Additive main effects and multiplicative interaction analyses of yield performance in rice genotypes for general and specific adaptation to salt stress in locations in India

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Abstract The aim of this study was to identify stable rice genotypes tolerant to a salt stress environment and to identify ideal mega-environments using AMMI (additive main effects and multiplicative interaction) stability model analysis. A total of 13 rice genotypes and three salt tolerance checks were evaluated across 13 salt stress locations (alkaline and

saline) for the two kharif seasons of 2014 and 2015. Genotype CSR 36 (CHK3) was found to be the most ideal of those tested. Genotypes CHK2 (CST 27) and IR 87952-1-1-1-2-3-B (G05) were found to be the most stable, with above average yields. The check CSR 36 (CHK3) genotype was the best performer in the majority of the environments studied, followed by

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CSR 27 (CHK2) and IR 87952-1-1-1-2-3-B (G05) which were the best genotypes in the mega-environment consisting of 21 environments evaluated across stress locations and year combinations. Overall, the most promising genotype (IR 87952-1-1-1-2-3-B) had high mean yield and stability and could be used for commercial cultivation or used as donor for breeding programs across salt-affected soils. The genotypes GN13 (IR 87938-1-1-2-1-3-B) and GN11 (IR 87938-1-2-2-1-3-B) showed 60–80% yield advantage at specific salt stress locations, showing that these genotypes could be used for specific environments of salt-affected soils in India.

Keywords Salt · Rice · Additive main effects and multiplicative interaction (AMMI) model · Mega-environment

Introduction

Soil salinity is adversely affecting agricultural productivity in approximately 900 million ha worldwide (FAO 2014). In India, 6.73 million ha are current affected by salt degradation, with the extent of salt-affected areas predicted to increase due to the repercussions of climate change, thereby threatening

future food security (Mondal et al. 2009). With increasing temperature, the low-lying coastal areas will be inundated more frequently by the sea water, exposing yet more land to salinity. In inland areas, salt accumulation is becoming an increasing challenging to crop production due to the build-up of salts and interactions with temperature as a consequence of improper drainage and the use of poor-quality irrigation water, particularly in arid and semiarid regions (Munns and Tester 2008; Tack et al. 2015). Consequently, the need to address this problem is urgent. The deployment of salt-tolerant crop varieties is the most effective, economic and environmentally friendly approach. Rice is inherently a salt-sensitive crop, with an electrical conductivity of soil-saturated extract (ECe) of 3 dS m⁻¹ being considered as the salinity tolerance threshold for rice (Mohammadi et al. 2013). In terms of limiting rice production, soil salinity is considered to be a major abiotic stress, after drought, limiting rice production in about 30% of rice growing areas (Wu and Garg 2003). The differential response of different rice genotypes to salinity and alkalinity at different growth stages and the lack of correlation between these responses (Krishnamurthy et al. 2016c), low selection efficiency of agronomic characters, lack of effective evaluation methods for salt tolerance among genotypes and the complexity of salinity tolerance phenotypes among genotypes are all factors impeding rice breeding programs for salt tolerance (Singh and Flowers 2010). Despite these challenges, several salt-tolerant rice varieties have been released in India and other rice-producing countries.

In addition to variable salinity levels, location-specific weather conditions also contribute significantly to genotype × environmental (G × E) interaction, with the result that identifying tolerant and stable genotypes is tricky. The intensity of salinity stress may increase with higher temperature, thereby effecting more grain yield loss in rice (Tack et al. 2015). Rice is most sensitive to salt stress at the early seedling and reproductive growth stages. Grain yield and salinity are governed by polygenic traits, and the effect of environment is more pronounced in polygenic traits than monogenic ones. Hence, analysis of such polygenic traits for salt tolerance across different locations is quite difficult. In order that meaningful conclusions can be drawn, a robust statistical analysis is required when genotypes are evaluated under different levels of salt stress at multiple locations

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across seasons. An understanding of the nature and causes of such genotype-by-environment interactions (GEI) across locations affected by salinity will help us to identify the genotype that is stable across the different salt stress locations (Krishnamurthy et al. 2017).

Among all the statistical models propounded for dealing with $G \times E$ data, the additive main effects and multiplicative interactions (AMMI) model (Zobel et al. 1988; Gauch 1992) and genotype main effect plus genotype by environment (GGE) biplot analysis (Yan et al. 2000) are the best fit to analyze such intricate datasets. These two models are supported by biplot (Gabriel 1971) visualizations that facilitate interpretation of the data. There has been much discussion and weighing of the advantages and disadvantages of these two models in terms of accuracy, reliability and superiority (Gauch 2006; Yan et al. 2007; Gauch et al. 2008; Yang et al. 2009; Yan and Holland 2010). According to Gauch (2006), the AMMI model is a singular value decomposition (SVD)-based statistical analysis that can be applied to yield trial data in agricultural research for two reasons. First, it offers a choice of model for visualizing data and partitions the overall variation of agriculture research into the main effects genotype (g in AMMI model) and environment (e in AMMI model), as well as the multiplication effect of GEI; consequently, complex variations can be handled easily and separately. Second, there is a prediction choice of model family members for gaining predictive accuracy. While AMMI and GGE are equivalent in terms of efficacy, best practices require model diagnosis for each individual dataset to determine which member is the most predictively accurate. AMMI is always superior or equal to GGE in this context, but best practices of model diagnosis are needed to determine which member family is the most predicative in terms of accuracy. The best practice of AMMI involves (1) analysis of variance (ANOVA), (2) model diagnosis, (3) mega-environment delineation, and (4) agricultural recommendations to exploit both broad and narrow adaptation to increase yields (Gauch 2013). Many earlier studies employed the AMMI stability model to identify general and specific adaptation of rice genotypes under salinity and alkaline stress conditions in India and Bangladesh (Krishnamurthy et al. 2015, 2016a, d; Islam et al. 2016) and in the coastal regions of southern Bangladesh (Islam et al.

2016). However, these studies did not implement the best practices of AMMI since they did not include model diagnosis to increase the accuracy of the model family. The $G \times E$ interaction coupled with the complex nature of salinity is a challenge to rice breeders as it complicates the testing and selection of superior genotypes and, thereby, significantly reduces progress in plant breeding.

Therefore, in the present study AMMI stability analysis was utilized to handle data generated from a multi-location trial (MLT) conducted across 13 salinity stress locations in 2 years (2014, 2015). The aim of the study was to identify superior test locations for the screening of salt-tolerant rice genotypes; to isolate stable rice genotypes with good yields for general and specific adaptation to saline and alkaline stress locations; and to investigate the options of grouping salt-tolerant locations so that mega-environment-specific genotypes can be employed for the management of soils affected by salinity.

Materials and methods

Plant materials and testing locations

The present investigation was conducted in 13 salt stress locations across India, representing five saline environments and eight alkaline environments, during the wet seasons of 2014 and 2015. The description of these locations is given in Table 1. The saline-challenged soils of the chosen experimental locations ranged from sandy loam to clay loam, with ECe ranging from 3.2 to 11.0 dS m^{-1} , while the alkaline-challenged soils ranged from sandy loam to clay loam, with pH ranging from 8.14 to 9.9. The ECe and pH values given in Table 1 were measured prior to transplanting, at the time of transplanting, at flowering and at maturity, and subsequently averaged. Thirteen putative salt-tolerant rice genotypes used in this study were obtained from the International Rice Research Institute (IRRI), Philippines, National Agricultural Research and Extension System (NARES) partners and Indian Council of Agricultural Research (ICAR) institutes of India. They were evaluated across 13 locations during the kharif season of 2014 and 2015, along with three checks, namely CST 7-1 (coastal salinity), CSR 27 (inland salinity) and CSR 36 (alkalinity). Details on these genotypes are given in

Table 1 Description and characterization of the locations used for the evaluation of rice genotypes during 2014 and 2015 (2 years)

Sl. no	Location	Latitude and longitude	Environment code	Stress type	Average ECe (dS m ⁻¹)	Average pH	Mean yield (kg ha ⁻¹)	
							2014	2015
1	Central Island Agricultural Research Institute (CIARI), Port Blair, Andaman and Nicobar Islands	11°37'N 92°43'E	E1-2014 E2-2015	Coastal saline	4.2	5.2	3457	3207
2	CSSRI RRS, Canning Town, West Bengal	22°32'N 88°67'E	E3-2014 E4-2015	Coastal saline	3.5	7.03	1788	3053
3	Central Coastal Agricultural Research Institute (CCARI), Ela, Goa	15°29'N 73°55'E	E5-2014 E6-2015	Coastal saline	5.0	6.35	2924	2383
4	Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth (BSKKV) Kharland Research Station, Panvel	18°99'N 73°12'E	E7-2014 E8-2015	Coastal saline	4.0	7.4	2160	3201
5	Central Soil Salinity Research Institute (CSSRI), Karnal saline microplot, Haryana	29°42'N 76°57'E	E9-2014 E10-2015	Inland saline	10	7.61	1208	1661
6	CSSRI, Regional Research Station, Lucknow, Uttar Pradesh	26°86'N 80°90'E	E11-2014 E12-2015	Alkaline	1.0	9.8	625	2585
7	Narendra Dev University of Agriculture and Technology (NDUAT), Faizabad, Uttar Pradesh	26°77'N 82°15'E	E13-2014 E14-2015	Alkaline	2.9	9.67	2546	3257
8	Chandra Shekhar Azad University of Agriculture and Technology (CSAUAT), Kanpur, Uttar Pradesh	26°29'N 80°18'E	E15-2014 E16-2015	Alkaline	1.4	10	1533	1866
9	Pandit Jawaharlal Nehru College of Agriculture and Research Institute (PAJANCOA), Karaikal, Puducherry	10°55'N 79°50'E	E17-2014 E18-2015	Alkaline	1.7	8.14 (RSC-8)	3533	4103
10	Punjab Agricultural University (PAU), Ludhiana, Punjab	30°53'N 75°48'E	E19-2014 E20-2015	Alkaline	1.3	8.6	6143	3917
11	Rajendra Agricultural University (RAU), Pusa, Bihar	25°58'N 85°38'E	E21-2014 E22-2015	Alkaline	1.5	9.2	2206	2897
12	CSSRI, Karnal sodic microplot, Haryana	29°42'N 76°57'E	E23-2014 E24-2015	Alkaline	1.1	9.9	674	1163
13	Anbil Dharmalingam Agricultural College and Research Institute (ADACRI), Trichy, Tamil Nadu	10°47'N 78°42'E	E25-2014 E26-2015	Alkaline	1.2	9.26	5051	4155

Table 2. Seeds were sown from the last week of May to the first week of June, depending on the location. Trials were laid out in a randomized complete block design (RCBD) with three replications. Observations on days to 50% flowering, plant height, productive tillers, spikelet fertility and grain yield were recorded at each testing location. Grain yield was determined from the whole plot and expressed in kilograms per hectare.

Data analysis

The AMMI model was used to analyze the $G \times E$ interactions. The procedures of Ebdon and Gauch (2002a, b) and Gauch (2013) were used for AMMI model analysis and accuracy gain. The AMMI model applies ANOVA to partition the variation into the main effects genotype (g in AMMI), environment (e in AMMI) and GEI, and then it applies principal components analysis (PCA) to the data. According to Gauch (2013), model diagnosis is useful to determine

Table 2 List of rice genotypes and their parentages used in the study

Genotype number	Genotype code	Genotypes	Parentage
1	CHK1	CST 7-1	CSR 1 × IR 24
2	CHK2	CSR 27	NONA BOKRA/IR 5657-33-2
3	CHK3	CSR 36	CSR 13/PANVEL 2//IR 36
4	GN01	IR 87830-B-SDO1-2-3-B	A 69-1/IR 73718-23-2-1-3
5	GN02	IR 87938-1-1-2-3-3-B	IR 4630-22-2-5-1-3/IR05N204
6	GN03	IR 87938-1-2-2-2-1-B	IR 4630-22-2-5-1-3/IR05N204
7	GN04	IR 87937-6-1-3-2-2-B	IR 4630-22-2-5-1-3/IR05N173
8	GN05	IR 87952-1-1-1-2-3-B	IR 4630-22-2-5-1-3/IR 72046-B-R-8-3-1-3
9	GN06	IR 84645-305-6-1-1-1	CHERIVIRUPPU/IR05F101
10	GN07	IR87848-301-2-1-3-B	A 69-1/IR 55179-3B-11-3
11	GN08	IR 87948-6-1-1-1-3-B	IR 4630-22-2-5-1-3/IR 61920-3B-22-2-1
12	GN09	IR 87938-1-1-3-2-1-B	IR 4630-22-2-5-1-3/IR05N204
13	GN10	IR 87830-B-SDO2-1-3-B	A 69-1/IR 73718-23-2-1-3
14	GN11	IR 87938-1-2-2-1-3-B	IR 4630-22-2-5-1-3/IR05N204
15	GN12	IR 87831-3-1-1-2-2-BAY B	A 69-1/IR02A201
16	GN13	IR 87938-1-1-2-1-3-B	IR 4630-22-2-5-1-3/IR05N204

the best AMMI model family for a given dataset, and it is advised to use the F_R -test (Cornelius 1993) to assess model diagnosis and to identify significant interaction principal components (IPCs) in the AMMI model using AMMISOFT software for the analysis of yield trial data. AMMI constitutes a model family, with AMMI0 having no IPC, AMMI1 having 1 IPC, AMMI2 having 2 IPC, and so on up to AMMIF (residual discarded). The AMMI model equation is:

$$Y_{ge} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} \quad (1)$$

where Y_{ge} is the yield of genotype g in environment e ; μ is the grand mean; α_g is the genotype deviation from the grand mean; β_e is the environment deviation; λ_n is the singular value for IPC n and correspondingly λ_n^2 is its eigenvalue; γ_{gn} is the eigenvector value for genotype g and component n ; δ_{en} is the eigenvector value for environment e and component n , with both eigenvectors scaled as unit vectors; and ρ_{ge} is the residual.

The interaction scores are commonly scaled as $\lambda_n^{0.5} \gamma_{gn}$ and $\lambda_n^{0.5} \delta_{en}$ so that their products estimate interactions directly, without the need of yet another multiplication by λ .

The ratio of yield for AMMI “winners” within each environment (identified in the first column of AMMI

ranks) was calculated by dividing the yield for the overall winner (Gauch 2013). According to Gauch (2013), a ratio of 1 represents a “winning” genotype across environments. This ratio is an assessment of the importance of narrow adaptation due to GEI effects, with a ratio of ≥ 1.10 indicative of narrow adaptation.

Results

ANOVA and identification of AMMI model families

Analysis of variance for grain yield using the AMMI model is presented in Table 3. Both the main effects genotype (G), environment (E) and their interaction (GEI) components were statistically significant at $p \leq 0.001$. The environmental component explains the largest proportion of variation (62.64%), followed by $G \times E$ interaction components (approx. 27.98% variation), with the genotypic component (G) explaining the least variation (about 2.81% of the total variation). The GEI effects were partitioned into seven IPCs (IPC1–IPC7) and found to be significant at $p \leq 0.01$ for grain yield in different salt-affected environments across the year. In terms of contribution to the

Table 3 Analysis of variance for grain yield in rice genotypes across saline and alkaline soil conditions during 2014 and 2015

Source of variance	df	SS	MSS	Proportion of variation			
				Total variation (%)	Main and interaction variation (%)	GEI variation (%)	GEI _s variation (%)
Treatment	415	3,151,205,668.41	7,593,266.67***	93.43			
Genotype (G)	15	94,926,605.22	6,328,440.34***		2.81		
Environment (E)	25	2,112,662,133.83	84,506,485.35***		62.64		
Interaction (G × E)	375	943,616,929.36	2,516,311.81***		27.98		
IPC1	39	256,738,554.94	6,583,039.87***			27.21	30.20
IPC2	37	192,580,282.15	5,204,872.49***			20.41	22.65
IPC3	35	121,522,574.05	3,472,073.54***			12.88	14.30
IPC4	33	97,483,574.60	2,954,047.71***			10.33	11.46
IPC5	31	63,217,535.86	2,039,275.35***			6.70	7.43
IPC6	29	50,788,574.47	1,751,330.15***			5.38	5.97
IPC7	27	43,119,809.33	1,597,029.97***			4.57	5.07
Residual	144	118,166,023.97	820,597.38***			12.52	13.90
Error	832	221,517,013.33	266,246.41	6.57			
Blocks/environment	52	27,507,734.42	528,994.89***		0.82		
Pure Error	780	194,009,278.92	248,729.84		5.75		
Total	1247	3,372,722,681.74	2,704,669.35	100	100	100	100

***Significant at $p \leq 0.001$ df, Degrees of freedom; GEI, genotype × environment interaction; GEI_s, genotype × environment interaction of signal; IPC, interaction principal component; MSS, mean sum of squares; SS, sum of squares

total GEI for grain yield, IPC1 and IPC2 cumulatively contributed 47.61% and IPC1–IPC7 contributed 87.47%. Based on statistical and practical considerations, model evaluation is essential to determine the best AMMI model family for grain yield. Seven AMMI model families were identified based on the F_R -test at $p \leq 0.01$ (since AMMISOFT is limited to 7 IPCs) for grain yield in the different salinity environments (Table 3). The AMMI model captured 90.12% of the GEI_s (GEI signal) and 9.88% of the GEI_N (GEI noise). Sum of squares for GEI_s and GEI_N was 8.96-fold and 0.98-fold, respectively, that of genotype main effect. The results clearly indicate that IPC1, IPC2 and IPC3 represent the AMMI model families AMMI1, AMMI2 and AMMI3, respectively, cumulatively covering 60.5% of the GEI variation and 67.13% of the GEI_s variation. AMMI biplot1 contained the variation of the principal additive effects of genotypes and environments (horizontal axis in Fig. 1) and the variation in the multiplicative effects of the GEI (vertical axis in Fig. 1). In contrast, the AMMI2 model

family delineated seven mega-environments with seven winner genotypes, namely CHK3, GN11, CHK1, GN13, GN05, GN03 and GN12 (Table 4). AMMI biplot2 shows the spatial pattern of the first two PC axes of the interaction effects, corresponding to the genotypes, and helps in visual interpretation of the GEI patterns and identification of the genotypes or locations that exhibit a low, medium or high level of interaction effects (Fig. 2).

Identification of winner genotypes from the AMMI model family

Winner genotypes identified using the AMMI model family for yield traits are shown in Table 4. The genotypes in the table are listed based IPC1 scores, with the top order and bottom order genotypes have contrasting GEI patterns. The AMMI constituted a model family from AMMI0 to AMMIF, with AMMI0 having one winner genotype in one mega-environment whereas the AMMIF consisted of 13 winner genotypes

Fig. 1 The scattered distribution patterns of 16 rice genotypes and 26 salt stress environments presented in the additive main effects and multiplicative interaction (AMMI) model biplot1, with grain mean yield (*Mean*, in kg ha^{-1}) shown on the abscissa

and interaction principal component 1 (*IPC1*) scores shown on the ordinate. See Table 1 for environmental codes (*E*) and Table 2 for genotype codes (*GN* and *CHK*)

with 13 mega-environments. The genotype CHK3 won in all AMMI model families, and it was also won in terms of maximum number of environments, with 26, 21, 13, 10, 8 and 8 in the AMMI0, AMMI1, AMMI2, AMMI3, AMMI4 and AMMI5 model families, respectively. According to the standard AMMI diagnosis model, an intermediate AMMI model, such as AMMI1 or AMMI2, is predicatively accurate; in the present experiment AMMI1 and AMMI2 delineated four and seven mega-environments based on IPC1 and IPC2 scores, respectively, with each environment having one genotype. According to AMMI1, in addition to genotype CHK3, the genotypes GN11, CHK1 and GN13 also won in one, two and two different mega-environments, respectively. Similarly, in the AMMI2 model family, the same genotypes won in four, three and one different mega-environments, respectively. In addition, the AMMI2 model family identifies another three genotypes, namely GN05, GN03 and GN12, which won in three, one and one different mega-environments, respectively. In the present study, the AMMI3 model family had the maximum predictive accuracy, representing ten environments with ten winning genotypes. According to the AMMI3 model family, genotypes CHK3, CHK2 and GN11 won in ten, four and three different mega-environments, respectively, with genotypes CHK1 and GN06 winning in two different mega-

environments and the remaining winner genotypes, namely GN13, GN02, GN03, GN05 and GN08, each winning in only one different environment. Among the ten genotypes of the AMMI3 model, three genotypes, namely CHK3, CHK2 and GN05, had maximum a grain yield of 3487, 3280 and 3086 kg ha^{-1} , respectively, which was more than overall mean yield of 2828 kg ha^{-1} under the different salt-affected environments across the years.

Delineation of mega-environments based on AMMI1

The ranking of the five top performing rice genotypes across the test environments based on AMMI1 and AMMIF ranking is presented in Table 5. The environments in the table are listed based on the IPC1 scores, with the top- and bottom-ordered environments have contrasting GEI patterns. According to AMMI1 model, 26 environments were delineated into four mega-environments. The first mega-environment was the largest and consisted of 21 different environments (Fig. 3). The second mega-environment consisted of two environments, namely E01 and E05, as did the third mega-environment (E12 and E14). The fourth mega-environment delineated by AMMI1 consisted of single environment (E21). The AMMIF model delineated 13 mega-environments with 13

Table 4 “Winner” genotypes and numbers of mega-environments for the additive main effects and multiplicative interaction (AMMI) model family for rice genotypes evaluated under 13 saline and alkaline soil conditions during 2014 and 2015

Genotype number	Genotype code	Grain yield (kg ha ⁻¹)	AMMI model family ^a										
			IPC1 score	AMMI0	AMMI1	AMMI2	AMMI3	AMMI4	AMMI5	AMMI6	AMMI7	AMMI8	AMMI9
16	GN13	2498.78	34.01		2	1	1	2	1	1	1	2	
5	GN02	2706.91	26.02				1			1	1	1	
15	GN12	2755.38	21.79			1							
6	GN03	2698.64	20.15			1	1	5	4	4	2	2	
7	GN04	2831.24	20.01						1	1	1	1	
9	GN06	2813.68	12.62				2	1	3	2	2	1	
10	GN07	2772.44	7.87					1	2	1	1	2	
8	GN05	3086.29	5.57			3	1		2	2	2	4	
4	GN01	2878.00	1.43										1
13	GN10	2941.35	- 4.11							2	2	1	
3	CHK3	3487.82	- 6.64	26	21	13	10	8	8	2	5	4	
2	CHK2	3280.14	- 12.43				4	2	1	3	3	1	
11	GN08	2759.14	- 17.22				1	1	1	4	3	4	
1	CHK1	2642.77	- 43.73		2	3	2	4	2	2	2	2	
14	GN11	2273.26	- 58.38		1	4	3	2	1	1	1		
Mega-environments				1	4	7	10	9	11	13	13	13	

^aAMMI0, No IPC; AMMI, 1 IPC; AMMI2, 2 IPCs....up to AMMI9, residual discarded

Fig. 2 The scattered distribution patterns of 16 rice genotypes and 26 salt stress environments presented in AMMI biplot12 showing IPC1 scores on the abscissa and IPC2 scores on the ordinate

genotypes. According to the AMMI1 model, genotype CHK3 was the winner genotype in 21 environments, followed by genotype CHK2, which was the winner in 18 environments. Genotypes GN05 and GN04 were ranked second and “won” in two and one environments, respectively. Genotype GN05 was the winner in CIARI, Port Blair for both study years (E1 and E2) and was also within the five top rankings in location CSSRI RRS Canning town for both years (E3 and E4). In the first mega-environment, the third ranking was achieved by three genotypes, namely GN05, CHK1 and GN04, in 14, five and two environments, respectively. In the second mega-environment, genotypes GN13, GN02 and GN12 ranked first, second and third, respectively; similarly genotype CHK1 ranked first in the third mega-environment. In comparison, genotype GN11 ranked second in the E14 environment and third in E12, and genotype CHK3 ranked second in the E12 environment and third in E14 of the third mega-environment. In the last mega-environment of AMMI1, genotypes GN11, CHK1, CHK3 and CHK2 ranked first to fourth, respectively. Genotypes CHK1, CHK2, CHK3, GN11 and GN08 were the top ranked genotypes of AMMI1 model and were the “winners” in the first, third and fourth mega-environments. Genotypes GN02, GN12 and GN04, the top ranked

genotypes of the AMMI1 model, were in the first and second mega-environments of the AMMI1 model.

Graphical representation of genotypes with broad and narrow adaptation suggested that genotypes CHK3, CHK2 and GN05, with an average grain yield of 3487, 3280 and 3086 kg ha⁻¹, respectively, were broadly adapted to the larger mega-environments which had 21 salt stress locations, while genotypes GN13, CHK1 and GN11 are genotypes with narrow adaptation, with an average grain yield of 2498, 2642 and 2273 kg ha⁻¹ over the environments, respectively (Fig. 4). Genotype GN13 exhibited a grain yield of $3487 \times 1.29 = 4498$ kg ha⁻¹, i.e. $4498 - 2498 = 2000$ kg ha⁻¹ (80%) yield advantage over genotypes with broad adaptation in the E01 environment and $3487 \times 1.19 = 4149$ kg ha⁻¹, i.e. $4149 - 2498 = 1651$ kg ha⁻¹ (66%) yield advantage over broad adaptation in the E25 environment. Similarly, genotype CHK1 showed $3487 \times 1.003 = 3497$ kg ha⁻¹ grain yield, i.e. $3497 - 2642 = 855$ kg ha⁻¹ (32%) yield advantage and $3487 \times 1.009 = 3518$ kg ha⁻¹, i.e. $3518 - 2642 = 876$ kg ha⁻¹ (33%) yield advantage over genotypes showing broad adaptation E12 and E14 environments, respectively. GN11 recorded $3487 \times 1.05 = 3661$ kg ha⁻¹ of grain yield, i.e. $3661 - 2273 = 1388$ kg ha⁻¹ (61%) yield advantage over genotypes with broad adaptation i then E21 environment.

Discussion

Evaluation of genotypes is a regular part of plant breeding activities, with the aim to identify stable genotypes across locations and seasons. Those genotypes which perform best during experimental station trials are promoted to MLTs to assess their suitability and adaptability to other regions of the country. Genotypes are evaluated across seasons to summarize their performance across different locations. In addition to genotype evaluation, the locations also have to be evaluated from time to time to identify useful or discriminating and redundant locations and to identify the stable genotypes. The interplay of genotype, location and season effects results in complex data, which calls for an efficient statistical analysis tool for better interpretations. Numerous statistical tools have evolved over the last three decades to handle such multifaceted datasets. With the advent of biplots, the AMMI and GGE biplot

Table 5 A ranking table showing the top five genotypes according to AMMI1 and AMMIF model families for 16 rice genotypes

Mega-environment	Environment code	IPC1 score	Ratio	AMMI1 ranks					AMMIF ranks				
				1	2	3	4	5	1	2	3	4	5
ME-2	E01	50.88	1.293	GN13	GN02	GN12	GN04	GN03	GN05	GN04	GN03	GN12	GN13
	E25	49.69	1.194	GN13	GN02	GN12	GN04	GN03	GN13	GN12	GN02	GN04	GN06
	E20	18.32	1.00	CHK3	GN04	GN05	GN02	GN12	GN02	GN05	GN08	GN04	GN03
	E05	15.16	1.00	CHK3	GN05	GN04	GN02	CHK2	GN07	GN12	GN05	GN03	GN09
	E07	15.15	1.00	CHK3	GN05	GN04	GN02	CHK2	GN06	GN01	CHK2	GN13	GN05
ME-1	E03	10.20	1.00	CHK3	CHK2	GN05	GN04	GN12	GN01	GN10	GN05	GN08	GN02
	E08	4.85	1.00	CHK3	CHK2	GN05	GN04	GN10	CHK1	CHK3	CHK2	GN04	GN03
	E17	4.64	1.00	CHK3	CHK2	GN05	GN04	GN10	GN05	GN04	GN13	CHK2	GN01
	E06	1.84	1.00	CHK3	CHK2	GN05	GN10	GN01	GN13	GN12	GN07	GN01	CHK3
	E02	1.79	1.00	CHK3	CHK2	GN05	GN10	GN01	GN05	GN06	CHK1	CHK3	GN12
	E16	0.31	1.00	CHK3	CHK2	GN05	GN10	GN01	GN08	GN13	GN01	GN10	GN11
	E15	− 0.59	1.00	CHK3	CHK2	GN05	GN10	GN01	GN04	GN09	CHK3	GN03	GN13
	E04	− 0.67	1.00	CHK3	CHK2	GN05	GN10	GN01	CHK3	GN12	GN05	GN13	CHK1
	E18	− 0.97	1.00	CHK3	CHK2	GN05	GN10	GN01	CHK3	GN04	GN12	CHK2	GN03
	E19	− 2.08	1.00	CHK3	CHK2	GN05	GN10	GN01	GN03	GN04	CHK2	GN08	GN11
ME-3	E11	− 2.20	1.00	CHK3	CHK2	GN05	GN10	GN01	CHK3	CHK2	GN09	GN08	GN07
	E13	− 5.31	1.00	CHK3	CHK2	GN05	GN10	CHK1	CHK1	CHK3	GN06	CHK2	GN09
	E24	− 7.90	1.00	CHK3	CHK2	GN05	CHK1	GN10	GN08	CHK3	GN10	CHK2	GN07
	E26	− 10.09	1.00	CHK3	CHK2	CHK1	GN05	GN10	CHK2	CHK3	GN07	GN10	CHK1
	E22	− 13.80	1.00	CHK3	CHK2	CHK1	GN11	GN05	GN05	GN10	CHK1	GN01	CHK3
	E23	− 17.24	1.00	CHK3	CHK2	CHK1	GN11	GN08	GN08	CHK3	CHK2	GN10	CHK1
	E10	− 18.22	1.00	CHK3	CHK2	CHK1	GN11	GN08	GN03	GN11	CHK2	CHK1	CHK3
	E09	− 20.25	1.00	CHK3	CHK2	CHK1	GN11	GN08	GN08	GN09	GN07	CHK2	GN05
	E12	− 23.10	1.003	CHK1	CHK3	GN11	CHK2	GN08	GN07	GN10	GN11	CHK1	GN08
	E14	− 23.82	1.009	CHK1	GN11	CHK3	CHK2	GN08	GN10	GN11	GN01	GN09	CHK2
ME-4	E21	− 26.60	1.053	GN11	CHK1	CHK3	CHK2	GN08	CHK3	CHK2	CHK1	GN08	GN01

method have become more popular. The pros and cons of these two models have been the subject of much discussion in recent years, particularly in terms of which model has the best reliability (Gauch 2006; Yan et al. 2007; Gauch et al. 2008; Yang et al. 2009; Yan and Holland 2010). The AMMI model separates G , E , and GE before applying SVD to GE for a least-square analysis. The GGE biplot method separates E before SVD and then attempts to separate G and GE after applying SVD to both. All SVD-based analyses, including the AMMI model and GGE method, are essentially equivalent. The AMMI model completely separates G , E , and GE , as is required for most agricultural research purposes and also separates signal from noise by practicing model diagnosis for the purpose of gaining accuracy (Gauch 2006; Gauch et al. 2008). The AMMI model is one of the most stability models employed to identify general and specifically adapted rice genotypes under the salinity and alkaline stress conditions of India (Krishnamurthy et al. 2015, 2016a, d) and coastal regions of southern Bangladesh (Islam et al. 2016). Krishnamurthy et al. (2016a) employed the AMMI and GGE models to identify a superior genotype for a particular trait using a genotype-by-trait biplot, and to compare the suitability of the AMMI and GGE biplot for identifying stable genotypes from 44 cultivars tested across seven salt stress locations. Hence, in the present study, we

used AMMI analysis to analyze a dataset derived from 13 putative salt-tolerant genotypes along with three checks tested across 13 different salt stress locations of India in two growing seasons (2014 and 2015).

ANOVA and model diagnosis ANOVA of the model provide an opportunity to determine whether selected AMMI analysis is appropriate for a set of experiments or not. The sum of squares (SS) for grain yield, G , E and GEI , all direct outputs from ANOVA, indicated that the main effects and interaction components were significant at $p \leq 0.001$. The environment and interaction component explains the larger proportion of variation, and the genotypic component (G) explains the least variation. The total variation of GEI consists of GEI_N and GEI_S , with GEI_N estimated simply by multiplying the error mean square (pure error in the study) by the number of degrees of freedom (df) of GEI , and GEI_S obtained by subtracting GEI_N from GEI (Gauch 2013). The SS for GEI_S and GEI_N was found to be 8.96- and 0.98-fold that of the genotypic (G) main effect, respectively. The results show that the AMMI model, as used in this study, was appropriate and worthwhile, since the SS for GEI_S is larger than G and datasets having substantial G and GEI_S and also SS for GEI are not buried in GEI_N . The significant contributions of G , E and GEI for grain yield under conditions of saline and alkaline soils in India were reported by Krishnamurthy et al. (2015),

Fig. 3 AMMI1 mega-environment display for 16 rice genotypes evaluated under 26 environments of saline and alkaline conditions. Environmental means are shown on the abscissa and IPC1 scores are shown on the ordinate

Fig. 4 Adaptive responses for rice genotypes according to the AMMI1 model. IPC1 scores for the 26 environments are shown on the abscissa and nominal yields for the 13 genotypes are shown on the ordinate

and Islam et al. (2016) reported the same result under conditions of saline soils of the coastal regions of southern Bangladesh.

AMMI is not a single model, rather it constitutes a model family, AMMI0 to AMMI6. AMMI0 captures no GEI_N and GEI_S whereas AMMI6, the full model, equals the actual data so it has no residual and captures all GEI_N and GEI_S . Therefore, model selection is one of the most important steps in AMMI analysis. Model diagnosis provides cues for selecting the best model family for a given dataset (Gauch 2013). The results of the present study show that total GEI can be divided into seven significant IPCs (IPC1–IPC7), contributing 87.47% of the total GEI with residual effect of 12.52% for grain yield. The AMMI model captures 90.12% of GEI_S and 9.88% of GEI_N . These results clearly indicate that IPC1, IPC2 and IPC3 represent AMMI model family AMMI1, AMMI2 and AMMI3, respectively, and that the SS of IPC3 is near to total SS of GEI, cumulatively covering 60.5% of GEI variations and 67.13% of GEI_S variations. These finding clearly indicated that it was better to not add IPC4. AMMI3 was found to be superior to AMMI4 in that in the former model IPCs capture a signal, whereas in the later model the IPCs capture noise. Discarding noise improves accuracy, increases repeatability, simplifies the drawing of conclusions and accelerates progress. Hence, in the present model diagnosis study, AMMI3 model optimizes predictive accuracy (Agahi et al. 2020).

A mega-environment is defined as a group of locations that consistently shares the best set of genotypes or cultivars across years (Yan and Rajcan

2002) or as a portion of the growing region sufficiently homogeneous to incite a similar response from the genotypes (Gauch and Zobel 1997). Mega-environment analysis has been applied mostly to yield-trial data, for which larger values are better. Mega-environments are distinguished by having different genotype “winners”. Increasingly complex AMMI models generally have more genotype “winners”, such as AMMI6, AMMI7 and AMMI8 which represent 13 winning genotypes with 13 mega-environments, but the accuracy of these models is relatively low since they consist of GEI_N . According to Gauch (2006), AMMI1 or AMMI2 is usually the most accurate because these two models can have substantially different accuracies for a given dataset, but in the present study it was AMMI3 that was the most accurate. Although AMMI3 achieves a greater accuracy than AMMI1, AMMI1 is still much more accurate than the raw data model AMMI0. Therefore, AMMI1 was taken to be the most suitable for mega-environment delineation, AMMI3 for optimizing predictive accuracy and AMMI0 for representing the raw data. The AMMI1 model delineated a total of 26 environments to four mega-environments, of which the first was E01, followed by E05 (second mega-environment), E12 and E14 (third mega-environment) and E21 (fourth mega-environment); the remaining 21 environments were classified in first mega-environment which is the largest one. The winning genotypes of AMMI1 were CHK3 in the first mega-environment, GN13 in the second mega-environment, CHK1 in the third mega-environment and GN11 in the fourth mega-environment. The AMMI biplot1 contains the variation of the principal additive effects of genotypes and environments. Genotypes that group together have similar adaptation while environments which group together influence the genotypes in the same way. In contrast, the AMMI2 model family delineates seven mega-environments with seven winning genotypes, namely CHK3, GN11, CHK1, GN13, GN05, GN03 and GN12. The AMMI biplot2 presents the spatial pattern of the first two PC axes of the interaction effects, corresponding to the genotypes, and helps in the visual interpretation of the GEI patterns and identification of the genotypes or locations that exhibit a low, medium or high level of interaction effects. Genotypes near the origin are non-sensitive to environmental interactive forces and those distant from the origin are sensitive to salt stress and have large

interactions. The points of either genotypes or environments that are close to each other have similar interaction patterns, while those that are distant from each other have different interaction patterns (Krishnamurthy et al. 2016d). The AMMI3 model family, diagnosed as being the most accurate for the present dataset, delineates ten mega-environments with ten winning genotypes, namely CHK3, CHK2, GN11, CHK1, GN06, GN13, GN02, GN03, GN05 and GN08 (Table 4). Among the winning genotypes of the AMMI 3 model family, genotypes CHK2 and GN05 achieved the second or third ranking in the majority of the environments of the first mega-environment, whereas GN02 ranked second in the second mega-environment of the AMMI1 model family. Finally, after combining all of the data of this model family, the overall winning genotypes were CHK3, CHK2, GN11, CHK1, GN13, GN02 and GN05, which were ranked either first or second in the mega-environment of the AMMI1 model family. The “winner” in 1 of the 2 years was not even among the top five genotypes in the other year in many locations. Since soil salinity is highly dynamic in nature, the level of salinity changes with fluctuating environmental factors, such as precipitation, temperature and relative humidity (Tack et al. 2015). In our experiment, this is evident by the effect of environment and GEI being very high compared to the genotypic effect. The rank of the genotypes and the performance of the genotypes under salt stress could be seen to be definitely altered with varying levels of salt stress (pH and EC of each location is given in Table 1). Location (CSSRI, Karnal sodic microplot, Haryana; namely environments 23 and 24) has four of five common genotypes between 2014 and 2015.

Selection or recommendation of the best genotypes involves two principal considerations. First, selection must be done in the context mega-environment scheme, which includes a single mega-environment exploiting only broad adaptation, or multiple mega-environments exploiting both broad and narrow adaptation. Second, selection is based on yield estimates using both the treatment and experimental designs (Gauch 2013). According to Gauch (2013), a ratio of 1 represents a winning genotype across environments. This ratio assesses the importance of narrow adaptation due to GEI effects, and a ratio of ≥ 1.10 is indicative of narrow adaptation. The ratio is the yield (or whatever the trait) of the winner within each environment,

divided by the yield for the overall winner (which is CHK3), with both yields estimated by the AMMI1 model, with the ratio automatically equal to 1 for the overall winner. This ratio assesses the importance of narrow adaptation, which are caused by $G \times E$ interactions. When a 5 or 10% yield increment has agricultural or economic significance, a ratio of ≥ 1.10 indicates that narrow adaptation offers substantial opportunities for yield increases, although at the cost of subdividing a growing region into two or more mega-environments. Therefore, CHK3, CHK2 and GN05 were the winning genotypes, with a ratio of 1; they are broadly adopted for different stress environments. In contrast, genotypes GN13 and GN02 showed narrow adaptation to E01, with a 29% yield advantage, and to E05, with a 19% yield advantage over the winning genotype (CHK3) under broad adaptation. Similarly, CHK1 adapted to E12 and E14 with negligible yield increment and GN11 adapted specifically to E21 with a 5% yield increment over the winning genotype (CHK3) under broad adaptation. The checks continued to dominate the genotypes in terms of high yields and stability, and this issue has to be seriously looked into by breeders. Stable rice genotypes have been identified across salt stress locations previously by Kumar et al. (2007, 2010, 2011), Anandan et al. (2009), Ali et al. (2013), Krishnamurthy et al. (2014) and Krishnamurthy et al. (2016b, 2017).

The genotypes GN13 and GN02 were narrowly adapted, with positive GEI in second mega-environment and negative GEI in the third and fourth mega-environments and also in the majority of the environments of the first mega-environment. Genotypes CHK3, CHK2 and GN05 were showed broad adaptation with neutral GEI and were less sensitive to the dynamic conditions of the salt stress condition. CHK1 and GN11 were narrow-adapted genotypes with positive GEI in the third and fourth mega-environment and in some of the environments of the first mega-environments, and with negative GEI in the second mega-environment. In the present investigation, the three broadly adapted, stable winning genotypes, namely CHK3, CHK2 and GN05, were identified, with a maximum grain yield of 3487.82, 3280 and 3086.29 kg ha⁻¹, respectively, which is more than grand mean yield of 2828.28 kg ha⁻¹. Genotypes GN13, CHK1 and GN11 were narrowly adapted to the second, third and fourth mega-environments,

respectively. Genotype GN13 recorded 80% yield advantage in the E01 environment and 66% yield advantage in E25. Similarly, GN11 provided 61% yield advantage in the E21 environment. Based on these findings, these three genotypes could be recommended for specific mega-environments.

Conclusion

The aim of the present study was to evaluate geographically and genetically diverse putative salt-tolerant rice genotypes across 13 salt stress locations representing inland salinity, alkalinity and coastal salinity conditions across India using the AMMI stability model. We found that the study locations themselves were significant factors accounting for the total variation in grain yield. This finding makes plant breeding efforts even more challenging, and a great deal of effect is needed to pool data from more number of years and to correlate it with weather changes and salinity dynamics during the period being studied. In our study, variety CSR 36 (CHK3) was found to be the most ideal and stable candidate, followed by IR 87952-1-1-1-2-3-B (G05). Overall, the most promising genotypes (CSR 36 [CHK3], IR 87952-1-1-1-2-3-B [GN05] and CST27 [CHK2]) had high mean yield and stability, and IR 87952-1-1-1-2-3-B (GN05) could be used for commercial cultivation across salt-affected soils. GN13 (IR 87938-1-1-2-1-3-B) and GN11 (IR 87938-1-2-2-1-3-B) were winning genotypes and are recommended for second and fourth mega-environments, with 61–80% yield advantages in narrow adaptation over broad adaptation.

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Author's contribution SLK, PCS, DKS, AMI and RKS conceptualized and designed the experiment. SLK, YPS, VKM, DB, BM, SM, SKS, RKG, PKS, KKM, BCM, KC, GP, PBV KDP, ST, OPV, AHK, ST, SG, RG, VKY, SKBR, MP and AA performed the field evaluations and recorded data. SLK and JB performed the data analysis. SLK drafted and revised the manuscript. PCS, DKS, AMI, RKS, YPS, VKM, DB, BM, SM, SKS, RKG, PKS, KKM, BCM, KC, GP, PBV KDP, ST, OPV, AHK, ST, SG, RG, VKY, SKBR, MP and AA edited the manuscript. All authors have read and approved the final manuscript.

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