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Stability analysis and GxE interactions in lowland rice promising genotypes

JP Bhatt*, JI Nanavati and AM Mehta

Main Rice Research Station, Anand Agricultural University, Nawagam, Gujarat, India
****Email: jpbhatt1987@gmail.com***

ABSTRACT

Genotype x environment interactions and stability parameter analysis are of major importance to sort out high yielding and stable promising genotypes. 48 diverse rice genotypes were evaluated in four different environments created by presence and absence of inoculation pressure for rice blast disease during wet season 2012 and wet season 2013 seasons to identifystability for grain yield per plant in rice.G x E (linear) and G x E (non-linear) were found significant for grain yield per plant. The preponderance of linear component noticed would help in predicting the performance of the genotypes across the environments with great precision.Three genotypes viz., GR-7 x NWGR-2002 (2-3-1-1-1), GR-7 x NWGR-3003 (3-1-2-1-1) and GR-7 x NWGR-3003 (4-1-1-1-1) were identified as most promising as it yielded higher than population mean performance coupled with unit regression coefficient and non-significant deviation from regression and therefore they should be recommended for wider cultivation after necessary testing. The genotypes, GR-7 x Ratna(1-1-1-1-1), GR-7 x IET-17429 (1-1-1-1-1-1), Gurjari x IR-72 (2-1-1-1-1) and Pankhali-203 due to mean value higher than overall mean, bi>1, and non-significant deviation from regression, hence considered as "genotypes with below average stability". Apart from these, Gurjari x IR-72 (4-1-2-3-1) was found with high mean performance than population mean, regression coefficient less than unity and non-significant deviation from regression was regarded as genotype with "above average stability and better adaptability to unfavourable environments".

Key words: *Lowland rice, stability, G x E interaction,genotypes, regression*

Rice is considered as one of the most important plants from *Poaceae*. Today, rice has special position as a source of providing over 75% of Asian population and more than three billion of world populations meal which represents 50 to 80% of their daily calorie intake (Amirjani, 2011). This population will increase to over 4.6 billion by 2050 (Honarnejad *et al.*, 2000) which demands more than 50% of rice needs to be produced what is produced at present to cope with the growing population (Srividya *et al.*, 2010). The yield stability is one of the most desirable properties of genotype to be released as a variety for cultivation. Stability is a complex product of genetic yield potential to stress conditions. Research on yield stability, or genotype x environment interaction is necessary to evaluate the consistency of rice grain yield and, for plant breeders, to develop cultivars that respond optimally and consistently across years and diverse agro-ecological conditions. The present study is an attempt to assess the possibilities of commercial exploitation of stable and high yielding genotypes of rice, through estimating genotype x environment interactions and stability parameter analysis.

The research material included 48 diverse rice genotypes comprising of rice blast resistant (IR-64), immune (GR-7), moderate resistant, moderate susceptible and susceptible genotypes and the elite lines derived by their hybridization for their differential response to blast of rice. The name of the genotypes is listed in Table 1. The experiment was conducted at the research farm of Main Rice Research Station (MRRS), Anand Agricultural University, Nawagam (Gujarat), India.The experimental material comprised of 48 genotypes was grown in randomized block design with three replications in four different environments created by presence and absence of inoculation pressure for rice blast disease *viz.*, protected field evaluation against blast in wet season 2012 (E_1), unprotected field and artificial screening for blast in wet season 2012 (E_2), protected field evaluation against blast in wet season 2013 (E_3) and unprotected field and artificial screening for blast in wet season 2013 (E_4). Each plot consisted of ten plants in a row keeping 20 and 15 cm inter and intra row spacing, respectively. The recommended package of practices was adopted to raise a good crop.

The observations were recorded for five randomly selected competitive plants from each genotype for all the characters except for days to 50% flowering which was recorded on plot basis. The most widely used approach is the regression technique, in which partitioning of G x E interactions component of variability into its linear and non-linear component for assessing the stability of genotypes over a range of environments. This is known as joint regression analysis. In the present study, the same approach as outlined by Eberhart and Russell (1966) has been used.

The results pertaining to analysis of variance for phenotypic stability for different characters are presented in Table 2. The mean sum of squares due to genotypes was highly significant for all the characters studied which indicated the presence of substantial amount of variation in the material studied. Highly significant variances due to environment (linear) indicated the existence of larger macro-environmental differences at the four environments for all the characters and also further suggested that these characters were influenced significantly by environments. The variances due to G x E were further partitioned in to two components *viz.*, (i) G x E (linear) and (ii) G x E (non-linear) i.e. pooled deviation.

The values of mean square due to environments + (genotypes x environments) were found to be significant for all the characters except number of effective tillers plant^{-1}, which suggested the distinct nature of environments and genotype x environment interactions in phenotypic expression. Highly significant estimates of mean square due to environments (linear) for all the characters except number of effective tillers plant^{-1}indicated that environments differed considerably

Table 1. Name of the genotypes and pedigree

Code	Cross combinations/ Genotypes	Line No./ Pedigree
G1	GR-7/IR-22	1-2-1-2-2
G2	GR-7/IR 59656-5K-2	2-2-1-1-3
G3	GR-7/IR 71730-51-2	3-2-1-1-1
G4	GR-7/9-YOU-138	2-1-1-1
G5	GR-7/CRMAS-2231-29	6-1-2-2
G6	GR-7/IR-64	5-1-1
G7	GR-7/CRMAS-2231-36	8-4-1-1-1
G8	GR-7/CRMAS-2231-36	1-1-2-1-1
G9	GR-7/NWGR-2002	2-3-1-1-1
G10	GR-7/NWGR-2002	3-1-1-1-1
G11	GR-7/NWGR-2002	2-3-1-2-1
G12	GR-7/NWGR-2002	4-2-1-2-1
G13	GR-7/Ratna	1-1-1-1-1
G14	GR-7/Ratna	3-1-2-1
G15	GR-7/NWGR-3003	3-1-2-1-1
G16	GR-7/NWGR-3003	4-1-1-1-1
G17	GR-7/IRBB-7	5-3-1-1-2
G18	GR-7/DDR-8	1-5-1-1
G19	GR-7/MahiSugandha	3-8-1-1-1
G20	GR-7/IET-17429	1-1-1-1-1-1
G21	GR-7/IET-17429	3-3-1-1-1
G22	GR-7/IET-17429	4-3-1-1-2
G23	GR-7/IET-17429	6-4-1-1-1
G24	IR-28/IET-16804	1-4-1-1-1-1,2
G25	IR-28/IET-16804	4-1-1-1-1,2
G26	IR-28/IET-16804	5-3-2-1
G27	IR-28/IET-17905	1-2-1-3-1
G28	IR-28/IET-16810	1-1-1-1-1,2
G29	IR-28/Gurjari	1-1-1
G30	IR-64/Gurjari	2-2-1
G31	IR-72/IR-38	1-1-1-2-1
G32	IR-72/ Pusa Sugandha-2 (IET-16310)	1-1-3-2-1
G33	Gurjari/IR-38	4-1-2-1-2,3
G34	Gurjari/IR-38	5-3-1-2-1
G35	Gurjari/IR-38	6-5-1-1-1
G36	Gurjari/IR-72	2-2-1-1-1
G37	Gurjari/IR-72	2-1-1-1-1
G38	Gurjari/IR-72	4-1-2-3-1
G39	GR-11/IR-64	3-1-1-1, 2
G40	GR-11/IR-64	4-1-3-1-2
G41	GAUR-100/IR-64	3-1-1-1
G42	Jaya/IR-64	52-2-3-2
G43	GR-7	GR-3/Basmati-370
G44	IR-64	IR5657-33-2-1/ IR2061-465-1-5-5
G45	Gurjari	Asha/Kranti
G46	GR-11	Z-31/IR-8-246
G47	GAR-13	GR-11/ IET-14726-22-1-8-1-1-1
G48	Pankhali-203	Selection from local land race Pankhali

Table 2. Analysis of variance (mean squares) for stability for grain yield and yield components in rice (Eberhart and Russell, 1966)

Source of variation	df	Days to 50% flowering	Plant height	Panicle length	Number of effective tillers plant^{-1}	Number of filled grains panicle^{-1}	Grain plant^{-1}
Genotype (G)	47	99.67**	436.95**	11.53**	4.68**	3495.93**	39.55**
Environment (E)	3	139.59**	1531.45**	63.43**	0.02	1357.93**	65.79**
G x E	141	8.38**	68.75**	2.29*	0.04	86.48*	7.27**
E + (G x E)	144	11.11**	99.22**	3.56**	0.04	112.97**	8.49**
Environments (Linear)	1	418.36**	4596.62**	190.23**	0.07	4073.75**	197.87**
G x E (Linear)	47	4.46*	96.06**	2.15*	0.04	138.07**	9.97*
Pooled deviation	96	10.13**	53.92**	2.30**	0.04	59.42**	5.80**
Pooled error	384	3.49	11.46	1.18	1.61	69.07	4.95
Pooled error for testing the pooled deviation	384	1.16	3.82	0.61	0.05	23.02	1.65

*, ** Significant at 5 and 1 per cent levels, respectively

among different years and locations for these traits. It revealed the genetic control of response of genotypes towards test years and locations and thus satisfying the requirement of stability analysis. The higher magnitude of mean squares for environment (linear) compared to genotypes x environments (linear) indicated that linear response of environment account for the major part of total variation for all the characters studied and which may be responsible for high adaptation in relation to grain yield and other traits. These results are akin with findings of Kumar *et al.* (2005) and Panwar *et al.* (2008).

Pooled deviation variances, the non-linear components of G x E interactions were significant for all the characters except number of effective tillers plant^{-1}. In this study, observed significant non-linear effects were of lower magnitude than linear component, which indicated that the characters registered significant G x E interaction had inconsistent/unpredictable performance over environments. The linear component of G x E interaction was found predominant for most of the characters, which indicated that a large portion of G x E interaction was accounted by linear regression, although non-linear regression component (pooled deviation) was also significant. The preponderance of linear component noticed would help in predicting the performance of the genotypes across the environments with great precision.These results are in conformity with those observed by Senapati *et al.* (2005) and Panwar *et al.* (2008).

Stability parameters for grain yield plant^{-1} are presented in Table 3. The data revealed that twenty five genotypes *viz.*, G3, G4, G5, G7, G9, G11, G13, G15, etc. exhibited high mean for grain yield plant^{-1}. The genotype G23 (24.75 g) registered the highest grain yield plant^{-1}. The average grain yield plant^{-1} over population and environments was 19.29 g. Hence genotypes with higher grain yield than 19.30 g were considered as better performing genotypes for grain yield.

The most important character grain yield plant^{-1} showed non-significant regression coefficient valuesfor35 genotypes when tested against hypothesis bi = 1, which suggested that these genotypes should be better suited for varying environmental situations may likely possess average stability. While 12 genotypes were found significant regression coefficient values when tested against hypothesis bi = 0 which showed that it can average stable in varying environmental situations.

The deviation from regression for grain yield plant^{-1} was found to be significant for 31 genotypes out of 48 genotypes, showing that their performance could not be predictable over years and locations. Even through these genotypes did not show stable performance over environment, out of 31, 18 genotypes gave higher yield on pooled basis as compared to population mean. While, remaining 17 genotypes had the non-significant deviation from regression indicating their predictable nature for grain yield plant^{-1} performance and adaptability to varying environmental situations.

Table 3. Stability parameters for grain yield plant^{-1} in rice

Genotypes	Mean	b_i	S^2d_i
G1	17.85	1.59*	0.29
G2	14.91	0.83	5.65**
G3	20.74	4.59**++	3.84*
G4	21.09	2.11	6.04**
G5	21.51	2.89*	6.45**
G6	14.18	-0.66	7.45**
G7	24.67	-1.35	7.88**
G8	16.53	1.7	5.65**
G9	24.19	0.5	3.04
G10	15.61	2.74**++	0.43
G11	23.38	-1.49+	6.1**
G12	18.75	2.85	12.51**
G13	20.57	4.14**++	2.1
G14	17.82	-0.64	7.27**
G15	22.75	0.83	1.83
G16	21.04	1.18*	0.88
G17	19.57	1.32	5.19*
G18	21.50	1.14	10.87**
G19	15.00	1.74**	1.21
G20	22.72	2.84**++	0.14
G21	18.34	0.81	2.65
G22	20.03	-1.68	11.74**
G23	24.75	-0.83	5.77**
G24	20.93	0.12	7.01**
G25	15.95	0.92	4.43*
G26	18.35	-0.71+	2.48
G27	16.79	2.07	5.01*
G28	10.29	0.37*++	0.1
G29	15.96	1.43	2.51
G30	21.06	0.99	13.99**
G31	18.90	2.55	7.03**
G32	22.85	-1.33	6.7**
G33	20.01	0.29	9.91**
G34	18.17	2.58	9.23**
G35	18.60	-1.01	7.2**
G36	16.97	3.28**+	3.83*
G37	21.94	2.76**++	1.29
G38	21.64	-1.02+	3.06
G39	21.09	1.05	12.36**
G40	23.52	-0.94	36.93**
G41	18.98	0.71	3.46*
G42	21.28	0.8	9.45**
G43	19.32	-0.66	4.78*
G44	14.91	2.15**	2.48
G45	20.93	0.28	4.71*
G46	14.97	2.21**++	0.34
G47	15.34	-0.43	3.31*
G48	19.89	2.37**++	0.04
Population mean	19.29	-	-
S. Em. ±	1.28	-	-

* = significant at 5% and 1% level for (b_i=0) and (S^2d_i=0)
\+ = significant at 5% and 1% level for (b_i=1)

Summarizing the stability parameters, it was seen that among all the genotypes which showed non-significant deviation from regression 3 genotypes *viz.*,G9, G15 and G16 were identified as most promising as it yielded higher than population mean performance coupled with unit regression coefficient and non-significant deviation from regression and therefore they should be recommended for wider cultivation, because the yield response of these varieties are almost parallel to the change of the mean yield in environments.

The genotype G13, G20, G37 and G48 due to mean value higher than overall mean, bi>1, and non-significant deviation from regression, hence considered as “variety with below average stability” which indicating that the genotypes were likely to be better adapted to favourable environments and yield reduction is likely in the unfavourable environments. The high yield potential of all these genotypes could be utilized through its cultivation under favourable environment (s) created through better management practices.

Apart from these, G38 was found with high mean performance than population mean, regression coefficient less than unity and non-significant deviation from regression are regarded as genotypes with “above average stability and better adaptability to unfavourable environments” where higher mean yield is sacrificed with changes in the environment or in other words where yield is not much affected by the changes in the mean yields over the environments. The eighteen genotypes *viz.*, G3, G4, G5, G7, G11, G17, G18, G22, G23, G24, etc. had high mean performance than population mean but had significant deviation from regression hence it’s performance could not be predicted and consider as unstable genotypes for this trait.

REFEERENCES

Amirjani MR 2011. Effect of salinity stress on growth, sugar content, pigments and enzyme activity of rice.*Int. J. Bot.*, 7(1): 73-81.

Eberhart SA and Russell WL 1966. Stability parameters for comparing varieties.*Crop Sci*., 6: 36-40.

Honarnejad R, Dorosti H, Mohammad Salehi MS and Tarang A 1998. Estimation of stability and adaptability of rice cultivars in different environmental conditions.*Seed and Plant*, 13 (4):32-43.

Kumar M, Singh NK and Kumar A 2005. Stability of yield in relation to components traits in rice under rainfed low land condition.*Madras Agric. J*., 92 (4-6): 193-199.

Panwar LL, Joshi VN and Ali M 2008. Genotype x environment interaction in scented rice.*Oryza*, 45 (1): 103-109.

Senapati BK, Roy SK, Sarkar G and Majumder ND 2005. Adaptability of some high yielding photosensitive rice genotypes to rainfed saline soils of Sunderban.*Oryza*, 42 (3): 220-221.

Srividya ALR, Vemireddy AS, Hariprasad M, Jayaprada and Sridhar S 2010. Identification and mapping of landrace derived QTL associated with yield and its components in rice under different nitrogen levels and environments. *Int. J. Plant Breed. Genet.*,4: 210-227.