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A STATISTICAL COMPARISON BETWEEN NON-PARAMETRIC AND PARAMETRIC STABILITY MEASURES

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ABSTRACT

The computation of type I error (α) and power of the test useful in evaluating the merits of various stability measures are discussed. Performances of non-parametric measures vis-a-vis parametric measures have been assessed based on these criteria.

Key words : Stability, parametric measures, non-parametric measures

Non-parametric measures are widely employed in the selection of crop varieties especially when the interest lies in genotypes, which excel in both yield and stability. However, it is a known fact that the non-parametric methods are less powerful than their parametric counterparts. Nevertheless, very little work has been done in the direction of comparing the performance of non-parametric measures *vis a vis* parametric measures. A comparative study will be quite useful because, if it is found that the loss in efficiency of the non-parametric approach is marginal in the situations, which are commonly encountered, these measures can be safely recommended.

Thennarasu[1] had proposed four non-parametric measures and shown that two of them performed better than other measures. He, however, did not consider their performance relative to the common parametric measures. In this paper we concentrate on the relative merits of non-parametric and parametric measures under different practical situations, the merits being judged on the basis of two criteria namely, (i) convergence of observed $\propto$ (Type-I error) to the postulated $\propto$ and (ii) the power of the test.

MATERIALS AND METHODS

Consider t genotypes having performance tested in s environments. In non-parametric analysis of GE interaction we deal with ranks of genotypes separately for each of these s environments. The rank of a genotype in a particular environment

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cannot be based purely on the phenotypic values (Y_{ij}) because the stability has to be measured independently of the genotypic effect. Therefore, r_{ij} the rank of the ith genotype in the jth environment is determined on basis of the corrected phenotypic values y_{ij}, namely $(Y_{ij} - \bar{Y}i.)$, $\bar{Y}i.$ being the mean performance of the ith genotype. The ranks obtained from these corrected Y_{ij}'s depend only on the GE interaction and error components and these are tabulated in Table 1.

Table 1. Ranks of t genotypes in s environments

Genotype	Environment							
	e_1	e_2	e_3	...	e_j	...	e_s	Mean
g_1	r_{11}	r_{12}	.	...	r_{1j}	...	r_{1s}	$\bar{r}_{1.}$
g_2	r_{21}	r_{22}	.	...	r_{2j}	...	r_{2s}	$\bar{r}_{2.}$
.	.	.	.	...	.	...	.	.
g_i	r_{i1}	r_{i2}	.	...	r_{ij}	...	r_{is}	$\bar{r}_{i.}$
.	.	.	.	...	.	...	.	.
g_t	r_{t1}	r_{t2}	.	...	r_{tj}	...	r_{ts}	$\bar{r}_{t.}$
Mean	$\frac{t+1}{2}$	$\frac{t+1}{2}$	.	...	$\frac{t+1}{2}$	...	$\frac{t+1}{2}$	$\bar{\bar{r}} = \frac{t+1}{2}$

Using the rank values and rank means defined in Table 1, Thennarasu[1] purposed the following stability measures:

$$NP_i(1) = \frac{1}{S} \sum_{j=1}^{s} | r_{ij} - M_{di} | \quad \ldots (1)$$

$$NP_i(2) = \frac{1}{S} \left[\sum_{j=1}^{s} | r_{ij} - M_{di} | / M^*_{di} \right] \quad \ldots (2)$$

$$NP_i(3) = \frac{\sqrt{\Sigma (r_{ij} - \bar{r}_{i.})^2 / S}}{\bar{r}^*_{i.}} \quad \ldots (3)$$

$$NP_i(4) = \frac{2}{S(S-1)} \left[\sum_{j=1j'=j+1}^{s-1} \sum^{S} | r_{ij} - r_{ij'} | / \bar{r}_{i.} \right] \quad \ldots (4)$$

In this investigation, these non-parametric measures are compared, for their performance, with Huhn[2] measure,

$$NP_i(5) = \frac{1}{S-1} \sum_j (r_{ij} - \bar{r}_{i.})^2 \quad \ldots (5)$$

as well as the parametric measures b_i, S^2_{di}, W_i, r_i^2 and σ_i^2. In the formulae, the quantities $\bar{r}_{i.}$ and M_{di} are the mean and median ranks respectively of the ith genotype, obtained from the corrected Y_{ij}s while $\bar{r}^*_{i.}$ and M^*_{di} are the same parameters computed from the uncorrected Y_{ij}s. For ranking purpose, the smallest y_{ij} in a particular environment is given rank one, the next higher value, rank two, and so on. Here, $NP_i(1)$ denotes magnitude of measure $NP(1)$ for the ith genotype, and similarly for the other measures. In the course of further discussion the parametric measures will be denoted by $P(1)$, $P(2)$, $P(3)$, $P(4)$ and $P(5)$ respectively. We shall now consider the simulation procedure involved in the computation of type I error and power of the test.

Determination of type I error and power of the test

To apply the test of significance of any measure through χ^2 test or by normal Z test, it is necessary that the stability measure should follow normal distribution. For ensuring non-erroneous selection of genotypes, the power of the test should be high. In order to find out a better stability parameter for a particular situation, comparison is carried out, making use of these distributional properties. To examine whether the normality holds or not a simulation programme is run and the observed and expected probability of type I error ($\propto$) for various stability measures, parametric as well as non-parametric, are compared. The soundness of the normal approximation for each of these measures is thereby assessed. A comparison is also made in terms of their power of the test. The essential details of the simulation procedure are given in the following paragraphs.

Simulation of variate values

According to Nassar *et al.*, [3] the ultimate distributional properties and the power of F test do not change much when the variate values are generated on computer and this is the motivation for the adoption of the procedure for the present investigation. The simulation of normal variate with general mean μ and error standard deviation σ_e is carried out in two stages. In the first stage, the standard uniform variates are generated which is further used to generate standard normal variates. The generation of standard uniform variate starts with the use of a random seed value, which allows the first function to generate a random number. The seed value used in the generation of first random number will change itself and produces

an entirely different random number, and this process continues. The generated random number in this function, every time, gets converted into a standard uniform variate, which will be used in second stage.

The second stage is the generation of normal variates with specified μ and σ_e values and this is achieved as follows. A second subroutine receives generated standard uniform variates from the first stage and converts them into a standard normal variates. These standard normal variates are used in the main programme to generate normal variables with a given mean and standard deviation. For generating a normal variate under the null hypothesis that all genotypes are equal in their effects, with mean μ and error variance σ_e, the model needs to include only the environmental and error effects. Therefore, in the generation of a single normal value (Y_{ij}), the programme invokes both the subroutines twice. But the generation of the variate values under the alternative hypothesis that the genotypes are not stable over the environments involves the inclusion of the effects of genotype, environment and GE interaction in the model. Thus the programme requires the invoking the subroutine four times one each for genotypic, environmental, interaction and error effects. The programme, therefore, takes more running time under alternative hypothesis than under null hypothesis. Adopting this procedure the probability of type I error and power of the test are studied in the following paragraphs.

Determination of type I error

The fact that the stability measures developed based on ranks can be approximated to normal distribution at least in the tail ends of the distribution [4] has helped in the development of the significance test for equality of stability values. The simulation procedure for the determination of Y_{ij} values under null hypothesis is considered in what follows:

Under the null hypothesis the performance of *i*th genotype in *j*th environment can be expressed as

$$Y_{ij} = \mu + e_j + \varepsilon_{ij} \qquad \ldots (6)$$

where, μ is the over all population mean,

e_j is the effect of environment j (j= 1, 2, ..., s)

ε_{ij} is the random error associated with *i*th genotype (i = 1, 2, ..., t) and *j*th environment and distributed with mean zero and variance σ_e^2

Since the environmental effect is same for all the genotypes, e_j has no influence on the null hypothesis in so far as the non-parametric measures are concerned and so in the generation of Y_{ij} values e_j can be conveniently assumed to be zero. For the simulation of the requisite data, the parametric values of μ and σ_e^2 were taken from the extensive data from All India Coordinated Project on Pearl millet. Assuming the grain yields to be normally distributed, the required normal variates (Y_{ij}) were generated as per the procedure, given above taking μ = 1984 and σ_e^2 = 152.22 and σ_E^2 = 1121.

The simulation programme is run for generating sets of $t \times s$ observations, coming from t genotypes (8, 10, ..., 24) and s environments (5, 10, 15). For each (t, s) combination the data are generated using three different random seeds thereby obtaining 3 sets of ts observations to serve as 3 replications. For each replication of a specified ts observations, the values of non-parametric stability measures $NP(1)$ to $NP(5)$ and also of the parametric measures considered are arrived at. This yields different sets of 3 × t values, one for each stability parameter, and each set is subjected to a one way ANOVA for testing the genotypic differences if any. For each (t, s) combination the entire procedures is repeated for 1000 (in a few cases, 5000 times) times and the number of times the observed F ratios exceed the table F value is determined. This number expressed as a proportion is our observed type I error. The observed $\propto$ is computed for different expected levels of significance ($\propto$ = 0.01, 0.05). For these expected $\propto$ levels the table values of F with degrees of freedom (t – 1) and $2t$ are taken as critical values. For the comparison of observed $\propto$ with a specified expected $\propto$ has been presented in Tables 2 to 13. These are tabulated for the different stability measures mentioned above for different combination of t and s.

Power of the test

For the comparison of the stability measures $NP(1)$ to $NP(5)$ with the parametric measures mentioned in the previous section in terms of their power efficiency a simulation programme was run under the full model

$$Y_{ij} = \mu + g_i + e_j + (ge)_{ij} + \varepsilon_{ij}$$

where the symbols have their usual meanings. The generation of variate values is carried out as explained earlier. For the simulation purpose the parametric values as determined from the real data on pearl millet have been made use of. Data are generated for different combination of t (8, 12, 16, 20 and 24) and s (5, 10 and 15). With the help of the $t \times s$ simulated normal values t genotypic stability values are

Table 2. Comparison between observed and expected Type I error (∝) for different number of genotypes (t) tested in s = 5 environments for various non-parametric measures

Expected ∝ = 0.01

t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.0167*	0.0170	0.0240	0.0231	0.0223
10	0.0171	0.0143	0.0217	0.0219	0.0167
12	0.0141	0.0137	0.0194	0.0193	0.0163
14	0.0140	0.0133	0.0181	0.0181	0.0150
16	0.0123	0.0130	0.0165	0.0162	0.0141
18	0.0117	0.0120	0.0141	0.0171	0.0141
20	0.0114	0.0121	0.0137	0.0132	0.0140
22	0.0122	0.0120	0.0129	0.0121	0.0123
24	0.0113	0.0099	0.0131	0.0115	0.0121

*An observed value represents Pr $[F > F_{.01,(t-1),2t}]$

Table 3. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 10 environments for various non-parametric measures

Expected ∝ = 0.01

t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.0240	0.019	0.027	0.031	0.023
10	0.0230	0.017	0.026	0.029	0.021
12	0.0200	0.013	0.023	0.028	0.021
14	0.0190	0.012	0.021	0.024	0.020
16	0.0170	0.011	0.019	0.019	0.021
18	0.0150	0.009	0.018	0.018	0.019
20	0.0120	0.011	0.018	0.015	0.017
22	0.0110	0.012	0.014	0.014	0.016
24	0.0130	0.013	0.015	0.016	0.015

*An observed value represents Pr $[F>F_{.01,(t-1),2t}]$

Table 4. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 15 environments for various non-parametric measures

	Expected ∝ = 0.01				
t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.0230	0.0190	0.027	0.0330	0.0270
10	0.0200	0.0200	0.028	0.0300	0.0260
12	0.0160	0.0180	0.029	0.0280	0.0220
14	0.0150	0.0170	0.022	0.0250	0.0230
16	0.0140	0.0160	0.019	0.0240	0.0170
18	0.0120	0.0160	0.018	0.0220	0.0160
20	0.0120	0.0150	0.014	0.0180	0.0150
22	0.0110	0.0130	0.012	0.0180	0.0150
24	0.0130	0.0110	0.017	0.0220	0.0150

*An observed value represents Pr $[F > F_{.01, (t-1), 2t}]$

Table 5. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 5 environments for various non-parametric measures

	Expected ∝ = 0.05				
t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.0650	0.0690	0.0890	0.0810	0.6730
10	0.0613	0.0590	0.0880	0.0840	0.0700
12	0.0631	0.0570	0.0740	0.0790	0.0720
14	0.0610	0.0587	0.0780	0.0720	0.0660
16	0.0590	0.0530	0.0710	0.0780	0.0650
18	0.0560	0.0460	0.0690	0.0720	0.0570
20	0.0570	0.0510	0.0670	0.0640	0.0590
22	0.0540	0.0540	0.0640	0.0670	0.0610
24	0.0530	0.0520	0.5900	0.0610	0.0610

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

Table 6. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 10 environments for various non-parametric measures

	Expected ∝ = 0.05				
t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.083	0.077	0.102	0.087	0.098
10	0.076	0.074	0.092	0.081	0.082
12	0.065	0.071	0.079	0.082	0.074
14	0.063	0.080	0.081	0.073	0.069
16	0.059	0.060	0.064	0.067	0.068
18	0.057	0.061	0.068	0.064	0.056
20	0.053	0.058	0.059	0.062	0.057
22	0.060	0.057	0.060	0.061	0.053
24	0.052	0.057	0.063	0.060	0.063

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

Table 7. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 15 environments for various non-parametric measures

	Expected ∝ = 0.05				
t	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	0.0920	0.066	0.089	0.1160	0.093
10	0.0810	0.065	0.082	0.092	0.094
12	0.0840	0.061	0.081	0.086	0.092
14	0.0820	0.062	0.075	0.072	0.089
16	0.0790	0.059	0.071	0.074	0.081
18	0.0770	0.057	0.062	0.069	0.076
20	0.0650	0.057	0.061	0.064	0.075
22	0.0620	0.052	0.058	0.063	0.068
24	0.0590	0.053	0.058	0.063	0.064

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

Table 8. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 5 environments for various parametric measures

	Expected ∝ = 0.01				
t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0164	0.0153	0.0186	0.0247	0.0274
10	0.0159	0.0146	0.0181	0.0221	0.0247
12	0.0143	0.0143	0.0174	0.0193	0.0276
14	0.0131	0.0137	0.0168	0.0182	0.0202
16	0.0127	0.0133	0.0163	0.0169	0.0163
18	0.0124	0.0121	0.0149	0.0154	0.0158
20	0.111	0.0120	0.0144	0.0147	0.0150
22	0.0112	0.0122	0.0139	0.0142	0.0167
24	0.0091	0.0126	0.0141	0.0137	0.0146
26	0.0117	0.0127	0.0132	0.0122	0.0131

*An observed values represents Pr $(F > F_{.01, t-1, 2t})$

Table 9. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 10 environments for various parametric measures

	Expected ∝ = 0.01				
t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0143	0.0156	0.0147	0.0167	0.0233
10	0.0143	0.0155	0.0147	0.0142	0.0211
12	0.0139	0.0147	0.0131	0.0131	0.0192
14	0.0137	0.0140	0.0137	0.0124	0.0171
16	0.0134	0.0134	0.0129	0.0113	0.0167
18	0.0121	0.0130	0.0133	0.0083	0.0151
20	0.0124	0.0127	0.0120	0.0081	0.0130
22	0.0119	0.0126	0.0124	0.0117	0.0124
24	0.0107	0.0121	0.0127	0.0116	0.0101

*An observed values represents Pr $(F > F_{.01, t-1, 2t})$

Table 10. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 15 environments for various parametric measures

Expected ∝ = 0.01

t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0152	0.0158	0.0201	0.0143	0.0221
10	0.0147	0.0156	0.0197	0.0142	0.0206
12	0.0147	0.0144	0.0194	0.0142	0.0174
14	0.0131	0.0143	0.0186	0.0134	0.0163
16	0.0134	0.0140	0.0177	0.0127	0.0170
18	0.0119	0.0139	0.0163	0.0119	0.0161
20	0.0107	0.0132	0.0160	0.0110	0.0156
22	0.0113	0.0130	0.0154	0.0126	0.0147
24	0.0117	0.0134	0.0154	0.0120	0.0144

*An observed values represents Pr $(F > F_{.01, t-1, 2t})$

Table 11. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 5 environments for various parametric measures

Expected ∝ = 0.05

t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0640	0.0611	0.0771	0.0744	0.0834
10	0.0621	0.0607	0.0723	0.0671	0.0810
12	0.0603	0.0600	0.0694	0.0663	0.0807
14	0.0574	0.0591	0.0641	0.0644	0.0741
16	0.0543	0.0570	0.0617	0.0610	0.0674
18	0.0531	0.0574	0.0609	0.0576	0.0631
20	0.0540	0.0539	0.0603	0.0549	0.0647
22	0.0529	0.0530	0.0584	0.0537	0.0614
24	0.0613	0.0517	0.0592	0.0532	0.0600

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

Table 12. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 10 environments for various parametric measures

Expected ∝ = 0.05

t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0634	0.0621	0.0723	0.0717	0.0804
10	0.0630	0.0601	0.0701	0.0642	0.0775
12	0.0567	0.0607	0.0664	0.0636	0.0713
14	0.0561	0.0602	0.0621	0.0619	0.0642
16	0.0547	0.0567	0.0617	0.0581	0.0531
18	0.0540	0.0566	0.0601	0.0580	0.0632
20	0.0531	0.0544	0.0602	0.0553	0.0606
22	0.0531	0.0540	0.0601	0.0551	0.0582
24	0.0546	0.0540	0.0600	0.0550	0.0580

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

Table 13. Comparison between observed and expected Type I error (∝) for different number of genotypes (*t*) tested in *s* = 15 environments for various parametric measures

Expected ∝ = 0.05

t	P(1)	P(2)	P(3)	P(4)	P(5)
8	0.0679	0.0622	0.0743	0.0736	0.0792
10	0.0664	0.0607	0.0712	0.0697	0.0687
12	0.0643	0.0606	0.0683	0.0692	0.0632
14	0.0611	0.0594	0.0642	0.0647	0.0631
16	0.0613	0.0590	0.0621	0.0627	0.0624
18	0.0600	0.0610	0.0624	0.0596	0.0622
20	0.0604	0.0616	0.0617	0.0582	0.0613
22	0.0597	0.0600	0.0623	0.0567	0.0607
24	0.0603	0.0600	0.0614	0.0569	0.0600

*An observed values represents Pr $(F > F_{.05, t-1, 2t})$

calculated for all the stability measures. In fact, we consider two additional set of $t \times s$ observations obtained from different seeds. These sets along with the first set serve as 3 replications of t genotypic stability values, which are analyzed by one way ANOVA for equal genotypic effects. The observed F value computed from the simulation is compared with the table F value with $(t - 1)$, $2t$ degrees of freedom. This procedure is repeated for 1000 times (5000, in a few cases) and the number of times the observed F statistic from ANOVA exceed the tabular F values at each level of significance, $\propto$ (0.01, 0.05) is worked out. The power of the test is determined there from. The values for different combinations of $\propto$, t and s are presented in Tables 14 to 17.

Table 14. Comparison of power of the test (in a one way ANOVA) for different combinations of number of genotypes (t) and number of environments (s) at $\propto$ = 0.01 for non- parametric measures

μ (Mean) = 1984 σ_e^2 = 152.22 σ_G^2 = 97.08 σ_E^2 = 1121 $\sigma_{G\times E}^2$ = 324.44

t	s	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	5	0.411	0.373	0.337	0.495	0.379
12	5	0.596	0.667	0.621	0.771	0.672
16	5	0.751	0.764	0.772	0.932	0.819
20	5	0.922	0.913	0.941	0.976	0.923
24	5	0.982	0.952	0.987	1.000	0.964
8	10	0.437	0.481	0.529	0.571	0.447
12	10	0.622	0.733	0.812	0.842	0.779
16	10	0.791	0.891	0.947	0.973	0.891
20	10	0.849	0.974	1.000	1.000	0.967
24	10	0.973	1.000	1.000	1.000	0.993
8	15	0.399	0.533	0.462	0.610	0.311
12	15	0.621	0.741	0.791	0.774	0.547
16	15	0.724	0.839	0.877	0.831	0.721
20	15	0.891	0.916	0.974	0.924	0.836
24	15	0.967	0.953	0.981	0.988	0.951

RESULTS AND DISCUSSION

As the non-parametric measures are distribution free, these measures can be computed even when the genotype-environment data do not follow normal distribution. These are also resorted to when the nonlinear component of GE interaction is so large that the parametric measures fail to provide any meaningful interpretation of the stability factor. It is against this background, a comparison between non-parametric and parametric measures have been made through the simulation procedure outlined in the previous section. The observed values of type-I error ($\propto$) for the non-parametric measures, for different levels of expected $\propto$, genotype (t) and environment (s) numbers are presents in Tables 2 to 7. Similar values for the parametric case are given in Tables 8 to 13. From these tables it is evident that the agreement between observed and expected $\propto$ is more striking in the case of non-parametric measures. As regards the convergence of observed to expected $\propto$ it is faster in the case of NP(2) than the

Table 15. Comparison of power of the test (in a one way ANOVA) for different combinations of number of genotypes (t) and number of environment (s) at $\propto$ = 0.05 for non- parametric measures.

μ (Mean) = 1984 σ_e^2 = 152.22 σ_G^2 = 97.08 σ_E^2 = 1121 $\sigma_{G\times E}^2$ = 324.44

t	s	NP(1)	NP(2)	NP(3)	NP(4)	NP(5)
8	5	0.531	0.613	0.597	0.671	0.556
12	5	0.771	0.741	0.839	0.883	0.839
16	5	0.783	0.831	0.984	0.944	0.971
20	5	0.881	0.961	0.981	0.979	0.986
24	5	0.942	0.982	0.987	0.999	0.991
8	10	0.562	0.601	0.655	0.757	0.677
12	10	0.692	0.799	0.891	0.917	0.834
16	10	0.872	0.917	0.937	1.000	0.951
20	10	0.937	1.000	0.981	1.000	0.973
24	10	0.974	1.000	1.000	1.000	0.982
8	15	0.566	0.572	0.743	0.641	0.531
12	15	0.673	0.811	0.873	0.939	0.666
16	15	0.754	0.970	0.962	0.968	0.837
20	15	0.873	0.967	0.981	0.996	0.941
24	15	0.913	0.960	0.974	1.000	0.954

remaining measures; for a small number of environments (s) it needs lesser number of genotypes to converge; though the values of s and t depend on the level of true $\propto$. In this respect the measure NP(1) is closely behind NP(2).

The powers of the test for the non-parametric cases are given in Tables 14 and 15 while the figures for the parametric case are in Tables 16 and 17. Thennarasu[1] had already reported that the power of the test increases as the magnitude of σ_{ge} decreases; therefore, this aspect was kept outside the purview of the present investigation. As expected the power of the test, in general, were higher in the parametric situations than in the non-parametric situations. It is also seen that the power increases rapidly with the increase in the number of genotypes. On the other hand the change of power from any increase in the number of environments, is rather small. A notable feature emerging from the data is that when the number of genotypes in the trial is fairly large the power efficiency of the non-parametric measures will be quite close to that of the parametric measures. So in these situations

Table 16. Comparison of power of the test (in a one way ANOVA) for different combinations of number of genotypes (t) and number of environments (s) at $\propto$ = 0.01 for parametric measures

μ (Mean) = 1984 σ_e^2 = 152.22 σ_G^2 = 97.08 σ_E^2 = 1121 $\sigma_{G\times E}^2$ = 324.44

t	s	P(1)	P(2)	P(3)	P(4)	P(5)
8	5	0.613	0.672	0.715	0.801	0.674
12	5	0.803	0.845	0.935	0.918	0.879
16	5	0.854	0.892	0.971	0.874	0.983
20	5	0.915	0.984	0.998	1.000	0.997
24	5	0.975	1.000	1.000	1.000	1.000
8	10	0.618	0.701	0.723	0.839	0.719
12	10	0.784	0.884	0.913	0.935	0.870
16	10	0.901	0.994	0.958	1.000	0.974
20	10	0.964	1.000	1.000	1.000	0.992
24	10	0.998	1.000	1.000	1.000	1.000
8	15	0.641	0.629	0.813	0.784	0.638
12	15	0.709	0.874	0.892	0.984	0.711
16	15	0.818	0.978	0.984	0.992	0.894
20	15	0.935	0.991	0.992	0.999	0.955
24	15	0.992	1.000	0.998	1.000	1.000

Table 17. Comparison of power of the test (in a one way ANOVA) for different combinations of number of genotypes (t) and number of environments (s) at $\propto$ = 0.05 for parametric measures

μ (Mean) = 1984 σ^2_e = 152.22 σ^2_G = 97.08 σ^2_E = 1121 $\sigma^2_{G\times E}$ = 324.44

t	s	P(1)	P(2)	P(3)	P(4)	P(5)
8	5	0.703	0.743	0.804	0.839	0.749
12	5	0.818	0.891	0.960	0.954	0.903
16	5	0.903	0.918	0.982	0.986	0.994
20	5	0.951	0.998	0.999	1.000	1.000
24	5	0.982	1.000	1.000	1.000	1000
8	10	0.709	0.739	0.834	0.872	0.813
12	10	0.818	0.982	0.934	0.992	0.917
16	10	0.953	1.000	0.965	1.000	0.991
20	10	0.992	1.000	1.000	1.000	0.998
24	10	1.000	1.000	1.000	1.000	1.000
8	15	0.754	0.715	0.891	0.835	0.705
12	15	0.845	0.913	0.902	0.989	0.819
16	15	0.919	0.991	0.994	0.997	0.911
20	15	0.972	0.997	0.998	1.000	0.992
24	15	0.997	1.000	1.000	1.000	1.000

the risk of selecting inferior genotypes from the use of non-parametric measures is minimal. Among the non-parametric measures, power of NP(2) is comparable to those of NP(3) and NP(4) and is definitely superior to both NP(1) and NP(5). We have already seen that the adequacy of normal approximation (in terms of $\propto$ convergence) in the case both NP(1) and NP(2). Now we have noted that in respect of power efficiency NP(2) is superior to NP(1). Accordingly, in situations involving a large number of genotypes, which are to be performance-tested in a set of environments, whose number is neither too small nor too large the measure NP(2) can be used for selecting stable genotypes.

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INHERITANCE OF STEM RUST RESISTANCE IN A WHEAT-RYE RECOMBINANT LINE 'SELECTION 212'

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ABSTRACT

Selection 212, a wheat-rye recombinant developed through homoeologous recombination between wheat and rye chromosomes using monosomic 5B of variety Chinese Spring was studied for inheritance of resistance against stem rust pathogen (*Puccinia graminis* f. sp. *tritici*). The F_1, the F_2, the F_3, the BC_1F_1 and the BC_1F_2 generations of the crosses involving 'Selection 212' and two susceptible lines Agra Local and Chinese Spring were tested in seedlings with pathotypes 122 and 40A of *P. graminis tritici*. A single recessive gene that controlled resistance to both the pathotypes was determined. Correlated behaviour of the F_2 backcross families of the cross (Sel.212 × AL) × AL with both the pathotypes revealed that the same resistance gene is providing resistance to pathotypes 122 and 40A. In addition, an adult plant resistance gene *Sr2* was also identified.

Key Words : Wheat, rye (*Secale cereale*), stem rust (*Puccinia graminis*), inheritance, recessive

Stem rust of wheat caused by *Puccinia graminis* Pres. f.sp. *tritici* Eriks. and Henn. is the most devastating disease of wheat crop in warmer climates. Breeding for rust resistance is the most feasible and practical approach to check losses caused by rust diseases. The evolution of new pathotypes on widely grown resistant cultivars necessitates identification of new sources of resistance for continuous process of resistance breeding. In an effort 'Selection 212', (Sel. 212) a line with new source of resistance was developed by homoeologous chromosome recombination between wheat and rye using monosomic 5B of variety Chinese Spring [1]. Sel. 212 when tested at seedling stage with 20 pathotypes of *P. graminis tritici* was found resistant to all the pathotypes [2]. The present study reports the inheritance of resistance to stem rust at seedling and adult plant growth stages using pathotypes 122 and 40A which identify resistance in Sel. 212, transferred from rye.