

AMMI Biplot analysis and Genotype x Environment interaction studies in rainfed upland rice accessions

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ABSTRACT

In present investigation, 18 new genotypes were tested for upland ecology at S. G. College of Agriculture and Research Station, Jagdalpur, Chhattisgarh, to identify promising genotypes and formulate phenological relationships at phenotypic and genotypic levels and estimate G x E interactions with uncertain weather parameters. The test populations exhibited enough variation for crop breeding research, however, genotypes responded differentially to water stress and late season drought with respect to morphological and yield traits. The first Interaction Principal Component Axis (IPCA1) explained 38.95% of total variation while IPCA2 explained 20.80%. Thus, the two axes together accounted for 59.75 % of the GGE variation for grain yield. According to the biplot, genotypes PM 6004, IR 84887-B-15 and IR 83381-B-B-137-3 were recorded vertex position. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the Biplot. Among the genotypes evaluated, IR-83381-B-B-137-3 and IR-86857-46-1-1-2 was found to be promising for rainfed breeding programme as parent material.

Key words: Biplot analysis, upland rice, Genotype X Environment, GGE

Rice production in Asia has witnessed 2.6 times gain since 1961, preliminary result of green revolution which dramatically increased the rice productivity in high input irrigated system. However, the rainfed rice which occupies 32 percent of Asian rice growing area has benefitted less from green revolution (Jambhulkar and Bose, 2014). Upland rice is grown in unpuddled fields where, by default, good soil drainage and uneven land surface renders the accumulation of water impossible. It is grown with little or no fertilizer input with direct seeded methodology in moisture deficit unsaturated soils (Aditya and Bhartiya, 2013). Further, poor ability of varieties to produce economic quantity of grain, due to the concomitant poor panicle yield, caused by varying degrees of water stress, makes rice production risky and unattractive due to low yield of 1 to 2 tones/hectare (Adewusi and Nassir, 2011). Therefore, genetic management strategies should be undertaken for cultivating rice with less water and maximizing extraction of soil moisture and its efficient use in crop establishment and growth to enhance biomass and yield.

The additive main effects and multiplicative interaction (AMMI) model (proposed by Gauch, 1992) is one of the most widely used statistical methods to understand and structure interactions between genotypes and environments (Hongyu *et al.*, 2014). In essence, the AMMI model applies the singular value decomposition (SVD) to the residuals of an additive two-way analysis of variance (ANOVA) model as applied to the genotype by environment interactins (GEI) table of means (Gauch, 2013; Rodrigues *et al.*, 2014). The main objective of AMMI analysis are: (i) understanding complex GEI, which includes delineating mega-environments and selecting genotypes to exploit narrow adaptations; and (ii) increasing accuracy to improve recommendations, repeatability, selections, and genetic gains. The widespread use of biplots exercise to quantify the genotype and environment is due to reason that GE effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environments. Later, the procedure was modified by Yan *et al.*, (2000) using biplots similar

to the AMMI technique, which has the advantage of decomposing the joint effect of genotype (G) and GE (G + GE) by principal component analysis (PCA), differing from the original AMMI analysis that decomposes only GE (Yan *et al.* 2007) and was referred as GGE Biplot analysis. The advantage of observing the effects of G + GE in a biplot graph signifies this technique as a reliable alternative to the AMMI analysis, in which the G effect can not be visualized directly in the biplot graphic (Balestre *et al.*, 2010). The differences between the GGE biplot and AMMI analysis is that, the GGE biplot analysis is based on environment-centered principal component analysis (PCA), whereas AMMI analysis is established on double centered PCA (Agyeman *et al.*, 2015). However, according to Yan and Tinker, 2006; AMMI could be misleading if used for “which-won-where” study (i.e., identification of mega-environments and their winning genotypes). Further, the GGE biplot is superior to the AMMI, because it provides more understandable interpretations than the AMMI, by allowing the visualization of any crossover GE interaction which is essential to breeding programmes (Ding *et al.*, 2007).

Upland rice is grown in a wide range of environments in India where it is subjected to the influence of G x E interactions which limits the effectiveness of selection of superior genotypes (Lakew *et al.*, 2014). Therefore crop breeders must use statistical techniques to accurately and efficiently measure the response of genotypes in multiple test environments (Yan *et al.* 2007). This paper attempts to define the current status of breeding for upland rice. Genetic and physiological mechanism contributing to maintain grain yield under upland conditions are discussed along with prevailing genotypic and environment interactions which is of utmost significance among unpredictable micro and macro environments.

MATERIALS AND METHODS

The experiment was undertaken with 18 Indian and Exotic genotypes under rainfed conditions during wet season 2013 and 2014 at Upland Rice Breeding Block of S. G. College of Agriculture and Research Station, Jagdalpur, IGKV, Raipur, Chhattisgarh. An upland ecology simulation model was created by choosing experimental plot completely rainfed condition, without standing water was maintained during entire

life cycle of crop. Sowing was completed by just onset of monsoon by direct seeding in agronomically standardized geometry in 10sq M plot with two replications. Trench was made in periphery of experimental plot to avoid no water accumulation. The data was recorded for 10 quantitative characters namely days to flowering, crop duration, plant height, and panicles per sq M, panicle length, spikelets per panicle, spikelet fertility, grain yield, biological yield and harvest index. The biennial trireplicated data was statistically analysed by Windostat Version 9.2 from Indostat Services, Hyderabad Licensed to Plant Breeding Division Sugarcane Breeding Institute Coimbatore.

RESULTS AND DISCUSSION

Looking for major role environmental interactions in genotypic response in upland rice growing ecology AMMI analysis was carried out to statistically predict the yield deviation. Since presently biplot analysis is considered as better option for genotype by environment interaction studies in comparison to AMMI, both the methods were deployed for accurate interpretation. With the inherent variability of upland rice ecologies for moisture levels, and the attendant interaction with environment for several traits, varieties and traits identified as having the potential for drought tolerance in a location may not necessarily exhibit consistency overtime and or over a large area (Nassir and Ariyo, 2006, 2007; Botwright *et al.*, 2008). Therefore, an attempt was made to assess interaction of genotype and environment based on biennial (wet season 2013 and 2014) experiments. The use of biplots to quantify the genotype environment interaction (IGE) is widespread since the GE effects can be visualized in a single graph, which facilitates the comparison of genotypes and their interaction with the environments (Balestre *et al.*, 2010). Recently, the IGE analysis using biplots similar to the AMMI technique, which has the advantage of decomposing the joint effect of genotype (G) and GE (G + GE) by principal component analysis, has been evolved that differing from the original AMMI analysis that decomposes only GE (Yan and Kang, 2003; Yan *et al.*, 2007; Gouch, 2006). The method is called GGE biplot analysis which identifies G x E interaction pattern of multi-environment data and clearly shows which variety performs best in which environments (Lakew *et al.*, 2014).

Analysis of variance for genotype by environment interaction for all the genotypes, traits and environment under study (Table 01) was found to be highly significant indicating the scope of study. In interaction biplot, the first Interaction Principal Component Axis (IPCA1) explained 38.95% of total variation while IPCA 2 explained 20.80% (Fig. 01). Thus, the two axes together accounted for 59.75 % of the GGE variation for grain yield (Balestre *et al.*, 2009a; 2009b. According to the biplot, genotypes PM 6004, IR 84887-B-15 and IR 83381-B-B-137-3 were recorded vertex position. These genotypes were the best or the poorest genotypes in some or all of the environments because they were farthest from the origin of the biplot (Yan and Kang, 2003). In this biplot, environments are also divided into different sectors. The first sector represents environment A, B and D; with genotype IR 83381-B-B-137-3 as the best yielder genotype and the second sector represents B; with genotype IR 84887-B-15 as the most favorable while the third sector represents C; with genotype R-RF-95 as the winner genotype. The other vertex genotype, R-RF-45 which was located far away from all of test environments, implied that it did not yield well at any of the test environments. The genotype x environment interaction revealed significant variation for days to flowering, crop biomass, spikelets fertility etc. ($p < 0.01$). AMMI analysis of variance for grain yield and associated traits revealed that effect due to environment; genotype and their interactions were significant showing that environment is divers of trait expression (Naveed *et al.*, 2007; Lakew *et al.*, 2014).

In multienvironmental graph, days to 50 percent flowering was found to have enough interaction with respect to Year X Genotype and Genotype X Year. Genotype IR-88287-B-B-141-1 shifted the flowering period from 85 DAS (wet season 2013) to 97 DAS (wet season 2014) while R-RF-95 shifted 75 DAS to 79 DAS (Fig 02). Similarly, in IR-88287- 677-60-3 flowering was eight DAS prolonged in comparison to wet season 2013. The study reveals the significant effect of rainfall frequency and duration upon flowering behavior over the years and role of Genotype and Environmental interaction in expression of the character. However, entry IR-86857-46-1-1-2 recorded very minimal differences in both the experimental years and can be concluded to have little interactive expression of flower biology. In consideration of spikelet fertility,

Table 1. Analysis of variance for genotype by environment interaction

	Df	DF	CD	PH	P/Sq M	PL	S/P	SF	GY	BY	HI
Year	1.00	1012.5	***	20.06	180.50	73.2	***	288.0	***	2.86	364.5
Genotype	17.00	42.32	***	370.3	5422.1	5.70	***	31.36	***	4.96	136.1
Year*Genotype	17.00	8.09	***	89.85	2083.6	1.38	**	2.47	0.17	1.24	1.50
Error (B)	36.00	0.81		39.69	744.01	1.30		4.44	0.12	0.78	8.44
Total	71.00	26.74		130.6	2176.9	3.39		14.41	0.25	1.92	42.35
General Mean	-9.00	84.72		89.69	269.75	20.9		90.39	2.31	6.43	36.39
C.V.	-9.00	1.06		7.02	10.11	5.45		2.33	14.7	13.7	7.99
CD(P<0.05)	-9.00										
Ai.- Aj (Year)	-9.00	0.43		3.01	13.04	0.54		1.01	0.16	0.42	1.39
Bi.- Bj; (Genotype)	-9.00	1.29		9.04	39.12	1.63		3.02	0.49	1.26	4.17

In Table: DF – days to 50 % flowering, CD – crop duration; PH – plant height; P/sq M – panicle per square meter; PL – panicle length; S/P – spikelet per panicle; SF – spikelet fertility; GY – grain yield; BY – biological yield; HI – harvest index
Significance level : 0.05(*); 0.01(**); 0.001 (***)

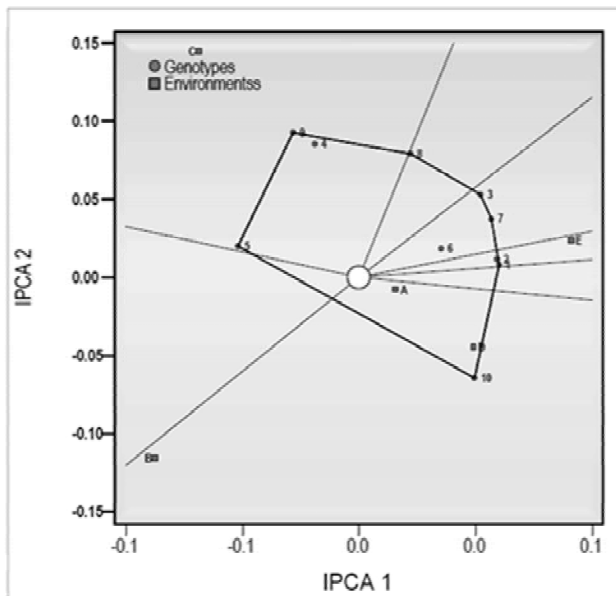


Fig. 1. Genotype x environment interaction plot

noticeable interaction was observed and IR-84859-B-41-1-2 recorded to most interactive followed by IR-86857-46-1-1-2. However, Sahbhagidhan and IR-84852-46-1-1-2 were relatively stable (Fig 03). While discussing environment drawn morphology *e.g.* days to flowering, crop duration, spikelet per panicle, spikelet fertility etc., its critical to consider prevailing weather phenomenon like rainfall and drought, because of being highly quantitative in nature. Moreover the genotypes

are interacting in positive direction hence, higher interaction doesn't always means to discard the genotype and further lesser interaction may yield of physiological threshold. The cause of environmental effect on genotype response also varies with crop genotype and location. Earlier Gunasekera *et al.*, (2006) reported rainfall and temperature to be cause of protein and oil content variation; Samonte *et al.*, (2005) identify heat index as discriminatory component of rice yield. Similar to present study Oak (2007); Shrestha *et al.*, (2012) and Nassir (2013) concluded hydrological factors as major role players.

Grain yield and biological was found to be quite variable component with respect to varying environment where, genotypes IR-86857-46-1-1-2 showed marked reduction in grain yield in wet season 2014. It's noticeable that despite of better precipitation made crop morphology and phenotypic reproductive performance, the grain yield and total crop biomass was reduced. Similar declination was observed for genotypes R-RF-69, R-RF-95, R-RF-45, PM-6004 and IR-83383-B-B-141-1 (Fig 04 and 05). This marked reduction is an indication of negative buffer of genotypes towards stress to nonstress shift. The results revealed that genotypes surely perform well under stress ecology but it normal rainfall prevails, the yield is reduced. In multi environmental graph for grain yield revealed that all genotypes followed approximate similar pattern except

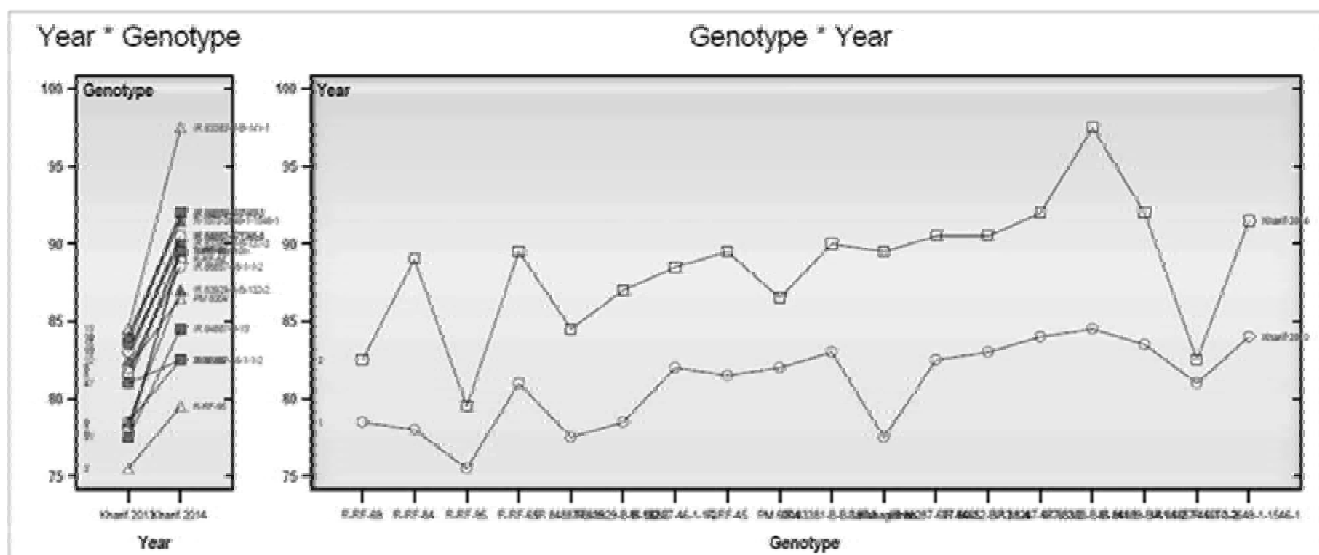


Fig. 2. Multienvironmental plot for days to 50 % flowering

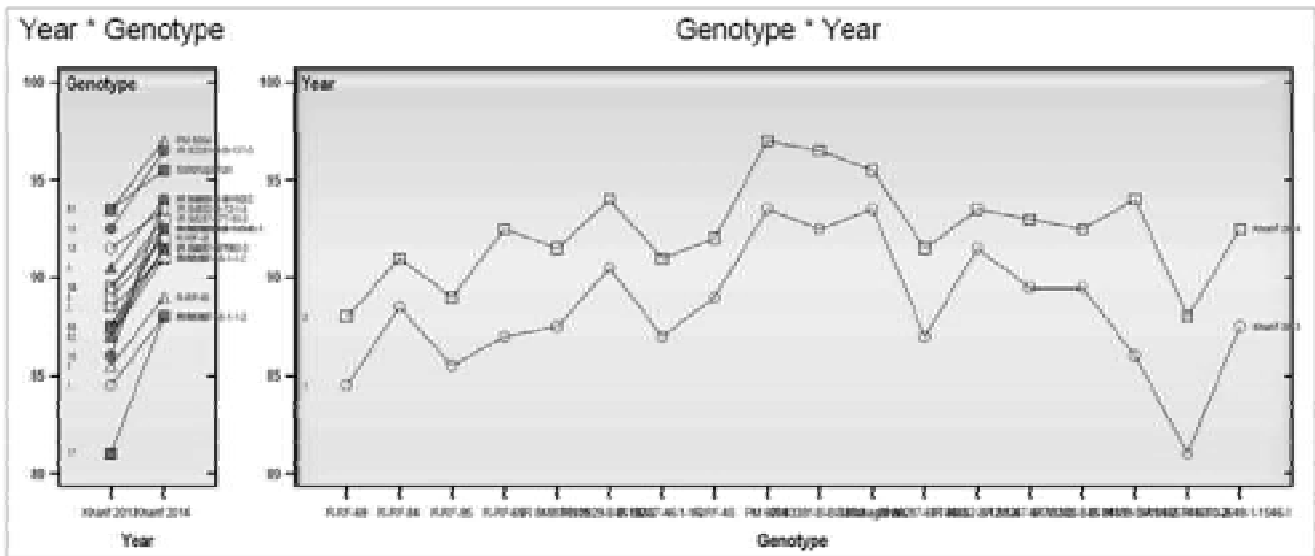


Fig. 3. Multienvironmental plot for spikelet fertility

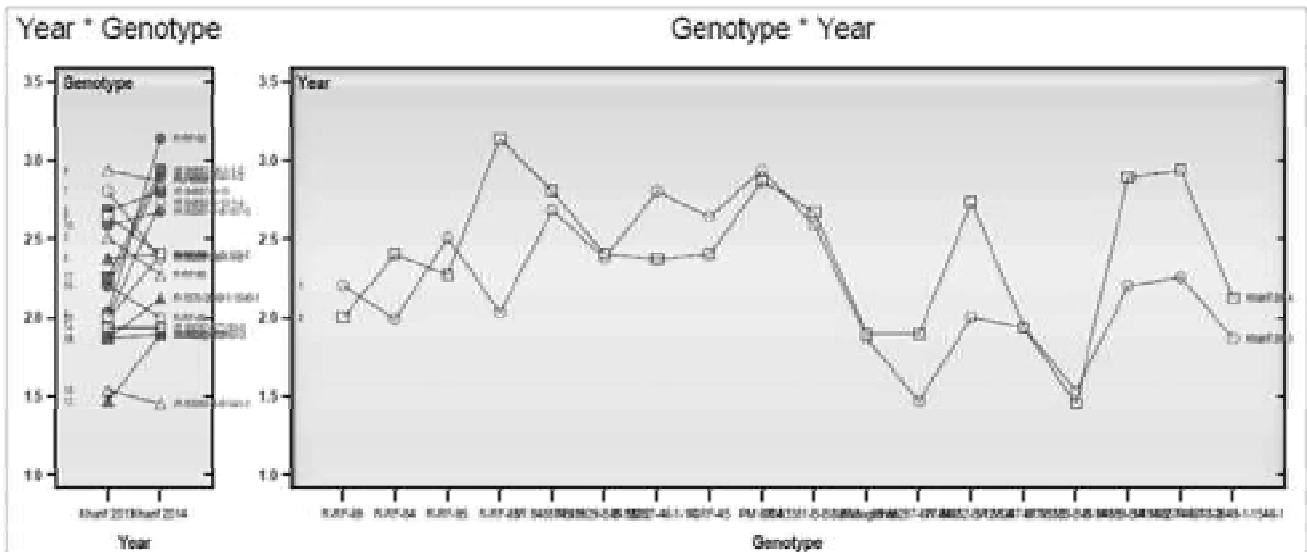


Fig. 4. Multienvironmental plot for grain yield

for R-RF-45, R-RF-95 and R-RF-65R which showed considerable alteration in grain yield. However, biological yield varied significantly with environment but followed similar genotypic pattern. Thus, despite of reduction on crop biomass, physiological buffering capacity of maintained the grain yield. The observation here are in consistent with those expressed by Samote *et al.*, (2005); Gouch (2006) and Nassir (2014) using

different crop data. The significant contribution of prevailing micro and macro environments in variable genotypic expression across locations and seasons are serious challenge for both crop management and crop breeding. Although, differential amount of variation is laid by environment but are large enough to emphasize the delineation of environment for stable response.

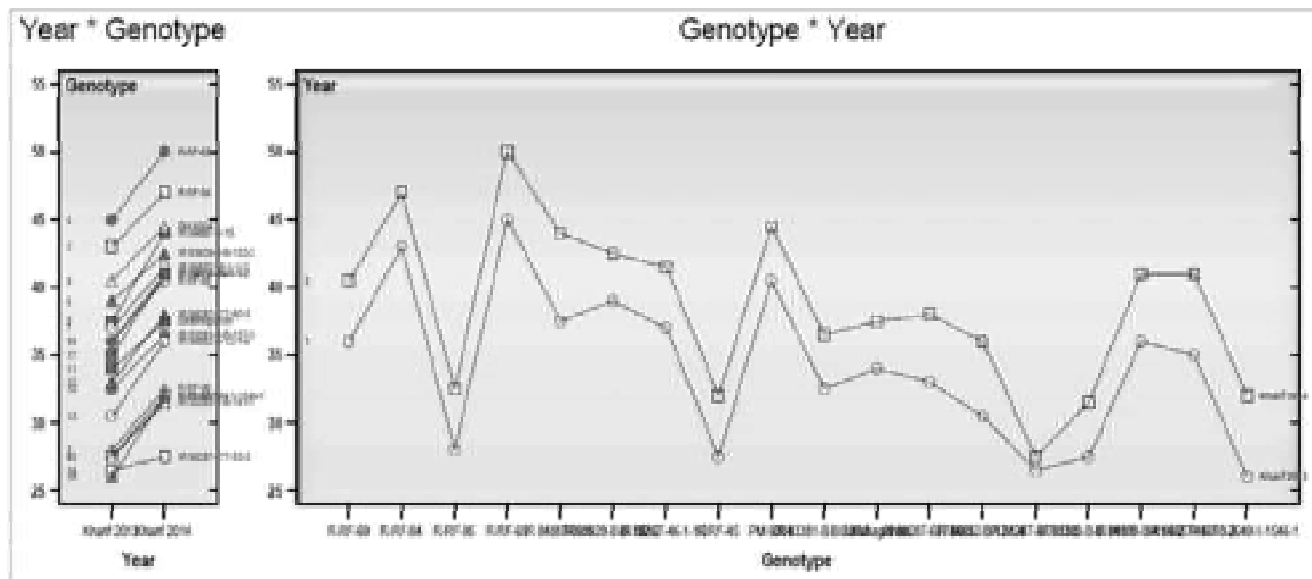


Fig. 5. Multienvironmental plot for harvest index

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