NARDI FUNDULEA, ROMANIA
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ROMANIAN AGRICULTURAL RESEARCH, NO. 32, 2015
Print ISSN 1222-4227; Online ISSN 2067-5720

NONPARAMETRIC STATISTICS FOR EVALUATING YIELD OF DIRECT SEEDED RICE GENOTYPES IN MULTI-ENVIRONMENTS

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ABSTRACT

Genotype (G) x Environment (E) interaction of 12 rice genotypes tested over six environments under direct seeded during optimal transplanting time for rice i.e. 15th January and 15th July of each year in dry and wet season respectively. The genotypes were grown in a randomized complete block design with three replications. The objective of this experiment was to identify stable high yielding genotypes. Combined analysis of variance showed genotype, environment and G×E interaction were significant. This indicates possibility of selection of stable genotypes across the environments. Huehn's non-parametric stability measures were used in both original datasets as well as after applying the correction to find out the stable rice genotypes. Based on original data genotype 12 was found stable whereas based on corrected data genotypes 11, 12 and 7 were found to be most stable under direct seeded rice. Principal component analysis was carried out to find out relationships among different stability measures. The first two principal components (PCs) PC1 and PC2 explained 83.58% (54.36 and 29.22% by PC1 and PC2, respectively) of the total variance.

Key words: non-parametric methods, rice, stability, genotype × environment interaction.

INTRODUCTION

Rice is the staple food for a large proportion of the world's population (Zhang, 2007). India is the second largest rice growing country in the world; however its productivity per unit area is low. In India, rice is cultivated on 44.01 million hectares with a production of 105.31 million tons and productivity of 2.23 t/ha. Among the rice production areas in the country, it is the most diverse in hydrology and other soil and climatic factors that combine to make a difference in rice yield (Singh et al., 1997). Analysis of interaction of genotypes with seasons would help in getting information on adaptability and stability performance of genotypes. Parametric statistics is the statistics which assume that the data follow some distribution, generally normal distribution. There are some statistical procedures which do not assume any distribution of the data; such statistical procedures are called non-parametric statistics. Parametric statistics uses interval and ratio scales for their parameter estimates. Non parametric statistical procedures make use of nominal and ordinal scales so that data are arranged in an ascending order and then assigned ranks according to those observations (Bredenkamp, 1974; Spearman, 1904). However, non parametric procedures are used less often than parametric procedures despite of certain advantages (Kubinger, 1986). Several nonparametric procedures have been developed to interpret the GEI in multi-environmental trial. Huehn (1979), Ketata et al. (1989), Fox et al. (1990), Huehn (1990b) and Thennarasu (1995) proposed several nonparametric indices of stability and GEI studies. Among these nonparametric procedures, Huehn's (1979; 1990b) statistics have been used widely to determine whether or not genotypes evaluated in multi environmental trails are stable (Flores et al., 1998; Hussein et al., 2000; Lin et al., 1986; Liu et al., 2010).

Huehn (1979) developed six nonparametric stability statistics using yield to rank genotypes in different environments. This method was then developed to incorporate the statistical properties and significance for the first two nonparametric methods (Z_1, Z_2) given by Nassar and Huehn

Received 12 February 2014; accepted 23 February 2015. First Online: March, 2015. DII 2067-5720 RAR 2015-35

(1987). Huehn (1990b) proposed the use of corrected means instead of original means for rank determination. Therefore, ranks of genotypes in each environment were corrected according to adjusted values. Although many authors (Dehghani, 2008; Kang and Pham, 1991) have used nonparametric measures of phenotypic stability introduced by Huehn (1979), only relatively few (Ebadi-Segerloo et al., 2008; Flores et al., 1998; Kaya and Taner, 2002; Sabaghnia et al., 2006) have used nonparametric measures of stability as proposed and discussed in Huehn (1990a; b). Therefore the objective of this paper was to study the stability of rice genotypes using Huehn's nonparametric statistics under varied environmental condition in direct seeded rice and to find the relationship among them.

MATERIAL AND METHODS

Plant material

This research data set involved 12 rice genotypes grown in 6 environments during dry and wet seasons. Genotype names and pedigrees are given in Table 1. Sprouted seeds were direct seeded in well puddle plots of 3m x 4m size during optimal rice growing season i.e. 15th January and 15th July.

Table 1. Mean yield and pedigree of the 12 rice genotypes, studied in 6 environments

Geno-type	Name	Yield (ton/ha)	Pedigree
1	Heera	3.13	CR-404-48 x Cr-289-1208
2	Vandana	3.68	C-22 x Kalakeri
3	KalingaIII	3.50	AC-540 x Ratna
4	Satyabhama	3.57	IR31238-350-3-2-1 x IR41054-102-2-3-2
5	Lalat	3.88	Obs.677 x IR-207 x Vikram
6	Naveen	4.37	Sattari X Jaya
7	Annada	5.21	MTU-15 x Yaikaku Nantoku (China)
8	Satabdi	4.79	CR-10-114 x CR-10115
9	Tapaswini	4.93	Jagannath x Mahsuri
10	IR 64	5.63	Gam Pai-15/Taichung Native 1
11	Satya Krishna	6.36	PHB-71 Doubled haploid
12	WITA 12	6.02	ITA 35/IR 9828-91-2-3 //CT 19

The seed rate was 12.5 g m^{-2} so that plant density becomes around 500 plants m^{-2}. The experiment was conducted in a randomized complete block design with three replications. The experiment was repeated in six consecutive dry-wet seasons from 2009-12 at the CRRI experimental farm with diverse environmental conditions. Need based cultural practices and plant protection measures were followed in each plot. In all trials, data were recorded on net plot grain yield. The harvested plot size was 10 m^{2}. At maturity, paddy yield was recorded and converted into t ha^{-1} after adjusting to 14% moisture level.

Non parametric stability statistics

Huehn (1979) proposed six nonparametric methods for assessing GEI and stability analysis. For a two-way dataset with *k* genotypes and *n* environments, the phenotypic value of *i*th genotype in *j*th environment was denoted as y_{ij}, where *i* = 1, 2, …, k, *j* = 1, 2, ..., n, r_{ij} as the rank of the *i*th genotype in the *j*th environment, and $\bar{r}_{i.}$ as the mean rank across all environments for the *i*th genotype. The genotype with highest yield was ranked first followed by next highest yielding genotype and so on. The statistics based on yield ranks of genotypes in each environment were expressed as follows:

$$S_i^{(1)} = 2\sum_{j}^{n-1}\sum_{j'=j+1}^{n}\left|r_{ij} - r_{ij'}\right| / \left[n(n-1)\right]$$

$$S_i^{(2)} = \sum_{j=1}^{n}\left(r_{ij} - \bar{r}_{i.}\right)^2 / \sum_{j=1}^{n}\left|r_{ij} - r_{i.}\right|$$

$$S_i^{(3)} = \frac{\sum_{j=1}^{n}\left(r_{ij} - \bar{r}_{i.}\right)^2}{\bar{r}_{i.}}$$

$$S_i^{(4)} = \sqrt{\frac{\sum_{j=1}^{n}\left(r_{ij} - \bar{r}_{i.}\right)^2}{n}}$$

$$S_i^{(5)} = \frac{\sum_{j=1}^{n}\left|r_{ij} - \bar{r}_{i.}\right|}{n}$$

$$S_i^{(6)} = \frac{\sum_{j=1}^{n}\left|r_{ij} - \bar{r}_{i.}\right|}{\bar{r}_{i.}}$$

Huehn (1990b) proposed the correction [$y_{ij}^* = y_{ij} - (\bar{y}_{..} - \bar{y}_i)$] where in a two-way dataset with k genotypes and n environments, it was denoted the phenotypic value of i^{th} genotype in j^{th} environment as y_{ij}, y_{ij} * is the corrected phenotypic value; $\bar{y}_{..}$ is the grand mean and $x_{i.}$ is the mean of genotype i in all environments. Huehn (1990b) used this correction on the two nonparametric measures consists on $S_i^{(1)}$ and $S_i^{(6)}$ and a new nonparametric statistics as $S_i^{(2)}$ while it was used term $S_i^{(7)}$ with this formula:

$$S_i^{(7)} = \sum_{j=1}^{n} \left(r_{ij} - \bar{r}_{i.}\right)^2 / (n-1)$$

These seven mentioned nonparametric measures of phenotypic stability were calculated according to original (uncorrected) and corrected datasets. For calculation of stability indices and other analysis statistical software SAS 9.2 and Microsoft Excel was used.

RESULTS AND DISCUSSION

Analysis of variance

A combined analysis of variance showed high significance of genotype × environment interaction (Table 2). Also all the main effects were highly significant. The environmental main effect explain 1.917% of the total variation; genotypic main effect explained 73.611% of the total variation and variation due to genotype × environment interaction explained was 11.611% of the total variation. Although the measured yield was a combined result of the effects of genotype, environment and their interaction, only G and GE were relevant to the genotype evaluation (Dehgahni et al., 2009; Sabaghnia et al., 2008).

Table 2. Analysis of variance for yield of 12 rice genotypes

Source	DF	Mean squares	TSS % explained
Env	5	1.182*	1.917
Rep(Env)	12	0.205	0.796
Genotype	11	20.475*	73.047
Gen* Env	55	0.651*	11.611
Error	132	0.295	

Nonparametric stability statistics

The present analysis on original data has been used with three descriptive statistics such as mean of ranks (MR), standard deviation of ranks (SD) and coefficient of variation of ranks (CV) (Table 3). Based on two ranking methods (MR and SD) over 12 genotypes across six environments (Ketata et al., 1989; *Cravero* et al., 2010) identified genotype 11 and 12 were more stable. Subsequently, MR and SD also identified genotype 1, 3, 6, 8 as most unstable across the environment which is in agreement with Thennarasu, 1995.

The original datasets of 12 genotypes were analyzed to estimate phenotypic stability by the statistics proposed by Huehn (1979; 1990b) with parameters ($S_i^{(1)}$, $S_i^{(2)}$, $S_i^{(3)}$, $S_i^{(4)}$, $S_i^{(5)}$, $S_i^{(6)}$ and $S_i^{(7)}$) and genotype 12 was identified as more stable and genotype 6 and 8, 1 and 5 were most unstable.

Table 3. Three descriptive statistics of ranks and seven nonparametric stability statistics based on original values for yield of 12 rice genotypes evaluated in 6 environments

Genotype	MR	SD	CV	S1	S2	S3	S4	S5	S6	S7
1	11.25	1.17	0.10	0.47	1.15	0.61	1.07	1.00	0.53	1.38
2	9.25	2.04	0.22	0.73	2.20	2.26	1.87	1.58	1.03	4.18
3	10.33	1.37	0.13	0.60	1.56	0.90	1.25	1.00	0.58	1.87
4	9.83	1.17	0.12	0.33	1.28	0.69	1.07	0.89	0.54	1.37
5	8.33	0.82	0.10	0.33	0.83	0.40	0.75	0.67	0.48	0.67
6	7.00	2.19	0.31	0.73	2.40	3.43	2.00	1.67	1.43	4.80
7	4.00	1.10	0.27	0.27	1.50	1.50	1.00	0.67	1.00	1.20
8	6.00	2.19	0.37	0.80	2.40	4.00	2.00	1.67	1.67	4.80
9	5.17	0.98	0.19	0.20	0.97	0.94	0.90	0.83	0.97	0.97
10	3.25	1.08	0.33	0.33	1.18	1.81	0.99	0.83	1.54	1.18
11	1.33	0.82	0.61	0.27	1.00	2.50	0.75	0.56	2.50	0.67
12	2.25	0.76	0.34	0.20	0.82	1.28	0.69	0.58	1.56	0.58

Analysis was made based to find out stability statistic values on the corrected ranks (CMR), standard deviation of corrected ranks (CSD), coefficient of variation of corrected ranks (CCV) and all seven Huehn's (1979, 1990b) stability statistics ($CS_i^{(1)}$, $CS_i^{(2)}$, $CS_i^{(3)}$, $CS_i^{(4)}$, $CS_i^{(5)}$, $CS_i^{(6)}$ and $CS_i^{(7)}$ (Table 4). Genotype 10 was ranking third in all the environments whereas genotype 1 was ranking twelfth and hence its stability index value was found to be zero using all stability index statistics. The ranking of other ten genotypes varied in different environments. Out of these genotypes, genotypes 11 and 12 were most stable based on CMR and genotypes 12, 11 and 7 were most stable based on CSD, whereas genotypes 1, 3 and 4 were most unstable based on CMR and genotypes 2 and 3 were most unstable based on CSD. Genotypes 11, 12 and 7 were found to be most stable using most of the Huehn's stability indices whereas genotype 2 was found to be most unstable using most of the stability indices.

Table 4. Three descriptive statistics of ranks and seven nonparametric stability statistics based on corrected values for yield of 12 rice genotypes evaluated in 6 environments

Genotype	CMR	CSD	CCV	CS1	CS2	CS3	CS4	CS5	CS6	CS7
1	12.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
2	9.00	1.41	0.16	0.60	1.67	1.11	1.29	1.00	0.67	1.67
3	10.33	1.21	0.12	0.47	1.38	0.71	1.11	0.89	0.52	1.22
4	10.00	0.63	0.06	0.13	1.00	0.20	0.58	0.33	0.20	0.33
5	8.33	0.52	0.06	0.27	0.50	0.16	0.47	0.44	0.32	0.22
6	7.00	1.10	0.16	0.47	1.50	0.86	1.00	0.67	0.57	1.00
7	4.17	0.41	0.10	0.13	0.50	0.20	0.37	0.28	0.40	0.14
8	6.00	0.89	0.15	0.33	1.00	0.67	0.82	0.67	0.67	0.67
9	5.17	0.75	0.15	0.27	0.85	0.55	0.69	0.56	0.65	0.47
10	3.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
11	1.17	0.41	0.35	0.13	0.50	0.71	0.37	0.28	1.43	0.14
12	1.83	0.41	0.22	0.13	0.50	0.45	0.37	0.28	0.91	0.14

Relationship among nonparametric statistics

To understand the relationships among nonparametric measures of phenotypic stability, principal component analysis was performed in accordance to the rank correlation matrix and explains 83.58% (54.36 and 29.22% by PC1 and PC2, respectively) of the total variance. The relationship among the different stability measures and mean yield was displayed graphically in a plot of PC1 versus PC2. The figure shows that the measures SD, S1, S2, S4, S5, S7, CSD, CS1, CS2, CS4, CS5,CS7 can be clubbed in one group; whereas CV, S3, S6, CCV, CS3 and CS6 was found to be distant from the that group. MR and CMR are away from rest of the measures because the genotype with highest yield was ranked first and so on.

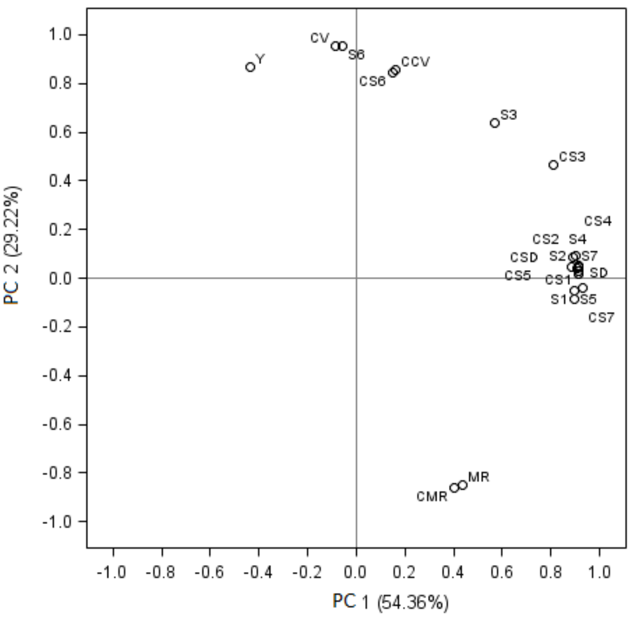

Figure 1. Principal component analysis (PC1 and PC2) plot estimated by 20 methods

CONCLUSIONS

Most plant breeders prefer simultaneous selection for mean yield and stability because the selected genotypes must have high mean values coupled with stable performance. In direct seeded rice crop, the Huehn's different stability measures showed similar results in both original datasets, as well as after applying the correction. There is good potential in nonparametric stability methods to identify favorable genotypes in plant breeding programs. The nonparametric method provided a lot of flexibility for plant breeders for simultaneous selection for yield and stability. According to Huehn's nonparametric statistics based on original data genotype 12 was best, whereas based on corrected data genotypes 11, 12 and 7 were found to be most stable under direct seeded rice. The principal component analysis was done to find out the relationship among all the stability measures and all the stability measures were classified into three groups with S1, S2, S4, S5, S7, CSD, CS1, CS2, CS4, CS5, CS7 in one group; CV, S3, S6, CCV, CS3, CS6 in second group and MR, CMR in other group.

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