Crossover and non-crossover G × E interactions for traits of economic importance in rice (*Oryza sativa* L.)

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Abstract

Thirty four advanced high yielding and long grained rice genotypes alongwith checks were evaluated in twelve environments for seven quantitative traits and data were subjected to regression analysis and also analyzed to detect the presence of crossover and non-crossover interactions. Six genotypes namely, Pusa R 1011, 1017, 1022, 1024, 1026, and 1030 were identified to be promising based on regression analysis, whereas genotypes Pusa R 1012, 1015, 1017, 1021, 1031, 1034 and 1035 were identified as potential ones by using crossover and non-crossover interactions concepts against standard check Pusa 44. Of these genotypes Pusa R 1017 was identified as high yielding genotype having specific adaptability and responsiveness to higher nitrogen regimes both by regression analysis and crossover and non-crossover interactions concept.

Introduction

To enhance the production of rice breeders look for environment specific genotypes responsive to input intensive agriculture. The regression technique describes the response pattern of individual genotype without differentiating the kind of g × e interaction involving change in magnitude of response or direction among the genotypes [1-2]. Baker [1] described a test, initially proposed by Gail and Simon [3] and illustrated its application to test the kind of interaction in crop plants. The concept of crossover and non-crossover interactions is important in decision making relating to crop improvement strategies [1], as the presence of crossover interaction is a substantial evidence in favour of breeding for specific adaptation. The genotypes exhibiting crossover interaction against a standard variety can be said to have specific adaptability and can replace that standard variety in the specific environments. In view of these facts, the present investigation was carried out with 34 genotypes in twelve environments created by manipulating the fertility status of soils in three planting dates over two years to identify sowing time

specific and high nitrogen responsive genotypes using regression analysis [4,5] and crossover and non-crossover interactions concept [3]. Information on this aspect in such type of generated materials in rice is scanty.

Materials and methods

Thirty four advance (F_6) breeding lines, selected on the basis of high grain yield/plant and possess long, slender, fine, translucent grains, alongwith most popular rice variety Pusa 44 were raised in the randomized block design with three replications. Environments were created by manipulating the fertility levels of soil by applying two doses of nitrogen i.e. 120kg/ha and 160kg/ha, superimposing in three dates of sowing (May 10, May 25 and June 10) over two years at the Crop Research Center of Division of Genetics, Indian Agricultural Research Institute, New Delhi. Thus, 12 environments were created, six during *kharif* 2002 i.e. Env. I (120 kg N/ha and May 10th sowing), Env. II (160 kg N/h and May 10th sowing) Env. III, (120 kg N/ha and May 25th sowing), Env. IV (160 kg N/ha and May 25th sowing), Env. V ((120 kg N/ha June 10th sowing) and Env. VI ((160 kg N/ha and June 10th sowing). Similarly six environments were created during *kharif* 2003. The initial soil fertility status of each environment with respect to available N, P and K was worked out and found similar. Each fertilizer dose *i.e.* 120kg/ha and 160kg/ha were split into three equal doses and applied at the time of transplanting, 20 days after transplanting and again 40 days after transplanting in each case. The nursery of each plot was given equal treatment with respect to inputs. Thirty days old seedlings were transplanted in each plot consisting of six rows of 2m length with row to row and plant to plant distances of 20cm and 15 cm, respectively. The data were recorded on ten randomly taken plants from each plot in each environment on grain yield/plant (g), biological yield/plant (g), harvest index (direct value were used for statistical analysis), grains/panicle, 1000-grain weight (g), plant height and productive tillers per plant and data were analyzed separately for each environment. Adjusted progeny means were used for

the combined analysis for the traits exhibiting the presence of gxe interaction. Regression analysis and analysis to detect the presence of crossover and non-crossover interactions were carried out as per Eberhart and Russel [4] and Perkins and Jinks [5] and Gail and Simon [3].

Results and disscussion

Analysis of variance revealed significant differences among genotyes for the seven traits in all 12 environments. The combined analysis revealed the presence of g × e interaction for grain yield/plant, biological yield/plant, harvest index, grains/panicle, 1000-grain weight, productive tillers/plant and plant height. Regression analysis enables breeders to select desirable genotypes with respect to the responsiveness and stability in different environments. In the present study, the genotypes Pusa R 1011, 1017, 1022 1024, 1026 and 1030 had above average performance and responsiveness with respect to grain yield/plant (Table 1). Among these high yielding genotypes, Pusa R 1011, 1022, 1024, 1026 and 1030 can be designated as stable one with average responsiveness. Though the genotype Pusa R 1017 is an above average yielder and also has shown above average responsiveness coupled with instability, it was the highest yielder in Env. X (year 2003, 160kg N/ha and 25th May sowing) followed by Pusa R 1011, 1024, 1026, 1022, and 1030 which were significantly superior to the best check. The genotype Pusa R 1017 showed above average

performance and instability for biological yield/plant and 1000-grain weight, being the best performer for these traits again in Env. X. The genotype Pusa R 1011 and 1030 showed average performance along with stability for harvest index.

The existence of prior scientific basis to explain crossover interaction is crucial [6]. Thus, it is advantageous to define the varietal combinations among which one has to look for qualitative interaction in advance. There will be enormous multiplicity of all possible varietal pairs for detection of crossover interaction if there is no prior basis for comparison. Such a practice will greatly increase the experimentwise error rate. In the present case, the new genotypes were therefore, compared with the standard check Pusa 44 for detection of crossover interaction since the aim was to find a suitable alternative to Pusa 44.

The H (heterogeneity of response) and Q^+ and Q^- (for the presence of crossover interaction) against the standard variety Pusa 44 were estimated for all the 34 genotypes for the traits exhibiting the presence of g × e interaction i.e. grain yield/plant, biological yield/plant, harvest index, grains/panicle, 1000-grain weight, tillers/plant and plant height and their significance was tested [1]. The genotype exhibiting either significant H or Q^+ and Q^- are given in Table 2. For grain yield/plant, H was significant for the 29 genotypes against Pusa 44. The presence of cross over interaction

Table 1. Heterogeneity (H) test of response for the comparison of mean grain yield/plant (g) against the standard variety Pusa 44 along-with Q^+ and Q^- value for crossover interaction and adaptability parameter for the genotypes

Genotypes (Pusa R)	Adaptability parameter			Against Pusa 44		
	$\mu + d_i$	$\beta_i \pm SE$	$\sigma^2 d_i$	H	Q^+	Q^-
1011	29.30*	0.16*±0.18	0.11	91.31#	112.56	80.13
1012	25.69	0.21*±0.12	0.19*	72.69#	98.79$	68.52
1015	23.10	0.01*±0.15	0.15	66.19#	76.12	52.92
1017	31.15*	1.01*±0.31	0.39*	156.95#	189.40$	60.13
1021	24.90	−0.60*±0.23	0.25*	52.12#	53.89	48.78$
1022	28.65*	0.12*±0.15	0.01	69.31#	49.60	43.12
1024	29.39*	0.04*±0.11	0.10	102.67#	92.90	95.91
1026	28.72*	0.12*±0.16	0.09	107.35#	84.78	80.19
1029	22.81	−0.41*±0.30	0.31*	69.21#	73.58	86.25$
1030	28.43*	0.10*±0.11	0.02	59.56#	56.71	44.78
1031	24.86	0.27*±0.17	0.16*	94.12#	103.85$	110.67
1033	22.25	0.35*±0.26	0.19*	103.69#	99.89	117.95$
1034	24.97	−0.41*±0.31	0.22*	72.70#	67.63	41.36$
1035	24.83	0.20*±0.27	0.25*	52.60#	61.58$	29.00
1039	23.93	−0.49*±0.26	0.12*	98.60#	105.61$	86.21
1040	23.98	0.61*±0.23	0.21*	84.0#	89.90	51.58$
1041	21.65	−0.69*±0.10	0.32*	44.08#	50.57	83.61$
1044	22.77	0.59*±0.29	0.35*	75.82#	69.83$	80.00
Grand mean (μ)	25.12±2.98					
Pusa 44	22.45±2.37					

*Significant at P < 0.05; # H was significant against χ^2 0.05 at s-1 df, where s is the number of environments, $ minimum of either Q^+ or Q^- was significant against "C" value given by [3].

Table 2. Genotypes exhibiting significant *, # H (heterogeneity of response) and Q^+ and Q^- against standard variety Pusa 44

Character	H	Q^+ and Q^-
Grain yield/Plant (g)	Twenty nine genotypes Pusa R 1011, 1012, 1013, 1014, 1015, 1017, 1018, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1030, 1031, 1032, 1034, 1035, 1036, 1037, 1038, 1039, 1041, 1042, 1043, 1044	Pusa R 1012, 1013, 1014, 1015, 1017, 1021, 1023, 1025, 1028, 1031, 1032, 1034, 1035 (twelve genotypes).
Biological yield/Plant (g)	All genotypes except Pusa R 1018, 1026, 1029, 1042	Pusa R 1013, 1017, 1036, 1039, 1040 (five genotypes)
Harvest index (%)	All genotypes except Pusa R 1015, 1018, 1021, 1027	Pusa R 1012, 1013, 1014, 1016, 1017, 1020, 1023, 1024, 1025, 1026, 1028, 1029, 1031, 1034, 1035, 1036, 1038, 1040, 1042, 1044 (twenty genotypes)
Grain/Panicle	All genotypes except Pusa R 1012, 1016, 1041, 1044	Pusa R 1013, 1017, 1021, 1022, 1025, 1026, 1028, 1029, 1030, 1031, 1036, 1039, 1040 (thirteen genotypes)
1000 Grain weight (g)	All genotypes except Pusa R 1021, 1022, 1026, 1035, 1036, 1042	Pusa R 1011, 1014, 1017, 1029, 1037, 1043, 1045 (Seven genotypes)
Plant height (cm)	All genotypes except Pusa R 1011, 1017, 1020, 1035, 1038, 1042, 1044	Pusa R 1013, 1015, 1016, 1019, 1021, 1029, 1036, 1039. 1041 (nine genotypes)
Tillers/Plant	All genotypes except Pusa R 1013, 1028, 1040, 1044	Pusa R 1012, 1015, 1017, 1018, 1021, 1023, 1026, 1029, 1037, 1039, 1041, 1043, 1045 (thirteen genotypes)

*H was significant against χ^2 0.05 at s-1 df, where s is the number of environments. # minimum of either Q^+ or Q^- was significant against "C" value given by [3].

was observed for 12 genotypes for grain yield/plant against Pusa 44. The five genotypes exhibited the presence of crossover interaction for biological yield/plant, 20 genotypes for harvest index and thirteen genotypes number of grain/panicle, seven genotypes for 1000-grain weight and nine genotypes showed the presence of it for plant height. Thirteen genotypes had the presence of g × e interaction of number of productive tillers/plant. All the genotypes failed to exhibit crossover interaction for all traits against Pusa 44 thus, presence or absence of crossover interaction was genotype and trait specific [7, 8]. The genotypes Pusa R 1011, 1017, 1021, 1023, 1025 and 1035 in environment IV had significantly higher grain yield/plant than check Pusa 44.

The conclusion drawn from regression analysis and crossover and non crossover interactions concepts about genotypes having specific adaptability differ considerably. The genotypes Pusa R 1011, 1017, 1022, 1024, 1026 and 1030 identified as potential yielder having specific adaptability for environment VI, on the basis of regression analysis failed to exhibit significant min (Q^+ or Q^-) against standard variety Pusa 44 except Pusa R 1017 which had significant min (Q^+ or Q^-) against Pusa 44. On the other hand seven genotypes Pusa R 1012, 1015, 1017, 1021, 1031, 1034 and 1035 identified as potential yielders having specific adaptability to higher fertility level. On the basis of crossover and non-crossover interaction concepts, these genotypes failed to exhibit stable above average performance and responsiveness for grain yield/plant except Pusa R 1017.

A mention may be made of the genotype, Pusa R 1017 that has been identified as a high yielding genotype having specific adaptability both by using regression analysis and crossover and non-crossover interactions concept. Pusa R 1017 gave significantly higher mean grain yield/plant than the standard variety Pusa 44. However, in environments V, VI, IX, XI and XII it had lower grain yield than Pusa 44. Thus genotype, Pusa R 1017 had specific adaptation to high yielding environment i.e. high nitrogen regimes rather than possessing general adaptation [7, 8].

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