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Genotype by environment interactions of grain yield performance and lodging incidence in advance breeding lines of rice across environments in Guyana

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**Mahendra Persaud¹,
Rajendra Persaud^{1*},
Nandram Gobind¹,
Ayub Khan²
Gomathinayagam
Subramanian³
and
Edgar Corredor⁴**

¹Guyana Rice Development Board (GRDB), Rice Research Station, Burma, Mahaicony, East ² Coast Demerara, Guyana.

² Faculty of Science and Technology, The University of the West Indies, St. Augustine, Trinidad and Tobago.

³ Faculty of Agriculture and Forestry, University of Guyana, Berbice Campus, Tain, Guyana.

⁴Fund for Latin America Rice/Central Institute for Tropical Agriculture, Cali, Colombia.

*Corresponding Author Email: rajpersaud25@yahoo.com, rpersaud@grdb.gy

Fifteen advanced rice (*Oryza sativa* L.) breeding lines along with three check varieties were assessed for lodging incidence and grain yield stability under six environments in Guyana. The trials were conducted in the spring and autumn seasons of 2018. A RCBD with three replication was employed. Descriptive statistics was used to look at the lodging incidence and AMMI & GGE analysis was utilized to study the genotype and environment (G x E) interactions. All genotypes (except G15-11, FG15-01, and check GRDB 10) recorded mean lodging incidence of less than 5 percent. The average grain yield of the 18 genotypes ranged from 5504.44 to 7499.21 Kg/ha. The biplot results showed genotype FG12-259 demonstrated consistently high stable grain yield performance followed by FG12-49, FG12-23, FG14-43, G13-126, G15-11, G14-10 and G16-104. Likewise, AMMI analysis found the environment at Rice Research Station, Burma, Region # 5, Spring crop, 2018 (E2) and Anna Regina, Region # 2, Autumn crop, 2018 (E4) to be the most representative environment with smaller average - environment axis (AEA) angle and closeness to the ideal test environment. Also, E4 followed by Lesbeholden, Black Bush Polder, Region # 6, Autumn crop, 2018 (E6) recorded low IPCA1 scores and showed small interactions. The what-won-where biplot pattern suggested the target environment consisted of three mega-environments since four environment falls in one sector and one each in another two sectors. The three check cultivars GRDB 10 GRDB 12 and GRDB14 also expressed a similar higher level of stable grain yields over all the test environments. Based on the consistently high and stable grain yield performance, along with other superior grain qualities and plant characteristics the genotypes *viz.* FG12-259 and FG12-49 were selected, developed, and released as commercial rice varieties called 'GRDB 16' and 'GRDB 15', respectively in Guyana for wider cultivation by the farmers.

Keywords: AMMI analysis; biplot; Stable grain yield; advance genotypes; genotype by environment interaction.

INTRODUCTION

Rice (*Oryza sativa* L.) has been cultivated as a major staple food crop for more than 60 percent of the world population and plays a key role in food and nutrition security globally (Pal and Mandal, 2021). As a cultivated cereal crop, it serves as a major source of income for persons in developing countries and many other parts of the world where it has been cultivated. However, to fulfill the daily

consumption and dietary intake of nearly millions of people in the world there is a need to develop and produce stable disease-resistant and high yielding cultivars (Persaud et al., 2021).

Plant lodging is basically the physical collapse of the plant canopy which can happen spontaneously because of mechanical instability or poor plant structure, through

external forces such as heavy rain falls and strong wind, or both (Shrestha et al. 2020). It is a major yield reducing factor in rice systems, particularly under intensified cultivation using high-yielding cultivars. At field level more than 50% yield reduction can be experience based on the field area affected by lodging. This is as a result of combined with reduced photosynthesis of the collapsed canopy, reduced grain recovery in mechanized harvesting systems, and pathogen complexes benefiting from high humidity in the collapsed canopy which also results in deuteriation and loss of grain quality. (Shrestha et al. 2020).

Multi-environment testing (MET) trials were used by plant breeders in different parts of the world where rice has been cultivated to understand the performance of new genotypes being developed for adoption to various environmental and biotic stresses conditions, meteorological components and cultivation practices, other such as soil conditions, field management or weather factors that influence the expression of genes for stable rice grain yield & lodging (Persaud et al. 2021). In order to have clear understanding of genotype by environment (GxE) interaction, many researchers have developed new and innovative analytical tools (Cooper and Delacy, 1994). Two such analytical tool developed was the Additive Main effects and Multiplicative Interaction (AMMI) model and the genotype main effects and genotype x environment interaction effects (GGE) model for understanding the interaction of the Genotype by Environment (Gauch 2006; Gauch, 2013; Mukherjee et al., 2013). The AMMI model analysis first accounts for the main effects and then applies the principal-component analysis to account for the interaction effects (Gauch, 2006). Many researchers have successfully demonstrated the potential utility of the AMMI models to understand G x E and to identify stable rice grain yield genotypes across varying environments (Persaud et al., 2021). The AMMI model analysis also identified the best and average environment, the winning genotypes within the various mega-environments and stable performance of the genotypes (Yan and Tinker 2006).

The rice industry in Guyana is one of the most important agriculture industries that contribute significantly with more than 22% to the country's GDP. It supports more than 10% of the Guyanese population directly or indirectly by providing a source of income for its people (Persaud et al., 2021). Rice is being cultivated primarily within five administrative regions (i.e., in regions number 2, 3, 4, 5, and 6) in Guyana, and recently a new expansion started with some quantity of rice cultivation in region number 9. In the different regions, each rice cultivar's grain yield performance varied within each geographical area. Therefore, it is important to identify high-yielding cultivars that can contribute to increasing the productivity of the rice industry in Guyana. In this regard, the Guyana Rice Development Board (GRDB) has embarked on a breeding program designed to support this effort of producing stable high-yielding cultivars for testing and releasing to farmers for cultivation within the different rice-growing environments across the country. In this study, fifteen advanced rice genotypes along with three commercial check varieties were evaluated in multiple locations and

or environments in Guyana to assess their grain yield stability under different environments.

MATERIALS AND METHODS

Genotypes utilized in this investigation

A total of eighteen rice entries were used in this study. These entries were selected from the Rice Breeding Program of the GRDB, Rice Research Station, Burma. Out of 18, 15 genotypes were collected from Advanced Yield Trials (AYT) and 3 popular rice varieties *viz.* GRDB 10, 12, and 14 (Table 1) were utilized as the check cultivars in the current study.

Experimental details

The research was carried out in 3 locations over two cropping seasons by the Guyana Rice Development Board in 2018. The six environments (E) were E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018). Fifteen advanced lines from the AYT were tested against three commercial varieties (Table 1). The experiment was set up using a Randomized Complete Block Design (RCBD) with four replications under lowland irrigated field conditions. The seed rate of 157.2 kg ha⁻¹ was utilized. Each entry was weighed out, placed in small poly bags soaked for 24 hours, taken out from the water, and incubated for 48 hours to be pre-germinated. The pre-germinated seeds were sown in a 24m² plots size. Fertilizer was applied at a rate of 185 kg N ha⁻¹ + 84 kg P₂O₅ ha⁻¹ + 84 kg K₂O ha⁻¹ with the N divided into three application splits of the half, quarter, a quarter at 18, 40, and 55 days after sown, respectively. All the P₂O₅ and K₂O were applied 18 days after sown (DAS). At 14 DAS weeds control done using Nomina at 250g ha⁻¹; early season pests control at 18 DAS using Pronto at 40g ha⁻¹, and disease control were carried out using Carbendazim at 740 ml ha⁻¹. Field sanitation and routine husbandry practices were followed throughout the trial duration. The temperature ranging from 24 to 32°C during the spring and autumn crop of 2018.

Studied characters

The two characters studies were the agronomic traits: Lodging Incidence (Lg). This indicates % of plants that lodged. (Standard Evaluation System for Rice (SES) 2002, and Grain Yield (Yld): the harvested area (less than 5 m²/plot), the grain yield were in kilogram per hectare at 14% moisture.

Data collection

At maturity percentage lodging incidence was recorded for

Table 1. List of advanced rice genotypes and checks

G.N.	Genotypes	Designation	Parentage
1	FG12-23	FL10891-13P-4-3P-1P-M	FL08428-6P-4-2P-3P/FL07462-3P-1-3P-1P-M-1P//FL06802-12P-2-3P-1P-M
2	FG12-49	FL10915-2P-4-2P-1P-M	FL08336-17P-2-3P-7P/FL08428-6P-4-2P-3P//FL05658-7P-1-5P-3P-M
3	FG12-259	FL10919-10P-5P-3P-1P-M	FL07495-16P-2P-2P-1P / FL07201-6P-5-3P-1P//FL04904-26P-3-2P-3P-M
4	G14-10	GR1630-40-47-2-1-1-1	FG07-127/G07-13
5	G15-02	GR1538-1-30-4-3-1-1-1-1-2	GROVENI/G04-8
6	G15-11	GR1627-31-27-3-1-1-1-2-1	FG07-125/G07-13
7	FG15-01	FL12017-2P-4-1P-1P-M	FL09156-4P-5-2P-1P/FL06747-4P-10-5P-3P-M//FL04674-3P-8-3P-2P-M
8	FG15-02	FL12032-2P-6-1P-2P-M	FL09474-12P-4-3P-3P/FL09382-20P-2P-1P-3P//FL08336-21P-2-5P-3P-M
9	G16-102	GR 1621-25-6-9-3-1-1-1-1-1-1	FG07-124/G07-2
10	G16-104	GR 1629-33-66-2-2-1-1-2-1-1-2	FG07-125/G08-112
11	G16-108	GR 1708-54-6-1-1-1-5-1-1-2	FG06-98/G07-2/FG07-35/G98-30-3
12	G16-112	GR 1739-1-77-1-3-1-1	IR 64/G07-2
13	FG14-43	FL13033-5P-4SR-1P-1P-M-M	FL09203-7P-3-2P-M/FL10030-12P-9-2P-1P//SD20A
14	FG15-35	FL14026-1P-3SR-2P-1P-M-MP	FL10127-7P-1-2P-2P-M-1P/OM 5629//FL08281-4P-4-3P-3P-M
15	G13-126	GR 1584-47-8-2-2-1-1	GR1117-12-2-3-4-3-2-1/FG07-90
16	GRDB 10	(Checks)	NA
17	GRDB 12	(Checks)	NA
18	GRDB 14	(Checks)	NA

G= Genotype number, NA= Not available

each experimental units and the entire plots were harvested manually using grass knives. Harvested samples were threshed using a small mechanical thresher with each plot sample harvested kept separately. The weight and moisture content of each sample were recorded. All weight was calculated and converted to 14% moisture content using the standard formula for conversion.

Statistical computations and AMMI analysis for the G x E interactions

The data obtained from each experiment were analyzed using the analytical software, Microsoft Excel 2013 and Statistix 8 to generate the means and tables. The AMMI statistical model structure and computational methods were used in the current study as described in Zobel et al. (1988); Gauch (2013); Mukherjee et al. (2013); Bose et al. (2014); Persaud et al. (2018). The Analysis of variance (ANOVA), AMMI biplot, and PC analysis was carried out using Plant Breeding Tools Version 1.4 software developed by IRRI (PBTools (Version 1.4) 2014). The additive analysis of variance (ANOVA) was utilized to partition the variations of the G x E interaction into several Interaction Principal Component analysis (IPCA). The genotype and genotype by environment (GGE) biplots analysis were utilized to ascertain the stability of genotypes over the six environments both numerically and graphically (Yan, 2001; Parihar et al., 2017; Persaud et al., 2019).

RESULTS

Lodging incidence of advanced breeding lines

All genotype (G) in Environment (E) 1- Anna Regina, Region # 2 (Spring crop, 2018) showed zero percent lodging

incidence; while the number of genotypes varied with the percentage of lodging incidence within the remaining five environments. Genotype G2 (FG12-49); G4 (G14-10); G8 (FG15-02); G11 (G16-108) and G12 (G16-112) demonstrate zero percent lodging incidence over all six environments (Table 2). With exception of G6 (G15-11) and G7 (FG15-01) along with the check G16 (GRDB 10), all other genotypes were observed with mean lodging incidence of less than 5 percent for the six environments studies. (Table 2). The highest average percent lodging incidence was recorded by G7 (FG15-01) and the check G16 (GRDB 10) in Environment 5- Rice Research Station, Burma, Region # 5 (autumn crop, 2018) as 93.33% and 68.33%, respectively.

Grain yields of advanced breeding lines

The grain yields of genotypes fluctuate for each genotype over each of the different environments (Table 2) however, E3 presented the highest grain yield for the majority. In Environment 1- Anna Regina, Region # 2 (Spring crop, 2018) the yield ranged from 6149.91 kg/ha (G10) to 7463.33 kg/ha (G6); Environment 2- Rice Research Station, Burma, Region # 5 (Spring crop, 2018) ranged from 7062.48 kg/ha (G9) to 9860.20 kg/ha (G2); Environment 3- Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018) ranged from 6678.49 kg/ha (G12) to 10417.24 kg/ha (check G17); Environment 4- Anna Regina, Region # 2 (Autumn crop, 2018) ranged from 5270.35 kg/ha (G9) to 6565.08 kg/ha (G7); Environment 5- Rice Research Station, Burma, Region # 5 (Autumn crop, 2018) ranged from 2559.00 kg/ha (G5) to 6456.64 kg/ha (G7) and finally Environment 6- Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018) ranged from 2572.61 kg/ha (G8) to 4400.13 kg/ha (G3) (Table 2).

Higher mean grain yield was recorded by genotype G3 (FG12-259) followed by G2 (FG12-49), G15 (G13-126), and

Table 2. Average lodging incidence and grain yields of advanced breeding lines evaluated under multiple environmental conditions, 2018

SN	Strain	*Av Percent Lodging Incidence						Mean	*Av Grain Yield (Kg/ha)						Mean (Kg/ha)	PC1	PC2
		Spring, 2018			Autumn, 2018				Spring, 2018			Autumn, 2018					
		E1	E2	E3	E4	E5	E6		E1	E2	E3	E4	E5	E6			
G1	FG12-23	0.00	15.00	0.00	0.00	8.33	0.00	3.89	6631.57	9319.57	8897.38	5417.10	4520.89	3914.87	6450.23	-6.16	-1.77
G2	FG12-49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6712.33	9860.20	10117.57	6315.15	4164.73	3763.49	6822.24	-12.32	-21.56
G3	FG12-259	0.00	13.33	0.00	0.00	0.00	0.00	2.22	7062.73	9563.53	10154.33	7357.92	6456.64	4400.13	7499.21	-16.82	8.85
G4	G14-10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6477.17	8818.30	8886.30	6226.82	4034.02	3421.12	6310.62	-2.17	-6.38
G5	G15-02	0.00	23.33	0.00	0.00	6.67	0.00	5.00	7278.45	7459.88	8157.97	4732.24	2559.00	2839.08	5504.44	25.14	-18.46
G6	G15-11	0.00	50.00	23.3	0.00	5.00	0.00	13.06	7463.33	8176.93	8189.47	6190.16	4103.68	3510.34	6272.32	18.69	2.55
G7	FG15-01	0.00	50.00	3.33	0.00	93.33	0.00	24.44	6774.21	8504.65	7598.77	6565.08	3662.10	2942.11	6007.82	13.34	4.35
G8	FG15-02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6003.11	8300.52	9221.03	5549.35	4234.74	2572.61	5980.23	-13.11	-10.22
G9	G16-102	0.00	6.67	0.00	0.00	0.00	0.00	1.11	7435.19	7062.48	8281.22	5270.35	3319.13	2804.75	5695.52	24.70	-9.68
G10	G16-104	0.00	0.00	0.00	0.00	3.33	0.00	0.56	6149.91	7906.01	9021.62	6013.63	4585.94	3355.49	6172.10	-6.31	0.85
G11	G16-108	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6287.07	7751.23	8006.91	6319.55	4105.36	3254.52	5954.11	6.36	8.04
G12	G16-112	0.00	0.00	0.00	0.00	0.00	0.00	0.00	6244.49	7857.77	6678.49	5482.12	4578.32	2941.86	5630.51	7.49	27.20
G13	FG14-43	0.00	10.00	0.00	0.00	0.00	0.00	1.67	6533.43	8885.98	9269.76	6175.72	4514.62	3968.59	6558.02	-5.54	-3.91
G14	FG15-35	0.00	0.00	0.00	0.00	6.67	0.00	1.11	6747.80	7581.52	9049.44	5849.37	4074.18	3303.99	6101.05	5.98	-7.12
G15	G13-126	0.00	0.00	0.00	0.00	13.33	0.00	2.22	6879.50	9257.88	8785.14	5697.90	5737.74	4188.86	6757.84	-8.38	15.04
G16	GRDB 10	0.00	18.33	0.00	0.00	68.33	3.33	15.00	6811.63	8481.32	8616.75	6359.05	5022.09	4026.16	6552.83	1.90	11.02
G17	GRDB 12	0.00	1.67	3.33	0.00	0.00	0.00	0.83	6611.61	9606.54	10417.24	6392.88	4975.81	2906.98	6818.51	-22.23	-18.07
G18	GRDB 14	0.00	0.00	0.00	0.00	13.33	0.00	2.22	6428.36	8521.31	8521.96	5823.84	5774.76	3532.19	6433.74	-10.56	19.27
																PC1	PC2
E1	Environment 1- Anna Regina, Region # 2 (Spring crop, 2018)															42.98	-7.54
E2	Environment 2- Rice Research Station, Burma, Region # 5 (Spring crop, 2018)															-18.73	-6.58
E3	Environment 3- Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018)															-21.21	-38.71
E4	Environment 4- Anna Regina, Region # 2 (Autumn crop, 2018)															7.17	5.43
E5	Environment 5- Rice Research Station, Burma, Region # 5 (Autumn crop, 2018)															-21.68	36.28
E6	Environment 6- Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)															11.46	11.13

SN= Serial number; *= average of 3 replication; Av.= Average; G= Genotypes; E = Environment; PC = principal-component analysis

check genotype G17 (GRDB 12) (Table 2).

AMMI analysis

The AMMI analysis of 18 genotypes evaluated for grain yield stability over six seasons (environment) showed the first principal component axis (IPCA1) accounted for 38.5% of the interaction of Genotype by Environment (G x E) SS at 21% of the interaction

degree of freedom (df). Similarly, IPCA2 explained 33.2% of the interaction SS. However, cumulatively the IPCA1, IPCA2, and IPCA3 contributed to 83.8% of the total interaction (Table 3).

AMMI1 Biplot display

The average grain yield (Kg/ha) of the 18 genotypes ranged from 5504.44 to 7499.21 Kg/ha with a greater

proportion of the genotypes showing more stable grain yield and a lesser proportion showing higher grain yield status. The three check cultivars viz. G16 (GRDB 10); G17 (GRDB12) and G18 (GRDB 14), recorded relatively higher mean grain yields over all the test environments (Figure 1). Genotypes or environments appearing almost on the perpendicular (broken) lines have similar means.

The genotypes viz., G6 (G15-11), G4 (G14-10), and G10 (G16-104) revealed similar means (Figure 1).

Table 3. Combined AMMI analysis

Source	df	SS	MS	^a Percent	^b Acum.
IPCA 1	21	10892961	518712.4	38.5	38.5
IPCA 2	19	9412888	495415.2	33.2	71.7
IPCA 3	17	3432323	201901.3	12.1	83.8
IPCA 4	15	3230028	215335.2	11.4	95.2
IPCA 5	13	1343428	103340.6	4.7	99.9
IPCA 6	11	0	0.0	0.0	99.9

Note: ^aPercent= Accounted for the percentage sum of squares; ^b Acum. = accounted for the accumulative percentage sum of squares; df =degree of freedom; SS= Sum of square; MS= Mean square; IPAC = Interaction Principal Components Analysis

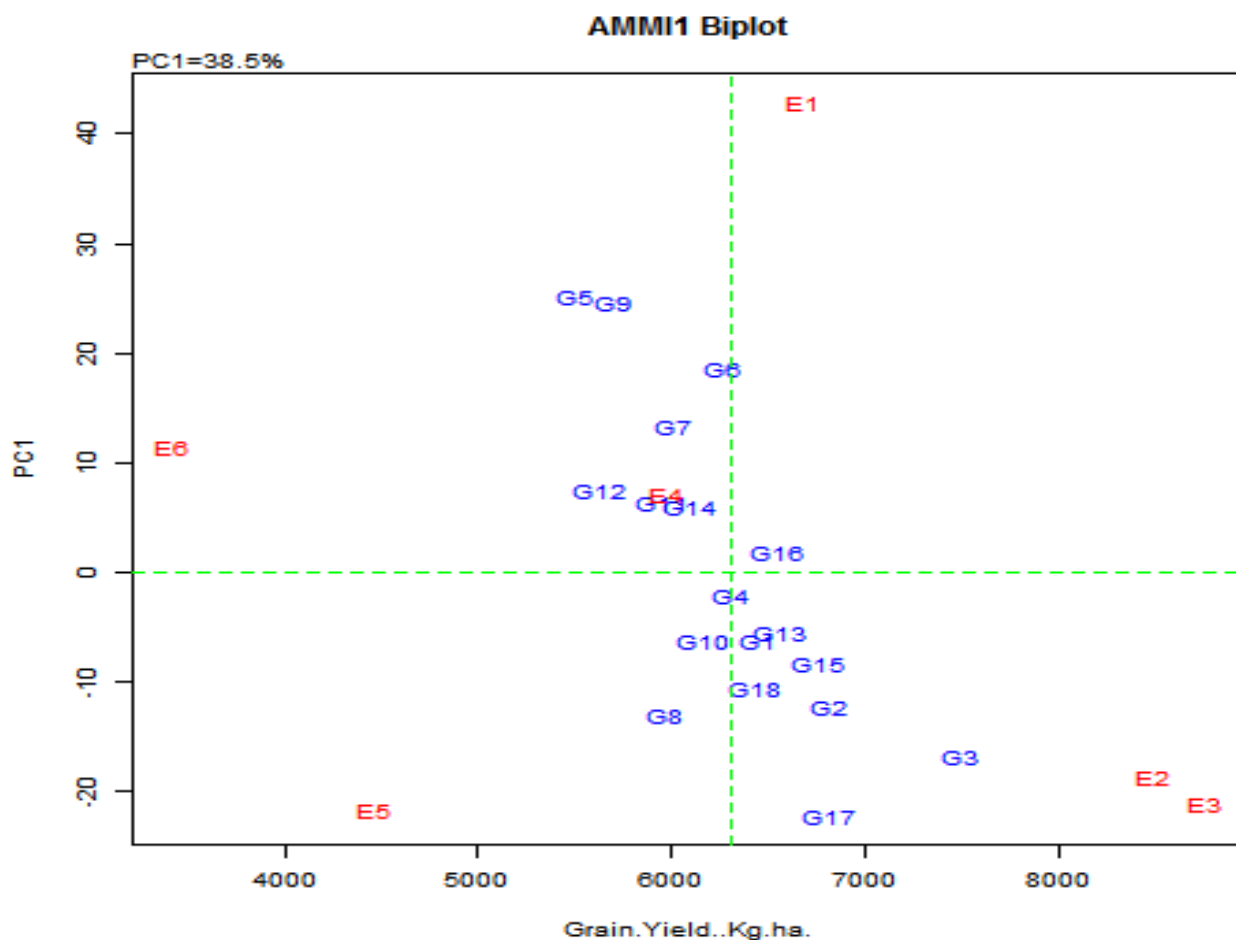


Figure 1: AMMI1 Biplot display for mean grain yield (Kg/ha) and IPCA 1 scores of the 18 advanced breeding lines/genotype (G) tested across six environments (E)

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

On the other hand, those genotypes falling almost on a horizontal line have similar interaction patterns. In this study, a few genotypes [G4 (G14-10), and G16 (GRDB 10)] were observed for similar interaction patterns (Figure 1).

Furthermore, genotypes or environments on the right side of the midpoint on the perpendicular (broken) lines

have higher mean grain yields than those on the left side. As a result, it is quite evident from the biplot that the genotypes, G1 (FG12-23), G2 (FG12-49), G3 (FG12-259), G13 (FG14-43), G15 (G13-126), along with the three check cultivars viz. G6 (G15-11), G4 (G14-10), and G10 (G16-104) demonstrated a higher level of stable grain yields. In

contrast, G5 (G15-02), G7 (FG15-01), G8 (FG15-02), G9 (G16-102), G10 (G16-104), G11 (G16-108), G12 (G16-112), and G14 (FG15-35) showed lesser stable average grain yields (Figure 1). Environment E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018) were also observed on the right-hand side of the midpoint of the main effect axis, suggesting that these environments were slightly more favorable for evaluation of advance rice genotypes; while E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018) and E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018) were slightly less favorable and the other remaining one environments *viz.* E4 - Anna Regina, Region # 2 (Autumn crop, 2018) appeared to be closer to an intermediary between the two (Figure 1).

Principal-component (PC) analysis

Genotypes or environments with IPCA1 scores of zero or near zero (either positive or negative) have small interactions and show greater stability and adoption over the test environment; while large IPCA1 scores have a high interaction effect and reflect more specific stability and adoption to specific environments. In the present case, Environment 4- Anna Regina, Region # 2 (Autumn crop, 2018) followed by Environment 6- Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018) observed with small PC analysis scores revealed lower interaction, greater stability, and adoption of genotypes over the test environments (Table 2). The higher PC analysis score in Environment 1- Anna Regina, Region # 2 (Spring crop, 2018), Environment 3- Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018), and Environment 5- Rice Research Station, Burma, Region # 5 (Autumn crop, 2018), indicated the high interaction effect and reflect more specific stability and adoption to a specific environment (Table 2); while intermediate interaction effect was observed from the remaining environment, *viz.* E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018) (Table 2; Figure 1).

Likewise, a relatively larger proportion of genotypes (55.6%) recorded relatively smaller PC1 scores ranging from 1.90 to 10.56 (either positive or negative) and showed smaller interactions (Table 2), which was one of the reasons for the appearance of the clustering together of the genotypes on the biplot (Figure 1); while a lesser proportion (44.4%) recorded higher IPCA1 scores > 10.56. The genotypes G 5 (G15-02), G 9 (G16-102), G 17 (GRDB 12), and G6 (G15-11) recorded the highest PC1 scores followed by genotypes, G3 (FG12-259) and G7 (FG15-01). The other genotypes recorded lower PC1 scores (either positive or negative). These genotypes implied the high interaction effect and reflected more specific stability and adoption to a specific environment (Table 2).

AMMI2 biplot display (IPAC 1 vs. IPAC 2)

In the AMMI2 biplot, the more responsive genotypes and environment were observed far away from the origin. E1 -

Anna Regina, Region # 2 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018) and E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018) were the most differentiating environment; while G5 (G15-02) were the most responsive genotypes followed by G9 (G16-102), G12 (G16-112), G18 (GRDB 14), G17 (GRDB 12) and G2 (FG12-49) (Figure 2).

The genotypes and environment fall in the same sector interacted positively; when located on the opposite side, they interacted negatively. The genotypes and environment observed in adjacent sectors had somewhat complex interactions (Figure 2). The genotypes *viz.* G1 (FG12-23), G4 (G14-10), G10 (G16-104), G11 (G16-108), G13 (FG14-43), G14 (FG15-35), and G16 (GRDB 10) were observed closer to each other and cluster near to the origin, indicate that those genotypes expressed more stable grain yield status and have similar performance. Those genotypes close to a particular environment indicated that they have better adoption to that specific environment. This is quite visible from the biplot that genotypes G2 (FG12-49) falling close E3 - Lesbeholden, Black Bush Polder, Region # 6 (spring crop, 2018) was particularly suitable and showed stable grain yield response in that environment. The genotype [G 11] was positioned intermediary between E4 - Anna Regina, Region # 2 (autumn crop, 2018) and E6 - Lesbeholden, Black Bush Polder, Region # 6 (autumn crop, 2018) indicating that it recorded highly stable grain yield response in those environments (Figure 2).

GGE- Biplot - Environment view for grain yields of advanced rice genotypes

The GGE biplot (Figure 3) demonstrated 78.1% of the total variation of the Genotype plus genotype-by-environment (GGE) from the perspective of the environment. The biplot displayed E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018), ; E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018) and E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018) to be the most discriminating (informative) environment, while E1 - Anna Regina, Region # 2 (Spring crop, 2018) showed as least discriminating (Figure 3).

Average-environment axis (AEA) and ideal environment view

The display of the Average Environment Axis (AEA) in Figure 4 was used to explain the ideal test environment for grain yield performance. The test environment E4 - Anna Regina, Region # 2 (autumn crop, 2018) and E2 - Rice Research Station, Burma, Region # 5 (spring crop, 2018) were considered as the better environments for testing and for the identification of genotypes with stable grain performance due to their placement in the biplot closest to the "average environment" and "ideal test environment". This is followed by E6 - Lesbeholden, Black Bush Polder, Region # 6 (autumn crop, 2018) which also showed a smaller angle with AEA and was observed to be the most representative environment. The environments away from AEA E3 - Lesbeholden, Black Bush Polder, Region # 6

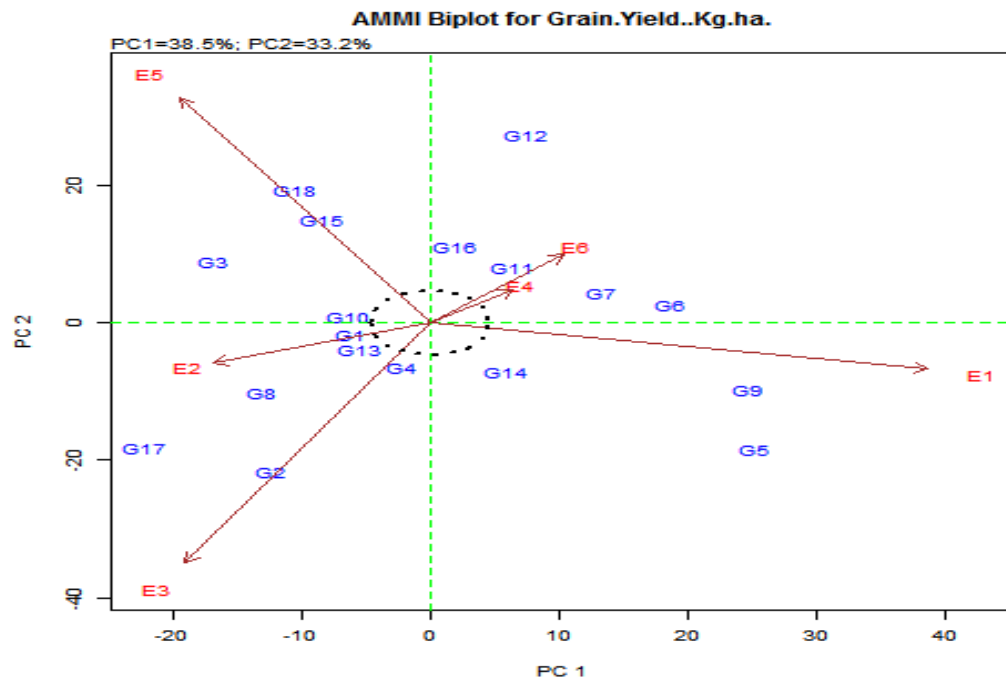


Figure 2: AMMI2 biplot for 18 breeding lines (G) and six environments (E) displayed on the first and second principal component axis (IPAC 1 vs. IPAC 2)

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

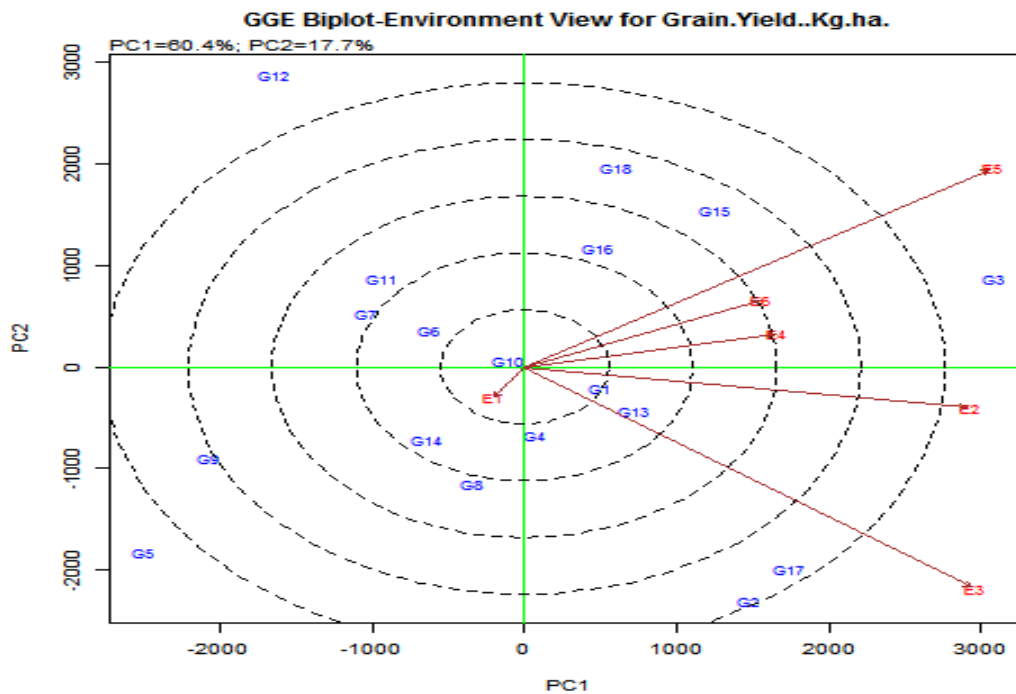


Figure 3: The GGE biplot showing the average grain yield performance of each genotype in each environment

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

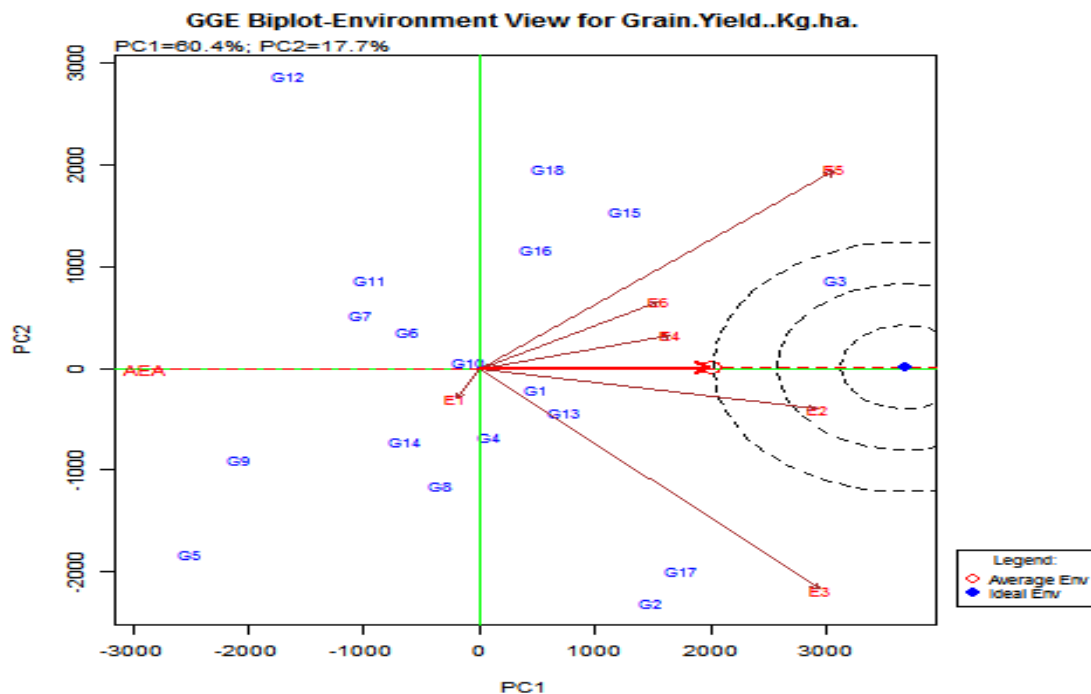


Figure 4: The average-environment axis (AEA) view shows the mean performance, ideal environment for testing the stability of genotypes

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

(spring crop, 2018) and E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018) were identified from the biplot as least representative (Figure 4).

GGE Biplot genotype view for grain yields of advanced breeding lines

Genotype G3 (FG12-259) was considered to be the most stable and ideal genotype since it is closest to the Average environment and ideal genotype; followed by G17 (GEDB 12) and G2 (FG12-49) (Figure 5). On the other hand G5 (G15-02), G9 (G16-102), and G12 (G16-112) were observed to be the furthest away from the Average environment and ideal genotype and thus considered to be the least stable genotypes in terms of grain yield performance (Figure 5).

What-won-where biplot for grain yield performance

The What-won-where biplot demonstrated that three mega-environment exist in the study (Figure 6). In the first mega-environment, four test environments fell into one sector *viz.* E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018), while the other two environments *viz.* E1 - Anna Regina, Region # 2 (Spring

crop, 2018); and E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018) fell in two opposite mega-environment sectors, respectively. Further, each mega-environment sector showed different winning genotypes (Figure 6). The winner, in this case, were referred to as those genotypes that consistently showed stable grain yield performance in each of the different environments. In this study, the genotype G3 (FG12-259) was identified as the winner within the mega-environment with the four environments *viz.* E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018) and E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018). Likewise, opposite to that in the mega-environment sector with E1 - Anna Regina, Region # 2 (spring crop, 2018), genotypes G5 (G15-02) and G 9 (G16-102) fell within that mega-environment were observed with stable grain yield performance. Also in mega-environment sector E3 - Lesbeholden, Black Bush Polder, Region # 6 (spring crop, 2018) genotype G2 (FG12-49) and check genotype G17 (GRDB 12) were identified as the winning genotypes within that environment (Figure 6). Further, the genotypes G1 (FG12-23), G4 (G14-10), G6 (G15-11), G8 (FG15-02), G10 (G16-104), G13 (FG14-43), and G14 (FG15-35) crowded together and clustered towards the origin of the biplot could be referred as genotypes with consistent and stable

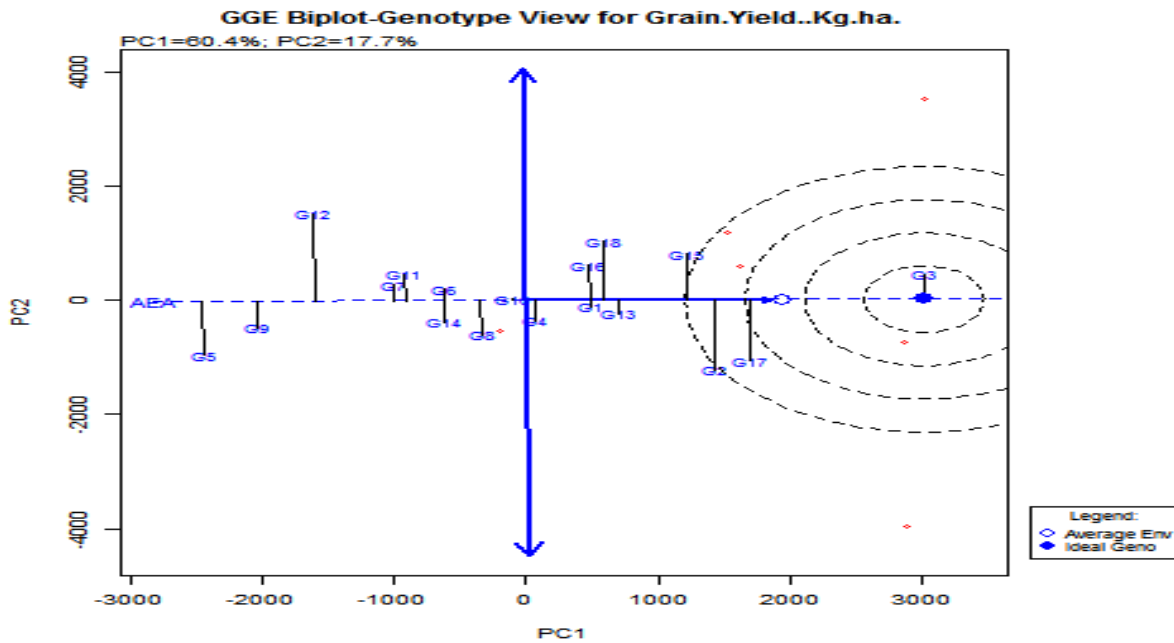


Figure 5: The GGE biplot showing the average environment, ideal and individual performance of each genotype

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

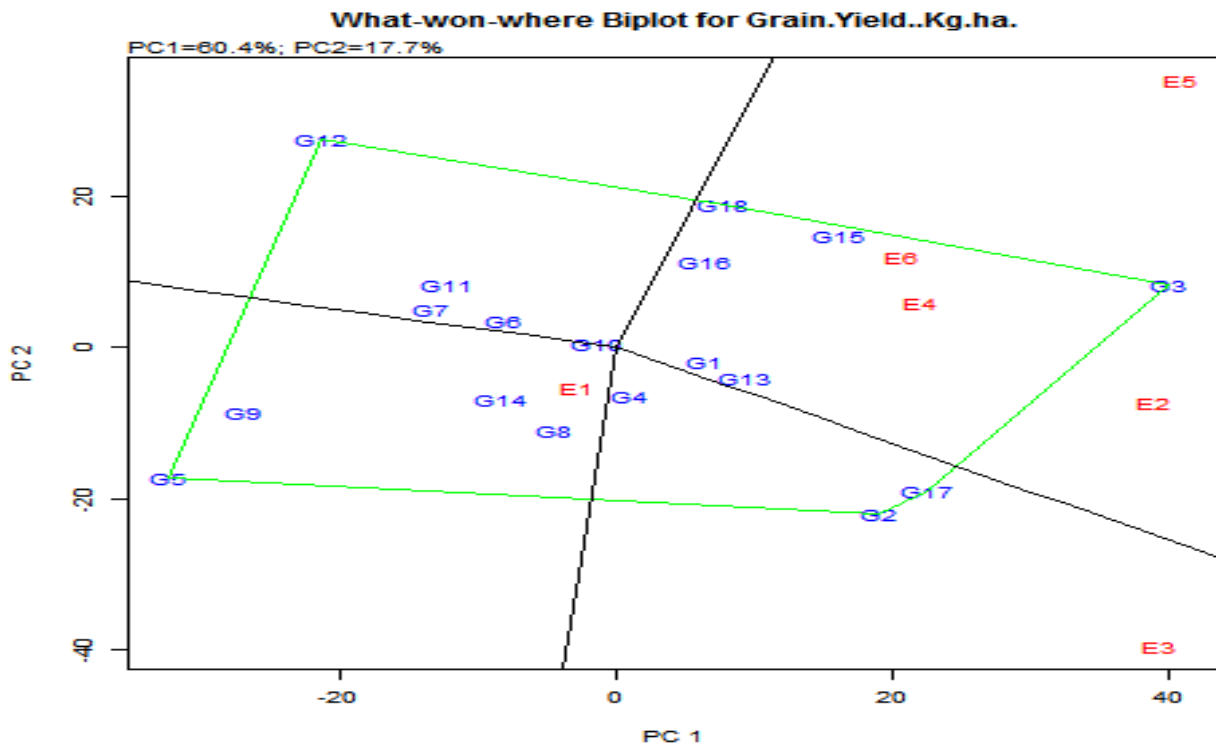


Figure 6: The what-won-where view of the GGE biplot to show which genotype performed best in which environments

G= Genotype; E= Environment; E1 - Anna Regina, Region # 2 (Spring crop, 2018); E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E3 - Lesbeholden, Black Bush Polder, Region # 6 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)

grain yield performance within all environments (Figure 6).

DISCUSSION

A potential rice breeding goal for many rice cultivating countries is the development of high-yielding cultivars combined with other important plant characteristics such as plant ideotype, tolerance to lodging and delay harvesting, disease resistance, or tolerance to major pests, grain and cooking qualities. The use of those high-yielding cultivars is known to be the most environmentally friendly and economical way to increase the productivity of the rice industry to meet the growing demands. Extensive research has been done over the years to identify rice germplasms with high grain yield and stable performances within the different rice cultivating environments. The current study identifies consistent expression of high stable grain yield performance of genotype FG12-259 as an ideal genotype since it is closest to the average environment; followed by FG12-49, FG12-23, FG14-43, G13-126, G15-11, G14-10 and G16-104 from the biplot over all seasons and all locations. Similar findings were reported by Islam et al. (2016) who evaluated eight and five newly released salt-tolerant rice varieties from 2010 to 2013 in South Bangladesh during the wet and dry seasons, respectively. These researchers found a variety BRR1 dhan54 to be the most suitable genotype with wider adaptability in the region during the wet season, followed by BRR1 dhan40 and BRR1 dhan53; while BRR1 dhan47 was the most stable variety followed by BRR1 dhan61 and BINA dhan8 for the dry season across all sites. Likewise, Torres and Henry (2018) found genotype *viz.* IR83142-B-7-B-B, Binuhangin, IR77298-14-1-2-13, IR70215-70-CPA-3-4-1-3, and IR77298-14-1-2 as the highest and most stable genotypes for grain yields from the AMMI1 biplot analysis for both well-watered and mild to moderately severe drought stress environments. Furthermore, Aryana and W. Wangiyana (2016) reported from the biplot analysis that G2(F2BC4A52-44) and G8(F2BC4A52-37) were stable genotypes across locations. In another similar study faba bean, Temesgen et al. (2015) reported that none of the varieties tested showed consistently superior performance across all environments, however, found that the genotype EK 01024-1-2 ranked in the top third of the test entries in 61.5% of the test environments and was identified as the most stable genotype, with type I stability and also showed a 17.0% seed size advantage over the standard varieties and was released as a new variety in 2013 for wide production and named "Gora". Similarly, based on the consistently high and stable grain yield performance, along with other superior grain qualities and plant characteristics the genotype *viz.* FG12-259 and FG12-49 were selected, developed, and released as commercial rice varieties called GRDB 16 and GRDB 15, respectively in Guyana for wider cultivation by the farmers. Similar findings were reported by Singh et al. (2012) who found variety, NDR 9542 can be adopted for cultivation by local farmers in all environments as the variety exhibited distinct yield superiority with good qualities. The other entries identified with stable grain yield

performance *viz.* FG12-23, FG14-43, G13-126, G15-11, G14-10, and G16-104 are still being studied in the advanced yield trials. Also, the three check cultivars *viz.* GRDB 10, GRDB 12, and GRDB14, also expressed a similar higher level of stable grain yields overall test environment. The performance of the check cultivars gives reliability to the grain yield stability performance expressed by the advanced breeding lines: FG12-259; followed by FG12-49, FG12-23, FG14-43, G13-126, G15-11, G14-10, and G16-104.

The AMMI analysis of 18 genotypes evaluated for grain yield stability over six seasons (environment) in this current study showed the IPCA1, IPCA2, and IPCA3 cumulatively contributed to 83.8% of the total interaction. Almost alike findings were reported by Roshandel et al. (2016). The researcher reported that the principal component analysis (PCA) of the three components accounts for up to 90% of G x E sum square (IPCA1, IPCA2, and IPCA3 with 70.72%, 18.99%, and 10.60%, respectively). While Bose et al. (2014) observed that the first two interaction principal component axes (IPCA) cumulatively explained 92 % of the total interaction effects.

In addition, from the present study, the AMMI analysis found the environment at Rice Research Station, Burma, Region # 5, Spring crop, 2018 (E2) and Anna Regina, Region # 2, Autumn crop, 2018 (E4) to be the most representative environment and closeness to the ideal test environment. Also, Anna Regina, Region # 2, Autumn crop, 2018 (E4) recorded low IPCA1 scores and showed small interactions. In a similar study carried out on barley by Miroslavljevic et al. (2014), it is evident that the environment had the highest effect on barley yield, and this factor explained 61.8% of treatment variation. Likewise, Roshandel et al. (2016) studied the grain yield stability of 20 soybean genotypes in four locations (Karaj, Gorgan, Moghan, and Shahrekord) in Iran. The researchers reported that Shahrekord, among the four tested locations, was identified as the ideal test location, due to being near the center of concentric circles of the biplot and Karaj as the lesser ideal location due to being far from the center of the concentric circles.

In this study also, the what-won-where biplot pattern suggested the target environment consisted of three mega-environments since four environment falls in one sector and one each in another two sectors. The genotype FG12-259 was identified as the winner within the mega-environment with the four environments [*viz.* E2 - Rice Research Station, Burma, Region # 5 (Spring crop, 2018); E4 - Anna Regina, Region # 2 (Autumn crop, 2018); E5 - Rice Research Station, Burma, Region # 5 (Autumn crop, 2018); E6 - Lesbeholden, Black Bush Polder, Region # 6 (Autumn crop, 2018)] that displayed in the right side of the biplot. That means that genotype FG12-259 demonstrated superior stable grain yield performance in those four environments. The genotype FG12-259 observed further away from the origin within those mega-environments showed greater stable grain yield status and contributed more to both GEN and G x E. While those genotypes *viz.* G1 (FG12-23), G4 (G14-10), G6 (G15-11), G8 (FG15-02), G10 (G16-104), G13 (FG14-43), and G14 (FG15-35), cluster closer to the origin in the what-won-biplot showed

consistent and stable grain yield performance within all environments. Those genotypes were also important from plant breeders' perspective.

Further, with exception of genotype *viz.* G15-11 and FG15-01 along with the check GRDB 10, all other genotypes were observed with lodging incidence less than 5 percent. This means that except for the 3 genotypes listed all the other genotypes expressed strong plant stand in the field and can be considered tolerant to lodging.

CONCLUSION

In this study, it was shown that AMMI and GGE model analysis is a practical and effective alternative for crop breeders to use successfully to identify superior genotypes of rice in different environment test conditions. The genotypes FG12-259 and FG12-49 were identified in this study as genotypes that expressed superior plant qualities (with lodging incidence below 5%) and consistently high and stable grain yield performance were selected, developed, and released as commercial rice varieties called 'GRDB FL 16' and 'GRDB FL 15', respectively in Guyana for wider cultivation by the farmers. The other genotypes with stable yields and excellent plant characteristics were also selected and placed in the advance yield trials for further screening and developmental work for possible release as commercial cultivars as well once found to be suitable.

Author's contributions

First author Mahendra Persaud designed and carried out the experiments with assistance from Nandram Gobind. Second author Rajendra Persaud analyzed the data, wrote the manuscript and made several revisions base on reviewers' comments. Other authors provide moral support, read, and agree with the content of the manuscript.

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Disclosure statement

There is no potential conflict of interest to declare.

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