

Non - Parametric Methods for Interpreting Genotype x Environment Interaction of Rice Genotypes (*Oryza Sativa* L.)

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Abstract

The promising rice genotypes were grown in different agro-ecological regions of Gujarat state to study their adaptability to varying climatic and soil conditions. Yield data of 21 rice genotypes grown at Nawagam, Vyara, Dabhoi and Thasra locations during *kharif*-2006 were collected from the Main Rice Research Station, Nawagam, Anand Agricultural University, Anand. Result of the combined or pooled ANOVA revealed that genotype, environment and genotype-environment interaction were highly significant. Significant genotypic variance indicated genetic diversity among genotypes yield.

Further the results of non-parametric stability analysis indicated that the genotypes IET-19147 and NWGR-3006 had the lowest value of $S_1^{(i)}$ and had higher grain yield as compared to overall mean grain yield thus genotypes IET-19147 and NWGR-3006 were stable over location while IET-19143, IET-19189 and IET-19132 were found to be highly unstable genotypes. In addition, it can be concluded from the plots portrayed by mean yield (kg plot⁻¹). Vs. $S_1^{(i)}$ and $S_2^{(i)}$ values also. Section 1 refers that genotypes (NWGR-3006, IET-19123, IET-19147) with high grain yield and small $S_1^{(i)}$ and $S_2^{(i)}$ values can be considered as stable and well adapted to all environments. Section 2 content genotypes possess high yield and large $S_1^{(i)}$ and $S_2^{(i)}$ values described as genotypes (NWGR-3132, NWGR-2018, IET-19140, IET-19160, IET-19143, IET-19189, IET-19117, IET-19146) with increasing sensitivity to environmental changes and greater specificity of adaptability to high-yielding environments. Section 3 referring poorly adapted genotypes to all environments which are NWGR-3026, NWGR-3215, NWGR-3199, NWGR-2032, IET-19148, IET-19132, GR-103. Section 4 exhibits that genotypes (NWGR-3113, NWGR-3213 and IET-19114) are low yielding and small $S_1^{(i)}$ and $S_2^{(i)}$ values indicative of greater resistance to environmental fluctuation and therefore increasing specificity of adaptability to low yielding environments.

Key words : Non-parametric stability method, G x E Interaction, Rice

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The primary responsibility of breeders is to evolve and identify superior and stable genotype. The stable genotype has consistent phenotypic performance over locations/environments. The resultant effect of genotype and environment may not be always independent. The stable genotypes can be identified by evaluating them over locations. This is subjected to pooled analysis over locations/environments. Interpretation of genotype x environment interaction (GEI) can be aided by statistical modelling. Models can be linear formulations such as joint regression (Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966) modelling). Modelling GEI in MLTs (Multi-location trials) helps to determine phenotypic stability of genotypes. This concept has been defined in different ways with increasing numbers of stability parameters (Gauch and Zobel, 1996).

Huehn (1996) indicated that there are two major approaches to study GxE interaction and determining adaptation of genotypes. The first and most common approach is parametric which relies on distributional assumptions about genotypes, environment and GxE effects. The second major approach is non-parametric approach. In non-parametric statistics as compared to parametric statistics no assumptions are needed about the distribution of analyzed values and homogeneity of variances. Additivity (linearity of effect) is not necessary requirements (Huehn, 1990) and they reduced the bias caused by outliers. Non-parametric stability measures are expected to be less sensitive to error measurements than parametric estimation and addition or deletion of one or a few observations is not likely to cause variation in the estimates as would be the case with for stability statistics (Nassar and Huehn, 1987). Therefore non-parametric methods were used to determine the stability of rice genotypes in the present study.

Materials and Methods

Data on multi-location trial on rice was selected from the Gujarat state for the present study. The test locations were Nawagam, Vyara, Dabhoi and Thasra for the multi-location trial. These multi-location trials were distributed over different agro-climatic zones of Gujarat.

Twenty one genotypes including check GR103 of late maturing group were tested at four locations during *kharif*-2006 in Small Scale Varietal Trial. The experiment was laid out in randomized complete block design (RCBD) with two replications for all the locations and standard agronomic practices were followed. Net plot size was 4.2m x 2.2m for each location under study. Data on grain yield (kg plot⁻¹) of rice genotypes grown at different test locations were collected and subjected to stability analysis by non-parametric methods which were proposed by Huehn (1979), Nassar and Huehn (1987). They were based on ranks of genotypes within environment. Genotypes with similar ranking across environments are classified as most stable.

Huehn (1979) and Nassar and Huehn (1987) proposed following four non-parametric measures of phenotypic stability.

1. Mean of the absolute rank differences (S_i⁽¹⁾) of a genotype

$$S_i^{(1)} = \frac{2 \sum_{j=1}^{q-1} \sum_{j=j+1}^q |r_{ij} - r_{ij'}|}{q(q-1)}$$

Where \bar{r}_i = mean of ranks over environments

r_{ij} = rank of genotypes in each environment based on $(Y_{ij} - \bar{Y}_i + \bar{Y}_{..})$

Ranks are assigned from lowest to highest

q = number of environments

2. Variance among the ranks over the q environments (S_i⁽²⁾)

$$S_i^{(2)} = \frac{\sum_{j=1}^q (r_{ij} - \bar{r}_i)^2}{(q-1)}$$

Where \bar{r}_i = mean of ranks over environments

r_{ij} = rank of genotypes in each environment

based on $(Y_{ij} - \bar{Y}_i + \bar{Y}_{..})$

Ranks are assigned from lowest to highest

q = number of environments

Testing of Significance

The statistical properties of S_i⁽¹⁾ and S_i⁽²⁾ have been investigated by Nassar and Huehn (1987). Approximate tests of significance based on the normal distribution are

developed for these two nonparametric measures. One computes the “statistic”

$$S^{(m)} = \sum_{i=1}^K Z_i^{(m)} = \sum_{i=1}^K \frac{[S_i^{(m)} - E(S_i^{(m)})]^2}{\text{Var}(S_i^{(m)})} \text{ where, } m = 1, 2$$

$$E(S_i^{(1)}) = (p^2 - 1)/3p$$

$$E(S_i^{(2)}) = (p^2 - 1)/12$$

$$\text{Var}(S_i^{(1)}) = (p^2 - 1)[(p^2 - 4)(q + 3) + 30]/45p^2q(q - 1)$$

$$\text{Var}(S_i^{(2)}) = (p^2 - 1)[2(p^2 - 4)(q - 3) + 5(p^2 - 1)]/360q(q - 1)$$

p = number of genotypes

q = number of environments

The statistic may be approximated by a chi-square distribution with p degree of freedom with E(S_i^(m)) expectation mean and variance Var(S_i^(m)). Under the null hypothesis that all genotypes are equally stable. The mean E(S_i^(m)) and variances Var(S_i^(m)) may be computed from the discrete uniform distribution (1,2,...,p).

3. Mean of the absolute rank differences (S_i⁽³⁾) of a genotype

$$S_i^{(3)} = \frac{\sum_{j=1}^q |r_{ij} - \bar{r}_i|}{\bar{r}_i}$$

Where, \bar{r}_i = mean of ranks over environments

r_{ij} = rank of ith genotypes in jth environment based on mean yield

Ranks are assigned from the lowest to highest

q = number of environments

4. Variance among the ranks over the q environments (S_i⁽⁶⁾)

$$S_i^{(6)} = \frac{\sum_{j=1}^q (r_{ij} - \bar{r}_i)^2}{\bar{r}_i}$$

Results and Discussion

Yield data of 21 rice genotypes grown at Nawagam, Vyara, Dabhoi and Thasra locations during *kharif*-2006 were collected from the Main Rice Research Station, Nawagam, Anand Agricultural University, Anand. These data were

subjected to analysis of variance for individual location as well as pooled over locations. The Analysis of Variance (ANOVA) for individual location (data not given) indicated that the variance for genotypes was found significant in all the locations except E3 (Dabhoi) location. This suggests the presence of genetic variability among the genotypes under study at most of the locations. Similar findings were reported by Anandan *et al.* (2009) in rice, Ozberk, (2005) in wheat, Sharma *et al.* (1998) in Pearl millet and Shinde *et al.* (2002) in pearl millet crop. The environment E1 was high yielding environment for the genotypes under study, whereas the environment E2, E3 and E4 were found to be low yielding environment as indicated by the environmental index.

Result of analysis of variance over locations presented in Table 1 gave the overall picture of the relative magnitude of the genotypes (G), locations (E) and genotype-environment interaction (GEI) variance. The combined ANOVA revealed that genotype, environment and genotype-environment interaction were highly significant and contributed 7.8, 80.1 and 12.1 per cent of trial or total variation. Gauch and Zobel (1997) reported that in normal multi-environment yield trials (MEYTs), E accounted for about 80% of the total variation, while GE accounted for 10%. Present findings are in agreement with these reports. Significant genotypic variance indicated genetic diversity among genotypes. The mean yield of genotypes over environment ranged from 3558kg ha⁻¹(G3) to 5872kg ha⁻¹(G10) (Table-2).

The parametric stability methods have good properties under certain statistical assumption like normal distribution of error and interaction effects however, they may not perform well if these assumptions are violated (Huehn, 1990). Parametric tests for significance of variance and variance related measures could be very sensitive to the underlying assumptions. Thus, it is wise to search for alternative approaches that are more robust to departures from common assumption, such as non-parametric measures (Nassar and Huehn 1987 and Huehn and Nassar, 1989).

Huehn (1979) and Nassar and Huehn (1987) proposed four non-parametric measures of phenotypic stability.

1. Mean of the absolute rank differences $S_i^{(1)}$ of a genotype and variance among the ranks $S_i^{(2)}$ over the environments

Non-parametric methods are based on the ranks of the genotypes across locations. They give equal weight to each location or environment. Genotypes with less change in ranks are expected to be more stable. The mean absolute rank difference $S_i^{(1)}$ estimates all possible pair wise rank

difference across locations for each genotypes. The $S_i^{(2)}$ estimates are simply the variance of ranks for each genotypes over environments. For the variance of ranks $S_i^{(2)}$, smaller estimates may indicate relative stability. Often, $S_i^{(2)}$ has less power for detecting stability than $S_i^{(1)}$. The $S_i^{(1)}$ may loose power when genotypes are similar in their interactions with the environments. Two rank stability measures proposed by Huehn (1979) were worked out and expressed as $S_i^{(1)}$ and $S_i^{(2)}$ are presented in Table 2. The genotypes G16 (IET-19114), G13 (IET-19147) and G7 (NWGR-3006) had the lowest value of $S_i^{(1)}$ and ranked 13th, 3rd and 8th for grain yield. G13 and G7 had higher grain yield as compared to overall mean yield thus genotype G13 and G7 were stable. The highest $S_i^{(1)}$ mean absolute rank was observed for genotype G17 (IET-19143), G18 (IET-19189) and G15 (IET-19132) indicating to be highly unstable genotypes.

For each genotype, $Z_i^{(1)}$ and $Z_i^{(2)}$ values were calculated based on ranks of the corrected data and summed over genotypes to obtain Z values (Table 2). $Z_i^{(1)}$ (20.38) and $Z_i^{(2)}$ (24.37) are distributed as χ^2 and were less than the critical value of $\chi^2_{(0.05, 21)}(32.67)$ which indicated the non significant differences among the ranks of stability of twenty one genotypes. Among the individual Z values, it was found that none of the genotypes were significantly unstable relative to other except G15, whose $Z_i^{(2)}$ value was greater than the table $\chi^2_{(0.05, 1)}(3.84)$.

Figures 1 and 2 represent plots portrayed by mean yield (kg plot⁻¹). Vs. $S_1^{(i)}$ and $S_2^{(i)}$ values. Mean $S_1^{(i)}$ and $S_2^{(i)}$ values and grand mean yield divide both figures into four sections. Section1 refers that genotypes (G7, G12 and G13) having high grain yield and small $S_1^{(i)}$ and $S_2^{(i)}$ values can be considered as stable and well adapted to all environment. Section 2 containing genotypes (G4, G8, G10, G14, G17, G18, G19 and G20) possess high yield and large $S_1^{(i)}$ and $S_2^{(i)}$ values are increasing sensitivity to environmental changes and greater specificity of adaptability to high-yielding environments. Section 3 referring poorly adapted genotypes to all environments capturing genotypes (G1, G3, G5, G9, G11, G15 and G21) in figure 1 and 2. Section 4 exhibits that genotypes (G2, G6 and G16) are of low yielding and small $S_1^{(i)}$ and $S_2^{(i)}$ values are indicative of resistance to environmental fluctuation and therefore increasing specificity of adaptability to low yielding environments.

2. Mean of the absolute rank differences $S_i^{(3)}$ of a genotypes and variance among the ranks $S_i^{(6)}$ over the environments

The Y_{ij} values must not be corrected for the genotypic effects before ranking because information about trait level would be lost. Huehn (1979) proposed two non-parametric

statistics for the simultaneous estimation of performance and stability which are $S_i^{(3)}$ and $S_i^{(6)}$. These statistics measure stability in units of the mean rank of the i^{th} genotype using $S_i^{(3)}$, the differences between rank and mean rank are weighted with themselves avoiding the possibility that a lot of smaller rank differences may lead to the same $S_i^{(3)}$ value as a few larger differences.

These $S_i^{(3)}$ and $S_i^{(6)}$ non-parametric measures were worked out by using the ranks which were assigned to genotypes on the basis of original mean data within environment and presented in Table 3. The results of $S_i^{(3)}$ and $S_i^{(6)}$ indicated that the genotypes G10 (IET-19140) and G12 (IET-19123) ranked first and second, respectively according to $S_i^{(3)}$ and $S_i^{(6)}$ and they occupied 1st and 2nd position in mean yield as well therefore these genotypes were found to be stable and adapted to all environments. According to $S_i^{(3)}$ and $S_i^{(6)}$, genotype G9 (NWGR-2032) was found to be most unstable followed by genotype G21 (GR-103) and genotype G15 (IET-19132). Huehn (1990) used three non-parametric measures $S_i^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$ for phenotypic stability of winter wheat grain yield in Germany. He concluded that one is interested in a simultaneous consideration of both stability and yield, $S_i^{(3)}$ can be applied and used on original (Uncorrected yield) data, because correction eliminates the genotypic effects from the data. Sabaghnia *et al.* (2006) worked out all four non-parametric stability measures for lentil genotypes in Iran and interpreted the similar type of results. $S_i^{(3)}$ measure was used to find the stable cowpea (*Vigna unguiculata* L.) genotypes by Aremu *et al.* (2007).

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Table 1: Analysis of variance for Pooled over locations (Plot base yield data)

Sources of variation	df	SS	SS (%)	MS
Repl/Environments	4	0.57	--	0.142
Environments	3	381.64	80.1	127.213**
Genotypes	20	36.97	7.8	1.849**
G x E	60	57.83	12.1	0.964**
Pooled error	80	15.30		0.191
Total	167			

** Significant at 1 per cent level of probability

Table 2: Mean absolute rank difference ($S_i^{(1)}$) and variance of ranks ($S_i^{(2)}$) for different rice genotypes over locations

Sr. No.	Genotypes	Mean Yield (kg ha ⁻¹)	Rank	$S_i^{(1)}$	Rank	$S_i^{(2)}$	Rank	$Z_i^{(1)}$	$Z_i^{(2)}$
G1	NWGR-3026	4508	17	9.500	16	54.250	13	1.11	0.63
G2	NWGR-3113	4347	18	6.167	4	26.917	5	0.12	0.19
G3	NWGR-3215	3558	21	9.833	18	70.250	19	1.42	2.30
G4	NWGR-3132	4907	7	9.333	14	57.667	15	0.97	0.90
G5	NWGR-3199	4616	16	9.500	16	62.250	17	1.11	1.33
G6	NWGR-3213	4690	11	6.500	5	26.250	4	0.04	0.22
G7	NWGR-3006	4838	8	4.667	3	14.000	3	0.94	1.05
G8	NWGR-2018	4773	10	9.000	12	59.333	16	0.71	1.05
G9	NWGR-2032	4232	19	9.000	12	50.000	12	0.71	0.36
G10	IET-19140	5872	1	8.667	11	46.667	10	0.50	0.20
G11	IET-19148	4630	15	8.000	9	40.000	9	0.18	0.02
G12	IET-19123	5791	2	6.667	6	28.667	6	0.02	0.13
G13	IET-19147	5015	3	4.500	2	13.583	2	1.08	1.08
G14	IET-19160	4956	4	7.833	7	38.917	7	0.13	0.01
G15	IET-19132	4683	12	10.167	19	90.917	21	1.77	5.99*
G16	IET-19114	4677	13	2.667	1	4.333	1	3.27	2.13
G17	IET-19143	4950	5	11.167	21	78.917	20	3.07	3.63
G18	IET-19189	4940	6	10.333	20	68.667	18	1.97	2.08
G19	IET-19117	4645	14	9.333	14	56.000	14	0.97	0.76
G20	IET-19146	4788	9	8.000	9	39.333	8	0.18	0.01
G21	GR-103	3804	20	7.833	7	48.250	11	0.13	0.27
		$E(S_i^{(1)})$	$V(S_i^{(1)})$	$E(S_i^{(2)})$	$V(S_i^{(2)})$	$Z_i^{(1)}$	$Z_i^{(2)}$	Tab. ²	Tab. ₂
		6.98	5.71	36.67	491.13	20.38	24.37	3.84	32.67

* Significant at 5 per cent level of probability

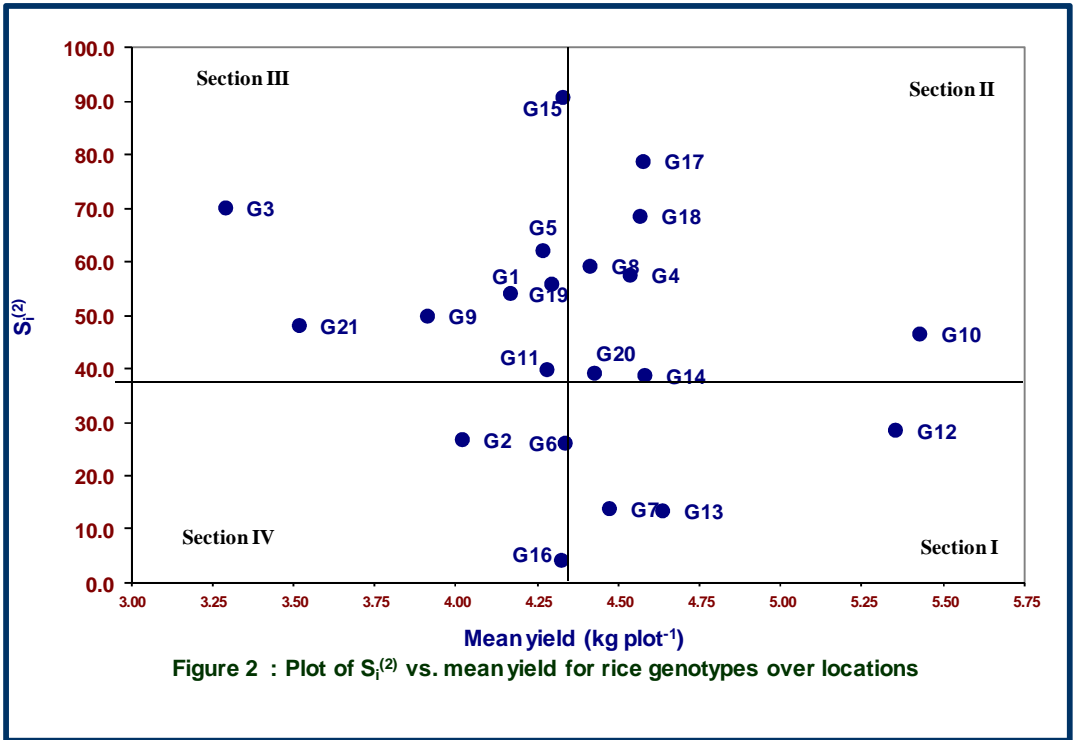
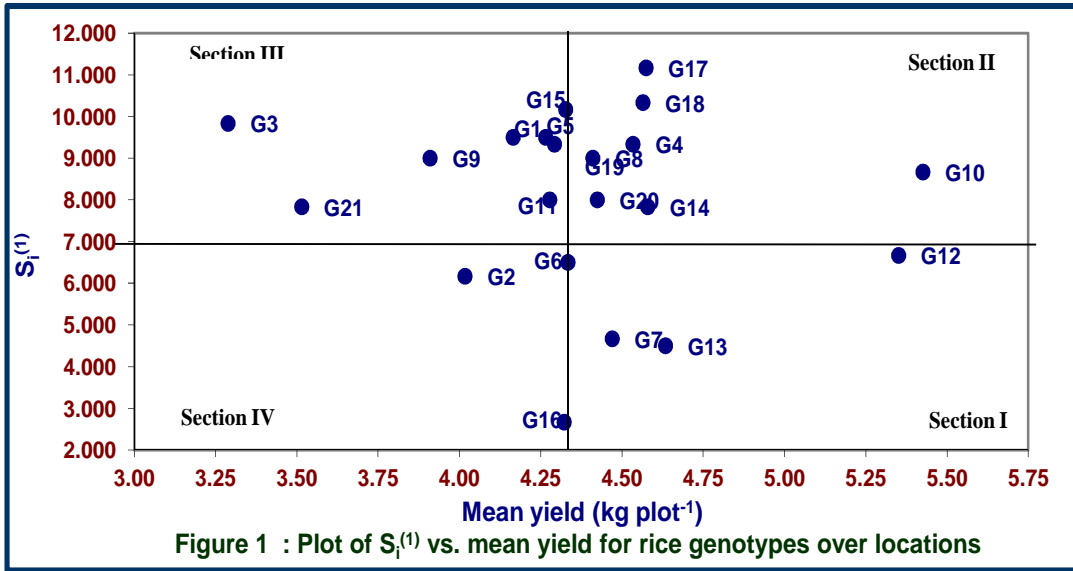


Table 3: Mean absolute rank difference ($S_i^{(3)}$) and variance of ranks ($S_i^{(6)}$) for mean yield of rice genotypes over locations.

Sr. No.	Genotypes	Mean Yield		Rank	$S_i^{(3)}$	Rank	$S_i^{(6)}$	Rank
		(kg ha ⁻¹)	(kg plot ⁻¹)					
G1	NWGR-3026	4508	4.165	17	2.000	18.5	13.111	17
G2	NWGR-3113	4347	4.017	18	1.667	12	6.333	11
G3	NWGR-3215	3558	3.288	21	1.818	13	3.182	6
G4	NWGR-3132	4907	4.534	7	1.447	11	6.191	10
G5	NWGR-3199	4616	4.265	16	2.000	18.5	12.889	16
G6	NWGR-3213	4690	4.334	11	1.156	7	4.511	7
G7	NWGR-3006	4838	4.470	8	0.640	3	2.000	4
G8	NWGR-2018	4773	4.410	10	1.818	13	14.000	18
G9	NWGR-2032	4232	3.910	19	2.645	21	19.194	21
G10	IET-19140	5872	5.426	1	0.074	1	0.037	1
G11	IET-19148	4630	4.278	15	1.268	9	5.927	9
G12	IET-19123	5791	5.351	2	0.154	2	0.154	2
G13	IET-19147	5015	4.634	3	0.642	4	2.019	5
G14	IET-19160	4956	4.579	4	1.224	8	6.755	12
G15	IET-19132	4683	4.327	12	1.852	16	17.259	20
G16	IET-19114	4677	4.322	13	0.842	5	1.789	3
G17	IET-19143	4950	4.574	5	1.846	15	16.769	19
G18	IET-19189	4940	4.565	6	1.957	17	12.830	15
G19	IET-19117	4645	4.292	14	1.415	10	7.683	14
G20	IET-19146	4788	4.424	9	1.022	6	5.400	8
G21	GR-103	3804	3.515	20	2.500	20	7.500	13

