Statistics and Applications **{ISSN 2452-7395(online)}**
Volume 14, Nos. 1&2, 2016 (New Series), pp 9-29

Parametric and Non-Parametric Methods to Describe Genotype by Environment Interaction and Grain Yield Stability of Bread Wheat

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Received October 15, 2015; Revised July 02, 2016; Accepted July 22, 2016

Abstract

Genotype by environment (G×E) interaction continues to be a challenging issue among plant breeders, geneticists, and production agronomists who conduct crop trials across diverse environments. GEI can reduce progress from selection. The methods of partitioning GEI into components attributable to each genotype measure the contribution of each genotype to GEI. Whenever an interaction is significant, the use of main effects, e.g. overall genotypes means across environments, is questionable. Stability of performance should be considered an important aspect of yield trials. Though large numbers of stability measures (parametric and non-parametric) are available in literature, the problem of plant breeder has been to decide which of the stability measure is to be chosen for the purpose of selecting stable genotypes? The objective of the present paper is to analyze genotype × environment (G×E) interaction of 20 Ethiopian wheat genotypes in 8 environments and compare the parametric and non- parametric methods of stability. The experiment was conducted during 2007/08 growing seasons in a randomized complete block design with four replications. Combined ANOVA and nonparametric tests (Kubinger, 1986 and Hildebrand, 1980) of G×E indicated the presence of significant interactions, as well as significant differences between genotypes and environments. However no cross-over andnon-crossover interactions were detected by the de Kroon/van der Laan(1981)and Bredenkamp (1974) procedure respectively. According to the parametric methods, genotype G11, G10, G5 and G12were found to be stable and according to the nonparametric methods, genotype G11, G10, G5, G18 & G12were found to be stable. The result shows that both the parametric and nonparametric methods gave a relatively same result but due to distribution free methods, the nonparametric stability measurements have advantages over parametric stability measurements. Mean yield performance across environments was significantly positively correlated with RS and TOP measures ($P<0.05$ and $P<0.01$ respectively) and there were significant negative correlations between mean yield and $s_i^{(3)}$,$s_i^{(6)}$,$NP_i^{(2)}$, $NP_i^{(3)}$.

Key Words: Genotype × Environment Interaction, Stability, Crossover and non-cross over interaction, Parametric methods, non-parametric methods.

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1. Introduction

Ethiopia is the largest producer of wheat in sub-Saharan Africa. Wheat occupies about 1.8 million hectares annually and ranks 4thin area and 2nd in productivity among the cereals (CSA, 2012). Bread and durum wheat are the major types of wheat grown. Bread wheat is of recent introduction; durum wheat is indigenous to the Ethiopia which is considered ‘the secondary center of diversity for tetraploid wheat’.

Wheat genotypes are generally evaluated in multi-environment trials (MET) to test their performance across environments and to select the best genotypes for specific environments. There are two major approaches to study genotype by environment interaction and determining the adaptation of genotypes (Hühn, 1996). The most common approach is parametric analyses, which are based on statistical assumptions about the distribution of genotypic, environmental and GEI effects. Another approach is nonparametric or analytical clustering, which makes no specific modeling assumptions about relating environments and phenotypes relative to biotic and abiotic environmental factors.

Several procedures have been proposed based on comparing ranks of genotypes in each environment, with genotypes with similar ranking across environments being considered stable (Hühn, 1979; Nassar and Hühn, 1987; Kang, 1988; Ketata et al., 1989; Fox et al., 1990). The four nonparametric measures of phenotypic stability have been proposed by Hühn (1979) and Nassar and Hühn (1987) for further reference see also Sabaghnia et al. (2006).

Many statistical procedures have been proposed tostudy G×E interactions (Westcott, 1986; Crossa, 1990;Lin and Binns, 1994; Kang and Gauch, 1996). Most of these procedures, however, fail to distinguish between significant crossover and non-crossover (usual) interactions(Baker, 1990). Nonparametric statistical procedures for the test of crossover interactions have been developed in the field of medicine and can be applied to G×E interactions in Multi-environment Trial (METs) (Truberg and Hühn, 2000). Hühn and Leon (1995) compared four nonparametric analyses of interactions and grouped them into two different concepts of interactions. While the Bredenkamp, Hildebrand, and Kubinger procedures depend on usual interactions, the de Kroon van der Laan method depends on crossover interactions. If some of the necessary assumptions are violated, the validity of the inferences obtained from the standard statistical techniques, for example, ANOVA, may be questionable or lost. In such cases, however, the results of nonparametric estimation and testing procedures, which are based on ranks, can be more reliable(Truberg and Hühn, 2000).

Stability analysis is only relevant if GEI is present (Hussain et al., 2000). Basically there are two broad categories of GEI: crossover and non-crossover (usual) interaction. A crossover interaction (discordance) exists if the ranking of the genotypes is not identical in different environments. If the ranking is identical, crossover interaction is nonexistent (concordance) (de Kroon &Laan,1981; Truberg&Hühn, 2000). Measures of GEI and stability are common tools applied by biometricians who have developed numerous methods to analyze it (Lin et al., 1986; Becker &Leon, 1988; Flores et al., 1998; Mohammadi&Amri, 2008).

2. Methodology

2.1. Material

Twenty wheat genotypes, listed in Table 2.1, were evaluated over a period of two years from 2007 to 2008in 4locations (Table 2.2) under irrigated condition. The experimental layout was a randomized complete block design (RCBD) with four replications. Planting method was on 30 cm apart at a seed rate of about 120 kg/ha. Plots were managed conventionally and followed the established local practices but usually the plot area ranged from 10 to 15m^2.

Table 2.1 Genotype codesof 20wheat genotypes.

No.	Genotype	Genotype code	No.	Genotype Code	Genotype code	No.	Genotype code	Genotype
1.	K6290Bulk	G1	8.	Kubsa(HAR-1685)	G8	15.	Shinna(HAR-1868)	G15
2.	K6295-4A	G2	9.	Galama(HAR-604)	G9	16.	HAR-407	G16
3.	ET-13.A2	G3	10.	Abola(HAR-1522)	G10	17.	HAR-416	G17
4.	ET12.D4	G4	11.	Magal(HAR-1595)	G11	18.	Gara	G18
5.	KKBB	G5	12.	Tusie(HAR-1407)	G12	19.	Batu	G19
6.	Mitikie(HAR-1709)	G6	13.	Tura(HAR-1407)	G13	20.	K6106-9	G20
7.	Wabe(HAR-710)	G7	14.	Katar(HAR-1899)	G14			

These wheat hybrids were selected based on their relative yield performance among the different experimental hybrids developed by the Ethiopian Seed Enterprise (ESE). These hybrids were released varieties adapted to the medium altitude wheat growing areas of Ethiopia. All the hybrids are categorized under the medium maturity group (between 140 and 145 days) and their broad adaptation zone is mid-altitude sub-humid which includes areas with an elevation range of 1000-2000m above sea level and an annual rainfall between 1000-1200mm.

The trials were conducted under irrigated conditions and fertilization at each site and other management activities were done according to the practices of each farmer (co-operator) for his farm and the specific field. The whole plot was harvested to estimate grain yields and to reduce border effects, data were recorded from the two central rows of each plot. Grain yields are expressed in kg/ha at 12.5 moisture content. The data being considered here are obtained from trials conducted by the Ethiopian Institute of Agricultural Research (EIAR).

2.2. Statistical Methods

2.2.1. Parametric Methods

In multi-environment yield trials of l genotypes (i=1,2,…,l), m environments(j=1,2,…m) and n replicates(k=1,2,…,n) arranged in RCBD, the linear model for the conventional analysis variance(ANOVA) is

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + B_{jk} + e_{ijk}$$

where

- $Y_{ijk}$is the observation of the i^{th}genotype in kth replication at the j^{th}environment.
- $\mu$is the overall mean yield of genotypes at all possible environments.
- $G_i$is the effect of i^{th}genotype; and $\sum_{i=1}^{l} G_i = 0$

- $E_j$is the random effect of the j^{th}environment drawn from a population with mean 0 and variance σ_E^2 and $E_j$is distributed as NID (0, σ_E^2)
- GE_{ij} is the interaction effect of the i^{th} genotype in the j^{th} environment. Since environments are random, this interaction is usually considered to be a random effect with mean 0 and variance $\sigma_{G\times E}^2$
- $B_{jk}$is the effect of the k^{th}replication in the j^{th}environment, and
- $e_{ijk}$is the usual random error term with mean 0 and variance $\sigma_e^2$and $e_{ijk}$is distributed asNID (0, σ_e^2)

2.2.2. Wricke's ecovalence (W_i)

Wricke (1962, 1964) defined the concept of ecovalence as the contribution of each genotype to the GEI sum of squares. The ecovalence (W_i) or stability of the ith genotype is its interaction with the environments, squared and summed across environments, and express as

$$W_i = [\bar{Y}_{ij} - \bar{Y}_{i.} - \bar{Y}._j - \bar{Y}_{..}]^2$$

Where $\bar{Y}_{ij}$is the mean performance of genotype i in the j^{th}environment and$\bar{Y}_{i.}$and$\bar{Y}_{.j}$are the genotype and environment mean deviations, respectively, and $\bar{Y}_{..}$is the overall mean. For this reason, genotypes with a low W_i value have smaller deviations from the mean across environments and are thus more stable.

2.2.3. Shukla's stability variance parameter (σ_i^2)

Shukla (1972) defined the stability variance of genotype $i$as its variance across environments after the main effects of environmental means have been removed. Since the genotype main effect is constant, the stability variance is thus based on the residual (GE_{ij}+ e_{ij}) matrix in a two-way classification. The stability statistic is termed "stability variance" (s_i^2) and is estimated as follows:

$$\hat{\sigma}_i^2 = \frac{1}{(G-1)(G-2)(E-1)}\left[G(G-1)\sum_j\left(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..}\right)^2 - \sum_i\sum_j(Y_{ij} - \bar{Y}_{i.} - \bar{Y}_{.j} + \bar{Y}_{..})^2\right]$$

Where $Y_{ij}$is the mean yield of the i^{th}genotype in the j^{th}environment, $\bar{Y}_{i.}$ is the mean of the genotype i in all environments, $\bar{Y}_{.j}$is the mean of all genotypes in j^{th} environments and $\bar{Y}_{..}$is the mean of all genotypes in all environments. A genotype is called stable if its stability variance (σ_i^2) is equal to the environmental variance (σ_e^2) which means that σ_i^2=0. A relatively large value of (σ_i^2) will thus indicate greater instability of genotype i. As the stability variance is the difference between two sums of squares, it can be negative, but negative estimates of variances are not uncommon in variance component problems. Negative estimates of σ_i^2may be taken as equal to zero as usual (Shukla, 1972). Homogeneity of estimates can be tested using Shukla's (1972) approximate test (Lin *et al*, 1986).The stability variance is a linear combination of the ecovalence, and therefore both W_i and $s_i^2$are equivalent for ranking purposes.

2.2.4. Nonparametric Genotype stability estimation

We denote: y_{ij} = phenotypic value of the ith genotypein the jthenvironment (i = 1, 2, . . .*l*; j = 1,2, . . ., *m*) . In this two-way table with l rows (genotypes)and m columns (environments) one ranksthe l phenotypic values y_{ij} within each column =environment separately (lowest value = rank of 1 and highest value = rank of l). Let r_{ij} be the rank of genotype *i* in environment *j*.A genotype *i* is stable over environments if its ranks are similar over environments, i.e. maximum stability = equal ranks over environments (Hühn, 1990).The statistics based on yield ranks of genotypes in each environment are expressed as follows:

(i)) <u>Average rank differences in different environments</u>, $S_i^{(1)}$. Mean of the absolute rankdifferences of a genotype *i* over the M environments. Genotypes ranking were done for each environment separately:

$$s_i^{(1)} = \frac{\sum_{j<j'}\left|r_{ij}-r_{ij'}\right|}{\binom{m}{2}} = \frac{2}{m(m-1)}\sum_j^{m-1}\sum_{j'=j+1}^{m}\left|r_{ij}-r_{ij'}\right|$$

(ii)) <u>Rank of variance</u>, $S_i^{(2)}$ across "m" environments:common variance of the ranks

$$s_i^{(2)} = \frac{1}{m-1}\sum_{j=1}^{m}(r_{ij}-\bar{r}_{i.})^2$$

$$\bar{r}_{i.} = \frac{1}{m}\sum_{j=1}^{m} r_{ij.}$$

$\bar{r}_{i.}$was interpreted as estimation of each "r_{ij}" under hypothesis ofmaximal stability (equal ranks). For a genotype "i" with maximumstability one obtains$s_i^{(1)} = s_i^{(2)} = 0$. The null-hypothesis of no genotype × environmentinteraction effects implies "all genotypes are equally stable"(with maximum stability). Tests of significance for both stabilitymeasures were done according to the following formula(Huhn and Nassar, 1989; 1991):

$$Z_i^{(v)} = \frac{\left[s_i^{(v)} - E\left\{s_i^{(v)}\right\}\right]^2}{var\left\{s_i^{(v)}\right\}}, v = 1,2$$

has an approximate χ^2 distribution with 1 degree of freedom.

(iii)) <u>Relative deviation in relation to the average rank</u>, $s_i^{(3)}$ (Huhn, 1979): sum of the absolute deviations of ther_{ij}'s frommaximum stability expressed in $\bar{r}_{i.}$ units

$$s_i^{(3)} = \sum_{j=1}^{m}\frac{\left|r_{ij}-\bar{r}_{i.}\right|}{\bar{r}_{i.}}$$

This parameter expresses stability in the units of yield. It expresses a sum of absolute deviations of ranks r_{ij} from their averagerank $\bar{r}_{i.}$, where deviations are expressed in the $\overline{r}_{i.}$ units. Thenumerator measures stability (= variability of ranks$\bar{r}_{i.}$), while thedenominator implies the yield level (= average values of ranksr_{ij}).

This set encompasses other measures, but the measure $s_i^{(3)}$is the simplest and mostly used.

(iv) <u>The sum of squares of rank for each genotype relative to the mean of ranks</u>:$s_i^{(6)}$

$$s_i^{(6)} = \sum_{j=1}^{m}\frac{\left(r_{ij}-\bar{r}_{i.}\right)^2}{\bar{r}_{i.}}$$

(v) Tests of significance

Approximate tests of significance based on the normal distribution are developed for these two nonparametric measures:

$$Z_i^{(v)} = \frac{\left[s_i^{(v)} - E\left\{s_i^{(v)}\right\}\right]^2}{var\left\{s_i^{(v)}\right\}}, v = 1,2 \tag{1}$$

would have an approximate chi-squared distribution with one degree of freedom and, similarly, the statistic

$$s^v = \sum_{i=1}^{k} Z_i^{(v)}, v = 1,2 \tag{2}$$

may be approximated by a chi-squared distribution with L degrees of freedom with E($s_i^{(v)}$) = expectation (= mean) of $s_i^{(v)}$ and V($s_i^{(v)}$) = variance of ($s_i^{(v)}$) .

Under the null hypothesis that all genotypes are equally stable the means E($\mathrm{s}_\mathrm{i}^{(\mathrm{v})}$) and variancesV($\mathrm{s}_\mathrm{i}^{(\mathrm{v})}$) may be computed from the discrete uniform distribution (1, 2, . . ., l). The following explicit formulae are derived and explained in Nassar and Hühn (1987):

$$E(s_i^{(1)}) = \frac{\mathrm{l}^2 - 1}{3\mathrm{l}}$$

$$E(s_i^{(2)}) = \frac{\mathrm{l}^2 - 1}{12}$$

$$V(s_i^{(1)}) = \frac{(\mathrm{l}^2-1)[(\mathrm{l}^2-4)(\mathrm{m}+3)+30]}{45\mathrm{l}^2\mathrm{m}(\mathrm{m}-1)}$$

$$V(s_i^{(2)}) = \frac{(\mathrm{l}^2-1)[2(\mathrm{l}^2-4)(\mathrm{m}-1)+5(\mathrm{l}^2-1)]}{36\mathrm{m}(\mathrm{m}-1)}$$

Thennarasu (1995) proposed another set of nonparametric statistics ($\mathrm{NP}_\mathrm{i}^{(1)}$, $\mathrm{NP}_\mathrm{i}^{(2)}$, $\mathrm{NP}_\mathrm{i}^{(3)}$and $\mathrm{NP}_\mathrm{i}^{(4)}$), based on ranks of adjusted means of the genotypes in each environment, and defined stable genotypes as those whose position remained unaltered in relation to the others in the set of environments assessed. These were calculated as follows:

$$NP_i^{(1)} = \frac{1}{m}\sum_{j=1}^{m}\left|r_{ij}^* - M_{di}^*\right|$$

$$NP_i^{(2)} = \frac{1}{m}\left(\sum_{j=1}^{m}\frac{\left|r_{ij}^* - M_{di}^*\right|}{M_{di}}\right)$$

$$NP_i^{(3)} = \frac{\sqrt{\sum\left(r_{ij}^* - \bar{r}_{i.}^*\right)^2/m}}{\bar{r}_{i.}}$$

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

The adjusted rank, $\mathrm{r}_{\mathrm{ij}}^*$, is determined on the basis of the adjusted phenotype values ($\mathrm{y}_{\mathrm{ij}}^* = \mathrm{y}_{\mathrm{ij}} - \bar{\mathrm{y}}_{\mathrm{i.}}$), where $\bar{\mathrm{y}}_{\mathrm{i.}}$ is the mean performance of the i^{th} genotype. The ranks, obtained from these adjusted values ($\mathrm{y}_{\mathrm{ij}}^*$), depend only on G×E interaction and error effects.

In the above formulas, r^*_{ij} is the rank of y^*_{ij}, and $\bar{r}^*_{i.}$: and M^*_{di} are the mean and median ranks for adjusted values, where $\bar{r}_{i.}$ and M_{di} are the same parameters computed from the original (unadjusted) data.

2.2.5. Relationship between non parametric estimators of stability

All the genotypes evaluated were respectively assigned stability values according to the procedure and definitions used, and were then ranked in order to determine Spearman's rank correlation coefficient between the different procedures. Let X_i indicates the ranking number of the i^{th} genotype and Y_i the ranking number of the i^{th} genotype, then $d_i = X_i - Y_i$ (i= 1,2,...l) and Spearman's rank correlation coefficient (r_s) can be described as:

$$r_s = 1 - \frac{6\sum_{i=1}^{l} d_i^2}{l(l^2-1)}$$

d_i = difference between two ranks of investigated trait;
l = number of correlated pairs.

2.2.6. Test of *G*×*E* interaction

Test of genotype × environment (G×E) interactions was performed using non parametric statistic HÜHN (1996):

2.2.6.1. Hildebrand's method (Huhn, 1996)

a) Transformation of original data for grain yield

y_{ijk} (*i*=1,2,…,*l*; *j*=1,2,…,*m*; *k*=1,2,…,*n*) in value of y^*_{ijk} performedby formula:

$$y_{ijk} - \bar{y}_{i..} - \bar{y}_{.j.} + 2\,\bar{y}_{...} = y^*_{ijk}$$

$\bar{y}_{i..}$ - Average yield of ith genotype;
$\bar{y}_{.j.}$ - Average yield in jth environment;
$\bar{y}_{...}$ - Generalmean yield;
y_{ijk} - yield of genotype "*i*" in "*j*" environment and "*k*" repetition.

b) Transformation of y^*_{ijk} values in R_{ijk} ranks(based on one single rank order)

$$R_{ijk} : y^*_{ijk} \rightarrow R_{ijk}$$

c)Test statistic for testing the significance of genotype× environment was calculated by formula:

$\frac{12}{l\,m(N+1)}\sum_{i=1}^{l}\sum_{j=1}^{m}(\bar{R}_{ij.} - \bar{R}_{i..} - \bar{R}_{.j.} + \bar{R}_{...})^2 \sim \chi 2$ with (l - 1) (m - 1) degrees of freedom
$N = nlm$
l - number of genotypes;
m - number of environments;
$\bar{R}_{ij.}$- Rank average per genotype/environment;
$\bar{R}_{i..}$- Genotype rank average;
$\bar{R}_{.j.}$- Environment rank average;
$\bar{R}_{...}$- Average rank overall (Hildebrand, 1980; Kubinger, 1986).

2.2.7. Kubingers method (Huhn, 1996)

a) Transformation of original data for grain yield:

y_{ijk}(i =1,2,…,l; j=1,2,…,m; k=1,2,…,n) in ranks (based on one single rank order)

$$\underline{R_{ijk} : y_{ijk} \rightarrow R_{ijk}}$$

b) Transformation of rank for genotype "i", environment "j" and repetition "k", (R_{ijk}) in R_{ijk}^{*} by formula

$$R_{ijk} \rightarrow R_{ijk}{}^{*} = R_{ijk} - \bar{R}_{i..} - \bar{R}_{.j.}$$

$\bar{R}_{i..}$- Genotype rank average;

$\bar{R}_{.j.}$- Environment rank average.

c) Transformation of R_{ijk}^{*} values in R_{ijk}^{**} ranks: (rank the R_{ijk}^{*} values)

$$R_{ijk}^{**} : R_{ijk}^{*} \rightarrow R_{ijk}^{**}$$

d)Test **s**tatistic for testing significance of genotype × environment interaction was calculated as: $\frac{12}{l\,m(N+1)}\sum_{i=1}^{l}\sum_{j=1}^{m}(\bar{R}_{ij.}{}^{**} - \bar{R}_{i..}{}^{**} - \bar{R}_{.j.}{}^{**} + \bar{R}_{...}{}^{**})^2 \sim$ χ^2 with $(l - 1)$ $(m - 1)$ degrees of freedom

$\bar{R}_{ij.}{}^{**}$ - Rank average of genotype "i" in particular environment "j";

$\bar{R}_{i..}{}^{**}$- Rank average of genotype i;

$\bar{R}_{.j.}{}^{**}$ - Rank average of environment j;

$\bar{R}_{...}{}^{**}$ -Over all Rank average.

2.2.8. Bredenkampmethod (1974)

Interactions detected by this method correspond to usual crossover interactions of parametric methods. In this method y_{ijk}-values for all environments and for all genotypes are transformed into ranks R_{ijk} of one single rank order (Hühn and Leon 1995).

2.2.9. Test of genotypes

The test statistic for testing genotypic differences was calculated as follows:

$$\chi^2_{(G)} = \frac{12l}{N^2(N+1)}\sum_{i=1}^{l} R_{i..}^2 - 3(N+1)$$

That is approximately χ^2-distributed, with l–1 degrees of freedom. $R_{i..}$ isrank average ofi^{th} genotype.

2.2.10. Test of environments

The test statistics for a test of environmental differences as follow is approximately χ^2-distributed, with m–1 degrees of freedom. $R_{.j.}$ is rank average of j^{th} environment.

$$\chi^2_{(E)} = \frac{12m}{N^2(N+!)}\sum_{j=1}^{m} R_{.j.}^2 \quad - 3(N+1)$$

2.2.11. Test of interaction effects (non-crossover interaction)

The statistic for a test of G×E interaction differences is approximately χ^2-distributed, with $(l–1)$ $(m–1)$ degrees of freedom. $R_{ij.}$ is the rank of i^{th} genotype in j^{th} environment.

$$\chi^2_{(G\times E)} = \frac{12lm}{N^2(N+1)}\sum_{i=1}^{l}\sum_{j=1}^{m}\left(R_{ij.}^2 - \frac{1}{m^2}R_{i..}^2 - \frac{1}{l^2}R_{.j.}^2) + 3(N+1)\right)$$

2.2.12. de Kroon Van der Laan method (1981)

Interactions detected by this method correspond to crossover interactions of parametric methods (Baker 1988). That means that interactions are used only insofar as they lead to different rankings of genotypes and/or environments. Therefore, this method requires rank orders for each environment or for each genotype separately (Hühn and Leon 1995).

a) Test of genotypes

The y_{ijk}-values are ranked for each environment separately into the ranksR_{ijk}. The test statistic for a test of genotypes differences is approximately χ^2-distributed, with *l*–1 degrees of freedom.

$$\chi^2_{(G)} = \frac{12}{lmn^2(mn+1)}\sum_{i=1}^{l} R^2_{i..} - 3(ln+1)$$

b) Test of environments

The y_{ijk}values are ranked for each genotype separately into the ranksR_{ijk}. The test statistic for a test of environmental differences is approximately χ^2-distributed, with *m*–1 degrees of freedom.

$$\chi^2_{(E)} = \frac{12}{lmn^2(ln+1)}\sum_{j=1}^{m} R^2_{.j.} - 3(mn+1)$$

c) Test of interaction effects (Crossover interactions)

The y_{ijk}-values are ranked for each environment separately into ranksR_{ijk}. The test statistic for the hypothesis of no rank changes of genotypes between environments (crossover interaction) is approximately χ^2-distributed, with (*l*–1) (*m*–1) degrees of freedom.

$$\chi^2_{(G\times E)} = \frac{12}{ln^2(ln+1)}\left(\sum_{i=1}^{l}\sum\nolimits_{j=1}^{m} R^2_{ij.} - \frac{1}{m}\sum_{i=1}^{l} R^2_{i..}\right)$$

The hypothesis of no environmentally caused changes in rank orders (within genotypes) can also be tested using this method (de Kroon and van der Laan 1981).

3. Result And Discussion

3.1. Combined Analysis of Variance

3.1.1. G×E Interaction Analysis

The combined ANOVA,the usual diagnostic plots-including a normal probability plot of residuals (i.e. for ANOVA for each environment and for combined ANOVA), a histogram of residuals, plot of residuals versus fitted values, plot of residuals versus level of regressor variable and other statistical procedures to assess model assumptions for ANOVAs (i.e. for yield data at each environment)including the LR test (for each genotype yield) were performed by using SAS software .The results do not reveal any serious violation of the assumptions. For homogeneity of residual variance, we applied the Bartlett’s test by considering genotypes as a group. Based on this, the p value for each of the separate ANOVA is much greater than 0.05 indicating the hypothesis that the residual variances in each of the separate ANOVA are homogeneous, cannot be rejected.

3.1.2. Analysis of variance and estimation of variance components.

The relative performance of genotypes based on the mean grain yield over environments is presented in Table 3.1. Yield performances are ranked. Grain yield is given in kg ha^{-1}.

Table 3.1: Mean grain yield (kg/ha) of 20 bread wheat genotypes over 8 test environments.

Genotype	Genotype Code	Mean grain yield	Rank
K6290Bulk	G1	3853.23	1
K6295-4A	G2	3570.28	6
ET-13.A2	G3	3673.42	3
ET12.D4	G4	3593.33	4
KKBB	G5	3186.36	15
Mitikie(HAR-1709)	G6	3329.14	12
Wabe(HAR-710)	G7	3313.60	13
Kubsa(HAR-1685)	G8	3513.09	7
Galama(HAR-604)	G9	3456.28	9
Abola(HAR-1522)	G10	3048.72	16
Magal(HAR-1595)	G11	3034.36	18
Tusie(HAR-1407)	G12	3030.58	19
Tura(HAR-1407)	G13	3454.74	10
Katar(HAR-1899)	G14	3273.31	14
Shinna(HAR-1868)	G15	3577.59	5
HAR-407	G16	3438.62	11
HAR-416	G17	3465.84	8
Gara	G18	3048.49	17
Batu	G19	3759.88	2
K6106-9	G20	2759.81	20

The combined analysis of variance (ANOVA) is shown in Table 3.2 and it revealed that there were significant differences among environments ($p<0.01$) and genotypes ($p<0.01$) for grain yield indicating the presence of variability in genotypes as well as diversity of growing conditions at different locations. The G×E interaction was highly significant ($p<0.01$) reflecting the differential response of genotypes in various environments.

Table 3.2: Combined ANOVA for yield and the percentage sum of squares of the 20 hybrids tested at 8 environments over a period of two years.

Source	DF	Sum of Squares	**%SS**	Mean Square	F Value	Pr> F
Env(E)	7	999543941.9	77.9	142791991.7	439.17	<.0001
Location (L)	3	623756478.2		207918826.1	639.47	<.0001
Year (Y)	1	5160646.2		5160646.2	15.87	<.0001
L×Y	3	370626817.5		123542272.5	379.96	<.0001
Rep(env)	24	14149904.6	1.1	589579.4	1.81	0.0112
Genotype(G)	19	48459603.8	3.78	2550505.5	7.84	<.0001
Env*genotype	133	72644063.7		546196.0	1.68	<.0001
G×L	57	35364200.2		620424.6	1.91	0.0002
G×Y	19	8002038.5		421159.9	1.30	0.1808
G×L×Y	57	29277825.0		513646.1	1.58	0.0064
Error	456	148264845	11.56	325142		
Corrected Total	639	1283062422				

The combined analysis of variance across locations and years showed highly significant differences among locations (L), year (Y) and genotypes (G) and their interaction (L×Y, G×L, G×L×Y). However, the interaction G×Y was not significant.

The restricted maximum likelihood (REML) estimates of variance components for environment, genotype and genotype × environment interaction are shown in Table 3.3. Estimated variance component due to environment ($\hat{\sigma}_E^2 = 1774767.5$) made the greater contribution to the total estimated variance for grain yield. Genotype × Environment interaction and residual components of variance were 55263.4 and 325142.1 respectively.

When individual estimates of variance for grain yield (Table 3.3) were expressed as a percent of the total variation$(\sigma_G^2 + \sigma_{G\times E}^2 + \sigma_e^2)$, the σ_G^2 component accounted for 14.14% of the total variation. The$\sigma_{G\times E}^2$was 12.47% of the total variation, indicating that the genotypes were less consistent over environments. This means that location selection needs more effort. All of the variance components were highly significant (p<0.01), and the importance of the $\sigma_{G\times E}^2$component indicates that factors such as rainfall, temperature, and disease incidence can result in conditions unique to each year location combination and that the genotypes respond differently to these conditions.

Table 3.3: Estimates of variance components for grain yield, genotypes and their interactions.

Variance Component	Estimate	% variance component
Var(env) $\hat{\sigma}_E^2$	1774767.5	
Var(rep(env)) $\hat{\sigma}_{R/E}^2$	13221.9	
Var(genotype) $\hat{\sigma}_G^2$	62634.7	14.14
Var(env*genotype) $\hat{\sigma}_{G\times E}^2$	55263.4	12.47
Var(Error) $\hat{\sigma}_e^2$	325142.1	73.39

The GEI is highly significant (p<0.01) accounting for 5.66% of the sum of squares implying the need for investigating the nature of differential response of the genotypes to environments. From the combined ANOVA in Table 3.2, G×E interaction is highly significant and hence superiority of genotypes across environments cannot be identified by considering their mean yield performance (see Table 3.1).

3.1.3. Parametric Stability Analysis

a)Wricke'secovalence (W_i)

The most stable genotypes according to the ecovalence method of Wricke (1962) were G10, G5 and G11. These genotypes were not the best ranked for mean yield, being 16th, 15th and 18th respectively.

The most unstable hybrids according the ecovalence method, higher W_i valueswere G20, G16 and G2 these hybrids were ranked 20th, 11th and 6th for mean yield respectively (Table 3.4).

Table 3.4: Wricke’secovalence value for 20 the hybrids at 8 environments.

Genotype	Ecovalence ($\mathbf{W_i}$)	Rank
G1	538363.71	10
G2	1786429.07	18
G3	1130443.87	16
G4	946303.10	15
G5	302434.95	2
G6	426586.25	8
G7	450989.95	9
G8	1601020.69	17
G9	929789.55	14
G10	286221.53	1
G11	311294.11	3
G12	635894.48	12
G13	382220.02	5
G14	384437.43	6
G15	365884.53	4
G16	2733767.87	19
G17	420613.95	7
G18	576063.53	11
G19	894997.34	13
G20	3057255.53	20

b) The environmental variance

The environmental variance (s_i^2) is one of the major stability measures for the static stability concept, i.e., the variance of genotype yields recorded across test environments. The smaller thes_i^2, the more stable the ith genotype. Genotype’s variance across environments and coefficient of variation are listed in Table 3.6.

Table 3.5: Genotype mean grain yield, environmental variance (s_i^2), and coefficient of variation (CV$_i$) for the 20 bread wheat varieties.

Genotype	Environmental _variance	Rank	CV$_i$	Environmental_variance	Rank	CV$_i$
G1	2405185.03	19	40.2484	2146490.02	16	42.2723
G2	2046790.55	13	40.0714	1539659.50	4	40.7031
G3	2258509.74	17	40.9110	2097619.78	14	38.5202
G4	1950761.93	9	38.8692	802702.02	1	32.4637
G5	1968419.49	10	44.0316			
G6	1802192.15	7	40.3245			
G7	2334427.18	18	46.1095			
G8	2859762.45	20	48.1366			
G9	1376777.48	2	33.9487			
G10	1971708.36	11	46.0579			
G11	1573821.98	5	41.3439			
G12	1496225.77	3	40.3620			
G13	1703592.37	6	37.7805			
G14	2112633.36	15	44.4042			
G15	1842655.07	8	37.9430			
G16	2002503.27	12	41.1531			

3.2. Nonparametric Method

3.2.1. Nonparametric Analysis Of G × E Interactions

The numerical values of the test statistic for the different statistical procedures to determine the significance of the effects of G×E interaction on grain yield of bread wheat genotypes are presented in Table 3.6. The null hypothesis for Bredenkamp is no non-crossoverG×E interactions and forde Kroon van der Laanis no crossover G×E interaction. The results indicated that significant interactions were found according to Hildebrand and Kubinger. In comparing the result of ANOVA with nonparametric analysis procedures, we found that both methods were in agreement, but nonparametric analysis provided more specific information about the nonexistence of crossover and non-crossover G×E interactions. For the de Kroon/van der Laan approach exceeding probabilities larger than 5% wereobtained implying No cross-over interactions were therefore detected by the deKroon/van der Laan procedure and also forBredenkamp approach exceeding probabilities larger than 5% were obtained implying No noncrossover interactions were therefore detected.

Table 3.6 Analysis of GEI using different nonparametric tests on 20 wheat genotypes grown in 8 environments.

Nonparametric tests	df	Statistic $\chi 2$	P-value
Bredenkamp	133	42.1193	0.9999
Hildebrand	133	187.7588**	0.0013
Kubinger	133	177.73416**	0.0058
de Kroon-van der Laan	133	148.5966	0.168

** Significant at the 0.01 level

3.3.2. Nonparametric Stability Analysis

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

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

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 environments for each genotype. The $S_i^{(2)}$ estimates are simply the variance of ranks for each genotype 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 $S_i^{(1)}$.

Table 3.7 Mean absolute rank difference ($S_i^{(1)}$) and variance of ranks ($S_i^{(2)}$) for yield of 20bread wheat varieties.

	$s_i^{(1)}$	Rank	$Z_i^{(1)}$	$s_i^{(2)}$	Rank	$Z_i^{(2)}$
G1	4.392857	6	2.934521	17.69643	8	1.621303
G2	7.178571	17	0.160926	38.55357	18	0.188513
G3	7.321429	18	0.259668	38.26786	17	0.168749
G4	5.178571	13	1.24709	19.41071	12	1.283605
G5	4.107143	4	3.724456	12.26786	4	2.950553
G6	5.214286	14	1.187285	19.42857	13	1.280294
G7	4.892857	11	1.778415	18.26786	11	1.504359
G8	7.821429	19	0.790407	43.125	19	0.653549
G9	6.535714	16	0.007523	30.69643	16	0.043702
G10	3.785714	2	4.725544	10.85714	2	3.360648
G11	3.25	1	6.658507	8.982143	1	3.946997
G12	4.785714	10	2.001908	17.71429	9	1.617581
G13	4.642857	9	2.320468	14.85714	5	2.267266
G14	4.964286	12	1.636767	18.125	10	1.533185
G15	4.464286	7	2.751729	15.26786	7	2.167138
G16	9.178571	20	3.682725	63.41071	20	6.09659
G17	4.571429	8	2.488564	15.07143	6	2.214743
G18	4	3	4.044928	11.42857	3	3.19132
G19	4.285714	5	3.219727	21.92857	14	0.859026
G20	5.785714	15	0.430263	26.21429	15	0.331757
	$E(S_i^{(2)})$	$V(S_i^{(2)})$	S^1	S^2	Tab. χ_1^2	Tab. χ_{20}^2
	33.25	149.209375	46.051421	37.280878	3.84	31.41

The $S_i^{(1)}$ may loose power when genotypes are similar in their interactions with the environments. Two rank stabilitymeasures proposed by Huhn (1979) were worked out and expressed as $S_i^{(1)}$ and $S_i^{(2)}$ are presented in Table 3.8 The genotypes G11, G10 and G18 had the lowest value of $S_i^{(1)}$ and ranked 18th, 16th and 17th for grain yield. G1 and G19 had higher grain yield as compared to overall mean yield, However, genotype G11, G10 and G18 were stable although they had the lowest mean yield. The highest $S_i^{(1)}$ mean absolute rank difference was observed for genotype G16, G8 and G3 indicating to be highly unstable genotypes. Since S^1 = 46.05 was higher than the critical value of χ^2= 31.41, there were significant differences in rank stability for grain yield among 20 wheat genotype grown in 4 locations during 2007-2008 (Table 3.8). And S^2 = 37.28 were higher than the critical value χ^2= 31.41, significant differences in rank stability among 20 wheat genotype grown in 4 locations during 2007-2008 (Table 3.8).

b) Relative deviation in relation to the average rank $S_i^{(3)}$ of a genotypes and the sum of squares of rank for each genotype relative to the mean of ranks $S_i^{(6)}$

Hühn (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 measurestability 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 $S_i^{(3)}$ valueas a few larger differences. These $S_i^{(3)}$ and $S_i^{(6)}$ non-parametric measures wereworked out by using the ranks which were assigned to genotypes on the basis of original mean data within environment and presented in Table 3.9

Table 3.8 The sum of the absolute deviations of rank ($S_i^{(3)}$) and the sum of squares of rank ($S_i^{(6)}$) for mean yield of 20bread wheat varieties.

	$S_i^{(3)}$	Rank	$S_i^{(6)}$	Rank
G1	5.081081	18	26.78378	15
G2	4.852459	17	35.39344	18
G3	5.830508	19	36.32203	19
G4	3.491525	13	18.42373	13
G5	1.652174	4	5.973913	4
G6	2.727273	9	12.36364	10
G7	1.978495	6	11	7
G8	4.051948	15	31.36364	16
G9	3.915493	14	24.21127	14
G10	1.225806	2	4.903226	2
G11	1.212598	1	3.96063	1
G12	1.870968	5	8	5
G13	3	11	13	11
G14	2.371134	8	10.46392	6
G15	3.017544	12	15	12
G16	5.844156	20	46.11688	20
G17	2.742857	10	12.05714	9
G18	1.333333	3	5.333333	3
G19	4.842105	16	32.31579	17
G20	2.098361	7	12.03279	8

The results of $S_i^{(3)}$ and $S_i^{(6)}$ indicated that the genotypes G11, G10 andG18 ranked first, second, and third respectively. According to $S_i^{(3)}$ and $S_i^{(6)}$ G11, G10 andG18 were found to be stable and adapted to all environments. But they occupied 18th, 16th and 17thposition in mean yield which implies stable genotypes with low yield.

According to $S_i^{(3)}$ and $S_i^{(6)}$ genotype G16 was found to be most unstable followed by genotype G3. Hühn (1990) used three non-parametric measures $S_i^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$ for phenotypic stability of winter wheat grain yield inGermany. He concluded that one is interested in asimultaneous 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. $S_i^{(3)}$ measurewas used to find the stable cowpea (Vignaunguiculata L.) genotypes by Aremu et al. (2007).

The nonparametric superiority parameter of Fox et al. (1990) consists of scoring the percentage of environments in which each genotype ranked in the top, middle and bottom third of trial entries. A genotype usually found in the top third of entries across environments can be considered relatively well adapted and stable. Thus, G19 was an adapted genotype, because it ranked in the top third of genotypes in a high percentage of environments (high top value, 87.5%), and was followed by G1 (75%) (Table3.10). The undesirable genotypes identified by this method were G10, G11, G12 and G18.

Kang's (1988) nonparametric stability parameter (rank-sum) uses both yield and Shukla's stability variance (Shukla 1972). The genotypes with the lowest rank-sum are the most favorable ones. According to the rank-sum statistic G15 had the lowest values for rank-sum and therefore were stable genotypes with high yield, followed by G1 and G17 (Table 3.9). According to the rank-sum statistic, the undesirable genotypes were G20, G12 and G16. The results of this method for stable genotypes are relatively in agreement with the TOP procedure.

Table 3.9 Genotype mean grain yield, Kang's rank-sum and TOP values with ranks for the 20 Bread wheat varieties.

	stability_variance	Rank	Kang's rank-sum	Rank	TOP (%)	MID (%)	LOW (%)	rank of top
G1	80379.35	10	11	2	75.0	25.0	0	2
G2	278484.96	18	24	15	50.0	37.5	12.5	3
G3	174360.32	16	19	7	50.0	25.0	25.0	3
G4	145131.63	15	19	8	50.0	37.5	12.5	3
G5	42930.34	2	17	6	0	62.5	37.5	16
G6	62636.89	8	20	10	12.5	50.0	37.5	12
G7	66510.5	9	22	13	12.5	75.0	12.5	12
G8	249055.06	17	24	15	25	50.0	25.0	11
G9	142510.43	14	23	14	37.5	50.0	12.5	8
G10	40356.78	1	17	6	0	37.5	62.5	16
G11	44336.55	3	21	12	0	25.0	75.0	16
G12	95860.42	12	31	19	0	37.5	62.5	16
G13	55594.63	5	15	3	37.5	62.5	0	8
G14	55946.60	6	20	10	12.5	37.5	50.0	12
G15	53001.70	4	9	1	50.0	50.0	0	3
G16	428856.20	19	30	18	50.0	12.5	37.5	3
G17	61688.91	7	15	3	37.5	50.0	12.5	8
G18	86363.44	11	28	17	0	37.5	62.5	16
G19	136987.86	13	15	3	87.5	0	12.5	1
G20	480203.44	20	40	20	12.5	37.5	50.0	12

Results of Thennarasu's (1995) nonparametric stability statistics, which are calculated from ranks of adjusted yield means, are shown in Table 3.10, with the ranks of genotypes according to these parameters. According to the first method ($\mathrm{NP}_i^{(1)}$), genotypes G15, G14 and G10 were stable in comparison with the other genotypes. The unstable genotypes based on $\mathrm{NP}_i^{(1)}$ were G20 and G16 followed by G3. Genotype G11 had the lowest value of $\mathrm{NP}_i^{(2)}$ and was stable, followed by G10 and G12. Because of the high values for $\mathrm{NP}_i^{(2)}$, the stabilities of G19 followed by G16 and G3 were low, although they had the highest mean yield (Table 3.10). $\mathrm{NP}_i^{(3)}$, like$\mathrm{NP}_i^{(2)}$, identified G11 as the most stable genotype, although it had the lowest mean yield. The next most stable genotypes were G10 and G5 both of which had low mean yield performances. The unstable genotypes based on $\mathrm{NP}_i^{(3)}$ were G19 followed by G1 and G3, which had the highest mean yield. Thus$\mathrm{NP}_i^{(3)}$ has a negative relationship with yield ($P < 0.01$).

Stability parameter $\mathrm{NP}_i^{(4)}$ identified G11 as a stable genotype, followed by G10 and G5; but like $\mathrm{NP}_i^{(2)}$and $\mathrm{NP}_i^{(3)}$, identified G19, G1 and G3 as unstable. The results of three NPs $\mathrm{NP}_i^{(2)}$, $\mathrm{NP}_i^{(3)}$ and $\mathrm{NP}_i^{(4)}$) were very similar to each other and identified G19, G1 and G3 as unstable, although they had the highest mean yield performances.

Table 3.10 Genotype mean grain yield and Thennarasu's nonparametric stability value for the bread wheat varieties.

	$NP_i^{(1)}$	Rank	$NP_i^{(2)}$	Rank	$NP_i^{(3)}$	Rank	$NP_i^{(4)}$	Rank
G1	4.5	7	1.285714	19	1.081081	19	1.343629	19
G2	4.5	7	0.642857	14	0.747656	15	0.946136	15
G3	6	18	1	17	0.924001	18	1.191283	18
G4	4.25	5	0.653846	15	0.748838	16	0.949153	16
G5	4.5	7	0.346154	6	0.350856	3	0.447205	3
G6	4.75	11	0.475	9	0.499483	8	0.623377	8
G7	4.25	5	0.369565	7	0.431717	7	0.55914	7
G8	5.75	16	0.638889	13	0.70657	14	0.90538	14
G9	5.75	16	0.71875	16	0.687116	13	0.885312	13
G10	3.875	3	0.242188	2	0.309303	2	0.394009	2
G11	4	4	0.228571	1	0.272309	1	0.346457	1
G12	4.5	7	0.257143	3	0.367445	4	0.456221	4
G13	4.875	14	0.609375	12	0.659775	12	0.852679	12
G14	3.625	2	0.258929	4	0.393242	6	0.474227	5
G15	3.25	1	0.5	10	0.639329	11	0.79198	10
G16	7.375	19	1.229167	18	0.833499	17	1.03525	17
G17	4.75	11	0.527778	11	0.618095	10	0.8	11
G18	4.75	11	0.306452	5	0.368179	5	0.47619	6
G19	4.875	14	1.392857	20	1.133413	20	1.43609	20
G20	7.375	19	0.460938	8	0.512606	9	0.639344	9

3.4. Rank Correlation among Stability Statistics and Yield

The results of the Spearman's rank correlation coefficient among the 15 parametric and non-parametric stability statistics and mean yield are presented in Table 3.11. Mean yield performance across environments was significantly positively correlated with RS and TOP measures (P<0.05 and P<0.01 respectively), but it was not significantly correlated with W_i, $S_i^{(1)}$, $S_i^{(2)}$ and $NP_i^{(1)}$ .However themean yield was found to have significant negative correlations with$s_i^{(3)}$, $s_i^{(6)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (P<0.01). The high correlation between mean yield and stability measures is expected as the values of these statistics were higher for high yielding genotypes. The non-significant correlation and negative significant correlation between yield and stability parameters suggest that stability parameters provide information that cannot be gleaned from average yield alone (Mekbib 2002).

Relationship among parametric and non-parametric methods

Ecovalance (W_i) was perfectly positively associated with Shukla and positively associated withs_i^2, $S_i^{(1)}$, $S_i^{(2)}$, $s_i^{(3)}$,$NP_i^{(2)}$and $NP_i^{(3)}$(P<0.01) and with $s_i^{(6)}$ and $NP_i^{(1)}$(P<0.05). Environmental variance (s_i^2), is significantly correlated with $s_{d_i}^2$(P<0.01) and with the methods of $s_i^{(3)}$(P<0.05). Stability variance (σ_i^2) had negative and significant correlations with, $S_i^{(2)}$and $NP_i^{(2)}$(P<0.05). The non-parametric method of $S_i^{(1)}$ was significantly positively correlated with $S_i^{(2)}$, $s_i^{(3)}$ and $s_i^{(6)}$(P<0.01) and with the methods of $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$(P<0.05). $S_i^{(2)}$had positive and significant correlations with $s_i^{(3)}$,$s_i^{(6)}$, $NP_i^{(1)}$, $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$ (P<0.01) and negative and significant correlation with RS (P<0.05). $s_i^{(3)}$, as well as $s_i^{(6)}$parameters were negatively correlated with TOP (P<0.01). TOP was negatively and significantly associated with $NP_i^{(2)}$, $NP_i^{(3)}$ and $NP_i^{(4)}$(P<0.01).

The most stable genotype according to the parametric methods was G11, G10, G5 and G12 while G11, G10, G5, G18 and G12 were stable according to the nonparametric methods. The most unstable genotype according to the parametric methods was G20, G16 and G2 while G3, G16, G19, G1 and G20 were unstable according to the nonparametric methods. The result shows that both the parametric and nonparametric methods gave a relatively similar result but it is based on one data set. So to prove that both the parametric and nonparametric methods give a relatively similar result, it needs simulation study.

Table 3.11 Spearman's rank correlation coefficients between different parametric and nonparametric stability parameters for grain yield of 20 bread wheat varieties.

	Y	W_i	σ_i^2	S_i^2	ASV	$S_{d_i}^2$	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	RS	TOP	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$
W_i	-0.24	1.00													
σ_i^2	-0.24	1.00**	1.00												
S_i^2	-0.58*	0.05	0.05	1.00											
ASV	-0.19	0.69**	0.69**	0.01	1.00										
$S_{d_i}^2$	-0.54*	-0.12	-0.12	0.95**	-0.1	1.00									
$S_i^{(1)}$	-0.25	0.77**	0.77**	0.17	0.52*	0.01	1.00								
$S_i^{(2)}$	-0.39	0.86**	0.86**	0.25	0.64**	0.08	0.91**	1.00							
$S_i^{(3)}$	-0.83**	0.62**	0.62**	0.46*	0.43	0.3	0.64**	0.75**	1.00						
$S_i^{(6)}$	-0.79**	0.67**	0.67**	0.41	0.48*	0.25	0.69**	0.81**	0.98**	1.00					
RS	0.56*	0.56*	0.56*	-0.42	0.38	-0.55*	0.43	0.38	-0.2	-0.13	1.00				
TOP	0.86**	-0.38	-0.38	-0.33	-0.29	-0.2	-0.33	-0.5*	-0.81**	-0.79**	0.38	1.00			
$NP_i^{(1)}$	-0.1	0.67**	0.67**	-0.06	0.39	-0.18	0.56*	0.6**	0.47*	0.53*	0.31	-0.15	1.00		
$NP_i^{(2)}$	-0.85**	0.58*	0.58*	0.38	0.46*	0.27	0.48*	0.65**	0.94**	0.93**	-0.29	-0.81**	0.53*	1.00	
$NP_i^{(3)}$	-0.86**	0.63**	0.63**	0.42	0.45*	0.31	0.52*	0.68**	0.95**	0.95**	-0.3	-0.84**	0.48*	0.98**	1.00
$NP_i^{(4)}$	-0.85**	0.64**	0.64**	0.42	0.46*	0.3	0.5*	0.66**	0.94**	0.94**	-0.26	-0.8**	0.51*	0.98**	0.99**

Critical value of the Spearman's rank correlation coefficients for n=20, α=0.05 is ±0.450 and for α=0.01 is ±0.591

Acknowledgements

We are greatly thankful to Associate Editor and Anonymous referee for his/her valuable comments, suggestions and supplying the literature to correct the chi-square formulas.

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