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Performance of Parametric and Non-Parametric Stability Measures

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SUMMARY

The presence of genotype-environment interactions necessitates the development of varieties or breeds suited or tailored to different agro-ecological environments based on their stability and adaptability characteristics. In many situations, the assumption about the normality and independence of observations as well as homogeneity of error variances is not fulfilled. This investigation aims to determine and compare, in terms of statistical power, the performance of different parametric and non-parametric methods for stability measures when the basic data are not normally distributed.

Keywords: Genotype environment interaction, Statistical power, Simulation, Stability measures.

1. INTRODUCTION

Crop and animal improvement would have been much simpler if there were no cross over genotype-environment interactions (GEI), which cause differential performance of different genotypes in different environments. The presence of genotype-environment interactions necessitates the developments of varieties or breeds suited or tailored to different, agro-environments based on their stability and adaptability characteristics. If possible, the breeder would like to have varieties, which show high performance for yield and other agronomic traits over as a wider range of environmental conditions as possible. However, the wide occurrence of GEI causes difficulty in the identification of superior varieties. In order to overcome this difficulty an attempt is usually made by the plant breeder to reduce the GEI, i.e. dependence of the genotypic ranking on environmental conditions through special breeding techniques like resistance breeding. For the final choice of varieties for general/specific adaptation, apart from the mean performance the stability characteristics of the trial genotypes have to be given due consideration.

Initially there were four different approaches to the statistical analysis of GEI (Prabhakaran and Jain, 1994). These are, the 'Variance component approach', 'regression approach', 'biometrical genetics approach' and the 'genetic correlation approach'. The choice among these methods depend on the particular situation in hand and the type of data that are collected. Subsequently various concepts of stability were advanced. Several procedures for analyzing GEI and yield stability were proposed. Most of these procedures (Prabhakaran and Mehra, 2002), however, were parametric methods performance of which were not quite satisfactory from the standpoint of breeders. The scientists therefore started looking for non-parametric measures

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which allow the selection of genotypes simultaneously for yield and stability.

There is hardly any study on the performance of non-parametric as well parametric measures when the basic data is not normally distributed. The objective of this study is therefore to investigate the performance of non-parametric as well as parametric measures when the basic data is not normally distributed.

2. NON-PARAMETRIC STABILITY MEASURES

There is ample justification for the use of non-parametric measures in the assessment of yield stability of crop varieties. Their chief advantages are (i) No assumptions about the distribution of phenotypic observations are needed, (ii) Sensitivity to measurement errors or to outliers are much less compared to parametric measures, (iii) Additions or deletions of one or a few genotypes do not cause distortions to non-parametric measures, (iv) Most of the time, the breeder, is concerned with crossover interaction, an estimate of stability based on rank-information, therefore, seems more relevant and (v) These measures are particularly useful in situations where parametric measures fail due to large non-linear GEI. In literature, non-parametric measures have been widely employed in the selection of crop varieties especially when the interest mainly lies in crossover interaction (Huhn 1996, Nassar *et al*., 1994, Thennarasu, 1995, Raiger and Prabhakaran, 2000, 2001).

The ranks based on uncorrected observations have been corrected to propose the mean rank difference and variance of ranks as stability statistics. Nassar *et al*. (1994) proposed six different stability measures, three based on ranks and the remaining based on phenotypic values and compared their distributional properties namely the power of the tests and their statistical significance simultaneously. Thennarasu (1995) proposed four non-parametric measures and showed that two of them performed better than the earlier measures. Raiger and Prabhakaran (2000, 2001) also conducted a detailed investigation on the utility of the non-parametric procedure for detecting genotype-environment interaction and assessing the stability of individual genotype. They computed type I error and power of the test which are useful in evaluating the merits of various stability measures. Performance of non-parametric measures vis-à-vis parametric measures was assessed on these criteria.

Consider t genotypes 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 cannot be based purely on the mean phenotypic values Y_{ij}, because the stability has to be measured independently of the genotypic effect. Therefore, r_{ij} the rank of the i^{th} genotype in the j^{th} environment is determined on basis of the corrected phenotypic values, namely $(Y_{ij} - \bar{Y}_{i.})$, $\bar{Y}_{i.}$ being the mean performance of the i^{th} genotype. Further, let $\bar{r}_{i.}$ and M_{di} be mean and median of ranks based on uncorrected values (r_{ij}) and $\bar{r}_{i.}^{*}$ and M_{di}^{*} be mean and median of ranks based on uncorrected values (r_{ij}). Some of the non-parametric measures from these considerations are given in Table 1.

It is a known fact that the non-parametric methods are less powerful than their parametric counterparts. The study conducted, against this background, by Raiger and Prabhakaran (2000) has shown 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 those of the parametric measures. So in situations which are commonly encountered, i.e. those involving a good number of genotypes being performance-tested in a set of environments whose number is, neither too small nor too large, the risk of selecting inferior genotypes from the use of non-parametric measures is minimal. It may, however, be noted that in all such studies the genotype by environment data were generated from normal populations. The behaviour of the various non-parametric and other measures under non-normality has never been considered in literature.

Table 1. Some of the Reported Non-parametric Stability Statistics** According to their Utility

Statistics measuring only stability:

$$S_i1 = 2\sum_{j<j'}^{s}\left|r_{ij} - r_{ij'}\right| / s(s-1) \qquad S_i3 = \sum_{j}(r_{ij} - \bar{r}_{i.})^2 / \bar{r}_{i.} \qquad NP_i(1) = (1/s)\sum_{j=1}^{s}\left|r_{ij} - Mdi\right|$$

Statistics combining stability & performance:

$$S_i4 = \sum_{j}(r_{ij} - \bar{r}_{i.})^2 /(s-1) \qquad S_i6 = \sum_{j<j'}^{s}\left|r_{ij} - r_{ij'}\right| / \bar{r}_{i.} \qquad NP_i(2) = (1/s)\sum_{j=1}^{s}\left|r_{ij} - Mdi\right| / M^{*}_{di}$$

$$NP_i(3) = \sqrt{[\sum(r_{ij} - \bar{r}_{i.})^2 / s]} / r^{*}_{i.} \qquad NP_i(4) = [2/s(s-1)]\sum_{j<j'}^{s}\left|r_{ij} - r_{ij'}\right| / \bar{r}_{i.}$$

** The *S* statistics (S_i1, S_i3, S_i4 and S_i6) were proposed by Huhn (1979) and the *NP* statistics (NP1, NP2, NP3 and NP4) by Thennarasu (1995)

Theoretical relationships of non-parametric measures, among themselves, and to the common parametric measures have not so far been elaborated. These, therefore, have to be judged on the basis of empirical (rank) correlations.

3. SIMULTANEOUS SELECTION FOR YIELD AND STABILITY

Integration of stability with performance through suitable measures will go a long way in selecting high yielding, stable cultivars. Several methods, for simultaneous selection for high yield and stability, and relationships among stability measures were discussed by Kang and Pham (1991). Kang (1993) discussed the reasons for emphasizing stability in the selection process. Generally, Type II errors constitute the most serious risk for growers (Johnson *et al.* 1992, Kang 1993) and an emphasis on stability during selection helps reduce such errors and is beneficial for growers. The development and use of *Yield-Stability statistic (YS_i)* has enabled incorporation of stability in the selection process (Kang 1993). A computer program (STABLE) for calculating this statistic is available free of charge (Kang and Magari 1995). Kang's Yield-Stability statistic (Kang 1993) has been evaluated and found to be useful for recommending varieties (Pazdernik *et al.* 1997, Hussein *et al*. 2000). However, Bajpai and Prabhakaran (1998, 2000) observed that Kang's rank-sum method has an inherent weakness that it is weighing heavily towards yield performance, apart from the arbitrariness in the scoring procedure. Accordingly they proposed three new indices (I_1, I_2, I_3), which were found to be superior to Kang (1993) indices. Dashiell *et al.* (1994) evaluated the usefulness of several stability statistics for simultaneously selecting for high yield and stability of performance in soybean. Fernandez (1991) also evaluated stability statistics for similar purposes. Other useful works in the area include, Kang (1990), and Gravois *et al.* (1990).

Several non-parametric measures were also proposed [Huhn 1996, Thennarasu 1995, Raiger and Prabhakaran 2000, 2001]. Nassar *et al.* (1994) compared the performance of 3 parametric and 3 non-parametric measures based on 2 criteria, convergence of observed α (type-I error) to the postulated α and the power of the test, (1-β). But all these studies were based on normally distributed dataset. Based on this investigation they recommended the parametric measure, $\sum_{j}\left|x_{ij} - O\right| / s$ and the non-parametric measure $\sum_{j}\left|r_{ij} - O\right| / s$ [where x_{ij} is the phenotypic value of the i^{th} genotype in environment j, r_{ij} is the rank based on corrected x_{ij} and O is some

measure of optimum performance] for varietal selection. Based on the same criteria, Thennarasu (1995) and Raiger and Prabhakaran (2000) found that, in situations involving a good number of genotypes, which are to be tested in a set of environments, whose number is neither too small nor too large, the measure *NP*(2) (Table 1) is a useful combined-measure.

In the present investigation, an attempt has been made to compare the performance of stability measure for normal and no-normal data. The performance of non-parametric measure vis-à-vis parametric measures has also been considered for both normal as well as non-normal conditions.

4. METHODOLOGY

Variates from different distributions such as normal, gamma and beta, are generated. The variates so generated are used for computing different parametric as well as non-parametric stability measures. They are compared with the stability measures coming from normal observations. The type 1 error (α) and power of the test (1-β) are considered for empirical comparison. For simulation of data from non-normal population we used he following algorithms:

4.1. Standard Gama Distribution

1. Generate G(1) variates
2. Set $X = \sum_k X_k$ where each X_k is G(1)
3. Return X

Setting $Y = \beta X$ will generate variates from G (p, β), with p.d.f.

$$f(y) = \frac{1}{\Gamma(p)\beta^p} y^{p-1} e^{-y/\beta}$$

4.2 Beta Distribution

Initialization

1. Set α=a + b if (a, b) $\leq$ 1 set β = 1/min (a, b)

   Otherwise set $\beta = \{(\alpha - 2)/(2ab - \alpha)\}^{1/2}$

   Set $\gamma = a + 1/\beta$

2. Generate U_1 and U_2 and set V= β log $\{ U_1 / (1- U_1)\}$

   W=a.exp(V)

3. If $\alpha \log\{(\alpha + (b + W) \} + \gamma V - \log(4) < \log(U_1 U_2 U_3)$, go to (i)

4. Return X= W/ (b + W)

4.3 Stability Measures Considered

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 genotypes in a particular environment 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 i^{th} genotype in the j^{th} environment is determined on basis of the corrected phenotypic values Y_{ij}, defined as

$Y_{ij}=Y_{ij}-Y_i$

Y_i being the mean performance of the i^{th} genotype. The ranks obtained from these corrected Y_{ij}' s depend only on the GE interaction and error components and these are tabulated in the following table.

Genotype	Environment							Mean
	e1	e2	e3	…	ej	…	es	
g_1	r_{11}	r_{12}	.	…	r_{1j}	…	r_{1s}	$r_{1.}$
g_2	r_{21}	r_{22}	.	…	r_{2j}	…	r_{2s}	$r_{2.}$
.	.	.	.	…	.	…	.	.
g_1	r_{i1}	r_{i2}	.	…	r_{ij}	…	r_{is}	$r_{i.}$
.	.	.	.	…	.	…	.	.
g_t	r_{t1}	r_{t2}	.	…	r_{tj}	…	r_{ts}	$r_{t.}$
Mean	$\frac{t+1}{2}$	$\frac{t+1}{2}$			$\frac{t+1}{2}$		$\frac{t+1}{2}$	r= $\frac{t+1}{2}$

For ranking purpose, the smallest Y_{ij} in a particular environment is given rank one, the next higher value, rank two, and so on. Using the

rank values and rank means, Thennrasu (1995) proposed the following stability measures

$$NP_i(1) = (1/s)\sum_{j=1}^{s}\left|r_{ij} - Mdi\right|$$

$$NP_i(2) = (1/s)\sum_{j=1}^{s}\left|r_{ij} - Mdi\right| / M^{*}_{di}$$

$$NP_i(3) = \sqrt{[\sum(r_{ij} - \bar{r}_{i.})^2 / s]} / r^{*}_{i.}$$

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

are studied when the basic data are non-normal.

As regards parametric measures we used mainly on the following statistics

Wricke (1962) Ecovalence measure

$$W_i = \sum(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2 = \sum_j \hat{g}_{ij}^2$$

Shukla (1972) Stability variance

$$\sigma_i^2 = \frac{t}{(s-1)(t-2)}W_i - \frac{MS(GE)}{(t-2)}$$

Eberhart & Russell (1996) b_i

$$b_i = \sum_{\mathrm{j}}(\mathrm{Y_{ij}} - \bar{Y}_{i.})(\bar{Y}_{.j} - \bar{Y}_{..}) / \sum_j(\bar{Y}_{.j} - \bar{Y}_{..})^2$$

Perkins and Jinks (1968) deviation mean square

$$s^2_{d_i} = [\sum_j(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2 - \beta_i^2\sum_j e_j^2\ ]/(\text{s-2})$$

Pinthus (1973) r_i^2 measure

$$\mathrm{r}_i^2 = b_i^2\sum_j \hat{e}_j^2 / [\, b_i^2\sum_j \hat{e}_j^2 + \sum_j \delta_{ij}^2\,]$$

* $MS(GE) = \sum(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2/(s-1)(t-1)$ is the GE interaction mean square

P1= $b_i = \sum_{\mathrm{j}}(\mathrm{Y_{ij}} - \bar{Y}_{i.})(\bar{Y}_{.j} - \bar{Y}_{..}) / \sum_j(\bar{Y}_{.j} - \bar{Y}_{..})^2$

P2= $W_i = \sum(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2 = \sum_j \hat{g}_{ij}^2$

P3= $\sigma_i^2 = \frac{t}{(s-1)(t-2)}W_i - \frac{MS(GE)}{(t-2)}$

P4= $s^2_{d_i} = [\sum_j(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2 - \beta_i^2\sum_j e_j^2\ ]/(\text{s-2})$

P5= $\mathrm{r}_i^2 = b_i^2\sum_j \hat{e}_j^2 / [\, b_i^2\sum_j \hat{e}_j^2 + \sum_j \delta_{ij}^2\,]$

P6= $\beta_i = \sum_j(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2(\bar{Y}_{.j} - \bar{Y}_{..}) / \sum_j(\bar{Y}_{.j} - \bar{Y}_{..})^2$

4.3 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 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 (α) 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.

4.4 Simulation of Variates Values

According to Nassar *et al.* (1994) the ultimate distributional properties and the power of F test do not change much when the variates 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 variates 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 produce an entirely different random number, and this process continues. The generated random number in this function, every time, gets converted in to a standard uniform variates, 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 in to 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 variates under the null hypothesis that all genotypes are equal in their effects, with mean μ and error variance σ_e^2, 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 subroutine twice. But the generation of the variates values under the alternative hypothesis that the genotypes are not stable over the environment involves the inclusion of the effects of genotype, environment and GE interaction in the model. Thus the programme requires the invoking of 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 sections.

4.5 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 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

$$Y_{ij} = \mu + e_j + \in_{ij}$$

Where, μ is the overall population mean,

e_j is the fixed effect of environment j with variance σ_2.

$\in_{ij}$ is the random error associated with i^{th} genotype (l=1,2,…,t) in j^{th} environment and normally 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 discussed earlier, taking μ =1984 and σ_e^2 =152.22 and σ_e^2 =1121. It is to be noted that the value of μ and σ_e^2 will not have any specific effect on type I error thus any mean and error variance can in fact be used.

The simulation programme is run for generating sets of $t \times s$ observations, coming from t genotypes (8,12,16,20,24) and s environments (5,10,15,20). 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 specified *ts* observations, the values of non-parametric stability measures, developed non-parametric stability measures and also of the parametric measures considered are arrived at. This yields different sets of $3 \times t$ values, one for each stability parameter, and each sets is subjected to a one way ANOVA for testing the genotypic differences if any. For each (*t*,*s*) combination the entire procedures is repeated 1000 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 α is computed for different expected levels of significance (α = 0.01, 0.025, 0.05, 0.10). For these expected α levels the table values of F with degrees of freedom (*t*-1) and 2*t* are taken as critical values. The same procedures are followed for gamma and beta distribution. For the comparison of observed α with a specified expected α has been presented in the result and discussion section. These are exhibited for different stability measures mentioned above for different combination of *t* and *s*.

4.6 Power of the Test

The superiority of particular stability measure in a given situation is judged on the basis of the power of the test. A stability measure giving a higher amount of power is considered superior of another with lesser power. This study of power also helps in determining the number of genotypes and environments required for a given power. The following is the simulation procedure adopted for the computation of the power in various parameter combinations. For the comparison of the stability measures with the parametric and non-parametric measures mentioned in the previous section in terms of their power efficiency under the full model assuming same experimental design.

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

Where the symbols have their usual meanings. The generation of variates 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 used. Data are generated for different combination of *t* (8, 12, 16, 20 and 24) and *s* (5, 10, 15 and 20). With the help of the $t \times s$ simulated normal values, *t* genotypic stability values are 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), 2*t*] degrees of freedom. This procedure is repeated 1000 times (5000 in some cases) and the number of times the observed F statistic from ANOVA exceed the tabular F values at each level of significance, α (0.01, 0.025, 0.05 and 0.10) is worked out. The power of the test is determined therefrom. The values for different combinations of α, *t* and *s* are presented in following section.

5. RESULTS AND DISCUSSIONS

As mentioned earlier the non-parametric measures are distribution free and hence these measures can be computed even when the genotype-environment data do not follow normal distribution. These have also been 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 that a comparison between non-parametric and parametric measures have been made through the simulation procedure outlined in sections. The observed values of type-1 error (α) for the non-parametric measures, at expected α=0.05, and for different genotype (*t*) and environment (*s*) are presented in Fig. 1. Similar values for the parametric case are given in Fig. 5. From these Fig. it is evident that the agreement between observed and expected α is more striking in the case of non-parametric measures. As regards the convergence of observed to expected α it is

faster in the case of NP(2) than the 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 α. In this respect the measure NP(1) is closely behind NP(2). The power of the tests for the non-parametric cases as well as for the parametric cases is also reported.

5.1 Type 1 Error

The type 1 error for α = 0.01, 0.025, 0.05, 0.10 are obtained for normal distribution and only type 1 error for α = 0.05 is exhibited in Fig. 1 to save space. From the Fig. it is seen convergence of level of significance increasing with increase number of genotypes. Among the four nonparametric stability measures, all measure shows, all most same performance, NP_2 is the best.

5.2 Power of the Test

Gamma Distribution: The power of test in one way ANOVA for different combinations of genotype an environment for different level of significance α = 0.01, 0.025, 0.05, 0.10 are computed and only for α = 0.05 is tabulated in Fig. 3 to save space. It is noticed that with increase number of genotypes, the power increases. With increased level of significance, the power increases. NP_1 has better power then NP_3, NP_4 and NP_2.

Beta Distribution: In case of beta distribution the results are exhibited in Fig. 3. NP_3 shows better performance than NP_2, NP_1 and NP_4.

Normal Distribution: Results of normal distribution are shown in Fig. 4. NP_2 and NP_3 show better performance then NP_4 and NP_1.

5.3 Parametric Measures

Normal Distribution: In case of normal distribution the type1 errors are reported in Fig. 5 and powers are exhibited in Fig. 6. P_1, P_6 show better power in other and P_4 shows poor performance.

Gamma Distribution: The results in case of gamma distribution are tabulated in Fig. 7 and 8. Here it is noticed that P_4 shows poor performance where as P_1 is the best.

Beta Distribution: In case of beta distribution, the results are shown in Fig. 9 to 10. In case of power the only measure P_1 shows good performance whereas the rest measures show very poor result.

Thennarasu (1995) had already reported that the power of the test increases as the magnitude of $\sigma_{g\times e}$ decreases. So this aspect was kept outside the purview of the present investigation. As expected the power of the test was, in general, 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 for any increase in the number of environments is rather small. A notable feature emerging from the investigation is that when the number of genotypes in the trial is fairly large, the power of the non-parametric measures will be quite close to those of the parametric measure. So in these situations the risk of selecting inferior genotypes from the use of non-parametric measures is minimal. Among the non-parametric measures, power of NP(1) is comparable to those of NP(3) and NP(4) and is definitely superior to both NP(2). We have already seen that the normal approximation is adequate in terms of α convergence in the cases of both NP(3) and NP(2). Now we have noted that in respect of power efficiency, NP(3) is superior to NP(2). Accordingly, in situations involving a large number of genotypes, to be performance tested in a set of environments, whose number is neither too small not too large the measure NP(3) can be used for selecting stable genotypes. In comparison parametric and nonparametric measures it is noticed that in small sample parametric measures have better power than nonparametric measures. But in case of large sample they equally perform, even nonparametric measures have better power than

it counterpart. In some non normal distribution parametric measure failed where as the nonparametric shows better performance.

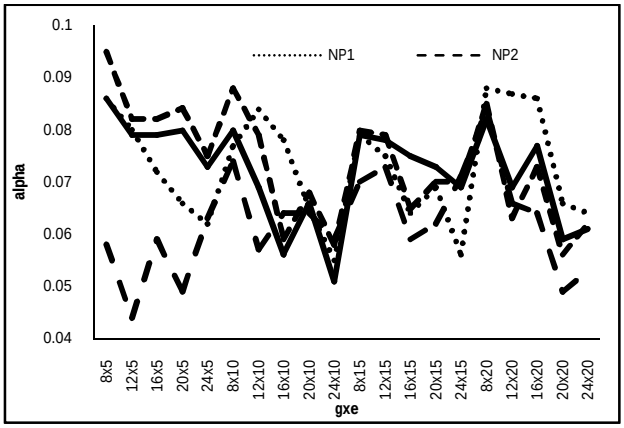

Fig. 1. Comparison between Observed and Expected Type I Error (α) for Different Number of Genotype (*t*) Tested in Different Environments for Various Non-parametric Measures (Expected α =0.05)

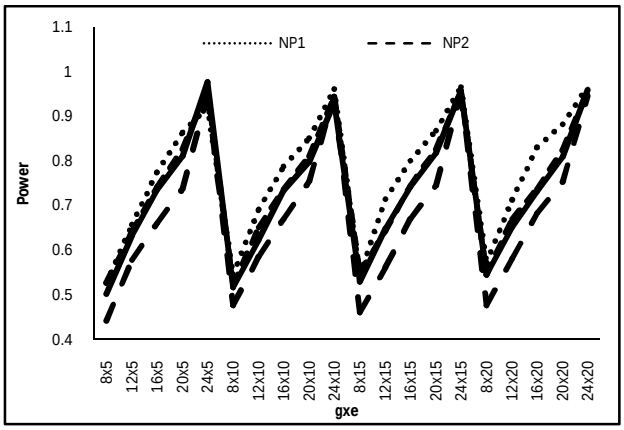

Fig. 2. Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Non-Parametric Measures in Case of Gamma Distribution

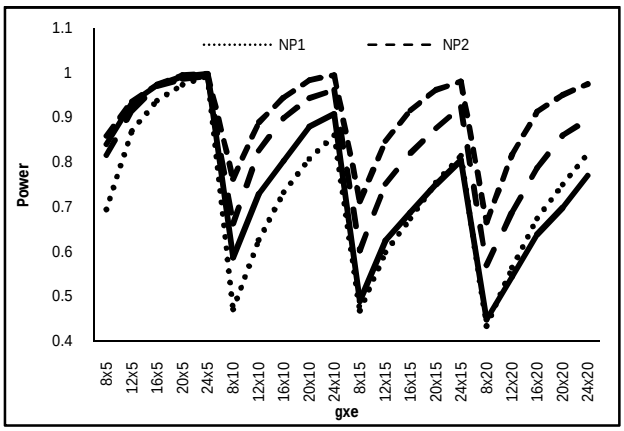

Fig. 3. Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Non-Parametric Measures in Case of Beta Distribution

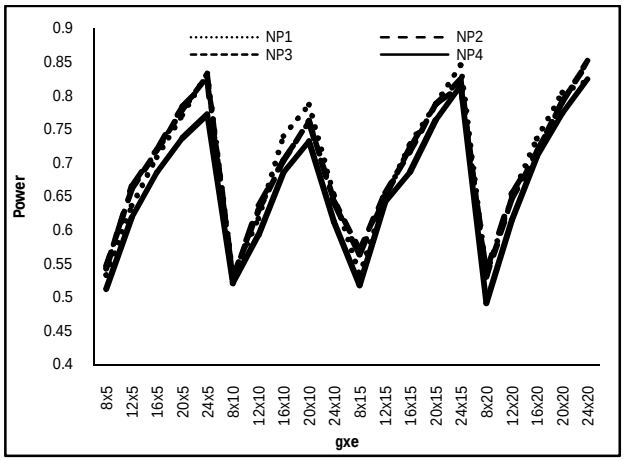

Fig. 4: Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Non-parametric Measures in Case of Normal Distribution

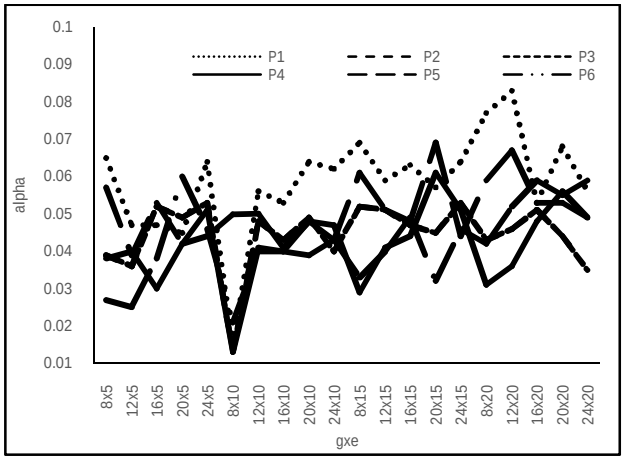

Fig. 5: Comparison between Observed and Expected Type I Error (α) for Different Number of Genotype (*t*) Tested in Different Environments for Various Parametric Measures in Case of Normal Distribution

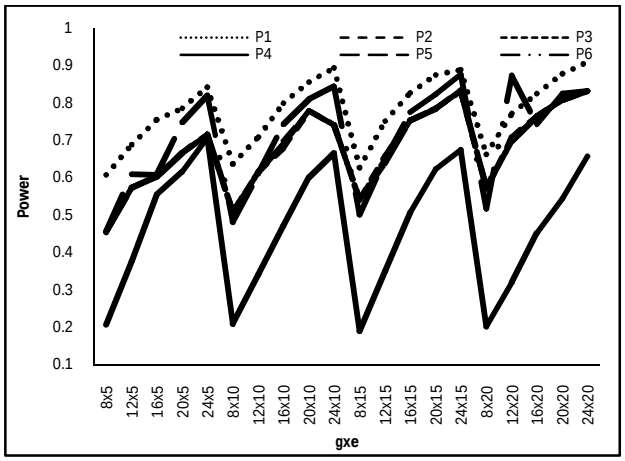

Fig. 6. Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Parametric Measures in Case of Normal Distribution

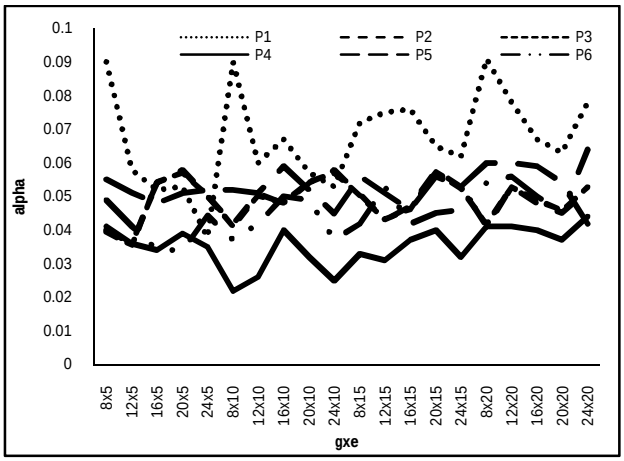

Fig. 7. Comparison between Observed and Expected Type I Error (α) for Different Number of Genotype (*t*) Tested in Different Environments for Various Parametric Measures in Case of Gamma Distribution

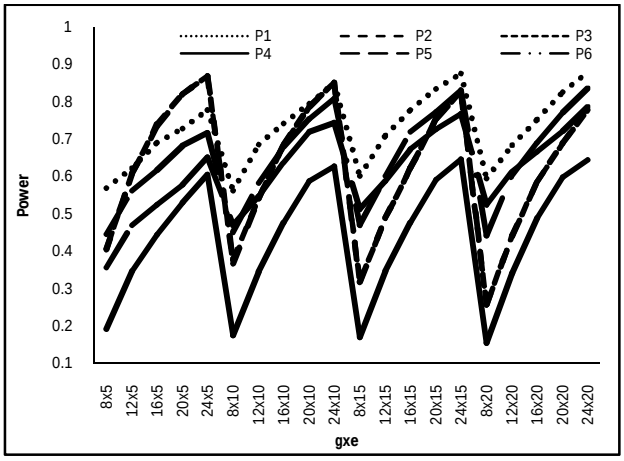

Fig. 8. Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Parametric Measures in Case of Gamma Distribution

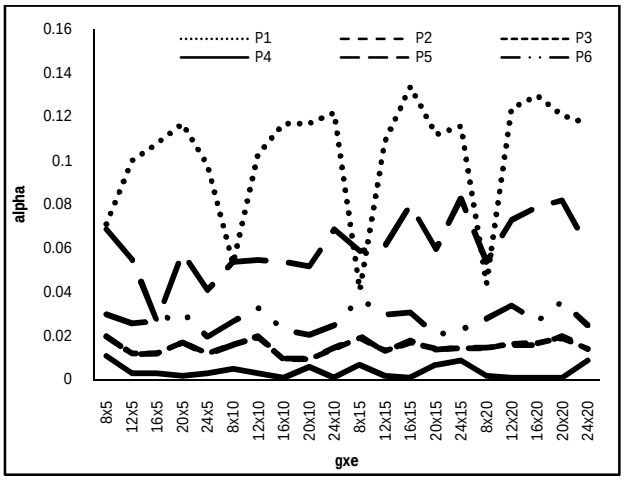

Fig. 9. Comparison between Observed and Expected Type I Error (α) for Different Number of Genotype (*t*) Tested in Different Environments for Various Parametric Measures in Case of Beta Distribution

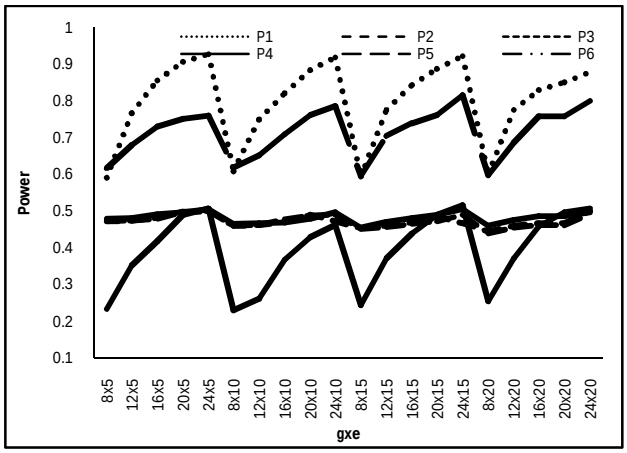

Fig. 10. Comparison of Power of the Test in a One Way ANOVA for the Different Combinations of Number of Genotypes (*t*) and Number of Environments (*E*) at α = 0.05 for Different Parametric Measures in Case of Beta Distribution

6. CONCLUSION

The paper is concerned with the comparison of non-parametric measures with parametric measures in their power efficiencies and stability assessments in case of normal as well as non-normal situation. Thennarasu (1995) proposed four non-parametric measures, and showed that two to them performed better than the measures proposed by earlier workers. However, there has been hardly any attempt to tackle the difficulties that arise when data are non-normal. The performance of non-parametric measures vis-à-vis parametric measures has also not been considered earlier in case of non normal data. The results of the investigation will be quite useful to the plant breeder and geneticists who would be able to select promising genotypes simultaneously for crop yield and crop yield stability. This in turn will promote sustainability of crop production, which the planners and policy makers are looking for, and will ultimately ensure greater food availability and security for our ever-increasing population. Type1 error and power of different nonparametric as well as parametric measures are obtained when data are normal as well as non-normal like gamma and beta distribution. With small sample sizes, the power of parametric measures was higher than nonparametric measures. When sample sizes were fairly large, the power was close to or higher for nonparametric measures.

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