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Genotype x Environment interaction effects on yield of rice hybrids in India

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Abstract

Performance of improved, high yielding varieties of rice over different agro ecological regions of India has been well documented by several workers. But the performance evaluation of rice hybrids which are recently evolved in India is yet to be assessed through multilocation trials. The objective of the present investigation was to analyse the pattern of Genotype x Environment Interaction for grain yield by Additive Main Effects and Multiplicative Interaction (AMMI) model using the data generated from a National Hybrid Rice Trial (NHRT) conducted over eleven locations in India involving 16 hybrids and two inbred check varieties. Results indicated a significant Genotype x Environment Interaction (GEI) that influenced the relative ranking of the hybrids across the locations. It was evident from AMMI analysis that genotype, environment and the first principal component of interaction effect accounted for 86.96% of treatment sum of squares and that the first five principal components of the interaction effect were found to be significant. The usefulness of the Procedure in selecting genotypes for general or specific adaptation is also brought out.

Key words : Rice hybrids, AMMI, biplot, GE interaction

Introduction

The Genotype x Environment Interaction structure is an important aspect of both plant breeding programmes and the introduction of new crop cultivars [1]. ANOVA which is an additive model is effective in partitioning the total sum of squares into i) the genotype main effect, ii) the environment main effect and iii) the GEI, but it does not provide insight into the GEI structure. To study the underlying interaction component, more advanced techniques such as principal component analysis are required. The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure. The AMMI model separates the additive variance from the multiplicative variance and then applies principal component analysis (PCA) to the interaction portion to extract a new set of coordinate axes which explain in more detail the interaction pattern. The estimation is accomplished using. the least-squares principle [2]. The effectiveness of AMMI procedure has been clearly demonstrated by various authors and more specifically by Zobel *et al.* [3] in soybean and Crossa *et al.* [4] in maize using multilocation trial data.

The main objectives of the present investigation are i) to determine the GEI effects on grain yield of rice hybrids for diverse agro-ecological regions in India, ii) to identify areas where hybrid rice is well adapted to give economic returns and iii) to select hybrids that are broadly adapted across the rice growing areas in India.

Materials and Methods

The data used in the present study pertain to National Hybrid Rice Trial conducted during Kharif season, 1993. The genotypes included in the trial were sixteen hybrids and two inbred check varieties, viz., Jaya and IR 36 which were evaluated at eleven locations. The locations were Maruteru, Mandya, Coimbatore in southern region, Karjat in western coastal region, Cuttack, Chinsurah, Faizabad in eastern region and Delhi, Karnal, Kapurthala and Pantnagar in north western region. The experiment was conducted by using RBD with three replications. Among the 16 hybrids included in the study, 9 were based on the CMS line IR 58025A, 3 were derived by using the CMS line IR 62829A and two were based on PMS 3A. The other two hybrids were from the private sector and their parentage was not known. The plot size was 10 m^2 with a plant density of 44 hills/m^2. The grain yield per m^2 was used for statistical analysis in this study.

The AMMI model is:

$$Y_{ij} = \mu + g_i + e_j + \Sigma\, hk\, \alpha_{ik}\, \tau_{jk} + R_{ij}$$

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where, Y_{ij} is the yield of ith genotype in the jth environment, g_i is the mean of the ith genotype as a deviation from the grand mean μ; e_j is the mean of the jth environment minus the grand mean (μ), h_k is the eigen value of the PCA axis k, α_{ik} and τ_{jk} are principal component scores for PCA axis k of the i^{th} genotype and the jth environment respectively and R_{ij} is the residual. The GE interaction sum of squares was subdivided into PCA axes, where axis k is regarded as having t + s-1-2k degrees of freedom and t and s are the number of genotypes and environments respectively. The data were analysed by using GENSTAT statistical package at the International Crops Research Institute for the Semi Arid Tropics (ICRISAT), Hyderabad, India.

Results and discussion

The AMMI analysis of variance is presented in Table 1. It clearly indicated that genotypes, environments and GEI components were significant and accounted for 7.12, 75.32 and 17.56% of the total treatment sum of squares. The proportion of variance due to GEI which is otherwise considered as residual in ANOVA was the second largest (17.56%). Thus, ANOVA accounted for only 82.44% of the treatment combinations SS attributable to genotypes and environment effects.

The GEI which was highly significant was further partitioned into five PCA axes (IPCA) with contribution of 25.74, 24.05, 19.86, 11.52 and 8.06 per cent to the total GEI variance. All the five IPCA axes representing the interaction pattern were significant and jointly accounted for 89.23% of interaction component with 64.71% of the df for GEI. The residual SS which accounted for only 10.77% of the interaction SS with 35.29% of df for GEI was non significant.

Table 1. AMMI analysis of variance for grain yield of 16 rice hybrids and two check varieties tested at 11 locations in India

Source	d. f.	Sum of squares	Mean squares	Percentage SS
Treatment combinations	197	2156.07	10.94*	100.00
Genotype	17	153.56	9.03*	7.12
Environment	10	1624.04	162.40*	75.32
GE interaction	170	378.47	2.23*	17.56
PCA 1	26	97.40	3.75*	$25.74
PCA 2	24	91.02	3.79*	$24.05
PCA 3	22	75.18	3.42*	$19.86
PCA 4	20	43.61	2.18*	$11.52
PCA 5	18	30.49	1.69*	$ 8.06
Residual	60	40.75	0.68	$10.77
Error	396	141.94	0.36	

* = Significant at 5% level.
$ = As percent of GE interaction SS.

Table 2 presents the mean yield data for sixteen hybrids and two inbred check varieties evaluated in this study across eleven locations. The means of the genotypes and the environments alongwith the first principal component scores corresponding the genotypes and the environments are also presented. The yields ranged from 1.23 t/ha to 10.67 t/ha.

In additive ANOVA model, the yield estimate for any genotype in any environment can be computed by adding the genotype mean to the environment mean and subtracting the grand mean. The AMMI estimates are then worked out by adding the ANOVA model estimates to the estimated GEI effect. For example, the ANOVA estimate for the hybrid IR 58025A/IR 46 in Maruteru is computed as 5.36 + 3.07 - 5.14 = 3.29 (Table 2), which deviated to the extent of nearly 26.54% from the actual yield. If only the first PCA axis corresponding to the hybrid IR 58025A/IR 46 in Maruteru is taken into account, the AMMI model estimate is then calculated by adding the product of 0.3005 and -0.7535 (which is part of the interaction effect) to this ANOVA estimate, which equals to 3.06. This AMMI estimate considering only the first set of PCA scores deviates to the extent of 17.69% from the actual yield. In the present study it was found that the fist five components were significant and each contributed a sizable proportion of the interaction effect and hence inclusion of only the first principal component was an over simplification of the matter. When the AMMI model includes more than one IPCA axes, assessment and presentation of genetic stability will become complicated compared to AMMI 1 model [5-8]. To overcome this, the second and higher order IPCA axes are normally pooled into residual [9] while presenting biplot assay. However, in the present study, the interaction effect was computed by including the first five PCA scores that correspond to the given genotype and environment which required limited extra calculations. For instance, the AMMI estimate for hybrid IR58025A/IR46 in Maruteru including all the five principal components was 2.58 which deviated to the extent of only 0.82% from the original value. Likewise, the ANOVA and AMMI estimates of all the genotype × location combinations were computed (detailed table not given for the sake of brevity). The results indicated that AMMI estimate differed from the actual value (in absolute terms) only to the extent of 5% or less in 64% cases; between 5-10% in 21% cases; between 10-15% in 12% cases and more than 15% in only 3% cases. This is in contrast with the deviation of the actual values from ANOVA estimates, where only 24% of the 198 cases registered less than or equal to 5% deviation; 23% of the cases registered 5-10% deviation; 17% registered 10-15% deviation and 36% of the cases registered

Table 2. Mean grain yield (t/ha) of 16 rice hybrids and 2 inbred checks grown in 11 locations and the first PCA scores for the GE Interaction effect as derived from AMMI analysis

Hybrid/variety	Maru-teru	Karjat	Pant-nagar	Cuttack	Coim-batore	Mandya	Delhi	Chin-surah	Faiza-bad	Karnal	Kapur-thala	Genotype Mean	First PCA
IR58025A/IR46	2.60	3.27	3.83	4.27	4.60	6.03	5.50	6.47	4.60	8.27	9.50	5.36	0.3005
IR58025A/IR21567	2.70	3.47	4.50	3.27	3.63	6.00	5.47	5.20	5.57	8.33	8.90	5.18	0.1187
IR58025A/IR34686	3.23	4.53	3.73	2.10	5.10	6.80	5.73	6.73	5.33	7.67	8.17	5.38	0.4094
IR58025A/IR40750	2.30	3.60	3.97	5.13	5.00	5.07	4.57	6.40	6.03	8.67	9.67	5.49	0.3356
IR58025A/IR54742	3.37	4.27	3.53	5.60	6.20	7.13	4.63	4.70	7.03	8.70	9.27	5.86	1.1102
IR58025A/29723	3.73	3.30	2.50	5.13	4.57	4.20	5.07	4.90	5.90	6.27	7.60	4.83	0.0503
IR58025A/Swarna	2.73	4.30	4.60	4.30	5.33	4.03	4.70	4.53	6.33	8.70	10.00	5.38	0.1040
IR58025A/Vajram	3.13	3.27	3.73	4.97	4.77	3.27	3.77	6.40	4.80	8.57	7.20	4.90	−0.2574
IR62829A/IR10198	2.63	3.40	3.93	4.67	3.93	4.00	5.83	4.60	5.07	7.13	6.77	4.72	−0.3527
IR58025A/IR35366	2.53	2.50	4.93	4.63	4.60	5.60	5.73	5.23	6.73	7.70	10.30	5.50	0.2182
IR62829A/IR35366	3.30	2.13	4.17	4.77	3.10	4.30	5.80	5.00	3.67	6.80	6.50	4.50	−0.5231
IR62829A/IR54742	2.27	2.33	3.30	3.73	4.47	5.67	4.30	5.00	5.57	7.63	8.60	4.81	0.6124
PMS3A/SL 51	3.30	2.73	3.63	1.90	3.23	1.23	5.30	5.10	4.23	7.83	7.90	4.22	−1.3839
PMS2A/IR31802	3.40	3.77	4.47	3.87	4.03	3.50	5.73	5.00	6.30	8.80	9.87	5.34	−0.6574
ORI 001	3.07	3.97	3.40	2.43	4.77	6.37	5.53	4.97	4.57	7.30	8.00	4.94	0.3895
ORI 161	4.07	3.87	4.30	5.47	6.70	6.27	5.30	6.90	7.20	9.33	8.80	6.20	0.5312
IR36	3.20	3.87	3.53	2.83	1.93	4.70	5.50	4.33	4.40	6.43	6.67	4.31	−0.4500
Jaya	3.73	3.07	5.09	3.37	4.86	4.47	6.63	5.00	6.20	8.13	10.67	5.56	−0.4554
Location Mean	3.07	3.42	3.95	4.02	4.49	4.92	5.26	5.36	5.53	7.90	8.58	5.14*	
First PCA	−0.7535	-0.1614	−0.7306	0.2066	0.7251	1.6990	−0.9701	−0.1800	0.3159	−0.1996	0.0486		

*Overall mean

deviations of 15% or more. The results clearly indicated that AMMI model provides a more reliable estimate of the performance of a given genotype at a given environment.

A comparison was also made between the observed means and the AMMI estimates with regard to the top ranked genotype within each location. While AMMI estimates concurred with the observed ranking in 8 out of 11 locations, the ANOVA estimate concurred with the observed ranking in 5 out of 11 locations, indicating that the GEI effect was more closely revealed by AMMI model as compared to the additive ANOVA model.

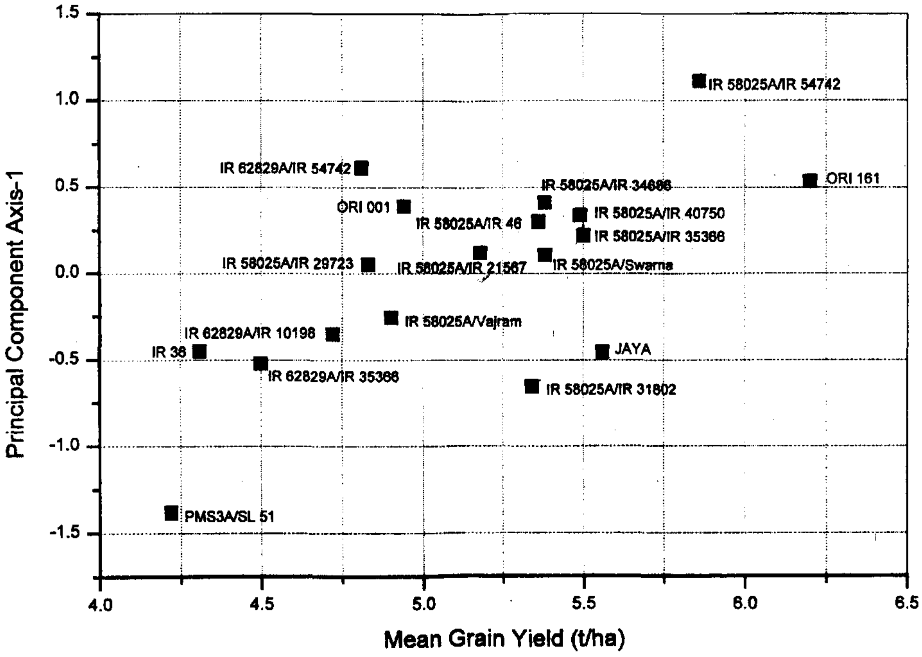

Fig. 1(a). Biplot of Genotypes and Interaction Component-1

Biplot assays of the AMMI results are presented in Figure 1(a) and 1(b). The main effects [genotype means in Fig. 1(a) and environment means in Fig. 1(b)] are shown along the abscissa (x-axis), and the ordinate (y-axis) represents the first PCA. Both main effects and interaction component are very clearly depicted in the figures. The usual interpretation of such a biplot assay is that if a genotype or an environment has a PCA score of nearly 'O', it has small interaction effects and when a genotype and an environment have the same sign on the PCA axis, their interaction is positive; if different, their interaction is negative. Figure 2 presents the spatial pattern of the first two PCA axes of the interaction effect corresponding to the genotypes. These biplots help in visual interpretation of the GE patterns and identify genotypes or locations that exhibit low, medium or high levels of interaction effects [3, 8, 10].

It is evident from Fig. 1(a) that the first principal component score was dominated by high interaction effect on yield of hybrids IR58025A/IR54742 and.PMS3A/ SL 51. Seven out of nine IR58025A based hybrids were on right-hand side of the grand mean. On the contrary, all the three IR62829A based hybrids had below average yields. Hybrids based on IR58025A differed from those based on IR62829A not only for mean yields, but also for their interaction effects. For instance, the hybrid IR58025A/ IR54742 had high yield and high PCA score, while the hybrid IR62829A/IR54742 was having below average yield with a moderate PCA score. Similarly, the hybrid IR58025A/IR35366 recorded above average yields and its PCA score was near to zero, while the hybrid IR62829A/IR35366 recorded below average yields and its interaction was negative. Hybrids IR58025A/IR40750 and IR58025A/IR35366 had mean yield levels as that of Jaya, the inbred check variety, but less influenced by the GEI effect as compared to Jaya indicating that hybrids are, in general mote widely adaptable. The variety Jaya had above average yield and was moderately influenced by GEI, whereas the other check variety IR36 with almost same interaction effect had below average yield. On the other hand, the hybrid ORI 161 which ranked first, was also influenced moderately by GEI effect. Hybrids IR58025A/ IR29723, IR58025A/Swarna and IR58025A/ IR21567 all based on CMS parent IR58025A were having zero score on the first PCA, indicating that these hybrids were less influenced by the interaction effect. However, the hybrid IR58025A/IR29723 was having below average yield. Hybrids grouped together in the biplot are supposed to have more or less similar pattern of interaction effect.

Figure 1b presents the biplot corresponding to location means and first PCA. It clearly indicated that locations Kamal and Kapurthala had excellent conditions for all hybrids and check cultivars, while at the same time, the PCA score for these two locations were near zero indicating that all genotypes performed well in the two locations. While the location Chinsurah and Karjat also had zero score on the PCA axis but their yield potential was only average and below average respectively. Both Mandya and Delhi had potential for

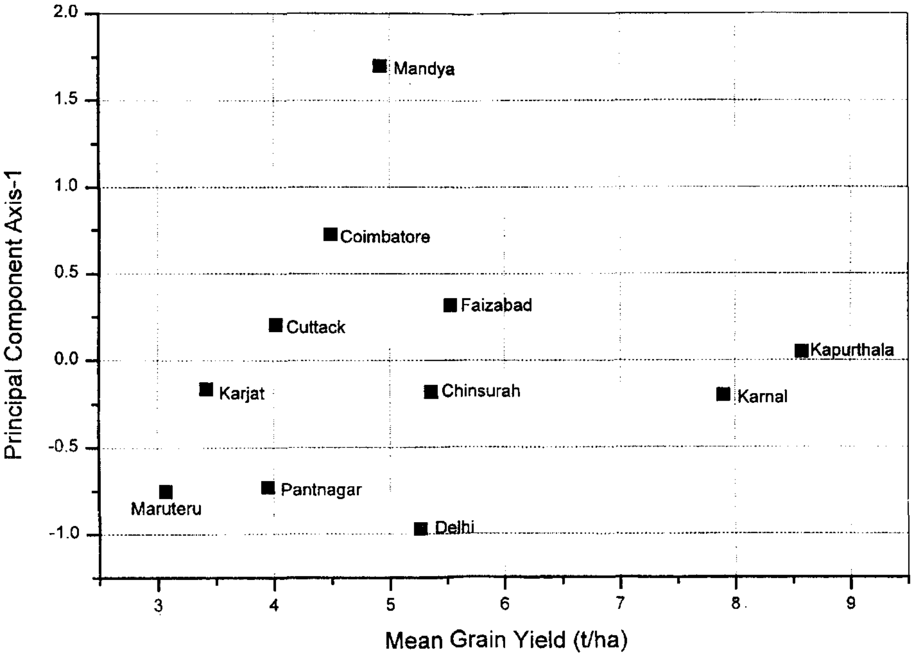

Fig. 1(b). Biplot of Locations and Interaction Component-1

average yield levels, but were exhibiting high interaction effects. The other locations had moderate interaction effect, but the pattern as revealed by this chart showed that six out of eleven locations had below average yield potential. Nevertheless, it should be noted that the first PCA axis which is considered for these two biplots contributed to the extent of only 26% of the interaction SS.

Biplot assay presented in Figure 1(a) thus identified two hybrids viz., IR58025A/Swama and IR58025A/IR21567 as having general adaptability at all locations. Hybrids ORI 161 followed by IR58025A/IR54742 were identified as specifically adapted to favourable locations. Favourable locations for these hybrids are those with high mean and high IPCA 1 score with the same sign as of genotype IPCA 1 score. Similar signs of IPCA 1 score for both genotype and the environment implies positive interaction and thus higher yield of the genotype at that particular location. For instance, locations, Faizabad, Coimbatore, Mandya and Kapurthala are most favourable for hybrids ORI 161 and IR58025A/IR54742. Interestingly, in the first three locations, these two hybrids were the highest yielding ones, while in Kapurthala it was not, because of low IPCA score of that location. On the other hand, the hybrids ORI 161 and IR58025A/IR54742 had low yields in Delhi, because they exhibited a higher magnitude of negative interaction at that location.

The locations Karnal and Kapurthala were not only highest yielding but also less interacting with almost zero score on PCA axis, and thus most suitable for growing rice hybrids. The growing conditions of these locations should be characterized so as to understand the factors responsible for stable yields. Another location with almost zero score on IPCA 1 axis was Chinsurah, but its yield potential was just above the average. The relative rankings of genotypes are expected to be fairly stable at this location. The locations, Faizabad and Delhi were highly interacting and therefore they are most suitable for specifically adapted hybrids or genotypes. On the other hand, the locations such as Coimbatore, Mandya, Cuttack, Maruteru and Pantnagar differed for both main effects and interactions. The relative rankings in these locations will be varying to a greater extent indicating that most of the genotypes/hybrids evaluated were not suitable for these locations. It was also evident from the figure 1(b) that all locations viz., Maruteru, Karjat and Cuttack in the coastal region had low mean yields implying that they were not suitable for most of the hybrids evaluated in the present study.

Figure 2 represents the biplot of first two PCA axes, which together account for 50% of interaction SS. Since the GEI effect is determined by the product of corresponding PCA scores, genotypes or environments with a small GEI will have small scores and be close to the centre of the axes. Genotypes occurring close together on the plot will tend to have similar yields in all environments, while genotypes far apart may either differ in mean yield or show a different

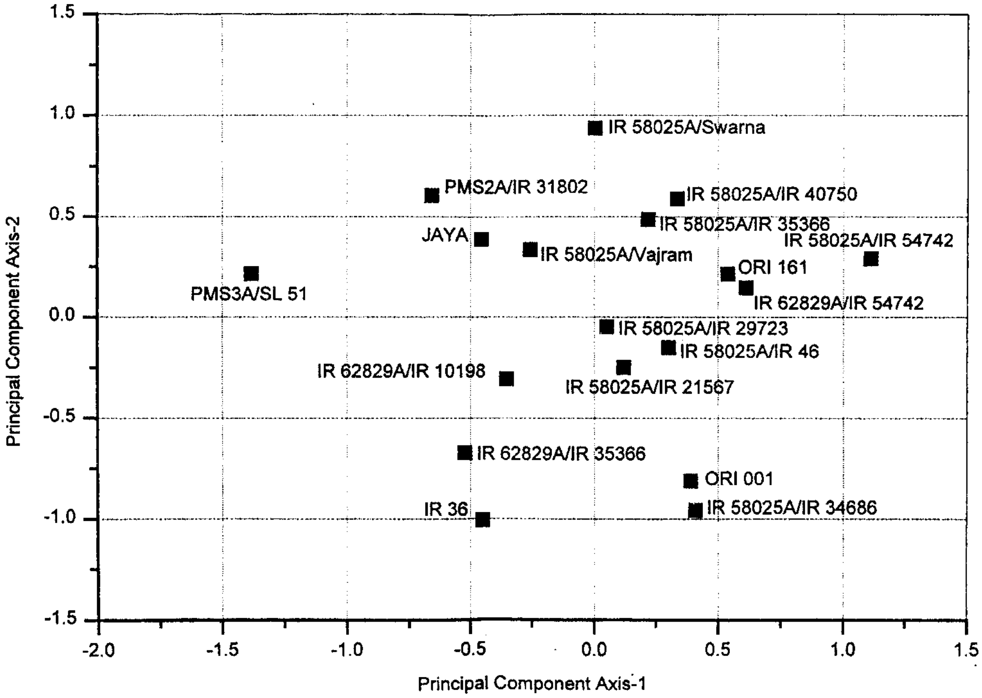

Fig. 2. Projection of Genotypes on the First two Principal Components of GxE Interaction Effect

pattern of response over the environments. Hybrids, IR58025A/IR29723, IR58025A/IR21567 and IR58025A/IR46 were close to the center of axes, while hybrids IR58025A/IR54742, PMS 3A/SL 51, IR58025A/Swarna, IR58025A/IR34686, ORI 161 and IR 36 are far away from the center. It is interesting to note that hybrid IR58025A/Swama which had zero score on axis-I (Fig. 1(a)) had a significant interaction component that pertains to axis-2. Also, hybrids IR58025A/IR34686, ORI 001; ORI 161 and IR62829A/IR54742; IR58025A/IR40750 and IR58025A/ IR35366; IR58025A/IR29723, IR58025A/IR21567 and IR58025A/IR46 which are in close groups tend to be influenced by same quantum of interaction effects across the locations. The direction of the genotypes from the center relative to each other is indicative of the correlations between them [10]. For instance, Jaya, IR58025A/Vajram, and PMS2A/IR31802 tend to have a positive correlation between their GEI effects, while negatively correlated with that of IR58025A/IR46, IR58025A/IR21567, IR58025A/ IR34686 and ORI 001. Likewise, hybrids IR58025A/IR40750, IR58025A/IR54742, IR58025A/IR35366, IR62829A/IR54742, and ORI 161 tend to have positive correlation in their interaction effect while negatively correlated with that of JR62829A/IRIOI98, IR62829A/IR35366 and IR 36.

AMMI analysis carried out for the first time for studying the performance and stability of rice hybrids has clearly indicated the usefulness of this model to have greater insight into the magnitude and nature of Genotype × Environment Interaction. This model is effective in identifying the genotypes that have specific adaptation (interacting) and those which are widely adaptable (non-interacting). It is also useful for characterizing the environment/locations which are suitable for growing a specific or a group of hybrids.

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