R-30-1-1 were dinamic stable and poorly adapted to all environments. Genotype FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4 and FG1-6-1-2 were specifically adapted to unfavourable environments. Genotypes FM1R-1-3-1, Fat-4-1-1, Situ Bagendit and Towuti were specifically adapted to favourable environments.

Key words: upland rice, new plant type, crossbreeding, multilocation test

INTRODUCTION

Indonesia, which extends along the equator, was awarded a varieties of food plants germplasm. Diversity of upland rice germplasm is a wealth of food crops that need to be explored and developed to make national superior upland rice varieties. At recent, the research and assembly of upland rice in Indonesia was directed to produce a new type of upland rice varieties (Abdullah *et al*., 2008; Dewi and Purwoko, 2012).

Landrace upland rice germplasms originating from Buru Island were Fulan Telo Gawa and Fulan Telo Mihat. They have superior characters such as short life age, long panicle, and good grain filling. Safitri *et al*. (2010) used them and crossed with a new type of lowland rice, Fatmawati and MR-BP360E-79-2. Their characters such as upright plant, stout trunk and dense panicles although cockpit for replenishing grain are still unfavourable. Another culture method used to speed up the formation of new type upland rice line with characters expected from its parent (Dewi and Purwoko, 2012). This method has acquired a number of dihaploid line of new type upland rice (Safitri *et al*., 2010). Those lines resulted must have well adapted and stable in different environmental conditions (Jambormias and Riry, 2008).

Adaptability and stability of a genotype can be determined by the interaction of its genotype with environment (Farshadfar *et al*., 2012). This interaction can also determined the adaptation region of genotype at particular environment and measure the role of environmental factor on the genetic potential of a genotype (Asad *et al*., 2009). Multilocation test needs to be done to know genotype x environment interaction pattern, adaptability and stability of a line (Hadi and Sa'diyah, 2004). The objectives of the research were to obtain information of genotype x environment interaction, yield potential, adaptability and stability of upland rice lines obtained from crossbreeding between Buru Island upland rice landrace and new plant type of lowland rice.

MATERIALS AND METHODS

This research was carried out in November 2010 – March 2012 in Bogor, Sukabumi and Indramayu (West Java), Purworejo (Central Java), Wonosari (DI Yogyakarta), Natar and Taman Bogo (Lampung). Upland rice lines used were ten lines of new type upland rice: FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-5, FG1R-30-1-4, FG1-6-1-2, FG1-65-1-2, FG1R-30-1-3, FG1R-30-1-1, FM1R-1-3-1, Fat-4-1-1; and two check varieties, Situ Bagendit and Towuti.

This research used design of completely rondomized blocks with four replications of nested in each location. There were forty eight experimental units in each location. The research consisted of land preparing, planting, intensive maintanance and harvesting. Harvest was done based on physiology maturity criteria marked by 80% yellowing panicle in a plot. Character used was yield grain per hectare.

Data analysis were done with anova each locations, pooled anova and yield stability. The pattern of tested genotype stability was known by using two stability analysis approaches, Finlay and Wilkinson (1963), and Additive Main Effect Multiplicative Interaction (AMMI) (Cornelius, 1993).

RESULTS AND DISCUSSIONS

Results pooled analysis of variance showed that environment, genotype and genotype x environment interaction for the mean yield of new type upland rice lines was significant. These factors contribute to variance of yield 48.5%, 14.9% and 16.6% (Table 1), respectively. Genotype x environment interaction caused by response changes of tested genotypes in each location (Mut *et al.*, 2010).

Table 2 showed the mean grain yield per hectare from twelve genotypes on seven locations. Line FG1R-36-1-1 in Bogor has the highest grain yield per hectare by 3.39 tons. Line FM1R-1-3-1 has higher yield than other lines, Sukabumi, Indramayu, Purworejo, Wonosari and Natar with 5.44, 1.76, 7.61, 5.76 and 3.92 tons, respectivelly, whereas Sukabumi, Indramayu and Natar were lower than check varieties. Line Fat-4-1-1 in Taman Bogo has the highest grain yield per hectare by 5.71 tons. Generally, line FM1R-1-3-1 showed the highest mean yield was 4.52 tons ha^{-1}.

Table 1 The pooled analysis of variance of mean yield twelve upland rice genotypes grown in seven locations

Source of variation	Degrees of Freedom	Sum of Squares	Mean Square	F-statistic	Contribute to variance (%)
Replicates within environments	21	12.55	0.60	4.29**	5.6
Environments (E)	6	108.65	18.11	129.97**	48.5
Genotypes (G)	11	33.37	3.03	21.78**	14.9
Interaction G x E	66	37.24	0.56	4.05**	16.6
Pooled Error	231	32.19	0.14		14.4
Total	335	224.00			

*Note : ** indicate significant difference at <0.01 probability level.*

Table 2 The mean yield (tons ha^{-1}) of twelve upland rice genotypes grown in seven locations

Genotype	Locations							Mean
	Bgr	Skbm	Idmy	Pwrj	Wnsr	Ntr	Tmbg	
FG1-70-2-1	2,97^{ab}	2,87^{cd}	1,73^{bc}	3,70^{b}	2,90^{bc}	1,67^{e}	4,04^{cd}	2,84^{cd}
FG1R-36-1-1	3,39^{a}	3,21^{c}	1,37^{bc}	3,74^{b}	3,38^{bc}	2,49^{d}	4,52^{c}	3,16^{c}
FG1R-30-1-5	2,25^{b-e}	2,75^{cd}	1,28^{c}	4,05^{b}	2,50^{bc}	2,89^{bcd}	4,06^{cd}	2,83^{cd}
FG1R-30-1-4	2,31^{bcd}	2,32^{d}	1,73^{bc}	3,77^{b}	3,03^{bc}	2,57^{d}	4,32^{c}	2,86^{cd}
FG1-6-1-2	2,87^{abc}	3,30^{c}	1,70^{bc}	3,34^{b}	3,10^{bc}	3,42^{abc}	3,22^{d}	2,99^{cd}
FG1-65-1-2	0,83^{f}	2,96^{cd}	1,45^{bc}	3,32^{b}	2,09^{c}	3,56^{ab}	4,68^{bc}	2,70^{d}
FG1R-30-1-3	2,02^{cde}	2,61^{cd}	1,51^{bc}	3,77^{b}	3,20^{bc}	2,65^{cd}	4,15^{cd}	2,84^{cd}
FG1R-30-1-1	2,12^{b-e}	3,14^{c}	1,06^{c}	3,79^{b}	2,30^{bc}	3,00^{bcd}	4,31^{c}	2,82^{cd}
FM1R-1-3-1	1,58^{def}	5,44^{ab}	1,76^{bc}	7,61^{a}	5,76^{a}	3,92^{a}	5,54^{ab}	4,52^{a}
Fat-4-1-1	1,40^{ef}	4,85^{b}	1,35^{bc}	7,38^{a}	4,39^{abc}	3,26^{a-d}	5,71^{a}	4,05^{b}
Situ Bagendit	2,00^{cde}	5,60^{a}	2,59^{a}	6,64^{a}	3,98^{abc}	3,67^{ab}	5,96^{a}	4,35^{ab}
Towuti	2,07^{cde}	4,92^{b}	2,16^{ab}	7,16^{a}	4,65^{ab}	4,04^{a}	5,69^{a}	4,38^{ab}
Mean*	2,15^{D}	3,66^{B}	1,64^{E}	4,86^{A}	3,44^{C}	3,09^{C}	4,68^{A}	3,36
CV(%)	25,41	11,84	29,98	13,91	41,69	16,04	13,75	16,11

Note: Bgr = Bogor, Skbm = Sukabumi, Idmy = Indramayu, Pwrj = Purworejo, Wnsr = Wonosari, Ntr = Natar, Tmbg = Taman Bogo. Numbers in one column followed the same letter showed not significant different at DMRT 5% test. * The numbers in a row which followed the same capital letters indicated not significant on DMRT 5% test. CV(%) = Coeficien Variance.

Finlay and Wilkinson Analysis

Genotypes FG1R-30-1-5, FG1-65-1-2, FG1R-30-1-3 and FG1R-30-1-1 showed the regression coefficient is not significant different from 1.0 ($b_i \cong 1$) with regression coefficients 0.84, 1.02, 0.78 and 0.96, respectively (Table 3). These genotypes had mean yield 2.83, 2.70, 2.84 and 2.82 tons ha^{-1} respectively. The results of these genotypes were lower than mean total of 3.36 tons ha^{-1}. According to Finlay and Wilkinson (1963), these genotypes were stable and poorly adapted to all environments. Figure 1 shows the relationship between regression coefficient and mean yield of genotypes above.

Table 3 The mean yield (tons ha^{-1}), regression coefficient and productivity in environmental index 1 ton ha^{-1} and 5 ton ha^{-1}

Genotype	Mean Yield (ton ha^{-1})	b_i	$\hat{Y}_i$ in environmental	
			1 ton ha^{-1}	5 ton ha^{-1}
FG1-70-2-1	2.84	0.58*	1.29	3.62
FG1R-36-1-1	3.16	0.68*	1.33	4.06
FG1R-30-1-5	2.83	0.84^{ns}	0.98	4.33
FG1R-30-1-4	2.86	0.67*	1.23	3.90
FG1-6-1-2	2.99	0.44*	1.59	3.34
FG1-65-1-2	2.70	1.02^{ns}	0.64	4.73
FG1R-30-1-3	2.84	0.78^{ns}	1.07	4.19
FG1R-30-1-1	2.82	0.96^{ns}	0.81	4.66
FM1R-1-3-1	4.52	1.62*	0.70	7.18
Fat-4-1-1	4.05	1.74*	0.33	7.29
Situ Bagendit	4.35	1.31*	1.05	6.28
Towuti	4.38	1.36*	1.00	6.42
Mean Total	3.36	1.00	1.00	5.00

*Note: b_i = regression coefficient, $\hat{Y}_i$ = productivity of genotype to-i, * indicate significant difference at the $t_{0.05\ .\ 66}$ and ^{ns} indicate not significant difference at the $t_{0.05\ .\ 66}$ tests.*

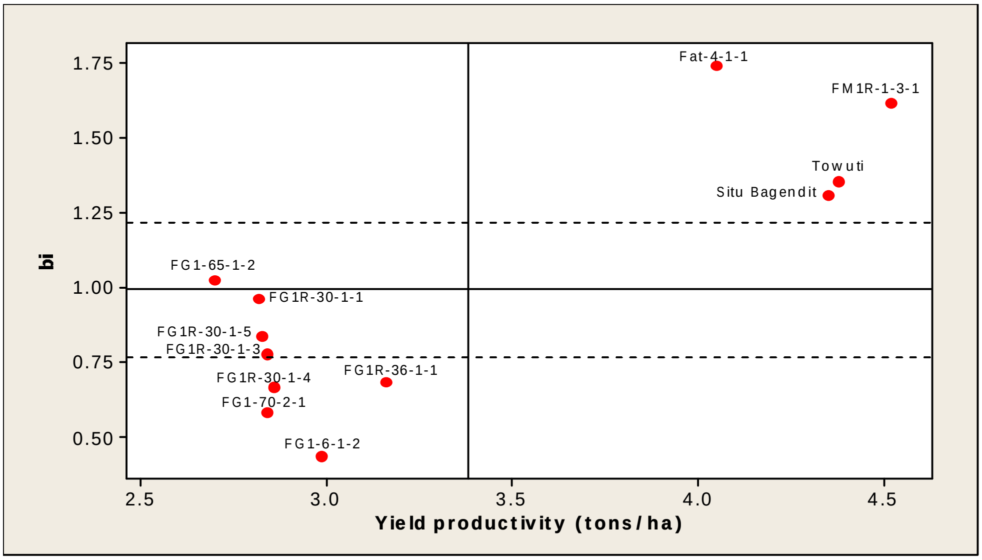

Figure 1 The relationship of regression coefficient (b_i) and yield productivity (tons ha^{-1}).

Genotypes FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4 and FG1-6-1-2 have regression coefficient lower than 1.0 (b_i <1) with each regression coefficient 0.58, 0.68, 0.67 and 0.44, and the mean results were 2.84, 3.16, 2.86 and 2.99, respectively (Table 3). Figure 1 shows these genotypes have regression coefficient less than 1.0 and mean results lower than mean total. They are stated as specifically adapted genotypes to unfavourable environments (Finlay and Wilkinson, 1963).

Genotypes FM1R-1-3-1, Fat-4-1-1, Situ Bagendit and Towuti have regression coefficient higher than 1.0 (b_i > 1) which values 1.62, 1.74, 1.31 and 1.36, respectively; mean results by 4.52, 4.05, 4.35 and 4.38, respectively (Table 3). Figure 1 shows these genotypes have regression coefficient higher than 1.0 and mean result overs the total mean. Thereby, they were specifically adapted genotypes to favourable environment (Finlay and Wilkinson, 1963).

Figure 2 shows the population pattern of twelve tested genotypes through the relationship between grain productivity with environmental index. Stable genotype (bi ≅ 1) lies parallel to the population mean of regression line. Genotypes FG1R-30-1-5, FG1-65-1-2, FG1R-30-1-3 and FG1R-30-1-1 with regression coefficient b_i ≅ 1 on environmental index 1 have productivity 0.98, 0.64, 1.07 and 0.81 tons ha^{-1}, respectively, whereas at index the 5 they are 4.33, 4.73, 4.19 and 4.66 tons ha^{-1}, respectively. The lies of genotype FG1R-30-1-3 in environmental index 1 was the same with lies of mean, whereas the three other genotypes were under population mean line. At the environmental index 2, 3, 4 and 5, the lies of four genotypes above were lower than total mean. It shows that they are stable genotypes with poorly adaption to all environments.

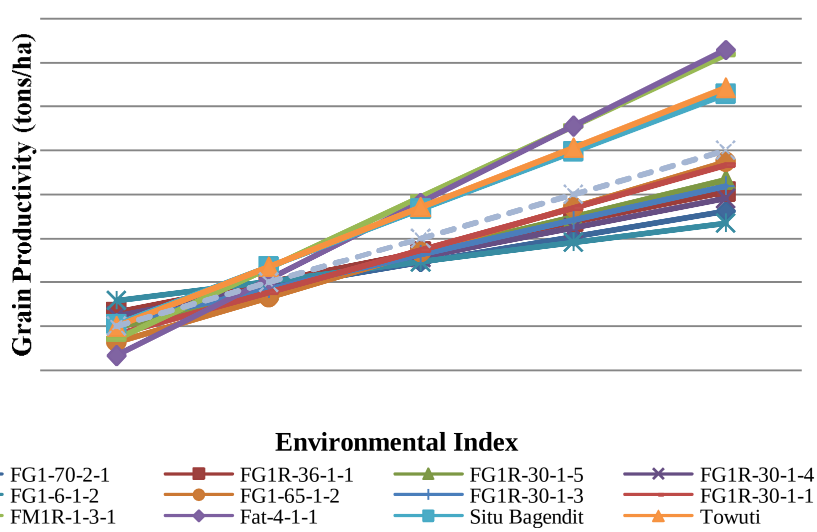

Figure 2 The pattern of genotypes tested by relationship between grain productivity and environmental index.

Finlay and Wilkinson (1963), stated that genotypes specifically adapted to poorly environments (b_i <1) will have mean yield above mean total in homely environment, whereas it is below in favourable environment. Genotypes FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4 and FG1-6-1-2 with regression coefficient lower than 1.0 (b_i <1) stated as specifically adapted genotypes to poorly environments. Their productivity were 1.29, 1.33, 1.23 and 1.59 tons ha^{-1}, respectively (above the total mean productivity of 1 ton ha^{-1}) at poorly environment on environmental index 1. Mean yield of these genotypes on environmental index 5 were below the productivity of mean total. They were 3.62, 4.06, 3.90 and 3.34 tons ha^{-1}, respectively.

Genotypes with specific adaptation to favourable environment (>b_i 1) have mean yield below mean total in homely environment, whereas it is above in favourable environment (Finlay and Wilkinson, 1963). Genotypes FM1R -1-3-1, Fat-4-1-1, Situ Bagendit and Towuti with regression coefficient higher than 1.0 (b_i >1) stated as specifically adapted genotypes to favourable environment. Genotypes FM1R-1-3-1 and Fat-4-1-1 have productivity 0.70 and 0.33 tons ha^{-1}, respectively, below productivity 1 ton ha^{-1} at homely environment on environmental index 1. Situ Bagendit and Towuti have productivity 1.05 and 1.00 ton ha^{-1}, respectively, close to mean total productivity 1 ton ha^{-1} on environmental index at homely environment. The mean productivity of FM1R-1-3-1, Fat-4-1-1, Situ Bagendit and Towuti were 7.18, 7.29, 6.28 and 6.42 tons ha^{-1}, respectively, above total mean productivity 5 tons ha^{-1}.

Additive Main Effect Multiplicative Interaction (AMMI) Analysis

AMMI analysis showed interaction principal component axis (IPCA1 and IPCA2) were significant different at opportunity level less than 1% of 0.00 opportunity. Contributions of diversity interaction effects that can be explained by components 1-6 were 67.62%, 16.97%, 7.17%, 4.37%, 2.65% and 1.22%, respectively (Table 4). Based on the value contribution of diversity can be seen that the first two components explained IPCA1 and IPCA2 can explain genotype x environment interactions to 84.59%. Thereby diversity can not be explained by the model is 15.41%.

Tabel 4 The analysis of variance AMMI for yield productivity

Source of variation	Degrees of Freedom	Sum of Squares	Mean Square	F-Statistic	Contribute to variance G x E (%)
Environments (E)	6	108.65	18.11	30.31**	
Replicates within environments	21	12.55	0.60	4.29**	
Genotype (G)	11	33.37	3.03	21.78**	
Interaction G x E	66	37.24	0.56	4.05**	
IPCA1	16	25.18	1.57	11.30**	67.62
IPCA2	14	6.32	0.45	3.24**	16.97
IPCA3	12	2.67	0.22	1.59 ns	7.17
IPCA4	10	1.63	0.16	1.17 ns	4.37
IPCA5	8	0.99	0.12	0.89 ns	2.65
IPCA6	6	0.45	0.08	0.54 ns	1.22
Error	231	32.19	0.14		
Total	**335**	**224.00**			

Note : ** indicate significant difference at <0.01 probability level and ns indicate not significant difference at >0,05 probability level; IPCA = Interaction principle componen axis.

The higher stability of a line can be demonstrated by the approach genotype point to 0.0 ordinate as the central axis (Arsyad and Nur, 2006). Figure 3 describes genotypes FG1R-30-1-5, FG1R-30-1-3 and FG1R-30-1-1 approaching the axis point 0.0. Therefore, those genotypes were grouped as stable and broad adaptable genotypes based on AMMI stability analysis.

Closed relationship between genotypes by environment indicated by the proximity of the genotypes point to tested environment line. It means there are well supporting environment for matching genotypes grown (Ganefianti *et al*., 2009). Genotypes FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4, FG1-6-1-2, FG1-65-1-2, FM1R-1-3-1, Fat-4-1-1, Situ Bagendit and Towuti were specifically and special adapted genotypes with grow well ability. This was demonstrated through the closeness relationship between genotype and environmental conditions. The relationship was shown between genotypes FM1R-1-3-1, Fat-4-1-1 and Towuti in Purworejo; Situ Bagendit in Sukabumi; FG1-65-1-2 in Natar; FG1-6-1-2 in Indramayu; and FG1-70-2-1, FG1R-36-1-1 and FG1R-30-1-4 in Bogor. Therefore, genotypes FM1R-1-3-1, Fat-4-1-1 and Towuti very suitable planted in Purworejo and Situ Bagendit fits planted in Sukabumi. Genotype FG1-65-1-2 was very fit planted in Natar, FG1-6-1-2 was most appropriate planted in Indramayu, whereas FG1-70-2-1, FG1R-36-1-1 and FG1R-30-1-4 were very fit planted in Bogor.

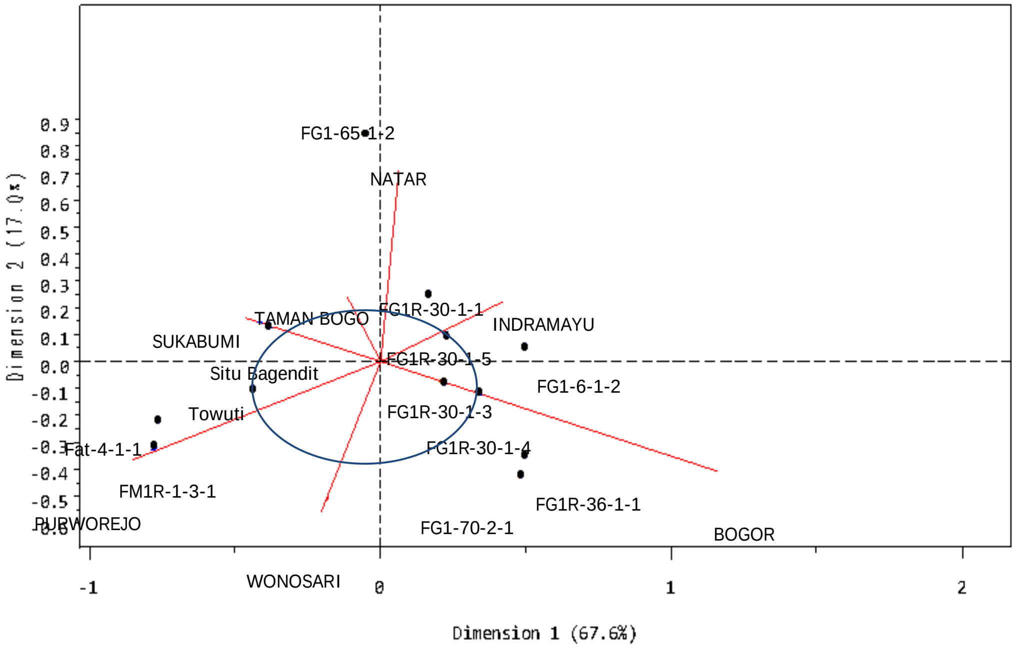

Figure 3. Biplot IPCA 1 and IPCA 2 interaction for yield productivity.

Relationship between Finlay-Wilkinson and AMMI analysis

Genotypes FG1R-30-1-5, FG1R-30-1-3 and FG1R-30-1-1 were stable by Finlay-Wilkinson and AMMI analysis, whereas FG1-65-1-2 was stable only by Finlay-Wilkinson (Table 5). Genotypes FG1R-30-1-5, FG1R-30-1-3, FG1R-30-1-1 and FG1-65-1-2 were genotypes that have dynamic stability. This dynamic stability was indicated by the regression coefficient (b_i) approaches to 1.0 in the regression graph (Figure 2). Those genotypes had yield below mean total, then they were dynamic stable genotypes with poorly adaption to all environments.

Finlay-Wilkinson's yield stability analysis stated that genotypes FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4 and FG1-6-1-2 were specifically adapted in unfavourable environment (Table 5). Based on the AMMI stability analysis, those genotypes were specific genotypes in spesific environment (Table 5). Genotypes FG1-70-2-1, FG1R-36-1-1 and FG1R-30-1-4 were spesific in Bogor, whereas genotypes FG1-6-1-2 in Indramayu. Thereby, they were specific genotypes with specific adapted to unfavourable environment.

Finlay-Wilkinson's yield stability analysis stated that genotypes FM1R 1- 3-1, Fat-4-1-1, Situ Bagendit and Towuti were specifically adapted to favourable environment (Table 5). Based on AMMI stability analysis, they were specific genotypes in a specific environment (Table 5). Genotypes FM1R 1-3-1, Fat-4-1-1 and Towuti were spesific in Purworejo while Situ Bagendit in Sukabumi. Then, they were specific genotypes with specific adapted to favourable environment.

Tabel 5 Criteria Finlay-Wilkinson and AMMI analysis

Genotype	Finlay-Wilkinson	AMMI
FG1-70-2-1	Unfavourable Environmental Adapted	Specific
FG1R-36-1-1	Unfavourable Environmental Adapted	Specific
FG1R-30-1-5	Stable-Poorly Adapted	Stable
FG1R-30-1-4	Unfavourable Environmental Adapted	Specific
FG1-6-1-2	Unfavourable Environmental Adapted	Specific
FG1-65-1-2	Stable-Poorly adapted	Specific
FG1R-30-1-3	Stable-Poorly adapted	Stable
FG1R-30-1-1	Stable-Poorly adapted	Stable
FM1R-1-3-1	Favourable Environmental Adapted	Specific
Fat-4-1-1	Favourable Environmental Adapted	Specific
Situ Bagendit	Favourable Environmental Adapted	Specific
Towuti	Favourable Environmental Adapted	Specific

CONCLUSION

Genotype x environment interactions contribute to yield diversity by 16.6%. Generally, the highest total yield from seven test locations indicated by line FM1R-1-3-1 by 4.52 tons ha^{-1}. Genotypes FG1R-30-1-5, FG1-65-1-2, FG1R-30-1-3, and FG1R-30-1-1 were dynamic stable genotypes with poorly adaption to all environments. Genotypes FG1-70-2-1, FG1R-36-1-1, FG1R-30-1-4 and FG1-6-1-2 were specifically adapted genotypes to unfavourable environment. Genotypes FM1R-1-3-1, Fat-4-1-1, Situ Bagendit and Towuti were specific genotypes with specific adaption to favourable environment.

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