International Journal of Chemical Studies 2020; 8(5): 410-415

International Journal of Chemical Studies

P-ISSN: 2349–8528
E-ISSN: 2321–4902
www.chemijournal.com
IJCS 2020; 8(5): 410-415

Received: 18-06-2020
Accepted: 20-08-2020

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Stability analysis for quality traits in rice hybrids using AMMI model

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DOI: https://doi.org/10.22271/chemi.2020.v8.i5f.10328

Abstract

Eighteen promising hybrids from different agro climatic zones *viz.*, Maruteru, Warangal, Jagtial and Ragolu of Andhra Pradesh, India were subjected to stability by using AMMI model for eleven quality characters. The pooled data was presented as per AMMI model. The analysis of variance indicated that the genotypes and environments were significant for all the quality characters except for milling per cent for genotypes indicating the diversity among the genotypes and environments studied. Among the AMMI components first IPCA axis explained most of the portion of G X E interaction for the characters under study. IPCA 1 was significant for head rice recovery per cent, gel consistency, alkali spreading value and protein content. The promising hybrid APMS 9A x MTU II-143-26-2 showed stability for head rice recovery per cent, milling per cent, volume expansion ratio and kernal elongation ratio whereas, APMS 6A x MTU II -187-6-1-1 reported stability for milling per cent, gel consistency, volume expansion ratio, protein content and amylose content. The highest yielding hybrid APMS 6A x MTU II-110-9-1-1-1-1 recorded stable performance for hulling per cent and milling per cent.

Keywords: AMMI model, GxE interaction and stability

Introduction

Rice (*Oryza sativa* L.) is the staple food for 65% of the global population and forms the cheapest source of food energy and protein. Besides yield, it is also important to look into the quality aspects of rice for better consumer preference. In hybrid rice breeding, grain quality traits are important issue to be addressed for acceptance of the hybrids. Grain quality attributes are important factor prior to variety adaptation and they vary among varieties and production environments (Jennings, 1979) [8]. Comprehensive study of adaptability of genotypes is an important goal in plant breeding programs (Das *et al.*, 2011) [4] this objective can be better understood and achieved by studying genotype x environment (GE) interaction. The additive main effects and multiplicative interaction (AMMI) model found more useful as it includes the additive variance and then applies principal component analysis to the interaction portion. The superiority of AMMI, compared to other models was explained by Gauch (2006) [6] for genotype specific breeding and selection for optimum performance. Very limited reports are available on the stability evaluation of rice grain quality traits. Thus present study was aimed to identify the genotypes having low G x E interaction with superior quality traits using AMMI model.

Material and Methods

In the present experiment 52 hybrids were developed in a line x tester design (Kempthorne, 1957) using four CMS lines and 13 restorers during *kharif*, 2010 at Andhra Pradesh Rice Research Institute and Regional Agricultural Research Station, Maruteru, Andhra Pradesh. During *rabi*, 2010-11 the 52 hybrids and three checks (*viz.*, MTUHR 2089-hybrid check, MTU 1075 and MTU 1010-varietal checks) were evaluated in a randomized block design with two replications by adopting a spacing of 20 x 15 cm over different agroclimatic zones of Andhra Pradesh *viz.*, Maruteru, Warangal, Jagtial and Ragolu for yield and yield contributing characters. Eighteen promising hybrids which recorded significant higher yield than high yielding check were subjected to quality analysis for eleven quality characters (physico-chemical) *viz.*, hulling per cent, milling per cent, head rice recovery, L/B ratio, water uptake, volume expansion ratio, kernel elongation ratio, gel consistency, alkali spreading value, amylose content and protein content (Table 1). Physico-chemical characters were recorded by standard evaluation methods (DRR 2006) [5]. Gel consistency was determined as described by Cagampang *et al.* (1973) [3]. A method as described by Little *et al*. (1958) [11] and Jennings *et al*. (1979) [8] used to determine alkali spreading value. Amylose content and protein content were estimated as per Juliano (1971) [9] and Piper (1966) [16], respectively.

The quality analysis data from four locations was subjected to pooled stability analysis as per AMMI model (Gauch, 1988) [7]. AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure. The AMMI model separates the additive variance and then applies principal component analysis to the interaction portion to extract a new set of coordinate axes which explain in more detail the interaction pattern. According to AMMI model the genotypes which are characterized by mean greater than the grand mean and the PCA scores nearly zero are considered as generally adaptable to all the environments. However the genotypes with high mean performance and with large value of IPCA scores are considered having specific adaptability to the environment (Sharma *et al.*, 1998) [17]. AMMI analysis permits estimation of interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations. In the present study, IPCA I was significant and contributed more than 50% of total G x E interaction sum of squares percentage for head rice recovery per cent, gel consistency, alkali spreading value and protein content. The interaction of eighteen promising hybrids along with three checks at four locations was best predicted by first interaction principal component (Pawar *et al.*, 2012) [14].

Results and Discussion

The analysis of variance of stability revealed that the genotypes and environments were significant for all the quality characters except for milling per cent for genotypes indicating the diversity among the genotypes and environments studied (Table 2). G×E interaction effects signify that genotypes behave differently across different environments. (Nayak *et al*., 2008 and Mahalingam *et al*., 2013 and Ashwini *et al*., 2019) [13, 12, 2]. It was found in present study that environmental mean variations were very higher than genotypic mean variations for most of the quality characters (Table 2). Hence, test locations were diverse and present results were in harmony with results of Adesole and Yetunde (2016) [1] and Ashwini *et al*., 2019 [2].

The first interaction principal component i.e IPCA (I) values predicts the stability of the studies genotypes over the target environments. Higher the values, lowest the stability over variable environments and vice versa, regardless the positive or negative value (Purchase *et al*., 2000) [15]. For hulling per cent, the biplot interaction (Fig.1) showed that the hybrids A_1R_3 (1), A_3R_5 (12) and A_3R_{10} (15) were stable with above mean (77.06%) and zero IPCA score. The mean performance of hulling per cent was high in Maruteru and Warangal locations with similar performance of hybrids as they recorded same PCA axis. Ragolu location PCA score was zero indicates the stable performance of all hybrids for hulling per cent. According to AMMI I biplot (Fig. 2) for milling per cent, the hybrids A_1R_3 (1), A_3R_7 (14), A_2R_5 (8), A_1R_5 (2), A_2R_7 (9) and check MTUHR 2089 (19) were stable with high mean (> 67.16%) and zero IPCA score. These results were in conformity with the results published by Mahalingam *et al*., 2013 [12]. Interaction of A_1R_3 (1) hybrid with Warangal location was positive. IPCA score of Warangal was zero with stable performance of all hybrids in this location for milling per cent. For head rice recovery IPCA I was significant and explained 68.52% of total G x E interaction sum of squares. From the biplot interaction (Fig. 3), the hybrids A_2R_7 (9) and A_2R_{12} (10) were stable with IPCA score zero and higher mean than grand mean (53.29%). These results for head rice recovery were confirmed by Mahalingam *et al*., 2013 [12]. Maruteru and Warangal locations had high mean with good conditions for most of the hybrids. On the other hand Jagtial location had low mean than grand mean and differed for main effects and interactions.

In the biplot presentation of L/B ratio (Fig. 4), the hybrids A_2R_5 (8), A_1R_7 (3), A_4R_3 (17), A_2R_3 (6) and MTU 1075 (20) had above general mean (3.06) with IPCA score zero and were stable for this character. Maruteru and Warangal locations had high mean with stable performance of all hybrids in these locations. For the character water uptake biplot interaction (Fig. 5) showed that the hybrids A_3R_5 (12), A_3R_1 (11) and A_3R_7 (14) were stable with IPCA score zero and above mean value (155.13 ml). Three locations *viz.*, Maruteru, Warangal and Jagtial had similar mean performance of hybrids for water uptake as they were placed on same axis.

According to AMMI I (Fig.6) for volume expansion ratio the hybrids A_2R_7 (9), A_1R_5 (2), A_1R_7 (3), A_3R_5 (12), A_3R_6 (13) and MTUHR 2089 (19) were stable with mean greater than average mean (4.35) and IPCA score near zero. The hybrid A_4R_6 (18) and Warangal location had same sign on IPCA axis indicating their positive interaction, *i.e*, the genotype was specifically adopted to particular location. The locations *viz.*, Maruteru, Warangal and Jagtial showed similar performance for this trait. Maruteru and Jagtial locations had favourable conditions for most of genotypes and IPCA score were nearly zero indicating stable performance of all hybrids.

For kernel elongation ratio biplot (Fig. 7), the hybrids A_1R_{12} (4), A_2R_7 (9), A_3R_1 (11) and A_3R_{12} (16) were stable with mean more than grand mean (1.79) and zero IPCA score. Favourable conditions were showed by both Maruteru and Warangal locations. IPCA score of Ragolu location was zero with low mean indicating stable performance of genotypes. Gel consistency was responsible for softness and the IPCA 1 axis was significant and explained 77.13% of the total G x E interaction sum of squares percentage. In the biplot presentation (Fig. 8), A_3R_1 (11), A_3R_6 (13) and A_1R_5 (2) hybrids were stable with above grand mean (72.14 mm) and near to IPCA score zero. Ragolu location IPCA score was zero with stable performance of hybrids. Whereas Maruteru location had good potential for gel consistency but exhibiting high interaction effects showing the suitability for specific adapted hybrids.

For alkali spreading value, the IPCA 1 was significant and contributed 63.19% of the total G x E sum of squares. From the AMMI I biplot (Fig. 9), A_3R_{12} (16) hybrid recorded high mean (2.96) and IPCA score near zero with stable performance over locations. In Maruteru and Warangal locations, hybrids had high mean performance for alkali spreading value. Amylose content was responsible for texture and appearance and from the amylose content biplot (Fig. 10) the hybrids *viz.*, A_1R_5 (2), A_4R_6 (18) and A_2R_4 (7) were stable with zero IPCA and low (<24.08%) mean. The performance of hybrids for amylose content was similar in Warangal and Ragolu locations. Jagtial location had high mean with IPCA score zero indicating all the genotypes were stable for expression of this trait whereas, Maruteru location had good conditions for genotypes but exhibiting high interaction effects indicate the suitability of specific adapted genotypes. With regards to protein content, IPCA 1 was significant with 63.75% of total G x E sum of squares. In AMMI I biplot (Fig. 11), A_1R_5 (2) and MTU 1010 (21) were stable with IPCA score near zero and above grand mean (8.18). Hybrids performance was same in Maruteru and Ragolu locations. Maruteru location had stable performance of hybrids for protein content as its IPCA score was near to zero.

AMMI analysis for quality traits revealed that the high yielding hybrids *viz.*, APMS 9A x MTU II-143-26-2 (A_2R_7), APMS 6A x MTU II -187-6-1-1 (A_1R_5), APMS 6A x MTU II-143-26-2 (A_1R_7), APMS 10A x MTU 1071 (A_3R_1), APMS 6A x MTU II-110-9-1-1-1-1 (A_2R_3) and APMS 9A x MTU II -187-6-1-1 (A_2R_5) also showed stability for most of quality characters like milling percentage, head rice recovery, L/B ratio, volume expansion ratio, kernel elongation ratio, gel consistency and amylose content. These may be exploited commercially after extensive testing in different environments.

Table 1: List of promising hybrids for quality traits in rice

S. No.	Promising hybrids	Code	Grain yield plant^{-1} (pooled locations)
1	APMS 6A x MTU II-110-9-1-1-1-1	A_1R_3	47.75
2	APMS 6A x MTU II -187-6-1-1	A_1R_5	41.75
3	APMS 6A x MTU II-143-26-2	A_1R_7	41.85
4	APMS 6A x MTU II-283-7-1-1	A_1R_{12}	38.30
5	APMS 9A x MTU 1071	$A_2 R_1$	39.03
6	APMS 9A x MTU II-110-9-1-1-1-1	$A_2 R_3$	42.06
7	APMS 9A x MTU II-110-11-1-1-1-6	A_2R_4	39.00
8	APMS 9A x MTU II -187-6-1-1	A_2R_5	41.91
9	APMS 9A x MTU II-143-26-2	A_2R_7	45.65
10	APMS 9A x MTU II-283-7-1-1	A_2R_{12}	4 1.75
11	APMS 10A x MTU 1071	A_3R_1	36.70
12	APMS 10A x MTU II -187-6-1-1	A_3R_5	36.15
13	APMS 10A x MTU II-190-1-1-1-1-1	A_3R_6	36.59
14	APMS 10A x MTU II-143-26-2	A_3R_7	41.20
15	APMS 10A x MTU II-290-42-1	A_3R_{10}	46.08
16	APMS 10A x MTU II-283-7-1-1	A_3R_{12}	39.36
17	IR 58025A x MTU II-110-9-1-1-1-1	A_4R_3	40.03
18	IR 58025A x MTU II-190-1-1-1-1-1	A_4R_6	41.10
Checks			
19	MTUHR 2089		30.25
20	MTU 1075		30.59
21	MTU 1010		27.21

Table 2: Analysis of variance of the AMMI model for quality characters in rice (*Oryza sativa* L.)

Source of variation	Hulling per cent			Milling per cent		Head rice recovery per cent		L/B ratio		Water uptake		Volume expansion ratio	
	Df	MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Genotypes	20	4.88*	30.57	5.87	28.56	37.30**	16.23	0.07**	78.12	7184.47**	91.80	0.49**	46.89
Environments	3	18.04**	16.96	22.75**	16.60	949.92**	62.00	0.02*	3.03	659.61*	1.26	0.57*	8.21
G X E interaction	60	2.79	52.47	3.76	54.84	16.68	21.77	0.01	18.84	180.85	6.93	0.16	44.90
PCA I	22	3.66	48.05	5.69	55.57	31.17*	68.52	0.01	5.83	265.59	53.85	0.20	47.26
PCA II	20	2.64	31.58	3.88	34.46	13.45	26.88	0.01	33.71	166.51	30.70	0.15	31.63
PCA III	18	1.90	20.37	1.25	9.96	2.56	4.60	0.00	10.46	93.23	15.46	0.11	21.13
Pooled Residual	60	2.79**		2.64**		8.29**		0.00**		180.85**		0.16**	
Error	84	1.21		1.15		1.31		0.00		21.85		0.04	
Total	167	2.52		3.04		28.18		0.01		948.23		0.14	

Source of variation	Kernal elongation ratio			Gel consistency		Alkali spreading value		Amylose content		Protein content	
	Df	MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Genotypes	20	0.04**	52.35	269.61**	68.89	2.95**	91.95	3.18**	43.88	0.23**	20.87
Environments	3	0.06**	12.07	191.40**	7.34	0.45**	2.12	11.35**	23.54	3.93**	53.30
G X E interaction	60	0.01	35.58	31.02	23.78	0.06	5.93	0.79	32.60	0.10	25.82
PCA I	22	0.01	51.58	65.26*	77.13	0.11*	63.19	1.01	46.85	0.17*	63.75
PCA II	20	0.01	30.70	21.28	22.86	0.04	22.99	0.82	34.71	0.07	25.16
PCA III	18	0.00	17.72	0.00	1.42	0.03	13.82	0.48	18.42	0.04	11.09
Pooled Residual	60	0.01**		11.20**		0.03**		0.79**		0.10**	
Error	84	0.00		7.14		0.01		0.29		0.01	
Total	167	0.01		50.47		0.39		1.01		0.14	

** Significant at1% level *Significant at 5% level

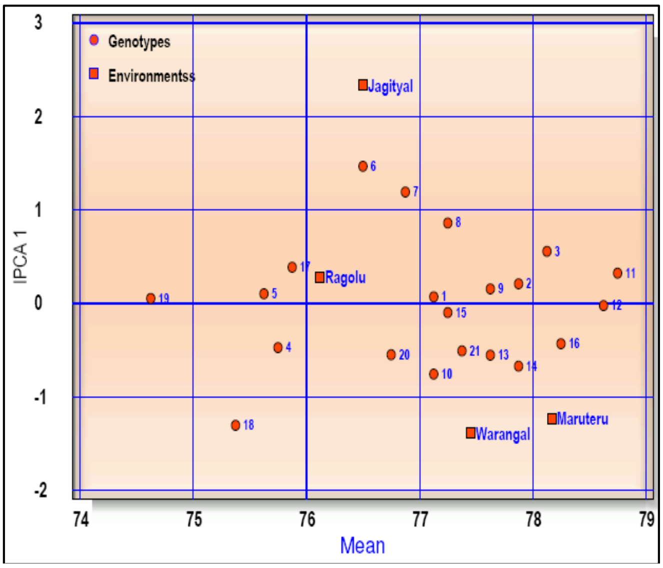

Fig 1: Biplot of interaction principal component analysis 1 against Hulling per cent for four locations

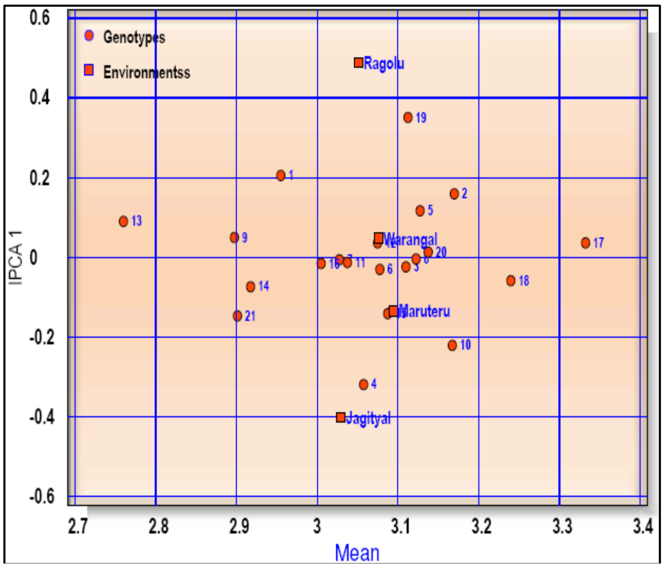

Fig 4: Biplot of interaction principal component analysis 1 against L/B ratio for four locations

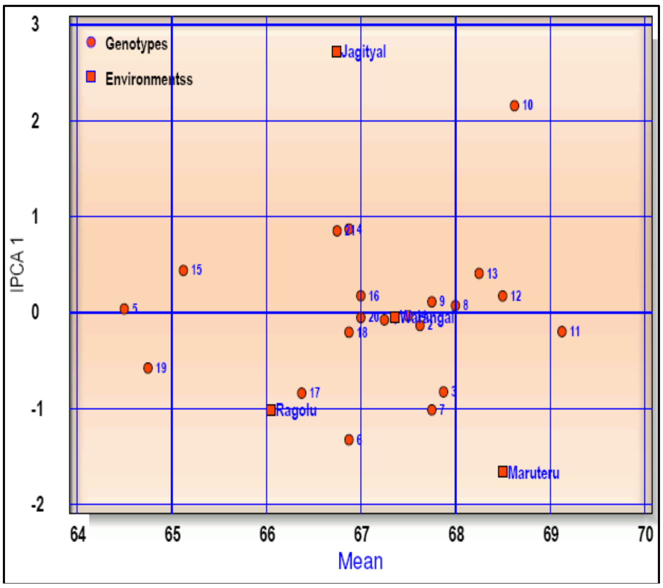

Fig 2: Biplot of interaction principal component analysis 1 against Milling per cent for four locations

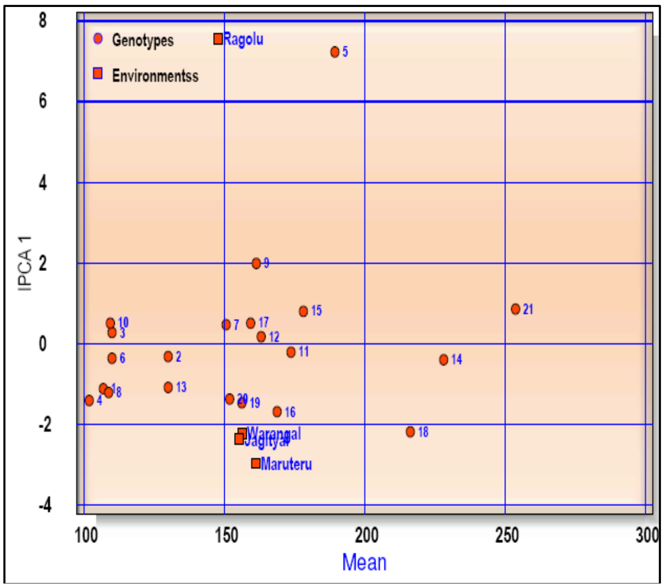

Fig 5: Biplot of interaction principal component analysis 1 against Water uptake for four locations

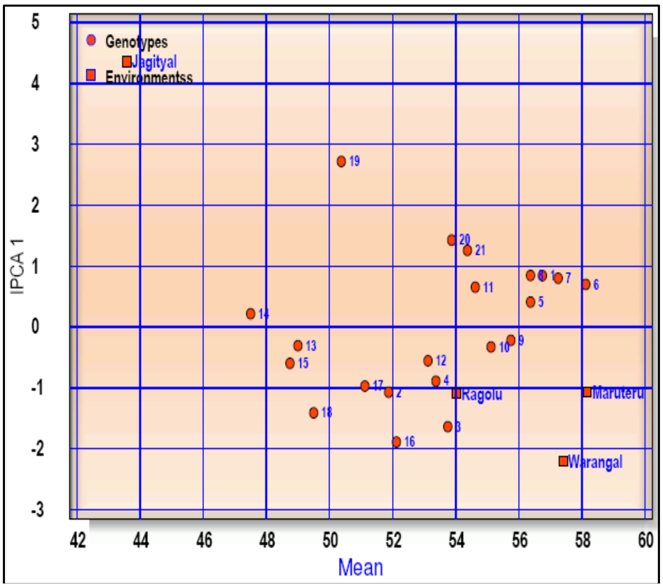

Fig 3: Biplot of interaction principal component analysis 1 against Head rice recovery per cent for four locations

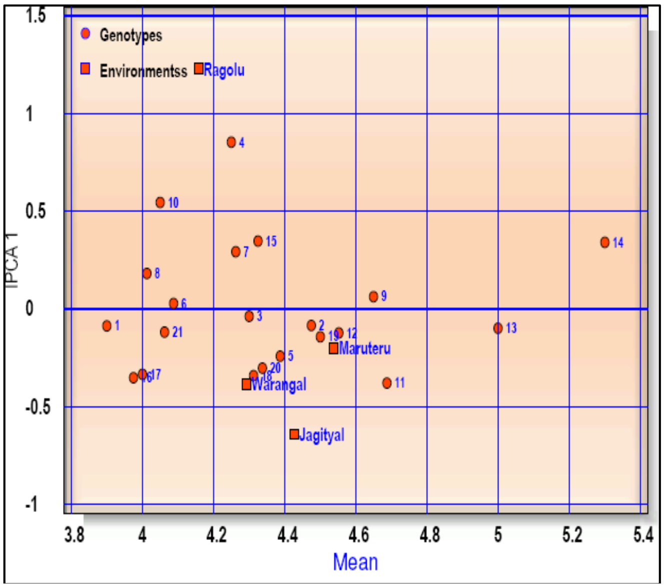

Fig 6: Biplot of interaction principal component analysis 1 against Volume expansion ratio for four locations

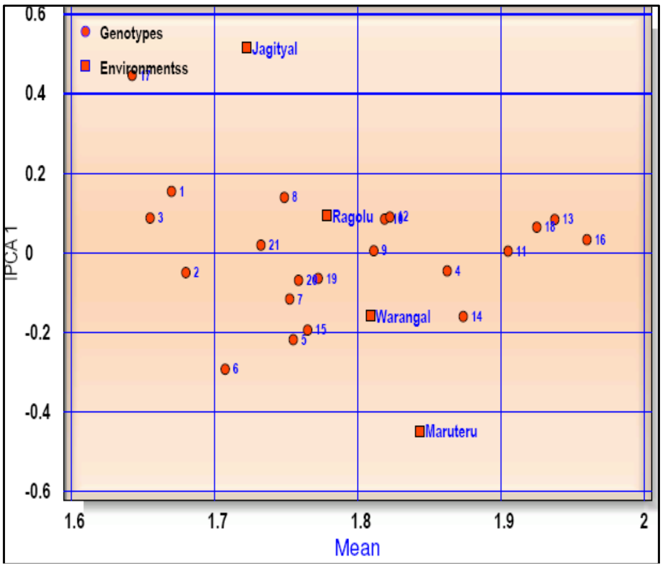

Fig 7: Biplot of interaction principal component analysis 1 against Kernel elongation ratio for four locations

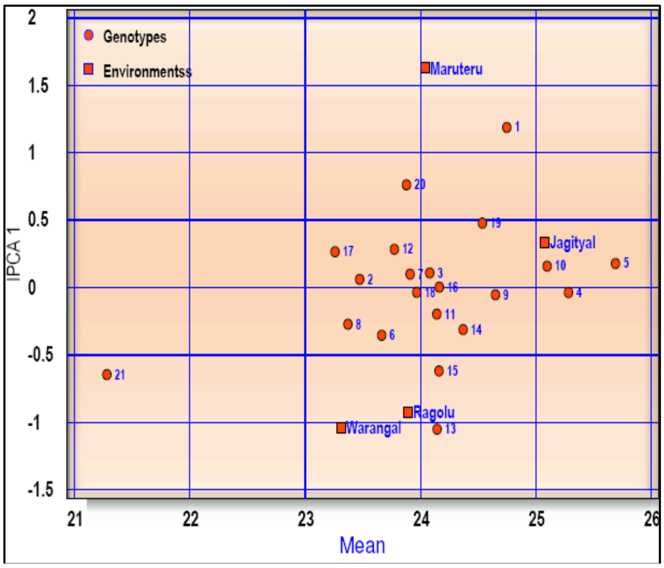

Fig 10: Biplot of interaction principal component analysis 1 against Amylose content for four locations

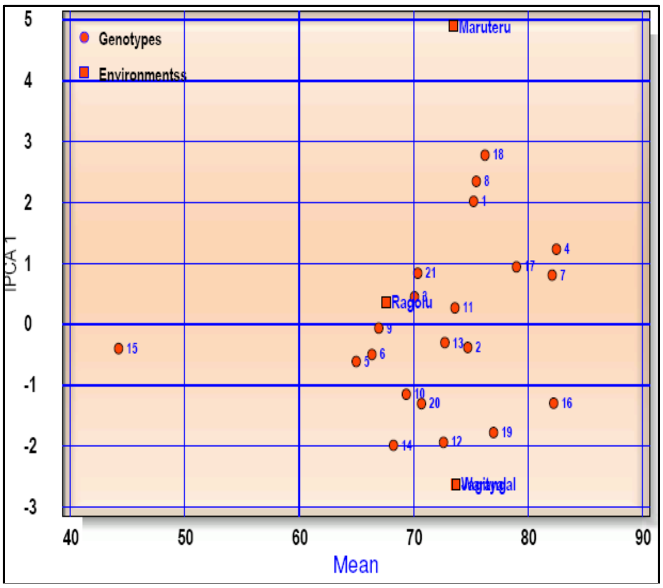

Fig 8: Biplot of interaction principal component analysis 1 against Gel consistency for four locations

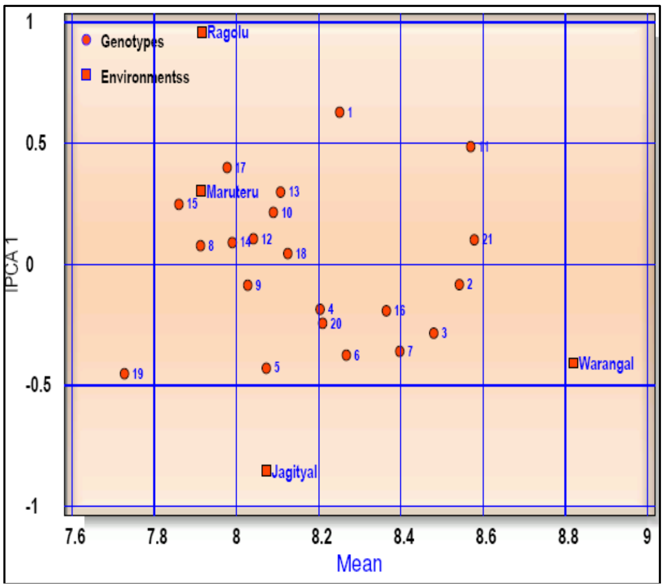

Fig 11: Biplot of interaction principal component analysis 1 against Protein content for four locations

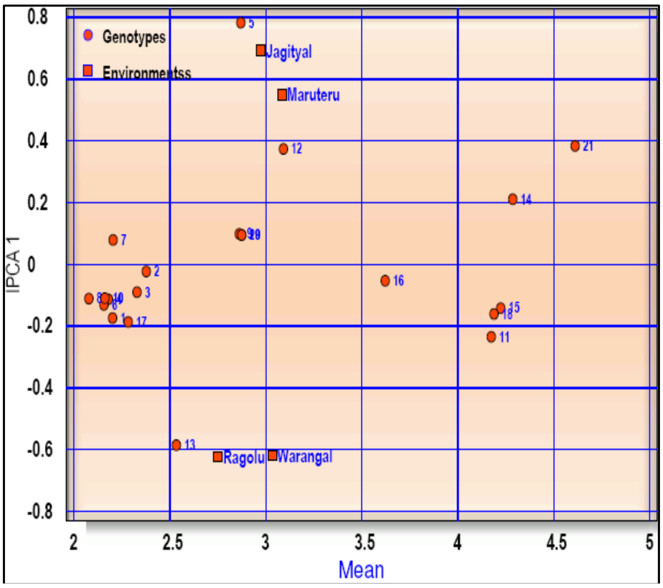

Fig 9: Biplot of interaction principal component analysis 1 against alkali spreading value for four locations

Acknowledgement

The first author is highly thankful to the Associate Directors of Research of Maruteru, Warangal and Jagtial Regional Agricultural Research stations and Head of Ragolu Research station for smooth conduct of the trial.

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