Assessment of Yield Stability of Rice Genotypes through Stability Analysis

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Abstract

Twenty promising short duration advance rice cultures along with three check varieties *viz.,* ADT 43, ADT (R) 45 and ASD 16 were evaluated for yield stability in three seasons *viz.,* navarai, 2012 (Dec-March), sornavari, 2012 (May-August) and navarai, 2013 (Dec-March) at Rice Research Station, Tirur. The stability analysis revealed significant differences among the genotypes and environments indicating the presence of wider variability among the genotypes and environment. Highly significant mean squares due to genotype × environment (G×E) interaction revealed that the genotypes interacted considerably with environmental conditions. Both linear (G×E interaction) and non-linear components (pooled deviation) of Environment + (G x Env.) interaction were found to be significant for grain yield revealed the importance of both regression co-efficient (*bi*) and deviation from regression (*S²d*) in determining the stability of grain yield. Based on stability analysis, the genotypes TM 10085, TM 10363 and TM 11118 with high mean grain yield are identified as stable genotypes because of their *bi* value around unity and showed non-significant deviation from regression. Hence, these cultures can be recommended for all the environments. The cultures TM 10225 and TM 10351 with high mean grain yield, *bi* value more than unity and non-significant deviation from regression are suitable for only favourable environments. The genotypes TM 10421 and TM 11310 with high mean and negative *bi* value are identified for poor environments.

Key words: Stability, G x E interaction, regression, grain yield

Introduction

Rice is grown over a wide range of agro climatic conditions and hence there is a need to develop genotypes with high yield potential and stable performance over a varied range of environments. The yield stability is one of the most desirable properties of a genotype to be released as a variety for cultivation. The adaptation of a cultivar over different environments is usually tested by the level of its interaction with different environments under which it is cultivated. Genotype x environment (GxE) interaction and yield stability analysis has continued to be important in measuring varietal stability and adaptability across seasons. G x E interactions greatly affect the phenotype of a variety, so the stability analysis is required to characterize the performance of varieties in different environments and to help plant breeders in selecting varieties (Dewi *et al.*, 2014). Grain yield depends on genotype, environment and management practices and their interaction with each other. A genotype is considered to be more adaptive or stable if it has high mean grain yield but a low degree of variation in yielding capacity when grown over varied environments. Hence, evaluation of genotypes for stability of yield under different seasons or locations has become an essential part in any breeding programme. The present investigation was aimed at identifying high yielding and high stable genotypes for irrigated ecosystem of Tamil Nadu.

Materials and Methods

Twenty promising short duration advance rice cultures along with three check varieties *viz.,* ADT 43, ADT (R) 45 and ASD 16 were evaluated for yield stability in three seasons *viz.,* navarai, 2012 (Dec-March), sornavari, 2012 (May-August) and navarai, 2013 (Dec-March) at Rice Research Station, Tirur. The experiment was conducted in Randomized Block Design (RBD) with two replications in a plot size of 8 m². Recommended management practices were followed. Observation was recorded on grain yield for each plot and calculated as tonnes/hectare. The mean yield data averaged over replications for genotypes from three environments for grain yield were subjected to stability analysis (Eberhart and Russell, 1966) using TNAUSTAT package. The parameters *viz.*, i. population mean; ii. regression coefficient (*bi*); iii. mean square deviation from regression (*S²di*) were estimated from the analysis.

Results and Discussion

The analysis of variance for grain yield revealed significant differences among the genotypes and environments indicating the presence of wider variability among the genotypes and environment (Table 1). Highly significant mean squares due to genotype × environment (G×E) interaction revealed that the genotypes interacted considerably with environmental conditions. This is in accordance with previous reports on rice by Panwar *et al*. (2008), Uma devi *et al*. (2011) and Sellammal and Robin (2013).

The variance due to Environment + (G x Env.) was partitioned into linear (i.e. variance due to G x E) and nonlinear components (i.e. variance due to pooled deviation). Both linear and non-linear components of Environment + (G x Env.) interaction were found to be significant for grain yield as indicated by high significant mean squares due to G×E (linear) interaction and pooled deviation revealed their importance in the expression of traits. These high significant differences are very important for determining G x E interaction. Relatively higher value of the linear component as compared to non-linear component suggested the possibility of prediction of performance for grain yield over the environments. The results confirm the earlier reports of Bose *et al*. (2012).

Therefore, linear (*bi*) and nonlinear (*S²di*) component of G x E interactions were considered while predicting the phenotypic stability of a genotype (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966). They have emphasized the use of deviation from regression as a measure of stability, whereas the linear regression could be treated as a measure of varietal response to environments. Accordingly, the mean and the deviation from regression of each genotype were considered for stability and linear regression was used for testing the varietal response.

The stability parameters such as mean, regression coefficient (*bi*) and mean square deviation from regression (*S²di*) for advance cultures along with the check varieties are presented in Table 2. Eberhart and Russell (1966) defined a stable genotype is the one which showed high mean yield, *bi* around unity and deviation from regression near to zero. Accordingly, i) Genotypes with high mean, *bi* around unity and deviation from regression near to zero are considered as stable genotypes. ii) Genotypes with high mean, bi >1 with non significant deviation from regression are considered as average genotypes. iii) Genotypes with high mean, *bi*<1 and non significant deviation from regression are identified as genotypes with low stability. iv) Genotypes with high mean and negative *bi* are identified for poor environments.

In the present study, the highest yielding genotype TM 10085 (6.62 t/ha), TM 10363 (6.22 t/ha) and TM 11118 (6.30 t/ha) are identified as stable genotypes because they exhibited *bi* value around unity and non-significant deviation from regression. Therefore, these cultures can be recommended for cultivation in all the environments.

The cultures TM 10225 and TM 10351 had high mean grain yield than the overall mean, regression value more than one (bi>1) and showed non-significant deviation from regression. Hence, these cultures are found suitable for favourable environments and there will be yield reduction in the unfavorable environments.

The second highest yielding culture TM 10421 with grain yield of 6.49 t/ha and another high yielding culture TM 11310 (6.17 t/ha) are identified for poor environments, because of its negative bi value. These cultures remain steady under poor environments but cannot exploit the positive improvement in the environment. Though the entry TM 10366 had *bi* value around 1.0, it was rejected because of its low mean performance.

The advance cultures identified for various environments are presented in Table 3. The genotypes differed considerably with respect to their stability for yield. Similar results were obtained in rice by Dushyantha kumar *et al*. (2007) and Bose *et al*. (2012).

Conclusion

The present study provided an evaluation of genotypic and environmental performance of 23 genotypes over a period of three seasons. Both linear and non-linear components contribute to the G x E interaction for grain yield indicating the importance of both regression co-efficient (*bi*) and deviation from regression (*S2di*) in determining the stability of grain yield. Based on the stability parameters, TM 10085, TM 10363 and TM 11118 are identified as suitable for all environments and TM 10225 and TM 10351 are found suitable for favourable environments. The culture TM 10085 (ADT 43 x IR 36) selected based on stability parameters was evaluated in Multi Location Trial (MLT) during 2013 and 2014 in different Rice Research Stations of Tamil Nadu. Based on the stable yield performance in MLT, it was promoted to Adaptive Research Trial (ART) and is being evaluated in all districts of Tamil Nadu. Based on the yield performance in station trials, MLT and ART, it will be nominated for variety release.

Table 1: Analysis of variance for stability of grain yield over environments

Source of variation	Df	Mean Sum of Squares
Genotypes (G)	22	0.7681**
Environments (Env.)	2	2.1707**
Env. + (G x Env.)	46	0.2031**
G x Env.	44	0.1136**
Environments (Lin.)	1	4.3414**
G x Env. (Lin.)	22	0.1674**
Pooled deviation (non-linear)	23	0.0573**
Pooled error	66	0.0506

**Significant against pooled error at 1%

Table 2: Mean performance and stability parameters for grain yield

S. No.	Designation	Cross combination	Mean grain yield (t/ha)	Bi	S^2di
1	TM 10085	ADT 43 x IR 36	6.62	0.914	0.169
2	TM 10205	ADT 39 x Karuna	5.26	0.047	0.999
3	TM 10223	ADT 43 x ADT 44	5.27	1.182	0.235
4	TM 10225	ADT 43 x ADT 44	6.37	1.239	0.193
5	TM 10231	TKM 9 x RTV 167	5.17	2.452	0.370
6	TM 10363	IET 19577 x Rupali	6.22	0.959	0.160
7	TM 10366	IET 19577 x GMS 48	5.60	1.118	0.312
8	TM 10332	BPT 5204 x GMS 48	5.32	0.294	0.082
9	TM 10351	IET 19577 x Jalaharaponni	6.03	1.210	0.570
10	TM 10380	IET 19577 x BPT 5204	5.75	2.027	0.552
11	TM 10382	IET 19577 x BPT 5204	5.46	2.185	0.019
12	TM 10411	BPT 5204 x CB 01001	5.46	1.469	0.118
13	TM 10421	ASD 19 x BPT 5204	6.49	-0.016	0.427
14	TM 11118	ADT 37 x ADT 43	6.30	1.002	0.212
15	TM 11216	ADT 39 x ADT (R) 45	5.62	2.160	0.043
16	TM 11253	ADT (R) 47 x BL 21	5.32	2.118	0.853
17	TM 11256	ADT 39 x TJ 1	4.98	2.450	0.683
18	TM 11260	ADT 39 x IET 20587	6.00	0.879	0.119
19	TM 11310	CB 04110 x TKM 6	6.17	-0.167	0.164
20	TM 11334	CB 04110 x RTV 167	4.98	0.350	0.097
21	ADT 43	IR 50 x White Ponni	5.30	1.362	0.767
22	ADT (R) 45	IR 50 x ADT 37	5.33	1.465	0.355
23	ASD 16	ADT 31 x CO 39	5.16	0.897	0.145
	Grand mean		**5659**		

Table 3: Genotypes recommended for various environments

Adaptive environments	Suitable genotypes
All environments	TM 10085, TM 10363 and TM 11118
Better environments	TM 10225 and TM 10351
Poor environments	TM 10421 and TM 11310

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