



## Study of different parametric stability measures when the basic data/variables are non-normal

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### ABSTRACT

The presence of genotype-environment interactions (GEI) necessitates the developments of varieties or breeds suited for different agro-environments based on their stability and adaptability characteristics. In many situations, the assumptions about the normality and independence of observations as well as homogeneity of error variances are not fulfilled. Therefore, there is a need to investigate the performance of different parametric methods for stability measures when the basic data is not normally distributed. This important aspect is taken up in the present investigation. Using simulation technique, power of the test has been computed for different sample sizes when the underlying dataset is normal as well as non-normal like gamma, beta, *t*, weibull, log normal etc. In most of the cases it is found that Eberhart and Russell parametric stability measure gives better performance.

**Key words:** Genotype environment interaction, Parameter methods, Probability distributions, Simulations, Stability measures

The wide occurrence of genotype-environment interactions (GEI) causes difficulty in the identification of superior varieties. In order to overcome this difficulty, an attempt is usually made by the plant breeders to reduce the GEI, i.e. dependence of the genotypic ranking on environmental conditions through special breeding techniques like resistance breeding. Since only a minor part of the GEI can be attributed to controllable environmental determinants, much reduction in the interaction cannot be achieved. The term "phenotypic stability" is used to refer to the fluctuations in the phenotypic expression of yield even as the genetic constitution of the varieties remains stable. This means that the breeder can no longer hope to find varieties which would excel everywhere and in all the years. 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. Therefore, "Stability" has become an important word in the lexicon of agronomists and breeders.

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 depended on the particular situation in hand and the type of data that are collected by the investigator. Several procedures for analyzing GEI and yield stability were proposed. Most of these procedures (Kang *et al.* 2002), however, were

parametric methods performance of which were not quite satisfactory from the standpoint of breeders. Some works regarding stability analysis may be found in Drazic *et al.* (2014) and Lal (2014). Verma and Solanki (2015) studied stability of seed yield and its component traits in fennel. Paul *et al.* (2015a and b) compared the performance of parametric and non-parametric stability measures and also assessed the performance of non-parametric stability for non-normal dataset. Dehghani *et al.* (2016) attempted to integrate the parametric and non-parametric measures to investigate genotype × environment interactions in tall fescue.

There is hardly any study on the performance of non-parametric measures when the basic data is not normally distributed. This indeed is serious when the ground reality is that, in many situations the assumptions about the normality and independence of observations as well as homogeneity of error variances is not fulfilled. There is, therefore, a strong case for investigating the performance of non-parametric measures when the basic data is not normally distributed. This important aspect is taken up in the present investigation, which will also consider the development of a few simultaneous selection measures, which could be used for selecting genotypes for both yield and stability.

### MATERIALS AND METHODS

Variates from different non-normal distributions such as log normal, gamma, beta, Weibull, and *t* 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

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normal observations. The type 1 error ( $\alpha$ ) and power of the tests are considered for empirical comparison purpose. Efforts are made for finding some new non-parametric measures. They are evaluated for their merits vis a vis other existing measures. The evaluation is based on the type I error, power of the test.

For simulation of data from non-normal population the following algorithms have been used:

*Lognormal distribution*

- i) Generate Y normally distributed with mean  $\mu$  and variance  $\delta^2$
- ii) Output  $X = \exp Y$

*Standard Gama distribution*

- i) Generate G(1) variates
- ii) Set  $X = \sum_k X_k$  where eachis  $X_k$  is G(1)
- iii) Return X

Setting  $Y = \beta X$  will generate variates from  $G(p, \beta)$ ,

with p.d.f.  $f(y) = \frac{1}{\tau(p)\beta^p} y^{p-1} e^{-y/\beta}$

*Weibull distribution*

The probability density function in this case is,

$f(x) = \frac{c}{b} (\frac{x-a}{b})^{c-1} \exp[-(\frac{x-a}{b})^c]$  and  $b, c > 0$ ,

The distribution function of Weibull can easily be inverted as to get the Weibull variate  $X = a + b[-\log(1-U)]^{1/c}$  from  $U(0,1)$ . When  $c=3.602$ , it closely approximates Normal.

*Thet distribution*

Let  $Y_1$  be standard normal variate

Let  $Y_2$  be independent of  $Y_1$  and Chi-square with  $n$  degrees of freedom.

Then  $X = Y_1 / \sqrt{Y_2/n}$  is t distribution with n d.f. where

$Y_2 = \sum_{i=1}^n Z_i^2, Z_i \sim N(0, 1)$

Alternatively we may use the TMX Algorithm using rejection and mixtures proposed by Kinderman *et al.* (1977) and Kennedy and Gentle (1980).

*Beta distribution*

Initialization:

- i) Set  $\alpha = a + b$  if  $(a, b) \leq 1$  set  $\beta = 1/\min(a, b)$   
Otherwise set  $\beta = \{(\alpha - 2)/(2ab - \alpha)\}^{1/2}$   
Set  $\gamma = a + 1/\beta$
- ii) Generate  $U_1$  and  $U_2$  and set  $V = \beta \log\{U_1 / (1-U_1)\}$   
 $W = a\{\exp(V)\}$
- iii) If  $\alpha \log\{(\alpha + (b + W))\} + \gamma V - \log(4) < \log(U_1, U_2, U_3)$ , go to (i)
- iv) Return  $X = W / (b + W)$

Consider t genotypes having performance tested in s environments. In non-parametric analysis of GE interaction the ranks of genotypes are considered 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

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

$Y_i$  is 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.

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, Thenrasu (1995) proposed the following stability measures when the basic data are non-normal

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

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

$NP_i(3) = \sqrt{[\sum_{j=1}^s (r_{ij} - r_i)^2 / s] / r_i^*}$

$NP_i(4) = [2 / s(s-1)] \sum_{j < j'} |r_{ij} - r_{ij'}| / \bar{r}_i$

Among the parametric measures following statistics have been used:

Wricke (1962) Ecovalence measure

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

Shukla (1972) Stability variance

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

Eberhart and Russell (1966)

$b_i = \sum_j (Y_{ij} - \bar{Y}_i)(\bar{Y}_j - \bar{Y}_{..}) / \sum_j (\bar{Y}_j - \bar{Y}_{..})^2$

Perkins and Jinks (1968) deviation mean square

$s_{di}^2 = [\sum_j (Y_{ij} - \bar{Y}_i - \bar{Y}_j + \bar{Y}_{..})^2 - \beta_i^2 \sum_j e_j^2] / (s-2)$

Pinthus (1973)  $r_i^2$  measure

$r_i^2 = b_i^2 \sum_j \hat{e}_j^2 / [b_i^2 \sum_j \hat{e}_j^2 + \sum_j \delta_{ij}^2]$

\*  $MS(GE) = \sum (Y_{ij} - \bar{Y}_i - \bar{Y}_j)^2 / (s-1)(t-1)$  is the GE interaction mean square

For simplicity we introduce the following notations for different measures.

$P1 = b_i = \sum_j (Y_{ij} - \bar{Y}_i)(\bar{Y}_j - \bar{Y}_{..}) / \sum_j (\bar{Y}_j - \bar{Y}_{..})^2$

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

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

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

$$P5 = r_i^2 = b_i^2 \sum_j \hat{e}_j^2 / [b_i^2 \sum_j \hat{e}_j^2 + \sum_j \delta_{ij}^2]$$

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

The evaluation is done mainly on the basis of type I error ( $\alpha$ ) and power of the test. For generation data from non-normal populations, to start with some standard distributions such as Gama and Weibull, Log normal,  $t$  and beta are considered. Some of these distributions are closer to Normal and some away from it.

The performance of various stability measures studied based on type I error ( $\alpha$ ) and power of the test,  $(1-\mu)$ . The performance of the newly evolved measures will be evaluated based on type I error and power of the test for the worse data situation.

*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  $\mu$  and error standard deviation  $\sigma_e$  is carried out. In the first stage, the standard uniform variates are generated which is further used to generate standard normal variates. The second state is the generation of normal variates with specified  $\sigma$  and  $\sigma_e$  values and this is achieved as follows. A second subroutine receives generated standard uniform variates from the first stage and converts them into 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  $\sigma_e^2$  and error variance  $\sigma_e^2$ , the model needs to include only the environmental and error effects. 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. Adopting this procedure the probability of type I error and power of the test are studied in the following sections.

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 (Nassar and Huhn 1987) 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  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment can be expressed as

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

where,  $\mu$  is the overall population mean,  $e_j$  is the effect of environment  $j$ ,  $\epsilon_{ij}$  is the random error associated with  $i^{\text{th}}$  genotype ( $i=1,2,\dots,t$ ) and  $j^{\text{th}}$  environment and distributed with mean zero and variance  $\sigma_e^2$ .

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  $\mu$  and  $\sigma_e$  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  $\mu=1984$  and  $\sigma_e^2=152.22$  and  $\sigma_E=1121$ . It is to be noted that the value of  $\mu$  and  $\sigma_e^2$  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 a specified

Table 1 Power of the test in a one way ANOVA for the different combinations of number of genotypes (T) and number of environments (E) at  $\alpha = 0.05$  for different parametric measures in gamma distribution.

| T  | E  | P1     | P2     | P3     | P4     | P5     | P6     |
|----|----|--------|--------|--------|--------|--------|--------|
| 8  | 5  | 0.5690 | 0.4050 | 0.4057 | 0.1930 | 0.3560 | 0.4450 |
| 12 | 5  | 0.6220 | 0.6060 | 0.6068 | 0.3470 | 0.4700 | 0.5630 |
| 16 | 5  | 0.6900 | 0.7330 | 0.7409 | 0.4440 | 0.5250 | 0.6170 |
| 20 | 5  | 0.7280 | 0.8200 | 0.8203 | 0.5290 | 0.5770 | 0.6820 |
| 24 | 5  | 0.7780 | 0.8680 | 0.8685 | 0.6050 | 0.6520 | 0.7170 |
| 8  | 10 | 0.5630 | 0.3670 | 0.3766 | 0.1760 | 0.4700 | 0.4510 |
| 12 | 10 | 0.6860 | 0.5420 | 0.5425 | 0.3450 | 0.5470 | 0.5820 |
| 16 | 10 | 0.7420 | 0.6860 | 0.6866 | 0.4760 | 0.6380 | 0.6780 |
| 20 | 10 | 0.7950 | 0.7860 | 0.7866 | 0.5880 | 0.7190 | 0.7540 |
| 24 | 10 | 0.8490 | 0.8510 | 0.8515 | 0.6280 | 0.7440 | 0.8080 |
| 8  | 15 | 0.6010 | 0.3180 | 0.3184 | 0.1700 | 0.5130 | 0.4690 |
| 12 | 15 | 0.7090 | 0.4890 | 0.4894 | 0.3470 | 0.5880 | 0.6010 |
| 16 | 15 | 0.7780 | 0.6220 | 0.6228 | 0.4770 | 0.6740 | 0.7190 |
| 20 | 15 | 0.8340 | 0.7540 | 0.7548 | 0.5920 | 0.7260 | 0.7720 |
| 24 | 15 | 0.8760 | 0.8260 | 0.8269 | 0.6460 | 0.7670 | 0.8310 |
| 8  | 20 | 0.5950 | 0.2570 | 0.2579 | 0.1550 | 0.5240 | 0.4420 |
| 12 | 20 | 0.6830 | 0.4410 | 0.4419 | 0.3420 | 0.6140 | 0.6030 |
| 16 | 20 | 0.7530 | 0.5860 | 0.5869 | 0.4880 | 0.6660 | 0.6910 |
| 20 | 20 | 0.8260 | 0.6890 | 0.6899 | 0.5980 | 0.7210 | 0.7710 |
| 24 | 20 | 0.8790 | 0.7780 | 0.7779 | 0.6450 | 0.7860 | 0.8360 |

Table 2 Power of the test in a one way ANOVA for the different combinations of number of genotypes (T) and number of environments (E) at  $\alpha = 0.05$  for different parametric measures in case of t distribution

| T  | E  | P1     | P2     | P3     | P4     | P5     | P6     |
|----|----|--------|--------|--------|--------|--------|--------|
| 8  | 5  | 0.8709 | 0.8130 | 0.8105 | 0.8090 | 0.8060 | 0.8100 |
| 12 | 5  | 0.8799 | 0.8200 | 0.8230 | 0.8230 | 0.8659 | 0.8230 |
| 16 | 5  | 0.9029 | 0.8309 | 0.8329 | 0.8309 | 0.8799 | 0.8309 |
| 20 | 5  | 0.9079 | 0.8409 | 0.8440 | 0.8440 | 0.8811 | 0.8440 |
| 24 | 5  | 0.9279 | 0.8540 | 0.8509 | 0.8509 | 0.8880 | 0.8509 |
| 8  | 10 | 0.8539 | 0.8300 | 0.8309 | 0.8309 | 0.8059 | 0.8609 |
| 12 | 10 | 0.8629 | 0.8409 | 0.8409 | 0.8490 | 0.8169 | 0.8109 |
| 16 | 10 | 0.8750 | 0.8590 | 0.8590 | 0.8569 | 0.8272 | 0.8390 |
| 20 | 10 | 0.8660 | 0.8669 | 0.8669 | 0.8650 | 0.8389 | 0.8469 |
| 24 | 10 | 0.9060 | 0.8740 | 0.8740 | 0.8790 | 0.8430 | 0.8540 |
| 8  | 15 | 0.8280 | 0.8109 | 0.8109 | 0.8100 | 0.8010 | 0.8209 |
| 12 | 15 | 0.8389 | 0.8280 | 0.8280 | 0.8259 | 0.8140 | 0.8380 |
| 16 | 15 | 0.8470 | 0.8340 | 0.8340 | 0.8300 | 0.8279 | 0.8440 |
| 20 | 15 | 0.8560 | 0.8429 | 0.8429 | 0.8500 | 0.8369 | 0.8529 |
| 24 | 15 | 0.8689 | 0.8559 | 0.8559 | 0.8640 | 0.8420 | 0.8659 |
| 8  | 20 | 0.8240 | 0.8090 | 0.8090 | 0.8069 | 0.8000 | 0.8390 |
| 12 | 20 | 0.8330 | 0.8140 | 0.8140 | 0.8300 | 0.8006 | 0.8440 |
| 16 | 20 | 0.8439 | 0.8399 | 0.8399 | 0.8459 | 0.8060 | 0.8599 |
| 20 | 20 | 0.8539 | 0.8409 | 0.8409 | 0.8559 | 0.8160 | 0.8609 |
| 24 | 20 | 0.8809 | 0.8580 | 0.8680 | 0.8640 | 0.8209 | 0.8780 |

Table 3 Power of the test in a one way ANOVA for the different combinations of number of genotypes (T) and number of environments (E) at  $\alpha = 0.05$  for different parametric measures in case of weibull distribution when  $c=3.602$

| T  | E  | P1     | P2     | P3     | P4     | P5     | P6     |
|----|----|--------|--------|--------|--------|--------|--------|
| 8  | 5  | 0.5720 | 0.4383 | 0.4389 | 0.2299 | 0.4380 | 0.3980 |
| 12 | 5  | 0.6680 | 0.4829 | 0.4720 | 0.3560 | 0.4820 | 0.5310 |
| 16 | 5  | 0.5450 | 0.3379 | 0.3399 | 0.2360 | 0.3360 | 0.4360 |
| 20 | 5  | 0.7880 | 0.6411 | 0.6456 | 0.5730 | 0.6440 | 0.6840 |
| 24 | 5  | 0.8000 | 0.6899 | 0.6889 | 0.6360 | 0.6810 | 0.7460 |
| 8  | 10 | 0.5850 | 0.5129 | 0.5020 | 0.2340 | 0.5020 | 0.4390 |
| 12 | 10 | 0.6870 | 0.5859 | 0.5750 | 0.3490 | 0.5850 | 0.5830 |
| 16 | 10 | 0.7850 | 0.6664 | 0.6669 | 0.4600 | 0.6660 | 0.6880 |
| 20 | 10 | 0.8170 | 0.740  | 0.7570 | 0.5390 | 0.7370 | 0.7510 |
| 24 | 10 | 0.8560 | 0.7899 | 0.7699 | 0.5760 | 0.7799 | 0.8000 |
| 8  | 15 | 0.5910 | 0.5249 | 0.5248 | 0.2050 | 0.5240 | 0.4310 |
| 12 | 15 | 0.7220 | 0.6680 | 0.6380 | 0.3190 | 0.6180 | 0.5760 |
| 16 | 15 | 0.7960 | 0.7440 | 0.7340 | 0.4650 | 0.7140 | 0.6890 |
| 20 | 15 | 0.8440 | 0.7588 | 0.7589 | 0.5240 | 0.7580 | 0.7670 |
| 24 | 15 | 0.8950 | 0.8480 | 0.8580 | 0.5980 | 0.8380 | 0.8000 |
| 8  | 20 | 0.5930 | 0.5437 | 0.5439 | 0.1910 | 0.5430 | 0.4620 |
| 12 | 20 | 0.7200 | 0.6518 | 0.6519 | 0.3120 | 0.6510 | 0.5990 |
| 16 | 20 | 0.7720 | 0.7170 | 0.7270 | 0.4180 | 0.7070 | 0.7110 |
| 20 | 20 | 0.8520 | 0.7919 | 0.7915 | 0.5290 | 0.7910 | 0.7740 |
| 24 | 20 | 0.8760 | 0.8285 | 0.8380 | 0.5990 | 0.8280 | 0.8160 |

ts observations, the values of 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  $\alpha$  is computed for different expected levels of significance ( $\alpha = 0.01, 0.025, 0.05, 0.10$ ). For these expected  $\alpha$  levels the table values of F with degrees of freedom (t-1) and 2t are taken as critical values.

The same procedures are followed for lognormal, gamma, beta, weibull and tdistribution case. For the comparison of observed  $\alpha$  with a specified expected  $\alpha$  has been presented in Tables 2 to 3. These are tabulated for the different stability measures mentioned above for different combination of t and s.

The adequacy of the test of stability of a genotype over environments depends on the number of genotypes and environments involved in the multi-location trials. 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 measures mentioned in the previous section in terms of their power efficiency a simulation programme was run under the full model

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

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 made use of. 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. They 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 1000 times (5000 in some cases) and the number of times the observed F statistic from ANOVA exceed the tabulated F values at each level of significance,  $\alpha$  (0.01, 0.025, 0.05 and 0.10) is worked out. The power of the test is

Table 4 Power of the test in a one way ANOVA for the different combinations of number of genotypes (T) and number of environments (E) at  $\alpha = 0.05$  for different parametric measures in case of beta distribution.

| T  | E  | P1     | P2     | P3     | P4     | P5     | P6     |
|----|----|--------|--------|--------|--------|--------|--------|
| 8  | 5  | 0.5910 | 0.4730 | 0.4730 | 0.2340 | 0.6170 | 0.4800 |
| 12 | 5  | 0.7680 | 0.4750 | 0.4750 | 0.3520 | 0.6800 | 0.4820 |
| 16 | 5  | 0.8560 | 0.4800 | 0.4810 | 0.4190 | 0.7310 | 0.4920 |
| 20 | 5  | 0.9070 | 0.4980 | 0.4990 | 0.4910 | 0.7510 | 0.4970 |
| 24 | 5  | 0.9280 | 0.5000 | 0.5000 | 0.5070 | 0.7610 | 0.5060 |
| 8  | 10 | 0.6080 | 0.4600 | 0.4610 | 0.2310 | 0.6190 | 0.4660 |
| 12 | 10 | 0.7500 | 0.4620 | 0.4630 | 0.2620 | 0.6530 | 0.4680 |
| 16 | 10 | 0.8220 | 0.4780 | 0.4710 | 0.3680 | 0.7100 | 0.4700 |
| 20 | 10 | 0.8850 | 0.4880 | 0.4910 | 0.4290 | 0.7620 | 0.4800 |
| 24 | 10 | 0.9200 | 0.4900 | 0.4720 | 0.4620 | 0.7860 | 0.4980 |
| 8  | 15 | 0.5950 | 0.4510 | 0.4530 | 0.2440 | 0.5970 | 0.4550 |
| 12 | 15 | 0.7760 | 0.4570 | 0.4610 | 0.3720 | 0.7040 | 0.4710 |
| 16 | 15 | 0.8440 | 0.4650 | 0.4690 | 0.4390 | 0.7390 | 0.4810 |
| 20 | 15 | 0.8880 | 0.4730 | 0.4850 | 0.4910 | 0.7630 | 0.4900 |
| 24 | 15 | 0.9220 | 0.4900 | 0.4680 | 0.5170 | 0.8170 | 0.5060 |
| 8  | 20 | 0.6010 | 0.4390 | 0.4450 | 0.2540 | 0.5990 | 0.4600 |
| 12 | 20 | 0.7770 | 0.4560 | 0.4610 | 0.3720 | 0.6880 | 0.4760 |
| 16 | 20 | 0.8310 | 0.4630 | 0.4680 | 0.4590 | 0.7590 | 0.4870 |
| 20 | 20 | 0.8510 | 0.4630 | 0.4680 | 0.4970 | 0.7590 | 0.4875 |
| 24 | 20 | 0.8790 | 0.4920 | 0.5000 | 0.5070 | 0.8000 | 0.4980 |

determined therefrom. The values for different combinations of  $\alpha$ , t and s are presented in Tables 2-3. For saving space, we have only reported the power of the test at  $\alpha=0.05$  for different measures of stability assuming normal as well as non-normal distributions. The other results have also been obtained and can be obtained from the author on request.

## RESULTS AND DISCUSSION

In case of normal distribution,  $P_6$ ,  $P_6$  show better power as compared to other measures; whereas,  $P_2$  shows poor performance. For lognormal distribution,  $P_2$  and  $P_4$  show better performance and  $P_4$  is the poorest. Due to lack of space, the tables for the normal and lognormal distributions are omitted but these can be obtained from the authors on request. The power of the test in a one way ANOVA for the different combinations of number of genotypes (T) and number of environments (E) at  $\alpha = 0.05$  for different parametric measures in Gamma distribution are tabulated in Table 1. Here it is noticed that  $P_1$  shows poor performance, whereas  $P_1$  is the best. Results are tabulated in Table 2 when the underlying distribution is considered to be t distribution. Here,  $P_6$  and  $P_6$  show better power than other measures. In case of Weibull distribution, results (Table 3) it is noticed that the measure  $P_1$  has attained maximum power, whereas  $P_4$  attained lowest power. For Beta distribution the results are shown in Table 4. Here only measure  $P_1$  shows good performance, whereas the rest of the measure shows very poor result.

Type I error and power of different parametric measures

are obtained when data are normal as well as non-normal like gamma, beta, lognormal, weibull and t distribution. 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.

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