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Research Article

Multivariate analysis of GGE and AMMI biplot graph to investigate genotype by environment interaction of rice hybrids at multiple locations in Malaysia

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Abstract

This study was conducted to investigate the genotype by environment (G×E) interaction of 20 rice hybrids tested in eight environments which include four locations and two different cropping seasons in Malaysia. The parameter was observed on yield per ha, number of panicles per plant, number of filled grains per panicle, and thousand-grain weight. Data analysis was used by ANOVA and stability measurement according to AMMI and GGE biplot graph. The ANOVA indicated that all studied phenotypic showed significantly different in variance genotypes, season, location, location × season, genotype × season, genotype × location × season. The most promising hybrids were G19, G3, G18, G13, G8, G7, and G14, resulting in a higher mean yield per ha. The multivariate stability analysis defined those hybrids divided into three categories. The first category is hybrids with high mean yield and wide adaptability (G19, G18, G3 and G4), the second category is the hybrid exhibiting high mean yield and is suitable for a specific environment (G12) and lastly, a hybrid with low yield and high stability (G9, G11 and G1). Hybrids with high yield and stable performance could be further evaluated in large-scale planting for prior release for commercial.

Introduction

To combat future population challenges, increasing current rice yield has received attention in recent decades. As a result, plant breeders, agronomists, weed scientists, and physiologists have employed a variety of techniques, such as the selection of the most suitable and adapted high-yielding varieties for the rice-growing environment, fertiliser management, weed management, nursery management, quality seed, crop establishment, and post-harvest management. Because these traits are heritable, breeding for high yielding has been identified as the most sustainable method

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among these. Plant breeders, however, found it difficult to directly select this ideal genotype due to the high influence of genotype by environment (GE) interactions on grain yield (i.e. high yielding cultivars). Genotypes evaluated in different seasons or locations frequently show phenotypic variation such as yield due to environmental factors such as temperature, humidity, pests, and diseases influencing genotypes. Although some hybrids may have wide adaptability across environments and some are highly influenced by the change in the environment which performs inconsistently in other locations (Akter et al., 2019). Environmental factors that contribute to hybrid rice yield include cool air temperature and high accumulative solar radiation during the grain filling stage (Jiang et al., 2016). According to Huang et al. (2017), the yield of super hybrid rice Zhunliangyou 527 and Liangyou 293 could reach more than 12 t/ha in Hunan and Guizhou provinces of China but averaged 7.5 t/ha in Gazipur, Bangladesh.

Stability analysis is necessary to define the adaptability of rice varieties, which may have a broad range of adaptability or a greater response in specific environments. Before being recommended for introduction and growth in diverse environments/locations, genotypes must be selected for stability and adaptability. Multivariate stability methods are the most recently used analysis in exploring and discovering patterns of GE interactions. The additive main effects and multiplicative interaction (AMMI) and genotype main effect (G) and GE, also known as GGE biplot, are the most commonly used multivariate approaches for the analysis of GE interactions. Both methods provide a graphical representation of the interaction patterns and describe the interrelationships between genotypes, environments, and GE interactions to identify stable genotypes and genotypes that have adapted to specific environments.

Information on GE interactions and stability factors for Malaysian environments can help to identify stable and high-yielding hybrids for cultivation across local rice granary areas, increasing national rice production and farmer income. The need to evaluate pre-release hybrids to identify high-yielding rice hybrids, better adaptability as well as their performance in local environment. To accomplish this, it is necessary to understand the factors that contribute to the phenotypic expression that could guarantee farmers a rice hybrid with superior yield performance. Therefore, a genotype by environment study was carried out on 22 MARDI rice genotypes, which included 20 rice hybrids and two check inbred varieties, across four locations and two cropping seasons to investigate stable hybrid performance in specific or across environments.

Materials and methods

Plant materials, location and crop management

In eight environment trials, a total of 20 newly produced hybrids and two locally popular inbred varieties namely, MR269 and MR263 (Table 1), were tested in a combination of two cropping seasons and eight environments. The trials were carried out in irrigated rice granaries in Peninsular Malaysia, specifically in the states of Penang, Perlis, and Kedah (Table 2). Similar descriptions of the weather, seasons, trial location, and soil texture were given in Elixon et al. (2022) earlier study. The experiment was layout using Randomised Completely Block Design in each environment, with plot sizes of 2.5 m × 2.5 m for each genotype. After transplanting, N, P_2O_5, and K_2O fertilisers were applied at rates of 120, 70, and 80 kg/ha during the early vegetative (10–15 days), active vegetative (30–35 days), panicle initiation (50–55 days), and grain filling (70–75 days). The grain yield of rice genotypes was determined by threshing 1.5 m× 1.5 m of crop cutting test of each genotype. The cleaned and dried grain was then weighed, and the final weight was 14% adjusted. Five representative sample plants were chosen at random from each genotype in each replication to record observations of yield component traits such as number of panicles per plant (NP), number of filled grains per panicle (FGP), and thousand grains weight (TGW).

Table 1. Malaysian rice hybrids used in study

Genotype code	Parents	Type
G1	IR79126A × 6165R	F_1 hybrid
G2	IR70369A × 6161R	F_1 hybrid
G3	0047A × P584	F_1 hybrid
G4	IR70369A × 6559R	F_1 hybrid
G5	IR70369A × ENT42	F_1 hybrid
G6	IR70369A × ENT19	F_1 hybrid
G7	IR70369A × YBL537	F_1 hybrid
G8	0047A × E54	F_1 hybrid
G9	0025A × MRQ97	F_1 hybrid
G10	0025A × 6117R	F_1 hybrid
G11	IR70369A × 6296R	F_1 hybrid
G12	0047A × 6161R	F_1 hybrid
G13	0025A × 6594R	F_1 hybrid
G14	0047A × 6187	F_1 hybrid
G15	0047A × MR152	F_1 hybrid
G16	0047A × 6301R	F_1 hybrid
G17	0025A × 6149R	F_1 hybrid
G18	0047A × YBL537	F_1 hybrid
G19	0047A × 6289	F_1 hybrid
G20	0025A × ENT19	F_1 hybrid
G21	MR263	Inbred (check variety)
G22	MR269	Inbred (check variety)

Table 2 Description of the trial plot based on location and season

No	Environment	State	Cropping Season	Ecosystem
1	Bukit Merah (BM1)	Penang	main season	Irrigated
2	Bukit Merah (BM2)	Penang	off-season	Irrigated
3	Telok Chengai ((TC1)	Kedah	main season	Irrigated
4	Telok Chengai (TC2)	Kedah	off-season	Irrigated
5	Bertam (BR1)	Penang	main season	Irrigated
6	Bertam (BR2)	Penang	off-season	Irrigated
7	Arau (AR1)	Perlis	main season	Irrigated
8	Arau (AR2)	Perlis	off-season	Irrigated

Notes: Main season (November 2016 to March 2017) and off-season (April 2017 to September 2017)

Statistical and stability analysis

A combined analysis was performed on the mean data from each location to generate mean data for the different statistical analysis methods (Table 3). For data analysis, the SAS programme version 9.3 was used. Genestat software was used to perform the AMMI and GGE biplot analysis. Seasons, locations, genotypes, and replication were studied as a random effect. If the interaction between genotype and environment was significant, an additional statistical analysis was required to determine genotype stability across eight environments.

Table 3. Analysis of variance analysis and mean square expectations for combined location

Source	**DF**	**MS**	**EMS**
Season (S)	s -1		
Location (L)	l – 1		
S×L	(s - 1) (l - 1)		
Rep in L and S	ls (r - 1)		
Genotype (G)	g -1	MS1	$\sigma^2_e + r\,\sigma^2_{g\ell S} + rl\,\sigma^2_{gs} + rs\,\sigma^2_{g\ell} + rls\,\sigma^2_g$
G×L	(g - 1) (l - 1)	MS2	$\sigma^2_e + r\,\sigma^2_{g\ell S} + rs\,\sigma^2_{g\ell}$
G×S	(g - 1) (s - 1)	MS3	$\sigma^2_e + r\,\sigma^2_{g\ell S} + rl\sigma^2_{gs}$
G×L×S	(g - 1) (l - 1) (s - 1)	MS4	$\sigma^2_e + r\,\sigma^2_{g\ell S}$
Error	ls (g - 1) (r - 1)	MS5	σ^2_e

Notes: DF (degree of freedom), MS (mean squares) EMS (expected mean squares), σ (variance), s (season), l (location), g (genotype), r (replicate), σ^2_e (error variance), σ^2_{gls} (Genotypic variance due to genotype × location × season), σ^2_{gl} (Genotypic variance due to genotype × location) and σ^2_{gs} (Genotypic variance due to genotype × season)

Broad-sense heritability calculated as (h^2_B) = (σ^2_{pg}/σ^2_g)/100, where σ^2_g and σ^2_p are the genotypic and phenotypic standard deviation, respectively. The variance phenotypic calculated as (σ^2_p) = $\sigma^2_g + \sigma^2_{gl} + \sigma^2_{gs} + \sigma^2_{gls} + \sigma^2_e$ and variance genotypic (σ^2_g) = [(MS1+MS4) – (MS2+MS3)]/rls Heritability is classified as high, moderate and low, respectively when the values are above 60%, between 30% - 60% and lower than 30% (Johnson et al., 1955). The phenotypic (PCV) and genotypic (GCV) coefficients of variation are determined with PCV = ($\sigma^2 p/\bar{X}$) ×100% and GCV = ($\sigma^2 g/\bar{X}$) ×100%, where $\sigma^2 p$ and $\sigma^2 g$ are the phenotypic and genotypic variances, whereas, the $\bar{X}$ is the mean value of the trait (Singh and Chaudhary,1985). The PCV and GCV values are categorised as high, moderate, and low, respectively, when they are above 20, between 10 and 20, and less than 10 (Burton, 1952). Meanwhile, AMMI (Gauch, 2006) and GGE biplot were used in the stability analysis of all the characters to demonstrate the GEI effect (Yan et al., 2000).

Results and discussion

Combined analysis of variance, variance components and mean performances

The yield component traits FGP, EGP, and TGP were highly significant, indicating that each genotype is genetically diverse and reliable for character selection of these traits, which is consistent with the findings of Yadav et al. (2018). The ANOVA analysis revealed that the variances for genotype, season, location, location×season, genotype×season, genotype× location×season (G×E) showed highly significant differences for the YLD, NP, FGP, and TGW characters. The presence of genotype variability for all studied characters would increase the chances of selecting genotypes with desirable traits, particularly yield and yield-related traits. The significant interaction due to G×E is an indicator of the varying response of rice genotypes to quantitative characteristics across environments. This means that assessing genotypes for stability analysis is required for identifying genotypes with either general adaptability or specific adaptation (Lakew et al., 2017). The portioning of the total sum square inTable 4 explained the variation of all traits. Except for TGW, a large variation observed on YLD, NP and FGP (40.12%, 30.19% and 7.42%, respectively) indicative that locations were diverse which larges differences among location effects that cause the most variation. A large sum of the square for genotype on all traits (range from 20.67% to 60.89%) indicated that genotypes were diverse; in contrast, a small variation was observed due to season which range from 0.72% to 6.16%. For TGW, it found that variation due to season was larger than location indicative responses of genotypes across cropping seasons were determinant than locations. Generally, the magnitude of genotype found sizeable than G×L, G×S and G×E factors for all traits indicative that sufficient number of genes controlling the phenotypic expression. Among these interactions, the G×S had the least variation effects on YLD, NP, FGP and TGW (range from 2.37% to 3.83%) as compared to G×L and G×E which accounted about (4.99% to 10.85%) and 5.34% to 10.54%, respectively.

Table 4. Combined ANOVA for YLD, NP, FGP and TGW traits of the rice genotypes in eight environments

Source	DF	YLD		NP		FGP		TWG	
		MSS	ESS (%)	MSS	ESS (%)	MSS	ESS (%)	MSS	ESS (%)
Locations (L)	3	319.27**	40.12	820.57**	30.19	20380.62**	12.12	7.42**	0.80
Reps (S×L)	16	0.61**	0.41	18.09**	3.55	587.18**	1.86	0.72	0.41
Season	1	17.13**	0.72	99.93**	1.23	16292.59**	3.23	171.94**	6.16
Genotypes (G)	21	23.50**	20.67	87.86**	22.63	9161.19**	38.13	80.99**	60.89
S×L	3	71.21**	8.95	207.24**	7.62	19178.82**	11.40	15.11**	1.62
G×L	63	4.11**	10.85	10.16**	7.85	688.43**	8.60	2.21*	4.99
G×S	21	3.03**	2.67	9.22**	2.37	874.21**	3.64	5.09**	3.83
G×L×S	63	3.99**	10.54	8.76**	6.77	681.34**	8.51	2.37**	5.34
Error	336	0.36	5.07	4.32	17.79	187.79**	12.51	1.33	15.97
Total	527								

Notes: YLD (yield), NP (number of panicles per plant), FGP (filled grains per panicle), TWG (thousand grain weight), **(highly significant at the 1% level) and *(significant at the 5% level).

The estimated GCV for YLD, NP and FGP was moderate, but low for TGW (Table 5). For YLD, NP, and FGP, the PCV was high, but for TGW, it was low. A high PCV for yield trait is consistent with the finding by Ismaeel et al. (2018). Low PCV for TGW was contradicting from Kumar et al. (2018) and Tuhina-khatun et al. (2015), who reported high and moderate PCV for this trait, respectively. TGW has a low GCV, indicating that it performed under genetic control and has limited potential for trait improvement. Overall, there were significant differences between PCV and GCV in YLD, NP, and FGP traits, indicating phenotypic performance under environmental influences. Large variation in the YLD trait may be due to meteorological factors such as rainfall and temperature, which invariably control the crop's yield potential (Shrestha et al., 2020; Kanfany et al., 2021). According to Xuan et al. (2019), temperature factors have a significant impact on yield, particularly during the grain filling and flowering stages. Similarly to FGP, this trait is usually influenced by environmental factors (Li et al., 2019). The broad-sense heritability of the YLD and NP traits was moderate. This may be due to environmental influences on the polygenic nature of this trait (Gyawali et al., 2018). The broad sense (h^2_b) heritability of FGP and TGW characters was found to be high, with a sufficient amount of genotypic for further progeny selection. However, heritability is a secondary character in this study because all materials studied are F_1 hybrids with no further selection in segregate progenies.

Table 5. Genetic variance components and heritability

Traits	σ^2_g	σ^2_{gl}	σ^2_{gs}	σ^2_{gls}	σ^2_p	σ^2_e	GCV (%)	PCV (%)	h^2_B
YLD	0.85	0.02	0.00	1.21	2.44	0.36	14.17	24.03	58.96
NP	3.22	0.23	0.04	1.48	9.29	4.32	13.39	22.74	58.86
FGP	345	1.18	16.07	164.52	714.56	187.79	14.45	20.80	69.48
TGW	3.17	0.00	0.23	0.35	5.07	1.33	6.48	8.19	79.06

Notes: σ^2_g (Genotypic variance), σ^2_{gl} (Genotypic variance due to genotype) × location$_,$ σ^2_{gs} (Genotypic variance due to genotype × season)$_,$ σ^2_{gls} (Genotypic variance due to genotype × location × season)$_,$ σ^2_e (Error variance), σ^2_p (Phenotypic variance), GCV (Genotypic coefficient of variation), PCV (Phenotypic coefficient of variation), h^2_B (Broad-sense heritability), YLD (yield), NP (number of panicles per plant), FGP (number of filled grains per panicle) and TGW (thousand grain weight).

Mean performance of rice hybrid characters

The mean YLD of genotypes in different environments ranged from 4.81 to 8.21 t/ha (Table 6). The results showed that hybrids G19, G3, G18, G13, G8, G7, G14, and G12 had significantly higher mean YLD than check varieties MR263 and MR269. Secondary rice traits FGP, FGP, and TGW contribute to YLD production. The range of mean NP production across environments was 10.32 to 16.46 panicles. Overall, hybrids G18 and G3 produced significantly higher mean NP than check varieties MR263 and MR269 and lower production in hybrids G17, G11, G6, G4, G14, G20, and G2. The average FGP ranged from 109.13 to 184.08 grains per panicle. It was discovered that hybrids G14, G19, G12, G17, G20, and G10 produced significantly higher mean FGP than the control varieties. The TGW ranged from 24.45 to 30.85 g on average. Rice hybrids G6, G20, G5, G7, G11, G4, G2, G14, G3 and G18 are desirable because they have significantly heavier grain than check varieties. In contrast, hybrid G8 had significantly lower TGW than control varieties.

Table 6. Mean for yield and yield components of 22 rice genotypes tested over the mega environment

Genotypes	YLD (t/ha)	NP	FGP	TWG (g)
G1	5.07^{ij}	13.98^{cde}	115.38^{fghi}	23.64^{k}
G2	5.50^{ghij}	12.15f^{ghi}	121.96^{efghi}	28.26^{def}
G3	8.10^{ab}	16.21^{a}	127.54^{defgh}	28.09^{def}
G4	4.81^{j}	11.34^{hij}	120.71^{efghi}	28.59^{cdef}
G5	5.83^{fghij}	12.56^{defgh}	108.54^{i}	29.93^{abc}
G6	5.56^{ghij}	10.99^{hij}	115.54^{fghi}	30.85^{a}
G7	7.24^{abcde}	15.19^{abc}	113.96^{ghi}	28.94^{bcd}
G8	7.34^{abcd}	16.00^{ab}	132.08^{def}	24.45^{jk}
G9	6.53^{defg}	15.27^{abc}	121.00^{efghi}	25.75^{ij}
G10	6.81^{cdef}	12.53^{defghi}	135.63^{cde}	27.27^{fgh}
G11	5.68^{ghij}	10.93^{hij}	115.71^{fghi}	28.73^{cde}
G12	7.16^{bcde}	12.35^{efghi}	153.25^{bc}	27.53^{efg}
G13	7.49^{bcde}	13.52^{cdefg}	130.79^{defg}	27.79^{def}
G14	7.22^{bcde}	10.93^{hij}	184.08^{a}	28.16^{def}
G15	6.24^{efgh}	15.19^{abc}	121.50^{efghi}	25.06^{ij}
G16	6.53^{defg}	14.85^{abc}	109.13^{i}	25.96^{hi}
G17	5.48^{hij}	10.32^{j}	144.08^{cd}	27.95^{def}
G18	7.80^{abc}	16.46^{a}	122.54^{efghi}	28.09^{def}
G19	8.21^{a}	13.79^{cdef}	170.63^{ab}	27.26^{fgh}
G20	6.80^{cdef}	11.86^{ghij}	135.67^{cde}	30.21^{ab}
G21	5.90^{fghi}	14.24^{bcd}	114.71^{fghi}	26.23^{ghi}
G22	5.68^{ghij}	14.08^{cde}	112.63^{hi}	25.96^{hi}

Continued Table 6

Genotypes	YLD (t/ha)	NP	FGP	TWG (g)
Mean	6.50	13.40	128.50	27.49
CV (%)	9.23	15.52	10.66	4.19
LSD $^{0.05}$	2.34	1.82	17.75	0.96

Means in the same column with the same superscript are not statistically different at the 5% level of the LSD (Least Significant Different) test. YLD (yield), NP (number of panicles per plant), FGP (number of filled grains per panicle) and TWG (thousand-grain weight).

Multivariate analysis as explained by AMMI biplot graph

The magnitude of interaction using AMMI can be visualised using the IPCA 1 vs. mean trait and IPCA 1 vs. IPCA 2 biplot models for each genotype and environment (Yan et al., 1998). The IPCA score of genotypes is an indicator of environmental adaptability and the relationship between genotypes and environments (Mahalingam et al., 2006). The most stable genotypes have an IPCA score close to zero (Sudhir et al., 2017). According to Balakrishnan et al. (2016), the closer a genotype's IPCA score is to zero, the more stable it is; conversely, a genotype with a high IPCA score, whether positive or negative, indicates that the genotype has adapted to a specific environment.

In AMMI 2 biplot, genotypes located farthest from the biplot centre are more sensitive and have a high level of environmental interaction than those located closer to the biplot centre (Lakew et al., 2017; Oladosu et al., 2017). The genotype closer to the centre origin is more stable and would be criteria for selecting rice hybrids with good adaptation. In Figure 1, the AMMI biplot graph showed the presence of GEI on studied traits when the first two principal component interactions account for approximately 63.55%, 63.08%, 60.32%, and 50.18% of genotype and genotype by environment variation, respectively, for YLD, FGP, NP, and TGW traits. For the YLD trait, high-yielding hybrid G8 performed consistently, as shown near the biplot origin (Figure 1A). Other high-yielding hybrids, such as G19, G3, G18, and G7, performed similarly well. It has been suggested that the above hybrids are desirable due to their broad adaptability and relatively high YLD production. The hybrids G12 and G13 produced a high mean YLD but interacted with the environments TC2 and AR2. G16, G9, G8, and G18 hybrids performed well as they got closer to the biplot centre (arrow) and produced a lot of panicles. Hybrids G3, G7, and G15 were among the hybrids with the highest mean NP panicle production but were located farthest from the biplot centre, indicating instability (Figure 1B). Hybrid G15 is suitable for environment BM1, whereas hybrids G3 and G7 are suitable for environment AR1. Hybrids G14, G19, G12, G17, G20, and G10 hybrids produced a high mean FGP grain yield (Figure 1C). However, as shown in the biplot centre, these hybrids performed unstable for FGP grains. AR1 environment was found to be suitable for hybrids G19 and G17, hybrids G14 and G12 were found to be suitable for TC2, BM1 and TC1 were found to be suitable for G20, and TC2 was found to be suitable for G10. Hybrids G16, G15, G6, and G7 were stable genotypes that were closer to the biplot centre (Figure 1D). However, the mean performance of these hybrids was below average for FGP production. Hybrids G2, G3, and G14 are desirable for TGW weight and performed with less environmental influence, as shown closer to the biplot centre. The hybrids G6, G20, G11, and G11 had higher TGW and performed better under low environmental variation, as shown near the biplot centre. The hybrids G4, G5, and G7 performed unstable in TGW weight expression, as shown by the position closest to the biplot centre.

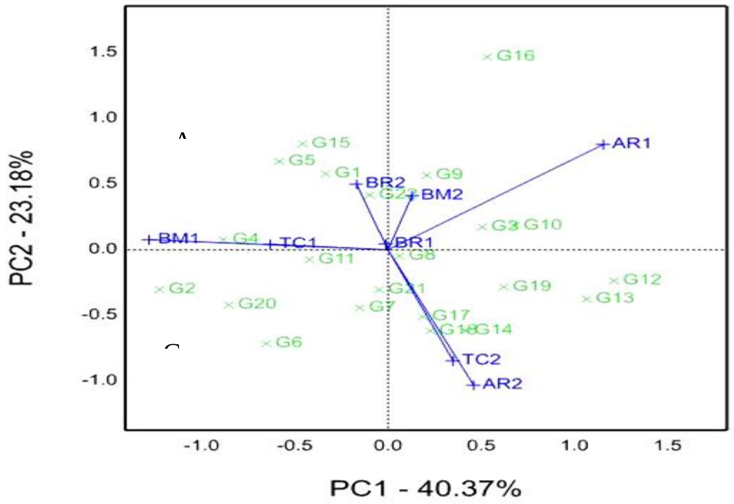

Figure 1A. AMMI biplot IPCA 1 vs. IPCA 2 on 22 rice genotypes for YLD per ha

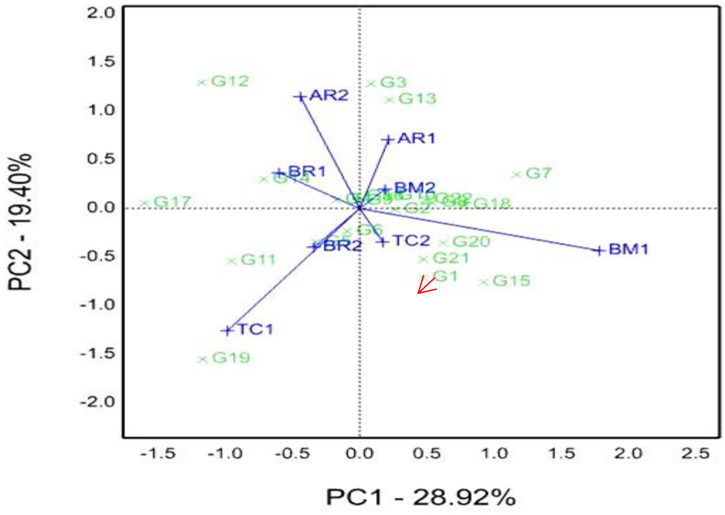

Figure 1B. AMMI biplot IPCA 1 vs. IPCA 2 on 22 rice genotypes for YLD NP panicles

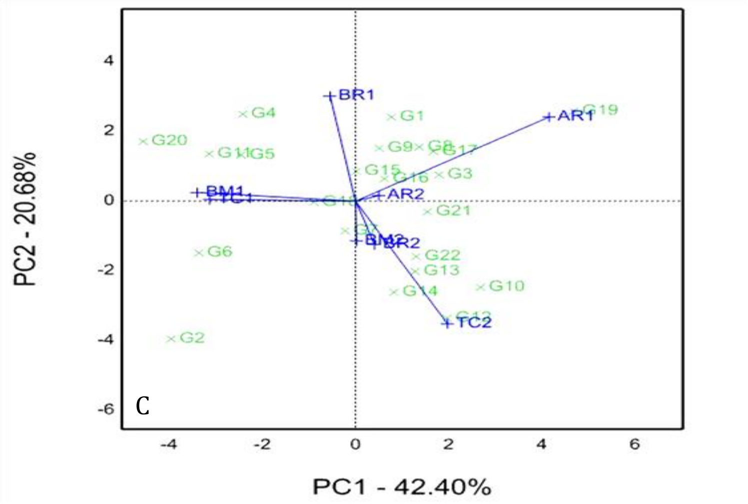

Figure 1C. AMMI biplot IPCA 1 vs. IPCA 2 on 22 rice genotypes for FGP grains production

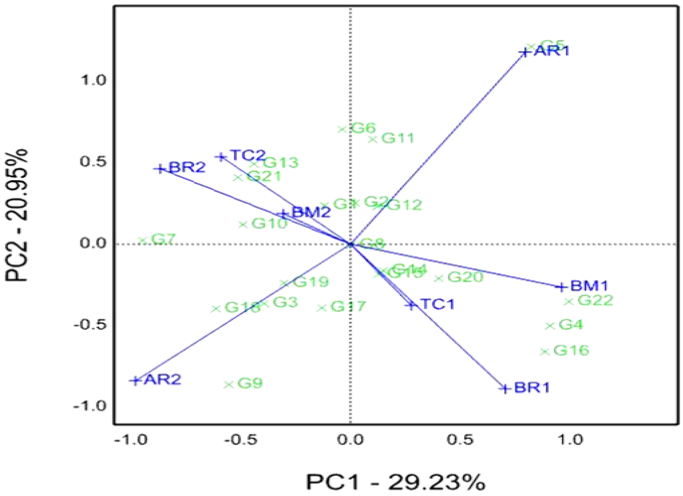

Figure 1D. AMMI biplot IPCA 1 vs. IPCA 2 on 22 rice genotypes for TGW grain weight in two seasons and eight environments

GGE biplot analysis of rice genotypes for yield and yield components

The genotype (G) primary effects and the genotype by environment interaction (GGE) are graphically represented in the GGE biplot graph (Yan et al., 2000). The G and GE are the two primary sources of variation for genotype evolution in a variety of environments. The GGE biplot analysis represents the G+GE of various environmental records obtained by plotting two (or more) PCA scores of G E interaction. The GGE biplot graph is divided into three parts: the polygon view of which-won-where pattern, which is useful for identifying the best genotypes for environments, the results of mean performance vs. stability of rice genotypes, and the third, which is used to identify better genotypes as they get closer to the concentric centre of the ideal genotype biplot.

GGE biplot graph for which-won-where view

The GGE biplot of the which-won-pattern pattern is explaining the specific genotypic adaptation in a limited environment or at each environment (Jain et al., 2019). A polygon was formed by connecting the vertex genotypes with lines and the genotypes were placed within the polygon (Sairekha et al., 2018). The polygon is divided into sectors confirming the existence of GEI. The vertex or winning varieties in each sector were the best or poorer in certain or in all tested environments because they are connected furthest from the origin (Neisse et al., 2018). The present study showed that the portioning of GEI of GGE biplot analysis accounted for 74.75%, 72.26%, 80.93% and 87.53% of total variance for YLD, NP, FGP and TGW traits, respectively (Figure 2). In Figure 2A, the YLD vertex genotypes were G12, G19, G18, G7, G2, G4, and G16. The GGE biplot graphically demonstrates that hybrid G19 is the vertex genotype in environments AR1, AR2, BR1, BM2, and TC2. In TC1, hybrid G18 was used as the vertex genotype, hybrid G7 in BM1, and hybrid G12 in BR2. Other hybrids that were not represented in any environments were concluded to be poor genotypes for YLD production and could be discarded. The polygon view for NP panicles (Figure 2B) revealed that hybrid G15 as the best vertex genotype for BM1, G18 as the best vertex genotype for TC1, TC2, BR2 and BM2, and G3 as the best genotype for AR1, AR2 and BR1. For the FGP trait (Figure 2C), hybrid G14 was a vertex genotype for environments BM1, BM2, BR1, BR2, AR2, TC1 and TC2, whereas G19 was a winning variety for AR1. The TGW weight polygon view (Figure 2D) showed hybrid G5 as the vertex genotype for environments BM1 and BR1, and hybrid G6 as the vertex genotype for BM2, TC2, AR2, BR2, AR1 and TC1.

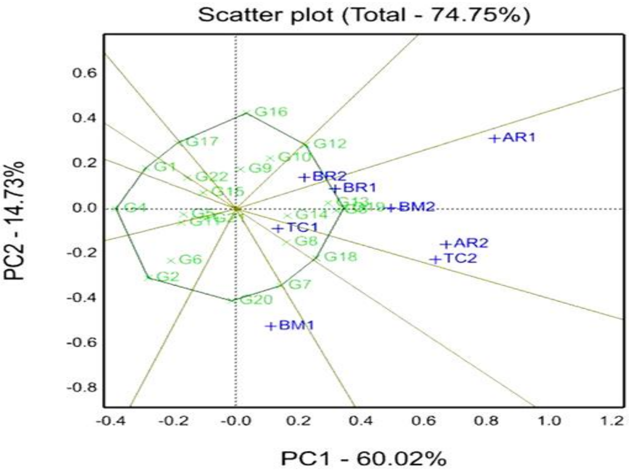

Figure 2A. GGE biplot polygon view which-won-where pattern of 22 rice genotypes for YLD per ha

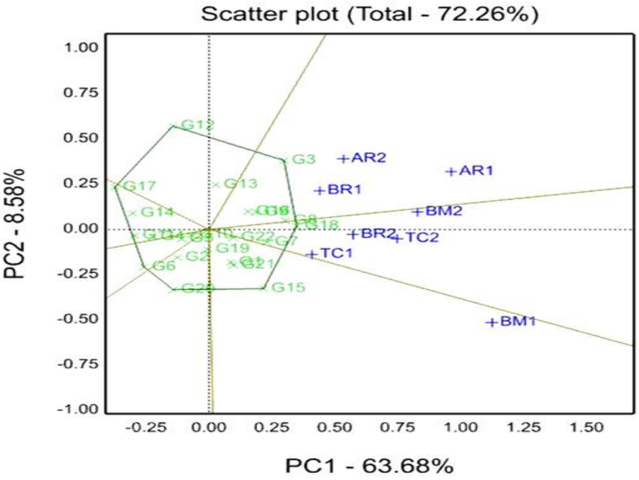

Figure 2B. GGE biplot polygon view which-won-where pattern of 22 rice genotypes for NP panicles

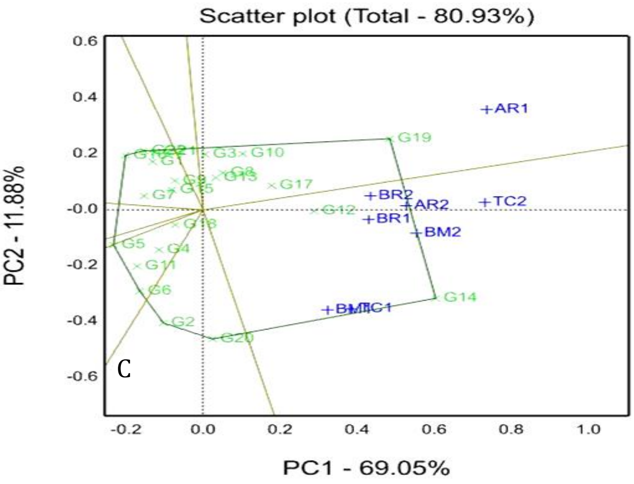

Figure 2C. GGE biplot polygon view which-won-where pattern of 22 rice genotypes for FGP grains production

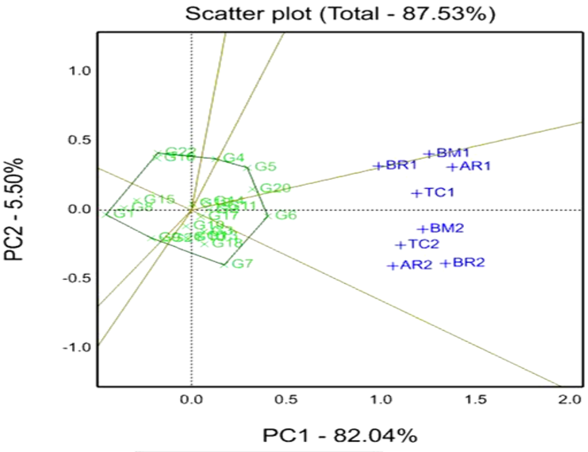

Figure 2D. GGE biplot polygon view which-won-where pattern of 22 rice genotypes for TGW grain weight in two seasons and eight environments

GGE biplot graph for mean performance vs. stability

The average environment coordinate (AEC) method was used to estimate trait performance and genotype stability (Yan, 2001). The average environment coordinate is the line that passes through the perpendicular line of biplot origin. The genotype mean yield is indicated by the direction in which the arrows point to a small circle (Neisse et al., 2018). The closer to the concentric circle, the higher the mean of the traits. Meanwhile, the perpendicular lines traverse the biplot origin, indicating genotype stability (Akter et al., 2015). Genotypes that are closer to the AEC line have higher genotype stability (Islam et al., 2020). The ideal hybrid has a high mean YLD per ha as well as stability. Hybrids with a high mean YLD per ha had G19, G3, G18, G13, G8, G7, G14, and G12 (Figure 3A). Hybrids G19, G3, G18, G13, G8, and G14 performed stable as their lines closer to AEC whereas G7 and G12 were unstable, as evidenced by longer lines length from AEC. Figure 3B showed that hybrids with higher mean NP panicles were G18, G3, G8, G9, G7, G15, and G14, meanwhile, G18, G8, G9, and G7 were found to be more closely related to AEC lines, indicating stable performance and a higher mean NP production. Hybrids G14, G19, G12, G17, G10, G20, G10, G8 and G13 were hybrids with higher mean FGP grain production (Figure 3C). Among them, hybrids G14, G19, and G10 were unstable as longer perpendicular lines from AEC. Hybrids G6, G20, G5, G7, G11, G4, G2, G14, G3, G18, G3, G13 and G12 were hybrids with higher TGW weights that performed above average (Figure 3D). The majority of them performed well in a variety of environments and had a higher TGW weight. However, hybrids G5, G4, and G7 were influenced by environmental variation and were shown to be the furthest away from the AEC line.

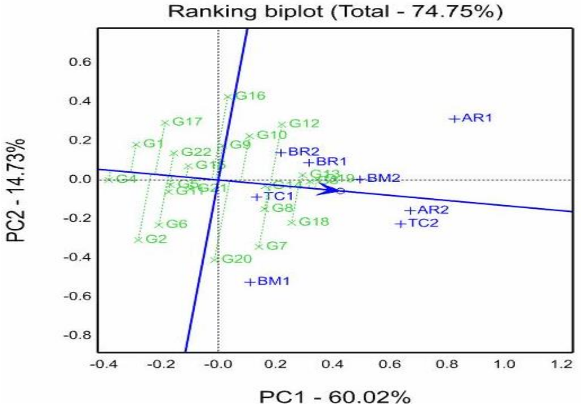

Figure 3A. Mean performance and ranking stability GGE biplot of 22 rice genotypes for YLD per ha

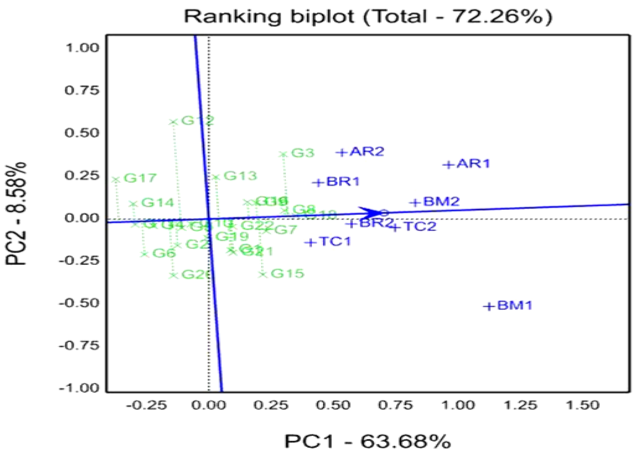

Figure 3B. Mean performance and ranking stability GGE biplot of 22 rice genotypes for NP particles

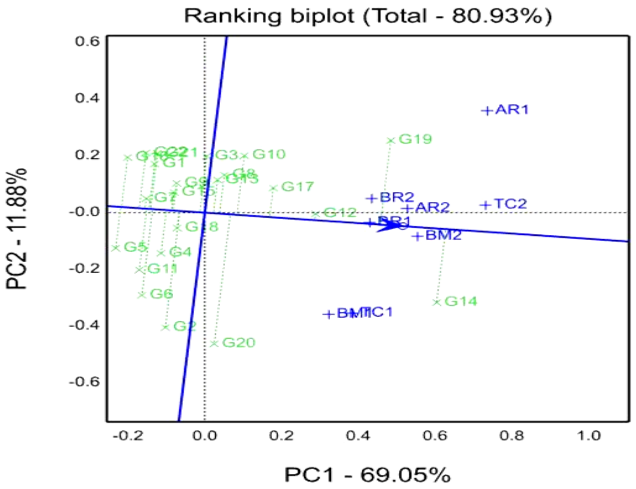

Figure 3C. Mean performance and ranking stability GGE biplot of 22 rice genotypes for FGP grains production

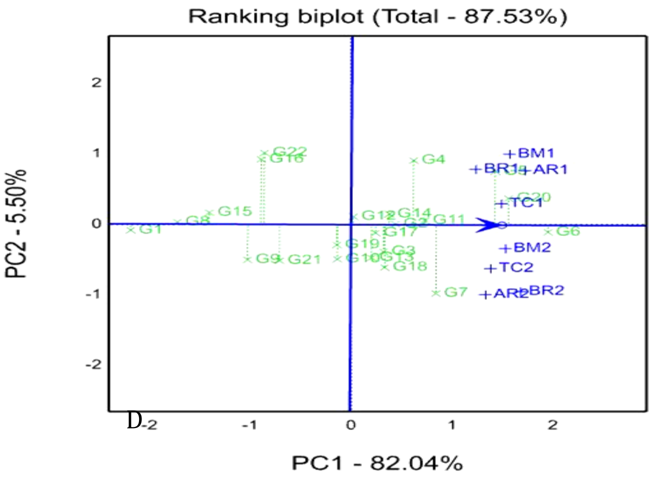

Figure 3D. Mean performance and ranking stability GGE biplot of 22 rice genotypes for TGW grain weight in two seasons and eight environments

Overall, the most promising hybrids discovered in G19, G3, G18, G13, G8, G7, and G14 produced higher mean YLD per ha in all environments. The multivariate method was able to perform stability analysis and aid in the selection of potential hybrids that performed well in the environment and had a high mean yield. In this study, hybrids were classified into three types based on their response to the environment: high yielding hybrids with broad adaptability to the environment, hybrids with responsiveness in a specific environment, and hybrids with stable performance but low YLD per ha. Other phenotypic traits, such as NP, FGP, and TGW, demonstrated a similar pattern of response over environment based on genotype. With a focus on the YLD trait, the AMMI and GGE biplot graphs show that hybrids G19, G8, G3, and G14 have broad environmental adaptability and are desirable with a high mean YLD per ha. Similarly, hybrid G12 had a higher mean YLD per ha than check varieties but were responsive in a specific environment.

Conclusion

A high-yielding hybrid is a major goal of the hybrid breeding programme. The desirable hybrid should outperform current popular varieties in terms of yield, adaptability, and have a low degree of environmental interaction. Furthermore, a hybrid that has been specifically grown to have a high degree of environmental influence would be more productive. The hybrids G19, G3, G18, G13, G8, G7, G14, and G12 had significantly higher mean YLD per ha than the control varieties MR263 and MR269. An ideal hybrid should be able to respond to both mean traits and stability at the same time. The AMMI and GGE biplot stability suggested that hybrids G19, G3, G18, G8, G14, and G12 performed well and had a wide range of adaptability, which would be beneficial for Malaysia, which has a high degree of unpredictability in its environment. Furthermore, hybrids G12 and G13 were developed specifically for environments/locations with a high degree of environmental variation. Yield component traits NP, FGP, and TGW react differently in different environments and compensate for yield productivity.

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Author 's declaration and contribution

The author declares that he has no conflicts of interest with regard to the publication of this paper. All authors contributed equally from research planning to data analysis, supervising the experimental work, and reviewing results.

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