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RESEARCH ARTICLE

Genotype by Environment (G×E) Interaction Study on Yield Traits in Different Maturity Groups of Rice

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Abstract

Rice production is affected by emerging problems of climate change and over-utilization of resources. To obtain consistent yield across diverse environments, a variety should have adaptability and stability to fit into various growing conditions. G×E interaction and stability performance of 59 rice lines of different maturity durations were investigated for grain yield-related traits in three environments. This study was carried out to identify stable lines for varietal development as well as to identify parental lines with stable contributing traits for further breeding programs. AMMI and GGE analysis showed significant genotype, environment, and G×E interaction indicating the presence of variability among the genotypes and environments. The G×E interaction effect showed that the genotypes responded differently to the variation in environmental conditions or seasonal fluctuations and explained that most of the traits were contributed mainly by genotype, followed by environment and their interaction. As per AMMI biplot analysis, environment1 was identified as the best suited for potential expression of grain yield and related traits. Results of stability analysis revealed that early and mid-early genotypes NH776, NH4371, 27K, NH686, 258S, NH219, and Tellahamsa were identified as the best stable genotypes across all the three seasons for single plant grain yield and hence suitable for wider environments. These selected genotypes can be suggested for hybridization in further breeding programs to develop early genotypes with high yield. The stable early and mid-early lines with high yield potential will be tested in multi-location trials for commercial cultivation.

Key words : Adaptability, biplot; G×E, mutants, wild introgression lines

Introduction

Despite having many varieties released so far in rice, most of them are obsolete and only few varieties show stable performance under diverse conditions across the years. Genotype by environment interaction studies play an important role in selection of stable varieties for grain yield and related traits across varied environments. AMMI and GGE biplot models are widely used to study G×E interactions, stability, and adaptability of genotypes. Highly populated Asian countries account for 95% of global production and consumption of the major staple food crop rice (*Oryza sativa* L.). Rice is a primary source of carbohydrates for more than half of the world's population. Global rice production is about 749.8 million tons (FAO 2015) from an area of about 158.8 million hectares with a per capita consumption of 57.5 kg per year (Statista 2015-16). Among the rice growing countries in the world, India has the largest area under rice crop of about 44 million hectares and ranks second in production with 103.61 million tons next to China with 207.44 million tons (Indiastat 2015-16). Rice contributes 42% of total food grain production and 45% of total cereal production in India.

The combined effects of escalating population, declining arable land, water, and resources will depress yield and increase production risks. Possible adverse effects from climate change and associated events are causing serious implications for meeting the food production targets per unit area as well as unit time. Further, due to urbanization, industrialization, and popularization of other crops there may be a decline of rice areas by 6-7 million hectares by 2050. About 55% of the rice area in India is under irrigated ecosystem. Rice requires more water per unit grain production compared to other cereal crops *viz.,* wheat, maize, sorghum. Absolute

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water scarcity is predicted for approximately 17% of the total population and 22% of the geographic area by 2050. To overcome these problems, there is a need to prioritize specific agronomic characters and their efficient utilization to improve productivity in rice.

Earliness is the key agronomic character which provides greater opportunity to varieties to fit into different ecosystems, in different cropping seasons (Bueno and Lafarge 2017: Lee et al. 2013) which helps in the escape of crops from various pests and diseases incidence and reduces crop loss. Short duration minimizes the utilization of water during the growing season and cuts down the cost of cultivation by limited use of inputs. Thus, it helps in escaping problems encountered from multiple stresses. Under existing scenario, in order to sustain rice production and to meet future demands, growing early high-yielding varieties is a feasible option. This will enhance rice productivity, resource- and input-use efficiency, profitability per unit area, and unit time. Serrano-Silva et al. (2014) simulated that early duration rice cultivars are the best adaptive strategy to lower methane emissions. Though more than 1,000 rice varieties have been released in India, many of which are not under cultivation due to inconsistent performance in diverse environments and only a few varieties with stable performance continue to be under cultivation even after 15-20 years of release (Bose et al. 2014).

Yield and heading date are complex characters, dependent on several contributing characters and highly influenced by genetic as well as environmental factors. For obtaining expected yield potential, it is necessary to identify the stable genotypes suitable for a wide range of environments. Stability of a cultivar is the consistency in performance across environments as an outcome of its genotype and environment interaction and this greatly affects the phenotype (Sharma et al. 1987). Wider adaptability and stability are prime considerations in formulating efficient breeding programs and selecting varieties (Cullis et al. 2010; Dewi et al. 2014; Filho et al. 2013; Worku et al. 2016). Suitability and adaptability of a variety to specific region or environment with stable performance can be detected by genotype by environment (G×E) interaction studies analyzed with AMMI and GGE biplot models. The additive main effects and multiplicative interaction (AMMI) model incorporates both the classical additive main effects model for G×E interaction and the multiplicative components into an integrated least square analysis. Thus, it becomes more effective in selection of stable genotypes (McLaren and Chaudhary et al. 1994) by estimating total G×E interaction of individual genotypes and partitioning interaction to each environment (Zobel et al. 1988). The GGE concept was used to visually analyze the yield from multi-environment trial (MET) data using biplots with factors of G and GE and source variation in GEI analysis of multi environment test data (Badu-Apraku et al. 2012: Yan et al. 2000). The GGE biplot is a graphical representation that displays the main genotype effect (G) and the genotype × environment interaction of multi-environment tests. Hence the present study was planned with the objectives to evaluate rice genotypes with varying yield levels and maturity duration for their stability and adaptability across growing seasons. GGE biplot and AMMI analysis was also employed to identify G×E interaction of grain yield and contributing traits in selected set of rice germplasm.

Material and Methods

Plant material

The experimental material comprised of 59 genotypes including popular varieties, introgression lines, and mutants obtained from the Crop Improvement Section, Indian Institute of Rice Research, Rajendranagar, Hyderabad (Supplementary Table 1). The genotypes used in present study varied in duration. The genotypes were classified based on days to 50% flowering as per DUS guidelines (PPV and FRA 2007). The genotypes showing days to 50% flowering between 71 to 90 days are classified as early genotypes, 91 to 110 days as medium duration, and 111 to 130 days as late genotypes.

Testing environments

The present investigation was carried out under three environments or three seasons during *Rabi* 2014-15, *Kharif* 2015, and *Rabi* 2015-16 at the Indian Institute of Rice Research Farm, Hyderabad, India. The farm is geographically situated at an altitude of 542.7 m above mean sea level at 17° 19′ N latitude and 78° 29′ E longitude. Trial in each season was considered as one environment for the multi environment analysis.

Experimental design

The experiment was laid out in a randomized complete block design (RCBD) with three replications. Each genotype was sown separately in raised nursery beds under three environments following uniform package of practices (http://www.rkmp.co.in/) across the seasons. Thirty-day-old seedlings were transplanted following a spacing of 15 x 20 cm for each entry. All the recommended package of practices was adopted besides providing necessary prophylactic plant protection measures to raise a healthy crop under three environments. Harvesting of each variety was done separately corresponding to maturity of each variety. Observations were recorded for yield and yield attributing characters on five randomly selected plants from each replication for each entry, while the data on days to 50% flowering and days to maturity were noted on plot basis following Standard Evaluation System (IRRI 2013). Average of phenotypic data on five plants per replication per entry was used for statistical analysis for each trait.

Statistical analysis

Analysis of variance was carried out for each environment (Supplementary Table 2). Test of homogeneity of variance was conducted by both the Barlette and Levene methods before conducting pooled analysis. Data of single plant grain

Table 1. Phenotypic variability of yield traits for the three seasons (Kharif 2014, Rabi 2014-2015, Rabi 2015-2016).

Variable	*Kharif 2014*							*Rabi 2014-2015*							*Rabi 2015-2016*						
	Min	Max	Mean	Var	SD	SE	CV	Min	Max	Mean	Var	SD	SE	CV	Min	Max	Mean	Var	SD	SE	CV
DM	100.00	155.00	128.84	149.87	12.24	0.92	9.50	118.00	164.00	138.16	126.43	11.24	0.85	8.14	99.00	166.00	125.77	231.76	15.22	1.14	12.10
PH (cm)	66.00	167.00	107.55	391.43	19.78	1.49	18.40	67.00	160.00	103.46	359.51	18.96	1.43	18.33	66.00	130.00	90.21	110.13	10.49	0.79	11.63
TN	6.00	37.00	15.02	30.51	5.52	0.42	36.78	6.00	37.00	16.58	35.87	5.99	0.45	36.13	6.00	36.00	18.37	35.42	5.95	0.45	32.39
PTN	6.00	37.00	14.10	30.29	5.50	0.41	39.02	6.00	36.00	15.45	37.54	6.13	0.46	39.67	6.00	33.00	16.63	25.45	5.04	0.38	30.34
PL (cm)	2.17	30.50	23.24	13.70	3.70	0.28	15.93	12.50	29.00	21.09	10.73	3.28	0.25	15.53	1.70	27.70	20.38	12.21	3.49	0.26	17.14
PW(g)	1.04	6.77	2.90	1.17	1.08	0.08	37.24	0.33	7.10	2.05	1.44	1.20	0.09	58.57	0.77	4.80	2.00	0.53	0.73	0.05	36.46
FG	5.00	383.00	145.27	3265.48	57.14	4.30	39.34	34.00	358.00	111.79	2552.25	50.52	3.80	45.19	41.00	244.00	100.04	1389.42	37.27	2.80	37.26
UFG	1.00	117.00	15.87	289.88	17.03	1.28	107.28	0.00	80.00	11.52	144.14	12.01	0.90	104.22	2.00	69.00	21.68	220.69	14.86	1.12	68.51
TGP	55.00	440.00	160.82	3498.22	59.15	4.45	36.78	39.00	372.00	123.31	2964.85	54.45	4.09	44.16	54.00	288.00	121.72	2088.53	45.70	3.44	37.54
SF (%)	4.27	99.28	89.76	147.31	12.14	0.91	13.52	52.11	100.00	90.39	86.97	9.33	0.70	10.32	45.56	98.65	82.74	87.03	9.33	0.70	11.28
SP (%)	0.72	46.38	9.39	67.17	8.20	0.62	87.32	0.00	47.89	9.60	87.17	9.34	0.70	97.28	1.35	54.44	17.26	87.03	9.33	0.70	54.04
TGW(g)	8.80	27.60	18.30	14.31	3.78	0.28	20.67	8.30	27.00	19.48	13.55	3.68	0.28	18.89	11.80	25.51	19.50	8.50	2.92	0.22	14.96
SPY (g)	2.62	65.53	26.10	169.33	13.01	0.98	49.87	0.40	83.40	21.17	170.08	13.04	0.98	61.60	3.52	41.57	17.94	42.14	6.49	0.49	36.18
BM(g)	4.00	85.00	26.65	164.35	12.82	0.96	48.10	7.00	83.90	28.32	97.90	9.89	0.74	34.93	8.30	48.10	20.03	49.32	7.02	0.53	35.06
BY (g)	8.74	139.53	52.75	569.99	23.87	1.79	45.26	10.80	149.90	49.50	445.43	21.11	1.59	42.64	12.32	78.67	37.97	144.85	12.04	0.90	31.70
TDM(g)	8.74	139.53	52.75	568.29	23.84	1.79	45.19	10.80	149.90	49.50	445.43	21.11	1.59	42.64	12.32	78.67	37.97	144.85	12.04	0.90	31.70
HI	8.95	71.26	48.67	91.08	9.54	0.72	19.61	1.63	55.87	40.24	137.91	11.74	0.88	29.19	20.21	55.64	47.19	53.70	7.33	0.55	15.53
PP (g)	0.02	0.48	0.20	0.01	0.10	0.01	48.67	0.00	0.62	0.15	0.01	0.10	0.01	62.16	0.03	0.34	0.14	0.00	0.05	0.00	36.53

DFF -days to 50% flowering, DM-days to maturity, PH- plant height, PL-panicle length, PW-panicle weight, FG- number of filled grains/panicle, UFG-number of unfilled grains/panicle, TGP- number of total grains/panicle, TGW- thousand grain weight, SPY-single plant grain yield TN- number of tillers plant, PTN-number of productive tillers/plant, SF- spikelet fertility, SP- sterility percentage, BM- biomass /plant, BY -biological yield /plant, HI -harvest index, PP -productivity/day, Var- Variance, SD-standard deviation, SE- standard error, CV- coefficient of variation

yield and 17 yield-related traits for all three seasons were then subjected to combined analyses via additive main effects and multiplicative interaction (AMMI) analysis of variance and genotype effect and genotype by environment interaction effect (GGE) using PB tools (Version 1.4, http://bbi.irri.org/products). AMMI uses ANOVA to analyze the main effects (additive part) and Principal Component Analysis (PCA) to detect the non-additive residuals by the ANOVA (Gauch 1993). The SS (%) was calculated comparing sum of squares (SS) from AMMI ANOVA. The results of the AMMI model analysis are interpreted on the basis of AMMI1 biplot where the graph is plotted with the main effect and first multiplicative axis (PC1) for both genotypes and environments and shows specific adaptation of genotypes and selection of environments (Ebdon and Gauch 2002). This provides a pictorial view of the transformed GEI for any interpretation. In a biplot where PC1 is on the vertical axis and mean yield on the horizontal axis, genotypes that appear almost on a perpendicular line had similar means and those on a horizontal line had similar interaction patterns. The same sign of a genotype and environment on their first PC axis shows a positive interaction, while negative interaction when signs are different (Tariku et al. 2013). Genotypes or environments with large PC1 scores, either positive or negative had large interactions, whereas genotypes with PC1 score of zero or nearly zero had smaller interactions (Crossa et al. 1990) and is considered as stable. The vertical line at the center of the biplot is the general grand mean. The AMMI model is a combination of analysis of variance (ANOVA) and principal component analysis (PCA). The analytical model is given as:

$$Y_{ij.} = \mu + \delta_i + \beta_j + \sum_{k=1}^{K} \lambda_k \delta_{ik} \beta_{jk} + \epsilon_{ij.}$$

GGE biplots display both G (genotype) and GE (genotype-environment) variation for traits under study (Kang 1993) and is based on the sites regression (SREG) linear–bilinear model (Cornelius et al. 1996; Crossa et al. 2002). The sites regression model as a multiplicative model in the bilinear terms shows the main effects of cultivars plus the cultivar x environment interaction (GGE) and the site regression model is:

$$Y_{ij.} = \mu + \beta_j + \sum_{k=1}^{K} \lambda_k \delta_{ik} \beta_{jk} + \epsilon_{ij.}$$

Where Y_{ij} is the mean yield of i^{th} genotype in j^{th} environment, μ is the overall mean, δ_i is the genotypic effect, β_j is the environment effect, λ_k is the singular value for PC axis k: δ_{ik} is the genotype eigenvector value for PC axis n, β_{jk} is the environment eigenvector value for PC axis k and ε_{ij} is the residual error assumed to be normally and independently distributed $(0, \sigma^2/r)$, σ^2 is the pooled error variance, and r is the number of replicates. The GGE biplot graphically represents

G and GEI effect present in the multi-location trial data using environment centered data and which-won-where plots.

The graphs generated were based on AMMI biplot for yield and yield related traits, GGE biplot environment view for yield and yield related traits (evaluation of suitable genotypes ideal for specific environment), GGE biplot genotype view for yield and yield-related traits (evaluation of stable genotypes relative to an ideal genotype) and polygon view of GGE biplot for identification of which won where. GGE biplot symmetric view was used in this study to explain the 'which-won-where' patterns for genotypes and environments. Different polygons composed of one or several environment(s) and one or more genotype(s) can be used to determine which genotype(s) is performing best in which environment(s). It is constructed by plotting the first two principal components (PC1 and PC2, also referred to as primary and secondary effects, respectively) derived from singular value decomposition of the environment-centered data. Options in GGE biplot analysis allow comparison among a set of genotypes with a reference genotype. This method defines the position of an ideal genotype, which will have the highest average value of all genotypes and be absolutely stable; that is, it expresses no genotype by environment interaction. A set of concentric circles are generated using the ideal genotype as the center. The ideal genotype is used as a reference to rank the other genotypes. A performance line passing through the origin of the biplot is used to determine mean performance of a genotype. The arrow on the line represents increasing mean performance. A stability line perpendicular to the performance line is also passing through the origin of the biplot; the two arrows in opposite directions represent decrease in stability. A genotype farther from the biplot origin on either side on the stability line represents relatively lower stability and those closer to the performance line are more stable.

Results

Combined analysis of variance showed highly significant difference for the characters among the genotypes in the present investigation after confirmation for homogeneity of variance using Bartlett and Levene test across the seasons, indicating the presence of inherent genetic variances among genotypes (Table 1). The significant mean sum of squares of genotype indicated that the genotypes were diverse with large differences for the mean yield potential. The significant genotype × environment interaction effect showed that the genotypes responded differently to the variation in environmental (seasonal fluctuations) conditions. The sum of square percentage (SS%) of AMMI and GGE showed that days to 50% flowering (DFF), days to maturity (DM), plant height (PH), panicle length (PL), panicle weight (PW), number of filled grains/panicle (FG), number of unfilled grains/panicle (UFG), number of total grains/panicle (TGP), and thousand grain weight (TGW) were contributed mainly by genotypic (G) effect followed by environment (E) and their interaction (G×E). But the characters *viz.,* single plant grain yield (SPY), number of tillers plant(TN), number of productive tillers/plant (PTN), spikelet fertility (SF), sterility percentage (SP), biomass /plant(BM), biological yield /plant (BY), harvest index (HI), and productivity/day (PP) were mostly affected by genotype by interaction (G×E). The principal component explains the contribution of genotype, environment and their interaction of the total sum of squares of the genotype × environment interaction.

First two principal components (PC1 and PC2) of AMMI analysis explained contribution of genotype and their environment, whereas the principal components of GGE analysis explained the contribution of the genotype, environment, and the interaction of the total sum of square. In the AMMI analysis, the PC1 value was higher than PC2 for all the traits explaining higher contribution of genotype in the total sum of squares. But compared to single plant grain yield PC1 (67.3) and PC2 (32.7), there was an increase in PC1 score and a decrease in PC2 score was observed for number of tillers/plant, number of productive tillers/plant, panicle weight, number of total grains/panicle, and biological yield/plant (Table 2). In GGE analysis, the PC1 value was higher than PC2 and PC3 for all the traits explaining higher contribution of genotype in the total sum of squares (Table 3).

Stability analysis of genotypes for yield and yield related traits across the environments

As per AMMI biplot model the mid early genotype G48 (NH4371) was identified as the most stable genotype for single plant grain yield across all the three seasons. From GGE biplot model, the genotype G52 (NH686), G19 (27K), and G54 (NH776) were identified as stable genotypes with high mean performance (Fig. 1). Among the seasons, E1 was found to be the most suitable season for potential expression of yield trait. The best suited genotypes were G19 in E1, G56 (Tellahamsa) in E2, and G5 (166-1) in E3. As per AMMI and GGE biplot model the late genotype G24 (95B) was identified as the stable genotype for days to 50% flowering across all the three seasons (Supplementary Fig. 1). Early lines G33 (Prasanna), G54 (NH776), and G36 (NH1637) were identified as stable in negative direction for days to 50% flowering as early to medium varieties are preferred than late genotypes. Among the seasons, E2 was found to be the most suitable season for expression of days to flowering for longer duration lines, whereas E3 was found to be favorable season for early lines. As per GGE biplot analysis the genotype G31 (Jaya) was best suited for E1 (*Kharif* 2015) and E2 (*Rabi* 2014-15). The late lines G16 (250K) and G10 (166-23-1) were best adapted to E3 (*Rabi* 2015-16). For days to maturity, a late introgression line G6 (166-2-11) was identified as a stable genotype with longest maturity duration across all the three seasons.

An early introgression line G4 (148S) was identified as stable for plant height and panicle length over the seasons. AMMI biplot model and GGE biplot model showed that a late line G21 (51B) was the best genotype, across the three

Table 2. ANOVA and Sum of Squares percentage on G, E and GxE derived from Analysis of variance for AMMI stability model.

Source of Variation	df	Days to 50 % flowering	Days to maturity	Plant height	Number of total tillers /plant	Number of productive tillers / plant	Panicle length	Panicle weight	Number of filled grains /panicle	Number of unfilled grains /panicle
Genotypes	58	67.63	67.78	57.91	30.04	29.87	44.97	43.69	48.12	34.49
Environments	2	17.41	14.17	16.27	4.57	3.12	14.22	13.67	14.44	9.17
G x E Interaction	116	14.47	17.45	21.56	43.83	44.57	21.29	20.41	17.25	27.22
IPCA1	59	66.18	67.00	58.10	69.50	68.50	67.00	72.90	65.30	57.30
IPCA2	57	33.82	33.00	41.90	30.50	31.50	33.00	27.10	34.70	42.70
Pooled error	348									
Total	530									

Source of Variation	df	Number of total grains /panicle	Spikelet fertility	Sterility percentage	Thousand grain weight	Single plant grain yield	Biomass /plant	Biological yield /plant	Harvest index	Productivity/ day
Genotypes	58	54.08	26.16	26.16	64.26	27.70	32.31	31.02	26.53	28.47
Environments	2	10.57	14.70	14.70	2.66	8.40	8.61	7.48	15.70	8.80
G x E Interaction	116	17.28	29.87	29.87	15.09	42.66	38.44	43.88	34.88	41.37
IPCA1	59	72.60	63.90	63.90	75.10	67.30	67.00	68.40	63.30	66.60
IPCA2	57	27.40	36.10	36.10	24.90	32.70	33.00	31.60	36.70	33.40
Pooled error	348									
Total	530									

Table 3. ANOVA and Sum of Squares percentage on G, E and GxE derived from Analysis of variance for GGE stability model.

Source of Variation	df	Days to 50 % flowering	Days to maturity	Plant height	Number of total tillers /plant	Number of productive tillers / plant	Panicle length	Panicle weight	Number of filled grains /panicle	Number of unfilled grains /panicle
PC1	59	85.7	81.4	79.5	48.3	53.4	68.8	79.5	75.4	53.4
PC2	57	8.4	11.9	15.6	33.6	28.9	21.5	15.6	16.9	28.9
PC3	55	5.9	6.7	4.8	18	17.7	9.7	4.8	7.7	17.7

Source of Variation	df	Number of total grains /panicle	Spikelet fertility	Sterility percentage	Thousand grain weight	Single plant grain yield	Biomass /plant	Biological yield /plant	Harvest index	Productivity/ day
PC1	59	61.6	76.3	48	81.5	49.2	57.5	50.9	45.9	49.4
PC2	57	19.9	17.5	33.6	14.2	40.7	27.7	37.6	35.9	39.4
PC3	55	18.5	6.2	18.4	4.3	10.1	14.8	11.5	18.2	11.2

seasons having highest tillering capacity. GGE biplot model indicated that best suited genotype in E1 was G3 (14S), in E2 was G23 (93B) and in E3 it was G14 (220S). Similar results were found for number of productive tillers also. From AMMI biplot model, an early line G4 (148S) was identified as the best genotype for panicle length however GGE biplot analysis identified a late line G8 (166-2-9) as the best genotype. Best suited genotype in E1 and E3 was G4 and for E2 the suitable genotype was G6, from GGE biplot model. A late genotype G11 (166-30) was identified as the stable genotype for panicle weight and filled grains per panicle, across the seasons, as per both AMMI biplot model and GGE model. Among the seasons E1 was found to be the most suitable season for expression of these traits. It was observed that late lines 166-23-1, 166-30, and 250K were the most adapted genotypes for highest number of filled grains per panicle in E1, E2, and E3, respectively. Similarly highest number of total grains/panicle were also found in late lines G11 (166-30) followed by G6 (166-2-11). Conversely, early genotypes like G43 (NH4071), G34 (Rasi), G4 (148S), G35 (Sahbhagidhan), and mid-early line G46 (NH4226) had high spikelet fertility and showed stable performance across the seasons.

The mid-early genotype G12 (166-9) and early line G4 (148 S) were identified as stable genotype for thousand grain weight. Stable performance for high biomass/plant was observed in late line G8 (166-2-9) followed by G56 (Tell-ahamsa). AMMI biplot and GGE models showed mid-early genotype G19 (27 K) was the best genotype for yield per plant across all the three seasons. Among the seasons E1 (Kharif) was found to be the most suitable season for expression of this trait. As per GGE biplot model the best suited genotype

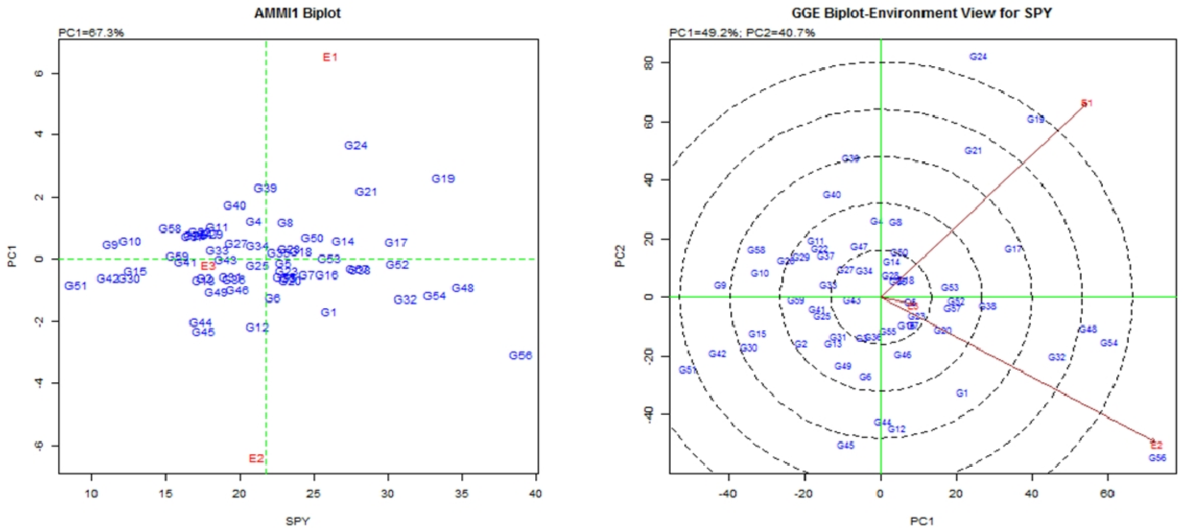

Fig. 1. AMMI1 biplot and GGE biplot for single plant grain yield of 59 genotypes tested in three seasons.

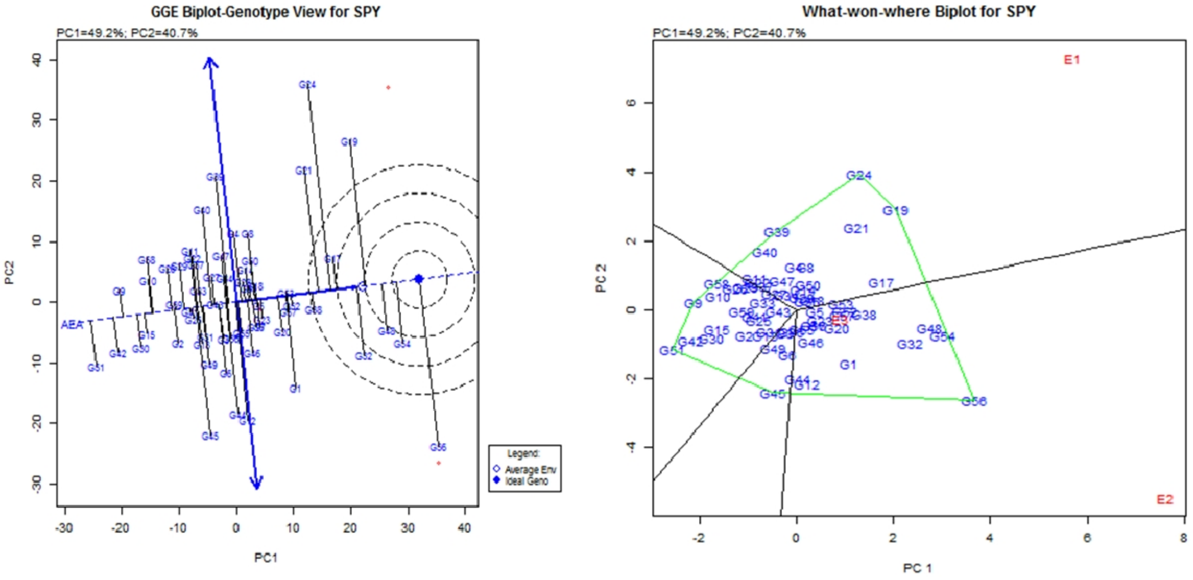

Fig. 2. GGE biplot of ideal genotype and comparison of the genotypes with ideal genotype along with 59 genotypes for single plant grain yield in three seasons based on which-won-where pattern.

in E1 was G19 (27 K), for E2, it was G54 (NH776), and for E3 the suitable genotypes were G52 (NH686), G57 (Tulasi), and G53 (NH73), belonging to early to mid-early maturity groups. Mid-early line G17 (258S) was identified as the best stable genotype for harvest index across all the three seasons by both AMMI biplot model and GGE biplot model. For productivity/day as per AMMI biplot model the genotype G19 (27K) was identified as the best stable genotype across all the three seasons. Based on GGE biplot model the genotype G24 (95B) was identified as the most stable genotypes across all the seasons.

Adaptability of genotypes across the three environments

Adaptability of genotypes across the environments was assessed based on GGE biplot-genotype view graph and GGE biplot polygon view graph (which-won-where graph). The ideal genotypes for traits were selected from GGE biplot genotype graph and the best suited genotypes for particular season was identified through GGE biplot polygon view graph (Supplementary Fig. 2). GGE biplot (Fig. 2) showed that G56 (Tellahamsa), a mid-early line is ideal genotype for single plant grain yield in all the seasons compared to other genotypes. G54 (NH776) which is next to G56 in ideal genotype graph and was more stable than G56; this can be considered as the best genotype across the seasons. The genotypes from early or mid-early maturation groups viz., G56 (Tellahamsa), G54 (NH776), G48 (NH4371), G19 (27K), G52 (NH686), G17 (258S), G21, and G38 (NH219) were identified as stable genotypes with high mean performance and suited for all the three seasons under study. The polygon view of GGE biplot (which won where graph) had shown that G24 was suitable to E1, followed by G19. These two genotypes were also high yielders in E1. G56 was best performer in both seasons E2 and E3.

Genotype view of GGE biplot showed that late line G24 (95 B) is ideal genotype for days to 50% flowering in all the seasons compared to other genotypes. The late genotypes G24 (95B), G13 (166S), G16 (250K), G6 (166-2-11), G10 (166-23-1), G5 (166-1), G22 (75 S), G8 (166-2-9), G9 (166-23), and G11 (166-30) are stable across the three seasons. As the early to medium varieties are preferred than late genotypes so we selected the genotypes in negative direction for days to fifty percent flowering. The genotypes G53 (NH733), G36 (NH1637), G54 (NH776), G50 (NH4406), G27 (Anjali), and G25 (Aditya) showed stable earliness. Similarly, the polygon view of GGE biplot (which won where graph) showed that genotypes G6, G13, G24, and G5 are suitable lines for the trait earliness. G6 (166-2-11) was found to be the ideal genotype for days to maturity in all the seasons compared to other genotypes from genotype view of GGE biplot. From GGE biplot, early line G4 (148S) was ideal genotype for plant height in all the seasons. For number of total tillers/plant, a late line G21 (51B) was identified as ideal genotype and the genotypes G21, G54 (NH776), G3 (14 S), G14 (220S), G23 (93B), G18 (263 K), and G19 (27 K) of varying maturity durations were found as stable lines. Similarly, G21 was found to be ideal genotype for number of productive tillers also. Genotype view of GGE biplot showed that early line G4 (148 S) and late line G8 (166-2-9) were ideal genotypes for panicle length in all the seasons.

From GGE biplot it was seen that late line G11 (166-30) was ideal genotype for panicle weight followed by late lines G8 (166-2-9), G6 (166-2-11), G16 (250 K), and mid-early line G12 (166-9). From the polygon view of GGE biplot (which won where graph) that genotypes G11 and G8 are suited genotypes across the three seasons. G11 was identified as ideal genotype in all the seasons for the trait, number of filled grains/panicle. G11 was identified as ideal compared to other genotypes having highest mean value for number of total grains/panicle. The late genotypes G11 (166-30), G6 (166-2-11), G8 (166-2-9), G10 (166-23-1), G16 (250 K), and G9 (166-23) were most stable genotypes for this trait. The late genotypes G24 (95 B), G21 (51 B), G23 (93 B), and G22 (75 S) and early lines G34 (Rasi), G35 (Sabhagidhan), G43 (NH4071), G42 (NH4029), G51 (NH4415), G47 (NH4231), and G27 (Anjali) were adaptable genotypes for spikelet fertility across the seasons. The polygon view of GGE biplot (which won where graph) showed that late genotype G24 was the best suited genotype for E1 and E3 and early genotypes G50 (NH4406) and G53 (NH733) were suitable genotypes for E2.

Genotype view of GGE biplot showed that early line G4 (148S) was the ideal genotype for thousand grain weight followed by mid early lines G19 (27 K) and G12 (166-9). The genotypes G4, G19, G12, G29 (IR64), G58 (Vandana), G25 (Adithya), G35 (Sahbhagidhan), G7 (166-2-3), G55 (Sona), G1 (130 K), G56 (Tellahamsa), and G33 (Prasanna) of early to mid early maturation were the stable genotypes across all the seasons for thousand grain weight. G56 was identified as ideal genotype for biomass/plant. The genotypes G56, G8, G5 (166-1), G4 (148S), G19 (27K), G39 (NH349), G48 (NH4371), and G16 (250K) are the best stable genotypes across all the seasons for biomass/plant. G56 (Tellahamsa) was identified as ideal genotype for biological yield/plant. Genotype view of GGE biplot showed that G17 (258S) was the ideal genotype for harvest index in all the seasons with highest mean value. The polygon view of GGE biplot (which won where graph) showed that genotype G1 (130 K, mid-early line) was the best suited genotype for E2 and G17 for E3. G56 (Tellahamsa) was identified as the ideal genotype for productivity/day and G54 (NH776) was also a stable genotype for this trait. The early-mid early genotypes G56 (Tellahamsa), G54 (NH776), G48 (NH4371), G32 (MTU1010), G19 (27 K), G38 (NH219), and G17 (258S) were the best stable genotypes across all the seasons for productivity/day. The polygon view of GGE biplot (which won where graph) showed that genotypes G24 (95 B) and G19 were the best suited genotypes for E1, and G56 and G54 were the suited genotypes for E2 and E3.

Discussion

Improvement of existing released varieties is a major challenge in breeding programs in the climate change scenario. In order to sustain rice production, cultivation of early high-yielding varieties is required as it will enhance resource- and input-use efficiency per unit area and unit time and thus the rice productivity. It is therefore necessary to select potential stable donors for yield in different maturity groups. Yield and yield-related traits are highly influenced by environment and its interactions, so it is essential to study G×E interaction for identification of stable genotypes in breeding programs. The quality of selection was enhanced in breeding trials when the stability variance was assessed along with yield (Kang 1993). In the present study G×E interaction was mainly studied by two widely used models, i.e. AMMI and GGE biplot models. AMMI and GGE biplot are excellent tools for visual data analysis of genotypic performance across different environments (Gauch 2006; Rakshit et al. 2016; Yan et al. 2000). Biplots helps in displaying genotypic stability statistics and clustering of genotypes based on performance across diverse environments (Balakrishnan et al. 2016; Rasul et al. 2017; Thillainathan and Fernandez 2001). The GGE biplots give more detailed graphical representation of mean performance and stability and display which-won-where pattern of genotypes (Yan and Kang 2003; Kang 1993).

Combined analysis of variance for the data showed significant genotype, environment, and genotype × environment interaction, indicating the presence of variability among the genotypes and environments and their role in phenotypic expression. The significant genotype × environment interaction effect showed that the genotypes responded differently to the variation in environmental (seasonal fluctuations) conditions. The PC1 value was higher than PC2 for all the traits and that explained higher contribution of genotype in the total sum of squares of the genotype × environment interaction. The SS% explained contribution of each trait and results revealed that days to 50% flowering, days to maturity, plant height, panicle length, panicle weight, number of filled grains/panicle, number of total grains/panicle and thousand grain weight were contributed mainly by genotype, followed by environment and their interaction. On the other hand, single plant grain yield, number of tillers/plant, number of productive tillers/plant, spikelet fertility, sterility percentage, biomass/plant, biological yield /plant, harvest index, and productivity/day were affected significantly by G × E interaction.

As per AMMI biplot analysis the season *Kharif* 2015 was the best suited environment for potential expression of following traits *viz.,* panicle length, panicle weight, filled grains/panicle, low unfilled grains/panicle, total grains/panicle, spikelet fertility, low sterility percentage, biological yield/plant, harvest index, and productivity/day. *Rabi* 2014-15 season was identified as best suited for expression of plant height, productive tiller number, low unfilled grains per panicle, spikelet fertility, and biomass/plant. *Rabi* 2015-16 was the best suited season for potential expression of reduced days to 50% flowering and early maturity, tiller number, thousand grain weight, and harvest index. It was previously reported that grain yield is significantly higher in dry season (rabi) than the wet season (kharif) under irrigated rice production in tropical conditions and variation was observed for the ideotype suitability for different seasons (Bueno and Lafarge 2017; Shahid et al. 2013; Wu et al. 2013; Yang et al. 2008). Even though, the AMMI model and GGE model explained similar results in case of stable genotypes and suitable seasons, there was a variation of magnitude in PC scores as previously reported by Yan et al. (2007) and Badu-Apraku et al. (2012).

Early introgression line, 148S was identified as stable best suited line across all the three seasons for plant height and panicle length. Another introgression line, 27K of mid early duration was identified as stable best suited line across all the three seasons for single plant grain yield, biological yield/plant and productivity/day. The late genotypes G11 (166-30), G6 (166-2-11), G8 (166-2-9) were found to be stable for number of grains per panicle, number of filled grains, and panicle weight. The genotypes Tellahamsa (mid-early line), NH776 (early line), NH4371 (early line), 27K (mid-early line), NH686 (mid-early line), 258S (mid early line), and NH219 (mid early line) were stable suited lines for single plant grain yield across all the three seasons.

Among early cultivars, Prasanna was as the best early line for thousand grain weight and harvest index. Early cultivar Rasi was identified for panicle length, low sterility percentage, and low unfilled grains/panicle. Sahbhagidhan was found to be stable line for spikelet fertility, thousand grain weight, harvest index, and low sterility percentage. Tellahamsa was identified as stable line for panicle length, single plant yield, biomass/plant, biological yield/plant, and productivity/day. Popular cultivar MTU1010 was identified for panicle length, biological yield, plant, harvest index and productivity/day. These are the potential *O. sativa* cultivars as donors for improving yield traits in breeding programs for the development early-high yielding varieties. There are only a very limited number of studies to identify the key traits contributing to grain yield based on crop duration (Bueno and Lafarge 2017) even though, the maturity duration is a major determinant for crop yield (Huang et al. 2013; Zhang et al. 2009). Ranawake and Amarasinghe 2014 reported that the quantitative effect of contributing traits for grain yield is not constant in different maturity groups of rice. The relevant traits for adaptation to varying seasons and conditions for different maturity groups were studied by Li et al. (2009), Huang et al. (2013) Wu et al. (2013), and (Bueno and Lafarge 2017) and found different growth dynamics strategies and contributing traits for each maturity groups in attaining potential yield. It explains the need to consider maturity groups for selection of specific traits in yield improvement programs.

Oryza nivara introgression line 166-9, 166-2-3, 148S, and 27K and mutant lines NH258S, NH219, NH4071, NH4029, NH4029, NH4415, NH4371, and NH776 were found to possess favorable phenotypic expression for multiple yield contributing traits across the seasons. This indicates the potential of mutants and wild introgression lines for yield improvement and gene identification. It was also found that early to mid-early duration lines are performing better and most stable in case of the major yield traits except in case of number of grains, number of filled grains, and panicle weight. Better adaptation across a wide range of environments and stable yield performance in climate change conditions is possible only through an understanding the genetics of traits across varying environments (Dixit et al, 2015). Selected stable early genotypes and genotypes with wider adaptability for grain yield using stability analysis are utilized in further breeding programs and to develop early genotypes with high yield.

Conclusion

The present research work reveals that the genotypes Prasanna, Anjali, Jaldidhan, NH776, NH1637, and NH4406 are the potential donors for earliness improvement and genotypes 166-30, 95B, 130K, Tellahamsa, and 27K for grain yield. Crosses between these genotypes may be a prospective research area in the current scenario with high demand and low inputs for developing short-duration, high-yielding lines. Secondly, mutants viz., NH219, NH686, NH776, and NH4371 and introgression lines 27K, 130K, and 148S which are stable for yield, earliness, and other agronomic traits and will be confirmed further through multi location and multi environmental trials. Breeding programs involving high-yielding varieties, mutants, and introgression lines of different maturity durations have the prospective to study the genetics, gene action and interactions controlling heading date traits and to obtain elite varieties with desirable agronomic characters.

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Supplementary Table 1. Details of genotypes and environments along with their codes used in AMMI and GGE analysis.

S.No	Genotype	Code used in AMMI and GGE analysis	Pedigree	Maturity group
Introgression Lines				
1	130(K)	G1	*Swarna* / *O. nivara*	Mid early
2	14-3	G2	*Swarna* / *O. nivara*	Late
3	14(S)	G3	*Swarna* / *O. nivara*	Mid early
4	148(S)	G4	*Swarna* / *O. nivara*	Early
5	166-1	G5	*Swarna* / *O. nivara*	Late
6	166-2-11	G6	*Swarna* / *O. nivara*	Late
7	166-2-3	G7	*Swarna* / *O. nivara*	Mid
8	166-2-9	G8	*Swarna* / *O. nivara*	Late
9	166-23	G9	*Swarna* / *O. nivara*	Late
10	166-23-1	G10	*Swarna* / *O. nivara*	Late
11	166-30	G11	*Swarna* / *O. nivara*	Late
12	166-9	G12	*Swarna* / *O. nivara*	Mid early
13	166(S)	G13	*Swarna* / *O. nivara*	Late
14	220(S)	G14	*Swarna* / *O. nivara*	Mid early
15	246(K)	G15	*Swarna* / *O. nivara*	Mid early
16	250(K)	G16	*Swarna* / *O. nivara*	Late
17	258(S)	G17	*Swarna* / *O. nivara*	Mid early
18	263(K)	G18	*Swarna* / *O. nivara*	Mid early
19	27(K)	G19	*Swarna* / *O. nivara*	Mid early
20	35(B)	G20	BPT5204 / *O. rufipogon*	Mid early
21	51B	G21	BPT5204 / *O. rufipogon*	Late
22	75(S)	G22	BPT5204 / *O. rufipogon*	Late
23	93B	G23	BPT5204 / *O. rufipogon*	Late
24	95B	G24	BPT5204 / *O. rufipogon*	Late
Cultivars				
25	Aditya	G25	M-63-83 / Cauvery	Early
26	ADT43	G26	IR-50 / Imp. white Ponni	Early
27	Anjali	G27	PR-19-2 / RR-149-1129	Early
28	Govind	G28	IR-20 / IR-24	Early
29	IR64	G29	IR 5657-33-2-1/ IR 2061-465-1-5-3	Mid early
30	Jaldidhan	G30	Kagalikai/Jaldidhan 8	Early
31	Jaya	G31	T(N)1 / T-141	Late
32	MTU1010	G32	Krishnaveni/IR64	Mid early
33	Prasanna	G33	RP-1667-301-1196-1562 IRAT-8 / N-22	Early
34	Rasi	G34	TN1 / Co.29	Early
35	Sahbhagi dhan	G35	IR55419-4*2/WayRarem	Early
Mutants				
36	NH1637	G36	N22	Mid early
37	NH1876	G37	N22	Early
38	NH219	G38	N22	Mid early
39	NH349	G39	N22	Mid early
40	NH363	G40	N22	Mid early
41	NH4014	G41	N22	Early
42	NH4029	G42	N22	Early
43	NH4071	G43	N22	Early
44	NH4076	G44	N22	Early
45	NH4078	G45	N22	Early
46	NH4226	G46	N22	Mid early
47	NH4231	G47	N22	Early
48	NH4371	G48	N22	Early
49	NH4385	G49	N22	Early
50	NH4406	G50	N22	Early
51	NH4415	G51	N22	Early
52	NH686	G52	N22	Mid early
53	NH733	G53	N22	Early
54	NH776	G54	N22	Early

Cultivars				
55	Sona	G55	N6 / PRN 48	Mid early
56	Tellahamsa	G56	HR12/TN1	Mid early
57	Tulasi	G57	Rasi/ Finegora	Early
58	Vandana	G58	C22 / Kalakeri	Early
59	Varalu	G59	Erramellalu /CR 544-1-2	Early

	Season	Code used in AMMI and GGE analysis
1	Kharif 2015	E1
2	Rabi 2014- 15	E2
3	Rabi 2015- 16	E3

Supplementary Table 2. Analysis of variance for single plant grain yield and its component traits in three different seasons.

Source of Variation	df	Season	Days to 50 % flowering	Days to maturity	Plant height	Number of total tillers /plant	Number of productive tillers / plant	Panicle length	Panicle weight	Number of filled grains /panicle	Number of unfilled grains /panicle
Replications	2	*Rabi* 15	0.073	0.006	0.073	0.023	0.107	0.148	1.356	1802.650	32.836
		Kharif 15	0.141	0.277	0.959	3.006	3.819	2.479	0.875	1465.379	46.311
		Rabi 16	0.006	0.023	0.262	11.407	9.475	2.389	0.080	89.972	9.768
Genotypes	58	*Rabi* 15	425.764**	378.395**	1055.585**	124.188**	127.228**	27.905**	3.544**	6503.481**	262.474**
		Kharif 15	478.356**	446.191**	1107.511**	71.992**	68.961**	18.526**	2.487**	6112.503**	327.446**
		Rabi 16	901.883**	701.132**	300.956**	80.277**	54.438**	27.912**	1.320**	3594.070**	524.706**
Error	116	*Rabi* 15	2.522	2.632	17.670	14.804	14.849	2.322	0.604	589.552	86.888
		Kharif 15	1.750	1.656	31.652	11.891	11.469	4.015	0.488	1546.827	102.305
		Rabi 16	1.040	1.063	16.615	13.401	11.233	4.524	0.144	309.506	72.326

Source of Variation	df	Season	Number of total grains /panicle	Spikelet fertility	Sterility percentage	Thousand grain weight	Single plant grain yield	Biomass /plant	Biological yield /plant	Harvest index	Productivity/ day
Replications	2	*Rabi* 15	1351.362	27.910	27.910	0.061	0.047	42.394	0.012	0.073	0.0002
		Kharif 15	1184.107	14.713	14.713	3.647	98.786	44.578	78.337	0.157	0.006
		Rabi 16	79.768	5.639	5.639	0.845	0.728	28.648	36.178	48.139	0.00007
Genotypes	58	*Rabi* 15	7893.964**	170.358**	170.358**	32.039**	406.671**	219.704**	1056.161**	325.736**	0.022**
		Kharif 15	7276.532**	113.602**	113.602**	34.585**	387.619**	409.325**	1321.165**	338.020**	0.022**
		Rabi 16	5438.737**	195.445**	195.455**	24.423**	93.073**	142.523**	341.181**	172.995**	0.006**
Error	116	*Rabi* 15	528.114	46.584	46.584	5.142	54.715	28.758	112.664	59.392	0.003
		Kharif 15	1587.659	43.577	43.577	4.425	60.11	62.558	148.841	73.511	0.003
		Rabi 16	448.062	34.235	34.235	0.678	17.380	19.233	56.297	22.121	0.001

* Significant at 0.05 level of probability** Significant at 0.01 level of probability

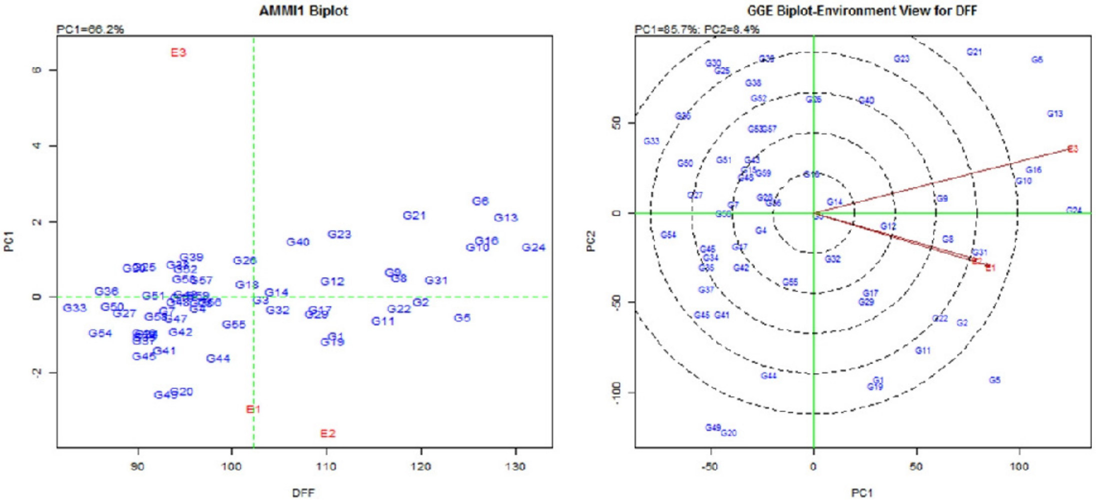
Supplementary Table 3. Test for Homogeneity of Variances.

Grp	Variable	Method	DF	Value	Pr(>Chisq)
Env	DFF	Bartlett	2	29.37	0
Env	DM	Bartlett	2	17.69	0.0001
Env	PH	Bartlett	2	74.17	0
Env	TN	Bartlett	2	1.4	0.4966
Env	PTN	Bartlett	2	6.68	0.0354
Env	PL	Bartlett	2	2.61	0.2706
Env	PW	Bartlett	2	43.59	0
Env	FG	Bartlett	2	31.62	0
Env	UFG	Bartlett	2	21.02	0
Env	TGP	Bartlett	2	11.76	0.0028
Env	SF	Bartlett	2	17.03	0.0002
Env	SP	Bartlett	2	3.83	0.1473
Env	TGW	Bartlett	2	13.52	0.0012
Env	SPY	Bartlett	2	92.67	0
Env	BM	Bartlett	2	60.52	0
Env	BY	Bartlett	2	79.53	0
Env	TDM	Bartlett	2	79.29	0
Env	HI	Bartlett	2	37.82	0
Env	PP	Bartlett	2	75.46	0

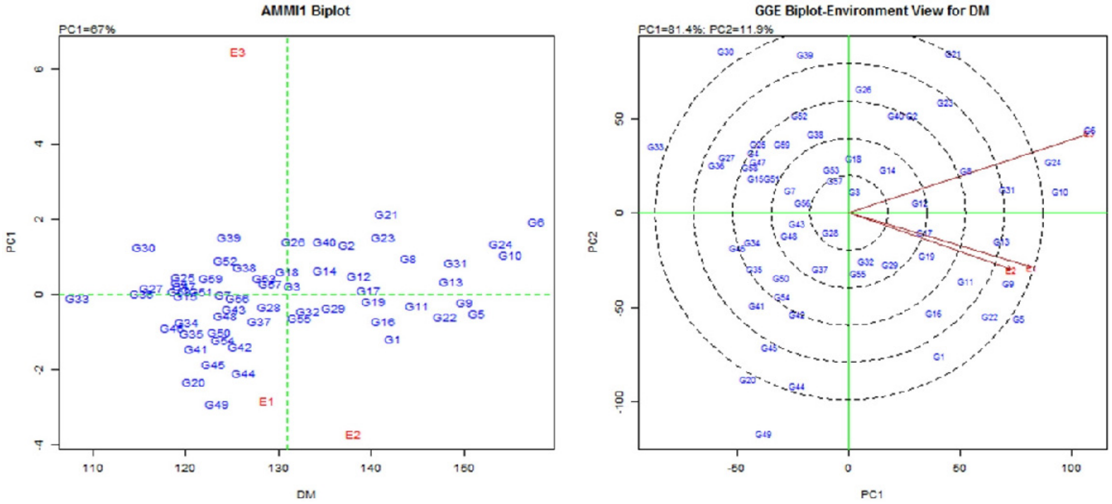
Grp	Variable	Method	DF	F Value	Pr(>F)
Env	DFF	Levene	2	7.77	0.0005
Env	DM	Levene	2	10.15	0
Env	PH	Levene	2	27.19	0
Env	TN	Levene	2	1.7	0.1832
Env	PTN	Levene	2	1.93	0.1457
Env	PL	Levene	2	0.03	0.9673
Env	PW	Levene	2	14.17	0
Env	FG	Levene	2	9.66	0.0001
Env	UFG	Levene	2	3.69	0.0256
Env	TGP	Levene	2	3.73	0.0247
Env	SF	Levene	2	0.35	0.7068
Env	SP	Levene	2	1.94	0.1445
Env	TGW	Levene	2	6.32	0.0019
Env	SPY	Levene	2	25.38	0
Env	BM	Levene	2	8.1	0.0003
Env	BY	Levene	2	15.8	0
Env	TDM	Levene	2	15.85	0
Env	HI	Levene	2	8.99	0.0001
Env	PP	Levene	2	23.5	0

Supplementary Table 4. Correlation Analysis using Pearson's product-moment correlation, Prob > |r|.

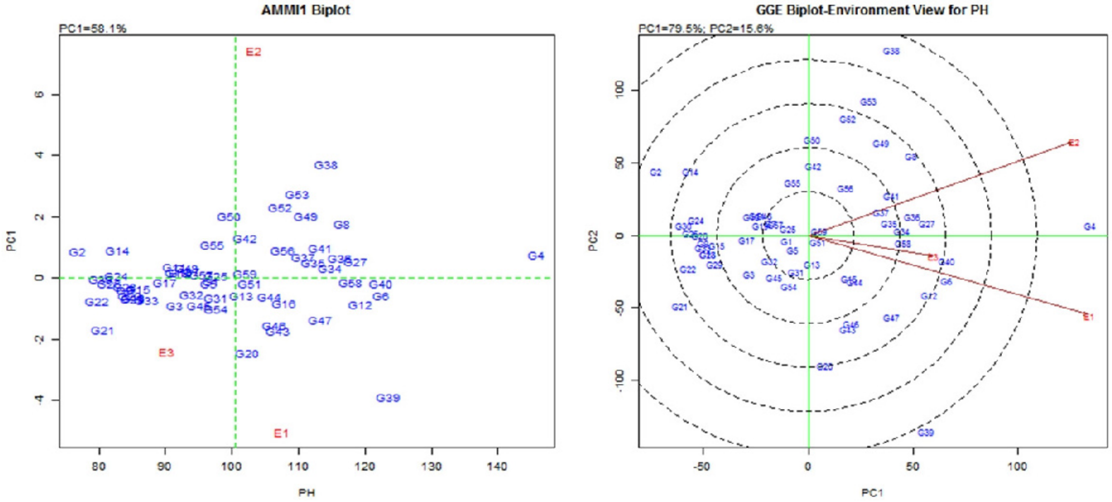
	DFF	DM	PH	TN	PTN	PL	PW	FG	UFG	TGP	SF	SP	TGW	SPY	BM	BY	TDM	HI	PP
DFF	1	0.92	-0.01	-0.16	-0.11	0.2	0.32	0.43	0.11	0.43	0.07	-0.11	-0.2	0.1	0.34	0.24	0.24	-0.27	-0.05
DM	0.92	1	-0.07	-0.11	-0.08	0.18	0.29	0.41	0.08	0.41	0.11	-0.08	-0.19	0.07	0.31	0.2	0.2	-0.29	-0.1
PH	-0.01	-0.07	1	-0.27	-0.25	0.19	0.18	0.15	-0.14	0.1	0.22	-0.26	0.11	0.13	0.29	0.23	0.23	-0.13	0.15
TN	-0.16	-0.11	-0.27	1	0.95	-0.15	-0.15	-0.14	-0.07	-0.15	-0.01	0.04	0	0.25	0.14	0.22	0.22	0.16	0.27
PTN	-0.11	-0.08	-0.25	0.95	1	-0.12	-0.12	-0.11	-0.09	-0.12	0.01	0.02	-0.03	0.29	0.17	0.25	0.25	0.19	0.3
PL	0.2	0.18	0.19	-0.15	-0.12	1	0.65	0.58	0.05	0.56	0.19	-0.06	0.27	0.27	0.24	0.27	0.28	0.13	0.25
PW	0.32	0.29	0.18	-0.15	-0.12	0.65	1	0.82	0.19	0.81	0.15	-0.16	0.12	0.26	0.26	0.28	0.28	0.1	0.21
FG	0.43	0.41	0.15	-0.14	-0.11	0.58	0.82	1	0.1	0.97	0.32	-0.29	-0.16	0.25	0.31	0.3	0.3	0.02	0.18
UFG	0.11	0.08	-0.14	-0.07	-0.09	0.05	0.19	0.1	1	0.36	-0.85	0.77	0.04	-0.03	-0.02	-0.02	-0.02	0.03	-0.04
TGP	0.43	0.41	0.1	-0.15	-0.12	0.56	0.81	0.97	0.36	1	0.08	-0.07	-0.14	0.22	0.29	0.27	0.28	0.03	0.16
SF	0.07	0.11	0.22	-0.01	0.01	0.19	0.15	0.32	-0.85	0.08	1	-0.91	-0.11	0.1	0.15	0.12	0.13	-0.07	0.08
SP	-0.11	-0.08	-0.26	0.04	0.02	-0.06	-0.16	-0.29	0.77	-0.07	-0.91	1	0.12	-0.1	-0.15	-0.14	-0.14	0.07	-0.09
TGW	-0.2	-0.19	0.11	0	-0.03	0.27	0.12	-0.16	0.04	-0.14	-0.11	0.12	1	0.14	0.09	0.12	0.12	0.16	0.16
SPY	0.1	0.07	0.13	0.25	0.29	0.27	0.26	0.25	-0.03	0.22	0.1	-0.1	0.14	1	0.67	0.92	0.92	0.57	0.98
BM	0.34	0.31	0.29	0.14	0.17	0.24	0.26	0.31	-0.02	0.29	0.15	-0.15	0.09	0.67	1	0.91	0.91	-0.14	0.62
BY	0.24	0.2	0.23	0.22	0.25	0.27	0.28	0.3	-0.02	0.27	0.12	-0.14	0.12	0.92	0.91	1	1	0.24	0.88
TDM	0.24	0.2	0.23	0.22	0.25	0.28	0.28	0.3	-0.02	0.28	0.13	-0.14	0.12	0.92	0.91	1	1	0.25	0.88
HI	-0.27	-0.29	-0.13	0.16	0.19	0.13	0.1	0.02	0.03	0.03	-0.07	0.07	0.16	0.57	-0.14	0.24	0.25	1	0.61
PP	-0.05	-0.1	0.15	0.27	0.3	0.25	0.21	0.18	-0.04	0.16	0.08	-0.09	0.16	0.98	0.62	0.88	0.88	0.61	1



AMMI1 biplot and GGE biplot for days to 50 % flowering of 59 genotypes tested in three seasons

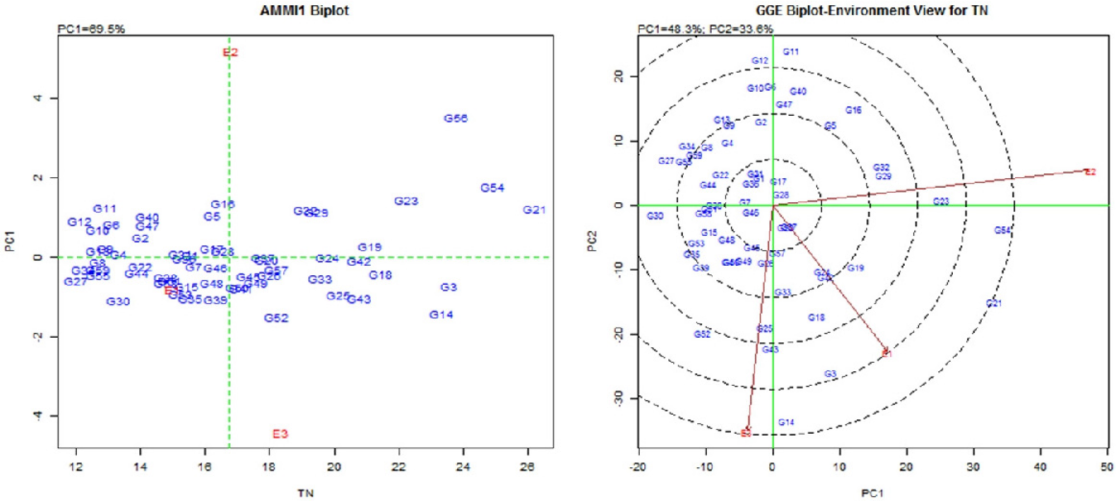


AMMI1 biplot and GGE biplot for days to maturity of 59 genotypes tested in three seasons



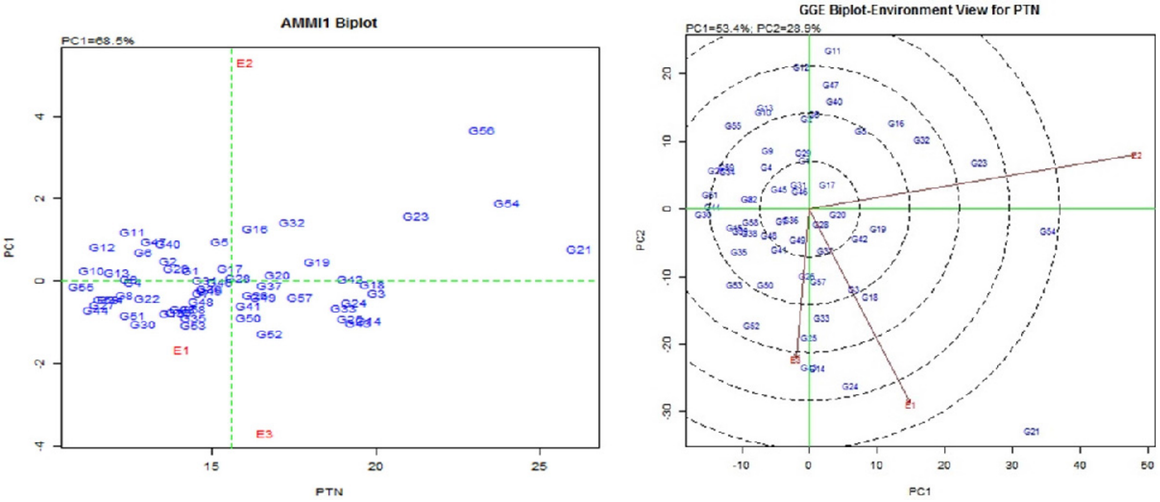
AMMI1 biplotand GGE biplot for plant height of 59 genotypes tested in three seasons

Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons.


AMMI1 Biplot

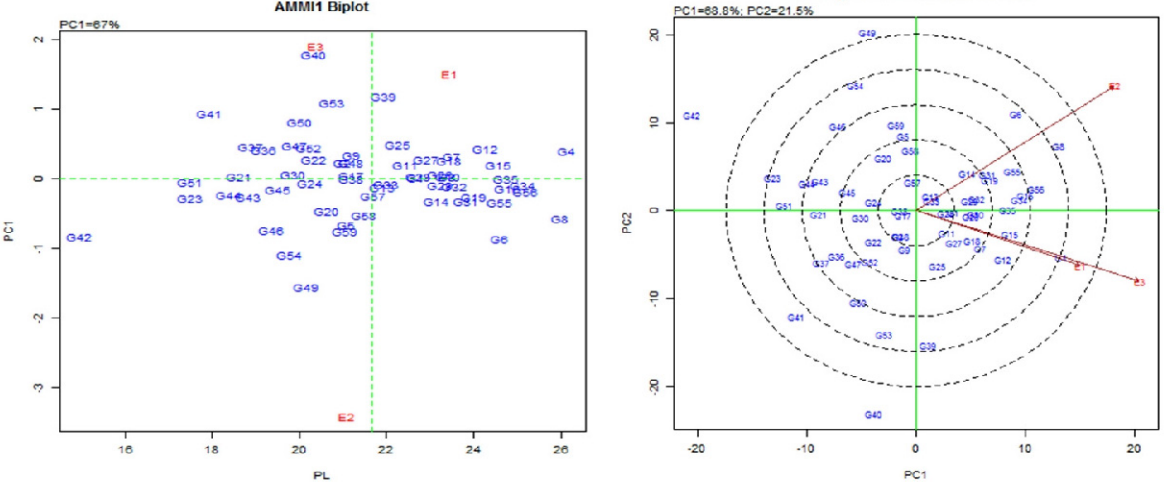
GGE Biplot-Environment View for TN

AMMI1 biplot and GGE biplot for number of total tiller per plant of 59 genotypes tested in three seasons


AMMI1 Biplot

GGE Biplot-Environment View for PTN

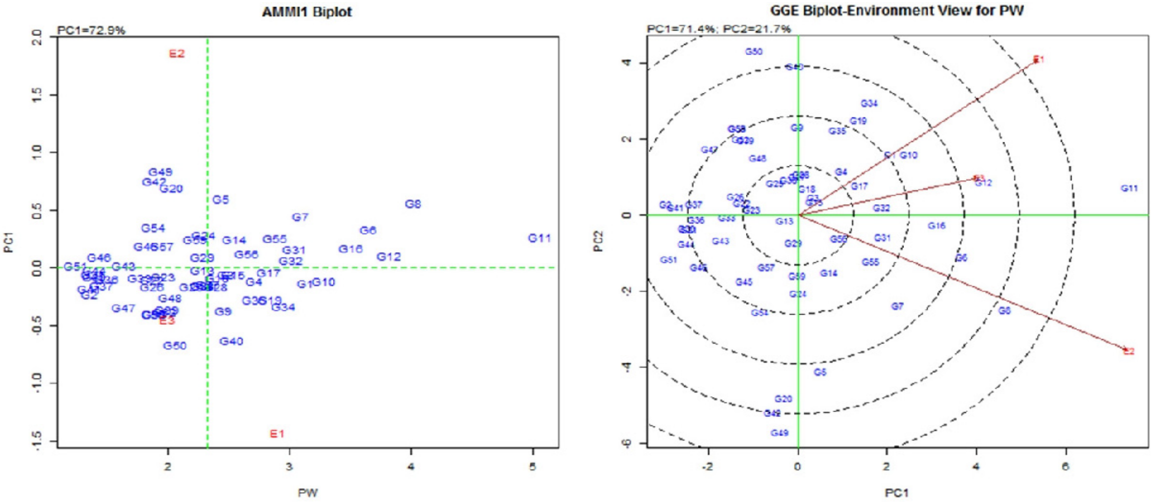
AMMI1 biplot and GGE biplot for number of productive tiller per plant of 59 genotypes tested in three seasons


AMMI1 Biplot

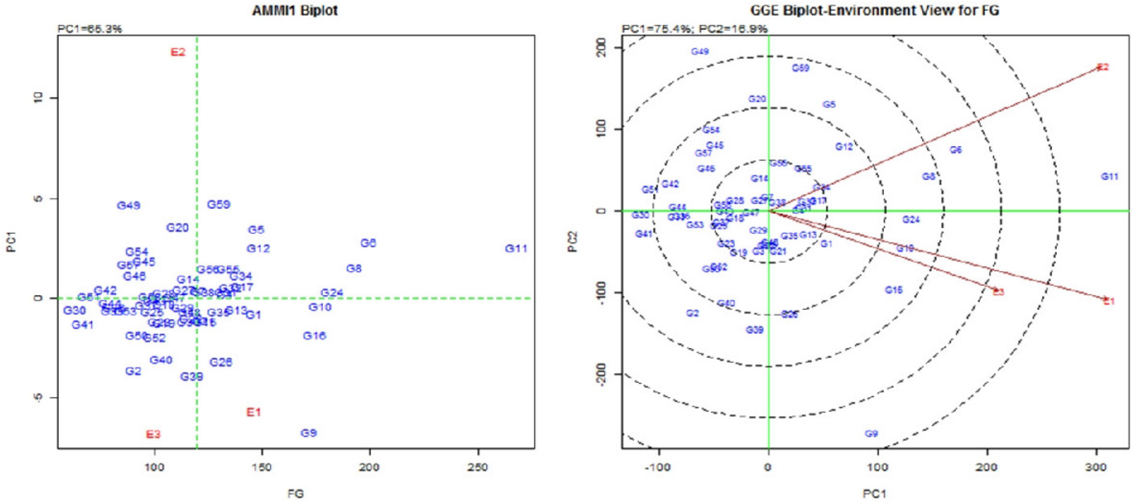
GGE Biplot-Environment View for PL

AMMI1 biplotand GGE biplot for panicle length of 59 genotypes tested in three seasons

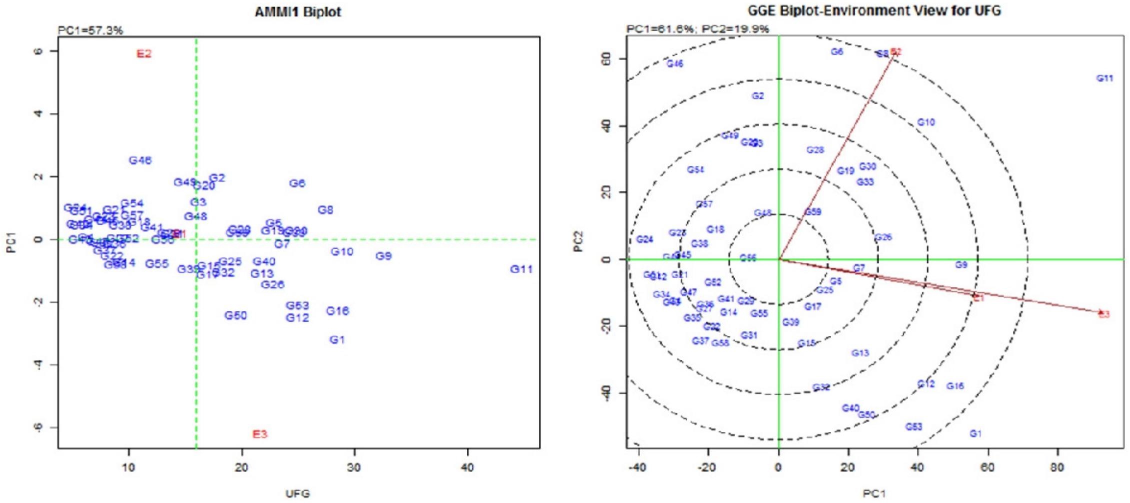
Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons. (Continued.)



AMMI1 biplot and GGE biplot for panicle weight of 59 genotypes tested in three seasons

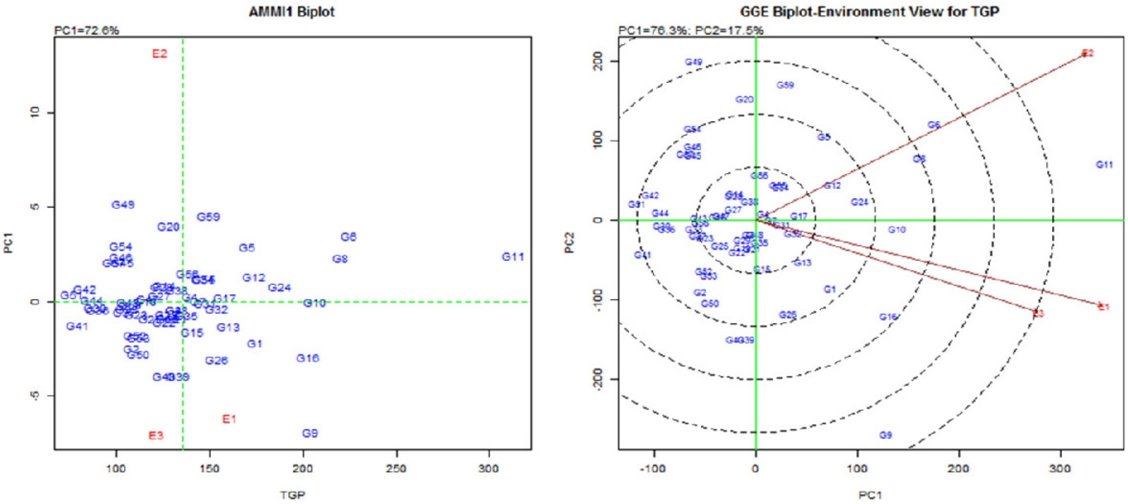


AMMI1 biplot and GGE biplot for number of filled grains per panicle of 59 genotypes tested in three seasons

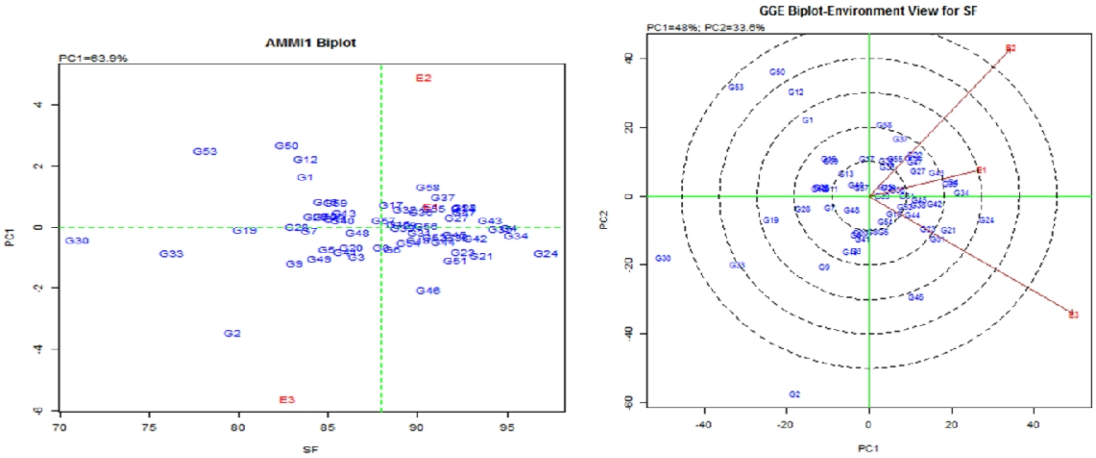


AMMI1 biplot and GGE biplot for number of unfilled grains per panicle of 59 genotypes tested in three seasons

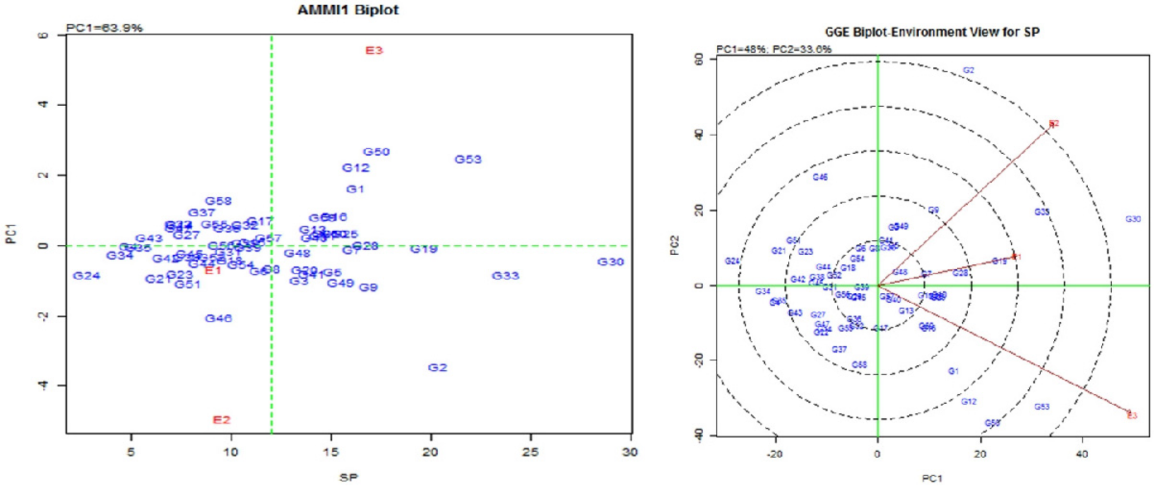
Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons. (Continued.)



AMMI1 biplotand GGE biplot for number of total grains per panicle of 59 genotypes tested in three seasons

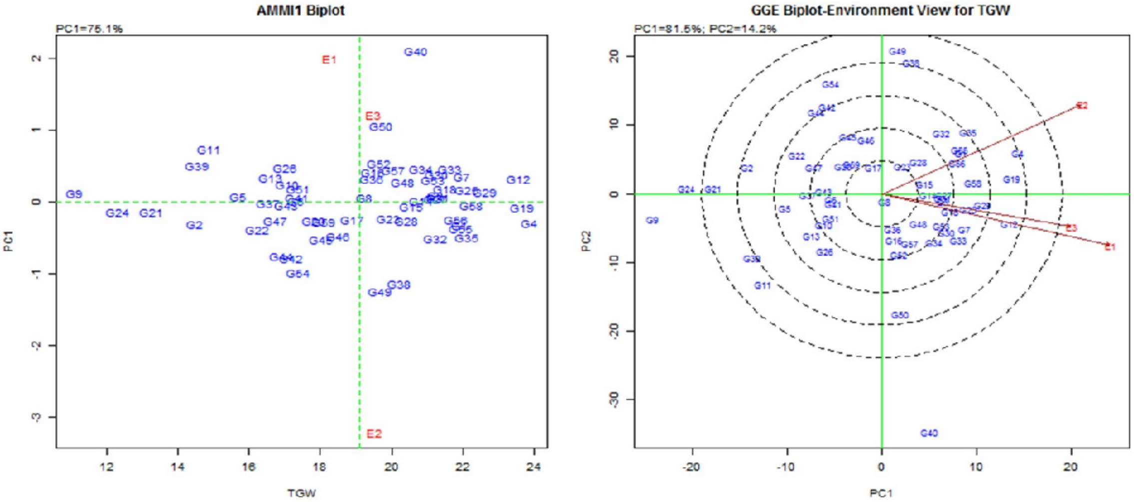


AMMI1 biplotand GGE biplot for spikelet fertility of 59 genotypes tested in three seasons

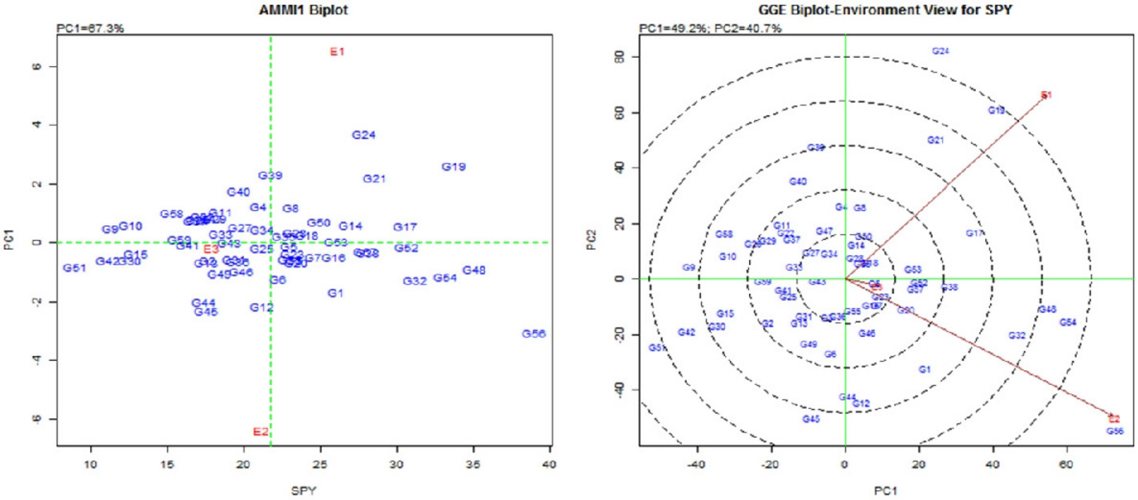


AMMI1 biplotand GGE biplot for sterility percentage of 59 genotypes tested in three seasons

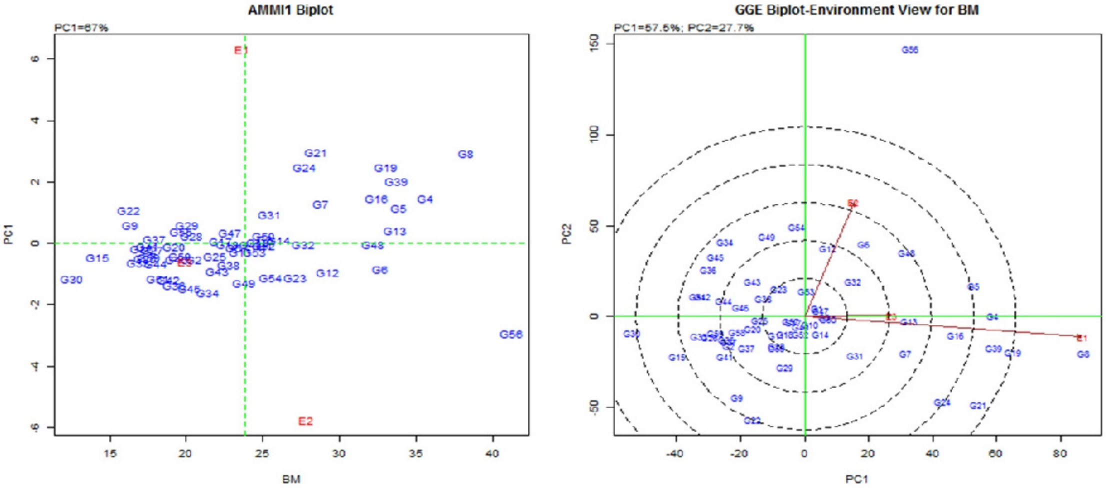
Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons. (Continued.)



AMMI1 biplotand GGE biplot for thousand grain weight of 59 genotypes tested in three seasons

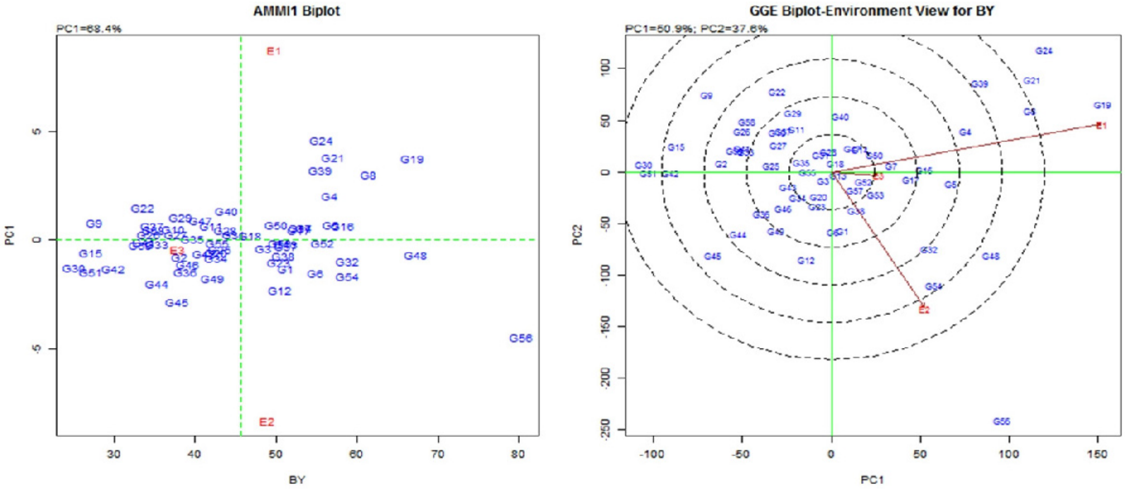


AMMI1 biplotand GGE biplot for single plant grain yield of 59 genotypes tested in three seasons

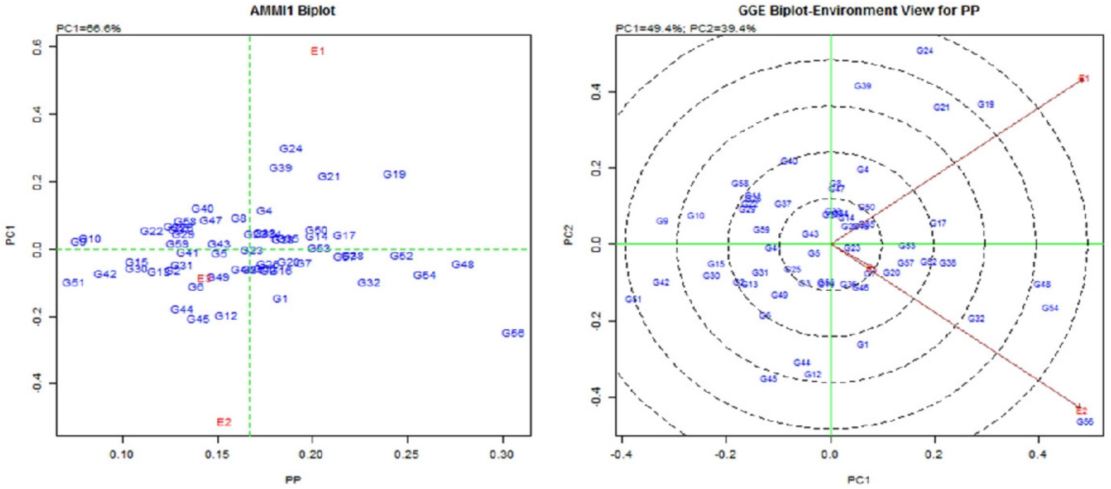


AMMI1 biplotand GGE biplot for biomass per plant of 59 genotypes tested in three seasons

Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons. (Continued.)

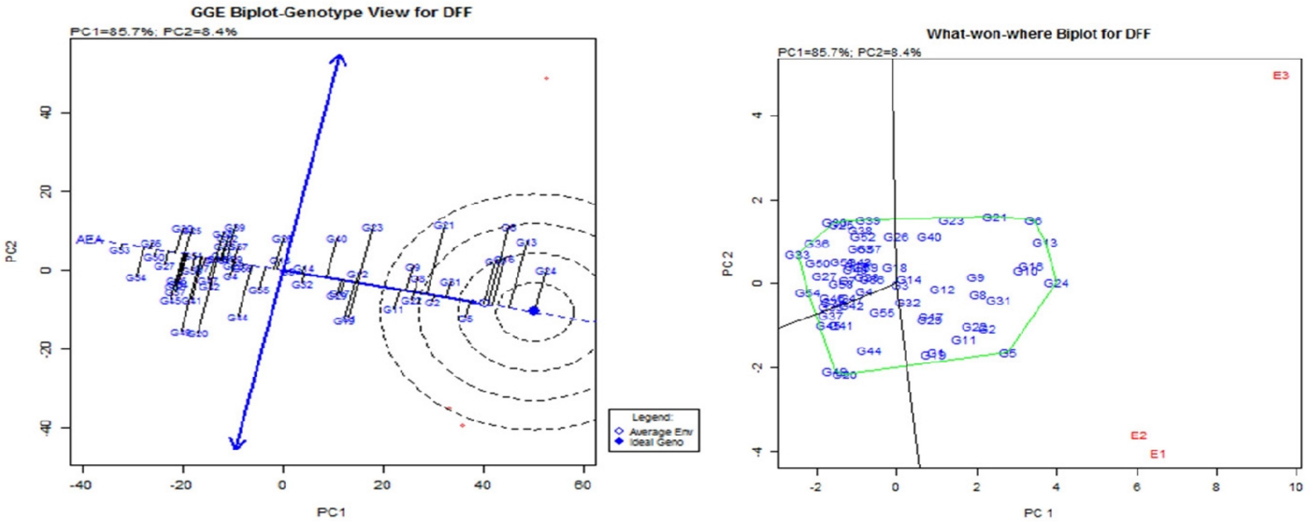


AMMI1 biplotand GGE biplot for biological yield per plant of 59 genotypes tested in three seasons

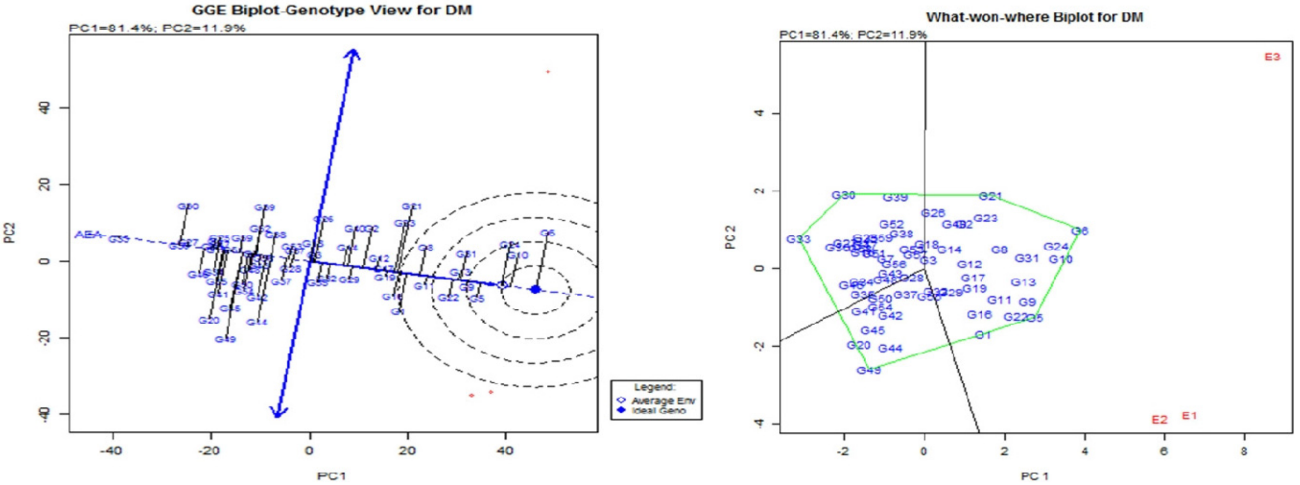


AMMI1 biplotand GGE biplot for per day productivity of 59 genotypes tested in three seasons

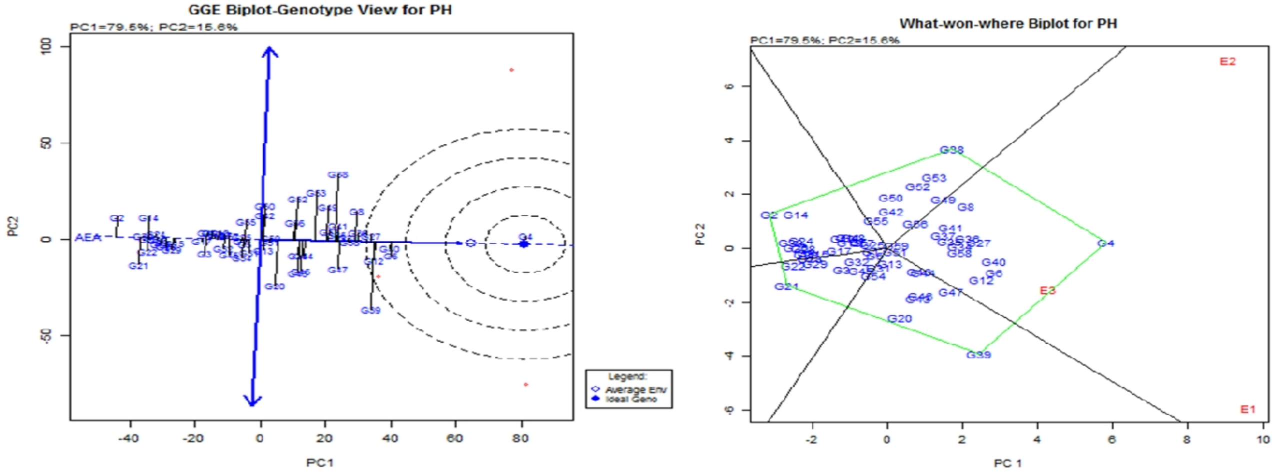
Supplementary Fig. 1. AMMI and GGE biplot for the primary component of interaction (PC1) and mean yield(t/ha) or main effect of rice genotypes in differet seasons. (Continued.)



GGE biplot of ideal genotype and comparison of the genotypes for days to 50 % flowering in three seasons based on which-won-where pattern

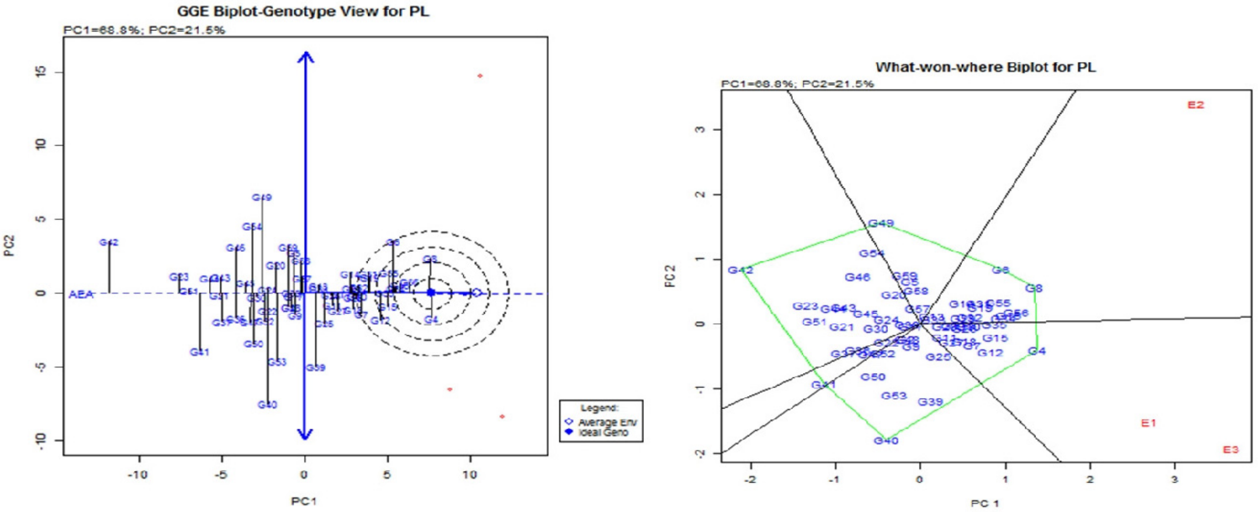


GGE biplot of ideal genotype and comparison of the genotypes for days to maturity in three seasons based on which-won-where pattern

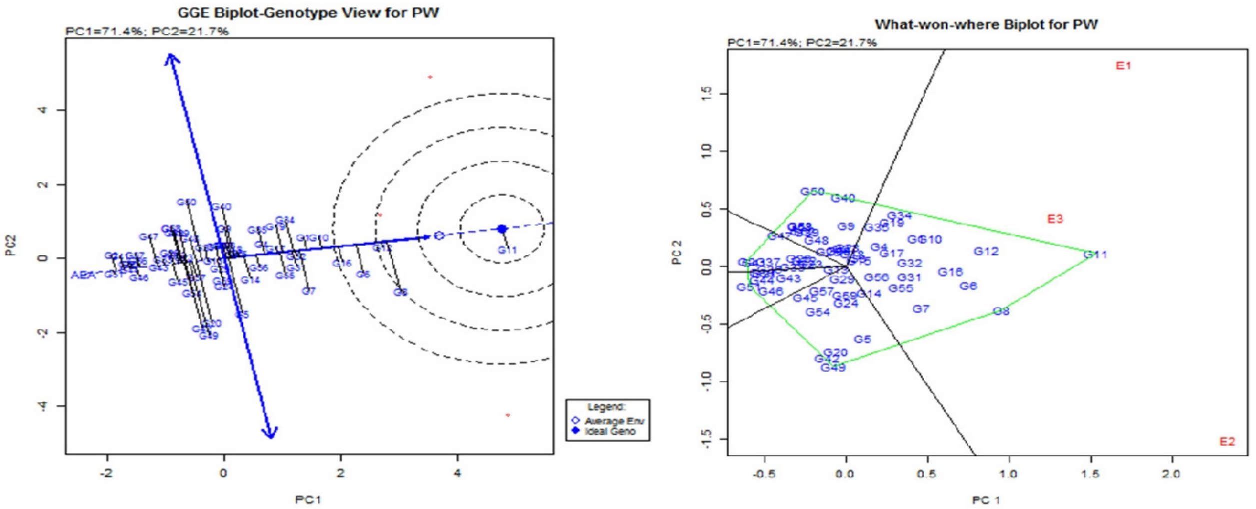


GGE biplot of ideal genotype and comparison of the genotypes for plant height in three seasons based on which-won-where pattern

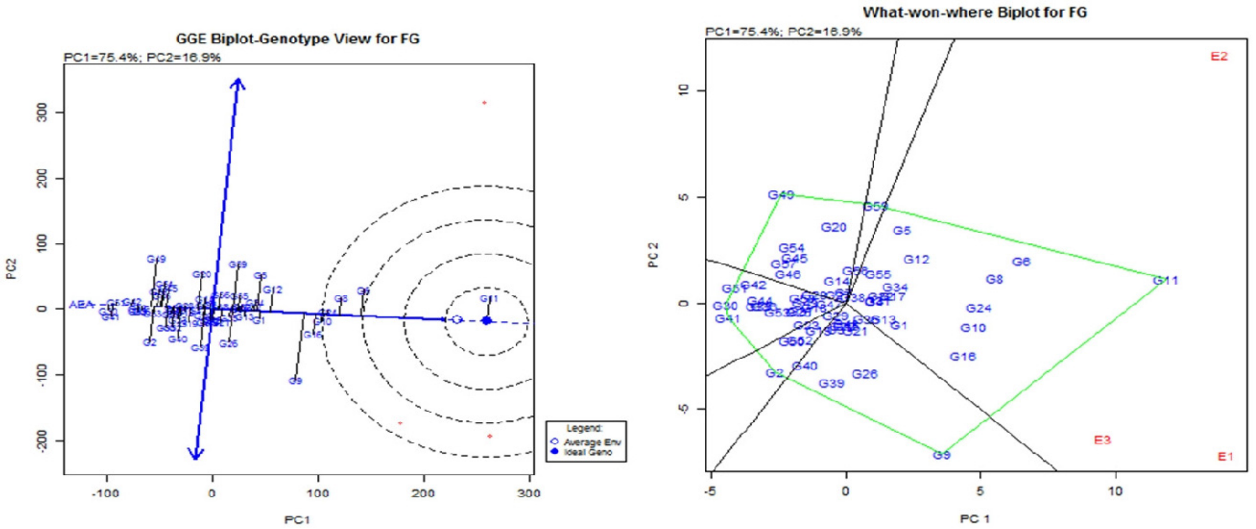
Supplementary Fig. 2. GGE biplot of ideal genotype and Polygon views of the GGE biplot based on symmetrical scaling for 'which-won-where' pattern of rice genotypes in three environments.



GGE biplot of ideal genotype and comparison of the genotypes for panicle length in three seasons based on which-won-where pattern

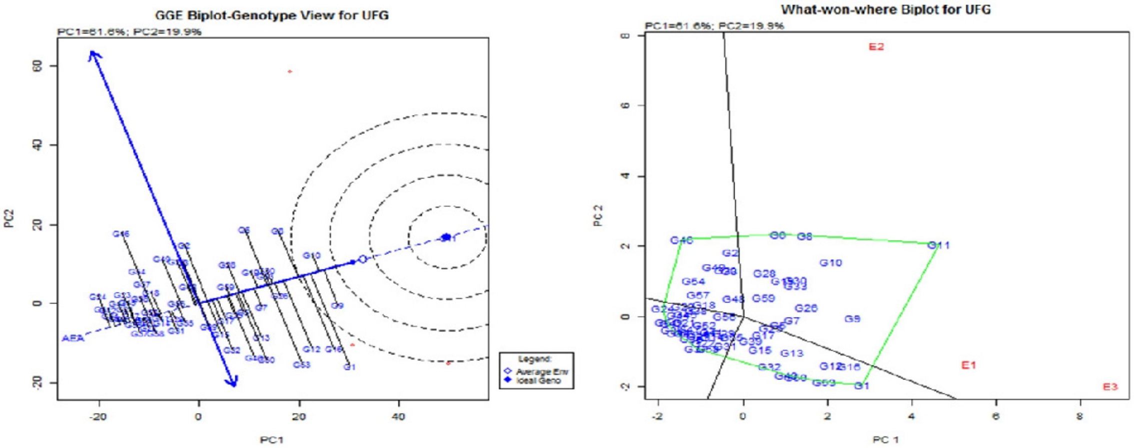


GGE biplot of ideal genotype and comparison of the genotypes for panicle weight in three seasons based on which-won-where pattern

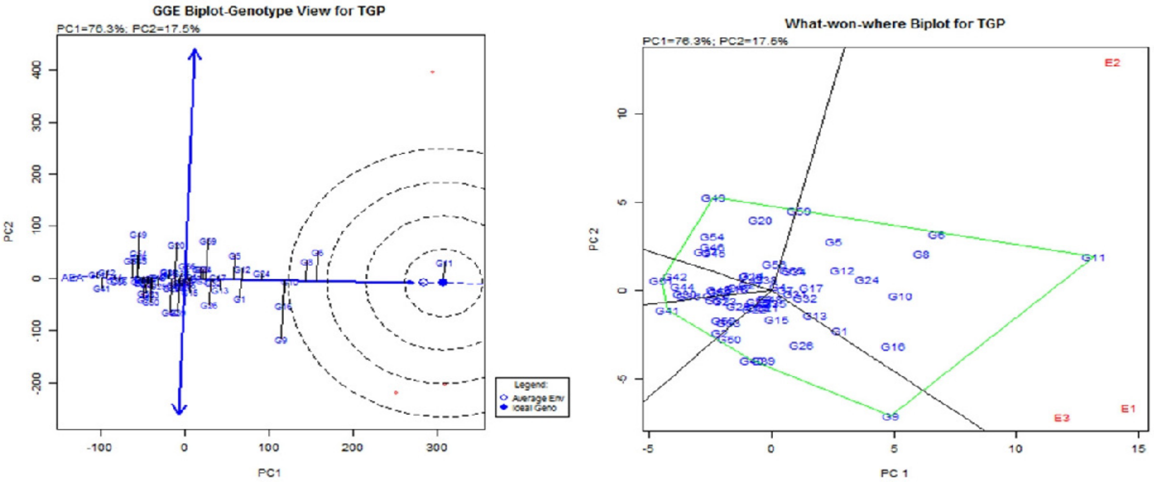


GGE biplot of ideal genotype and comparison of the genotypes for number of filled grains per panicle in three seasons based on which-won-where pattern

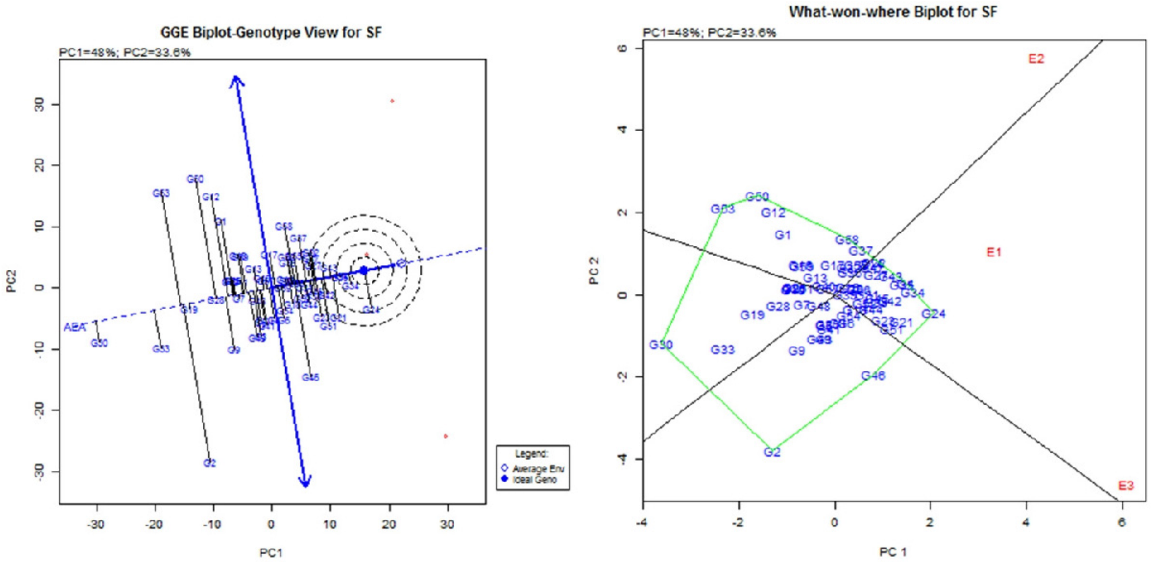
Supplementary Fig. 2. GGE biplot of ideal genotype and Polygon views of the GGE biplot based on symmetrical scaling for 'which-won-where' pattern of rice genotypes in three environments. (Continued.)



GGE biplot of ideal genotype and comparison of the genotypes for number of unfilled grains per panicle in three seasons based on which-won-where pattern

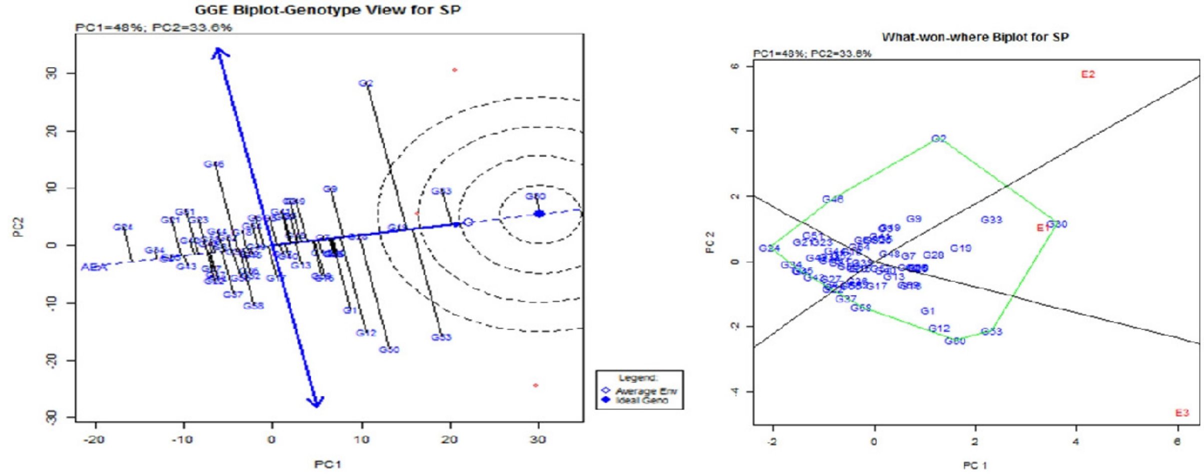


GGE biplot of ideal genotype and comparison of the genotypes for number of total grains per panicle in three seasons based on which-won-where pattern

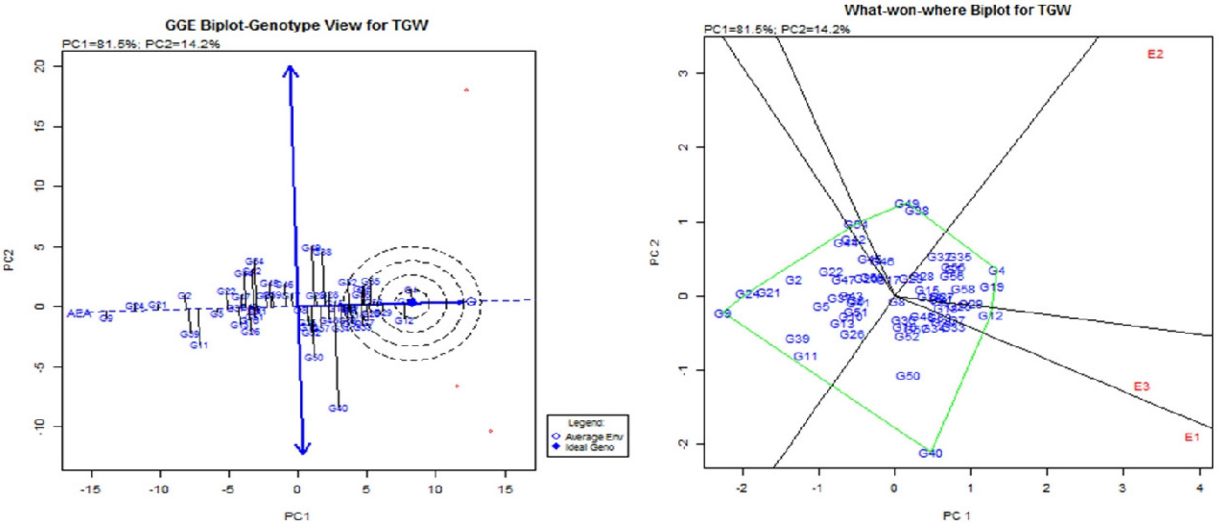


GGE biplot of ideal genotype and comparison of the genotypes for spikelet fertility in three seasons based on which-won-where pattern

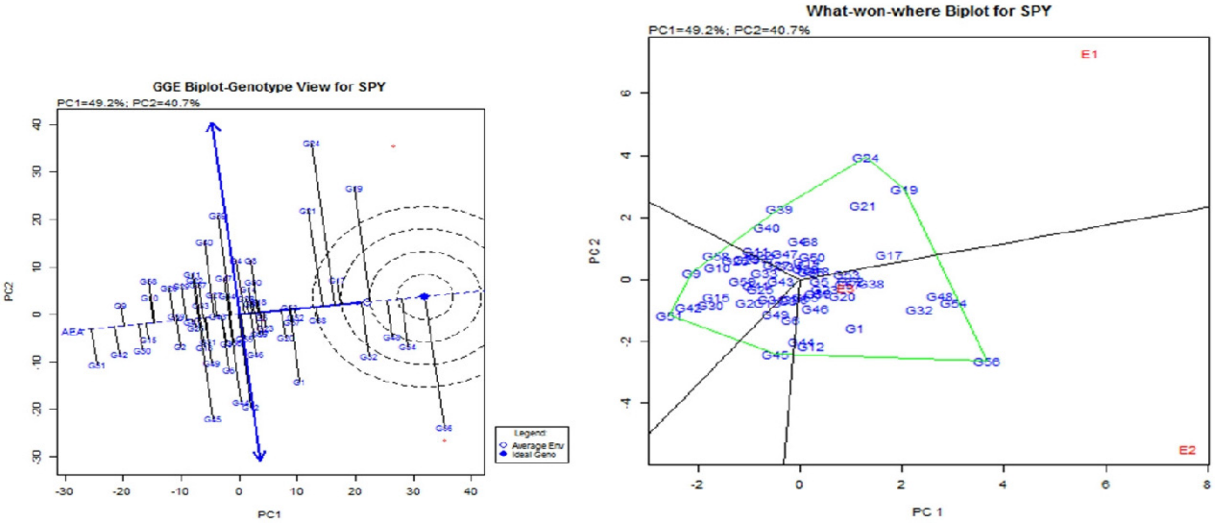
Supplementary Fig. 2. GGE biplot of ideal genotype and Polygon views of the GGE biplot based on symmetrical scaling for 'which-won-where' pattern of rice genotypes in three environments. (Continued.)



GGE biplot of ideal genotype and comparison of the genotypes for sterility percentage in three seasons based on which-won-where pattern

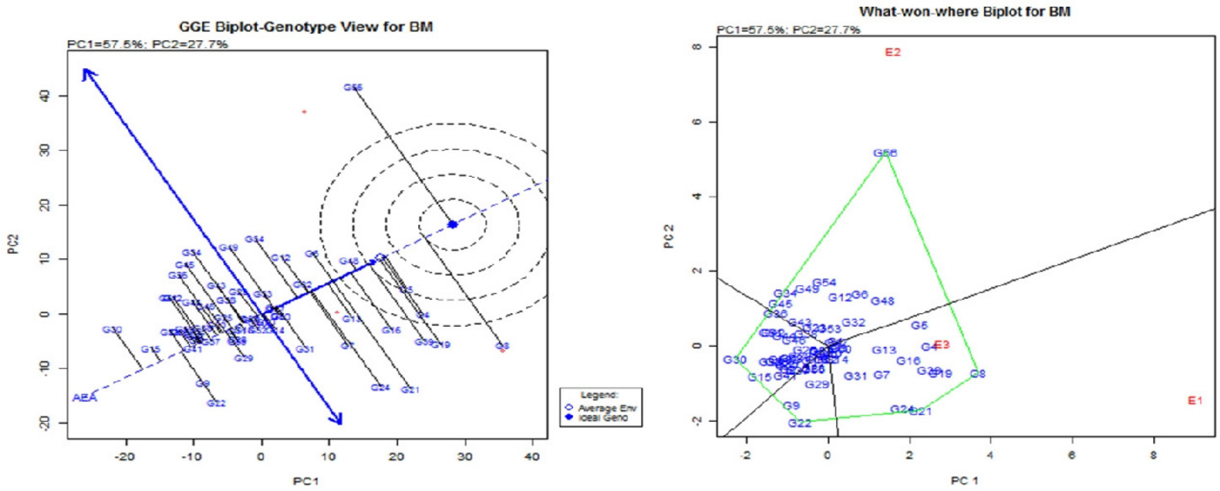


GGE biplot of ideal genotype and comparison of the genotypes for thousand grain weight in three seasons based on which-won-where pattern

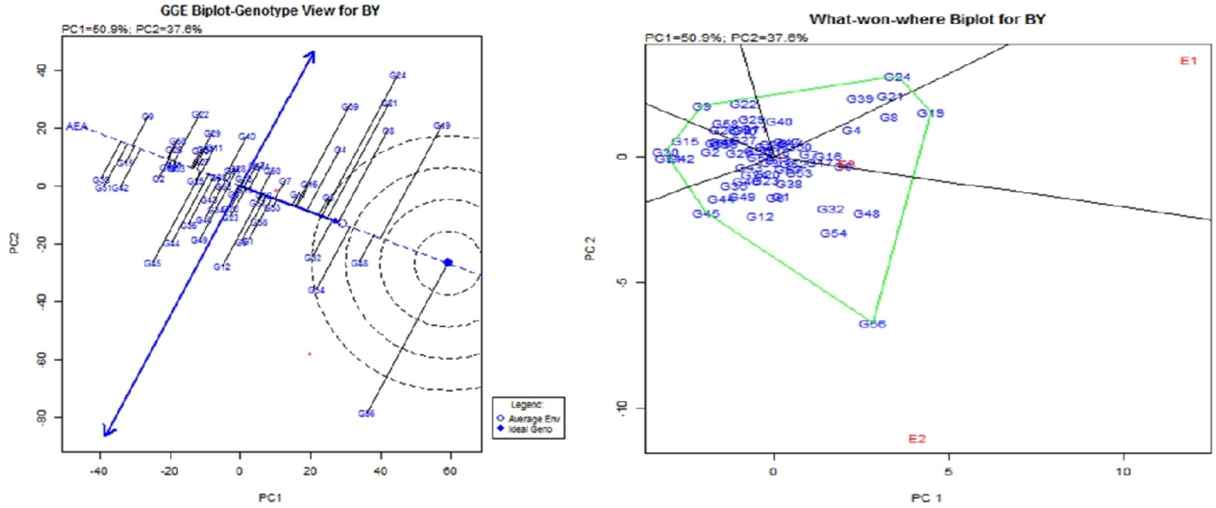


GGE biplot of ideal genotype and comparison of the genotypes for single plant grain yield in three seasons based on which-won-where pattern

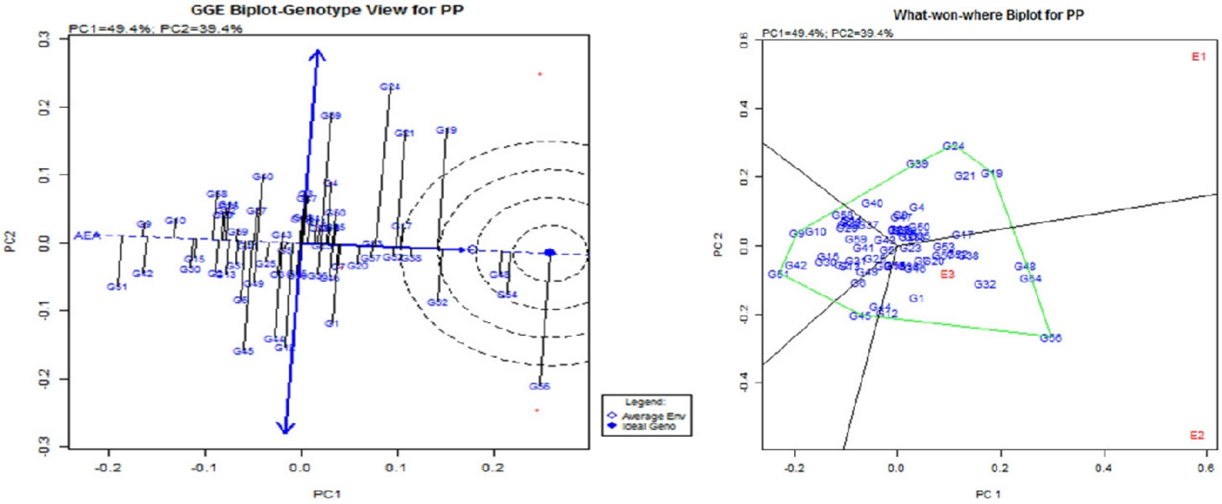
Supplementary Fig. 2. GGE biplot of ideal genotype and Polygon views of the GGE biplot based on symmetrical scaling for 'which-won-where' pattern of rice genotypes in three environments. (Continued.)



GGE biplot of ideal genotype and comparison of the genotypes for biomass per plant in three seasons based on which-won-where pattern



GGE biplot of ideal genotype and comparison of the genotypes for biological yield per plant in three seasons based on which-won-where pattern



GGE biplot of ideal genotype and comparison of the genotypes for per day productivity in three seasons based on which-won-where pattern

Supplementary Fig. 2. GGE biplot of ideal genotype and Polygon views of the GGE biplot based on symmetrical scaling for 'which-won-where' pattern of rice genotypes in three environments. (Continued.)