

A Nonparametric Analysis for Stability of Wheat Genotypes Tested in Southern Punjab, Pakistan

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Abstract

The objective of our study is to investigate the relationship amongst nonparametric stability statistics. Genotype environment interaction ($G \times EI$) of eighteen genotypes wheat, tested at seven locations was interpreted by non-parametric measures. Different nonparametric measures for ($G \times EI$) on the grain yield data of eighteen wheat's genotypes were selected from NUWYT in the year 2016-17 in Pakistan. The experiments were conducted in Randomized Completely Block Design (RCBD) and were replicated twice at each location. The nonparametric steps were used to attain improvement for $G \times EI$ at ($P < 0.01$) which recommended the various interaction of the wheat's genotype to be tested in each environment. Rank correlation by Spearman was applied to calculate the relationship amongst the stability of statistics with (PCA) biplot. The results of (PCA) and correlation analysis of nonparametric stability measures indicate to select stable and highly yield genotype by using S_i^1 , S_i^2 , S_i^3 and S_i^6 (Huehn, 1979), the NP_i^1 , NP_i^2 , NP_i^3 and NP_i^4 (Thennarasu, 1995) and rank sum (Kang's 1988). G16, G1 and G5, were found to be the most stable genotypes and G10 was unstable.

Keywords: ($G \times EI$) Genotype Environment Interaction, (PCA) Principal Component Analysis, ANOVA, Multi Environment Trial, Graphical.

Introduction

Wheat (*Triticum aestivum* L) is one of the most important staple food, which extensively grown crop in the world. It is the major dietary resource as well as an important agricultural product of Pakistan. Wheat is a major crop in Pakistan. 80 % farmers cultivate it on an area about nine million hectares (40 % of cultivated land of country) during "winter" season. The wheat crop is cultivated for food, feed, forage and breeding purposes. Wheat is grown at various agro-climatic atmosphere of the country. Interpretation of genotype-environment interactions facilitated by applying statistical methods as interaction complicates the identification of the best genotypes (Bertero et al., 2004). The nonparametric measures, based on ranks only, proved to be applicable substitute parametric measures (Dehghani, 2008). The rank order of genotypes is essential for applications, including testing programs and selection in breeding ((Huehn and Nassar, 1987), (Kang, 1988), (Thennarasu, 1995)). The success of crop progressive activities mostly depends on the identification of the superior genotypes for mass production.

Studying $G \times EI$ and determining the adaptation of genotypes requires two major approaches, the first approach is parametric which depends upon the distributional hypothesis about genotypic, environmental, and $G \times EI$ effects, and second nonparametric approach is analytical clustering,

which relate phenotypes and environmental concern to biological and inanimate environmental elements without making particular modeling hypothesis (Huehn, 1996).

The parametric measures possess good attributes under certain statistical hypothesis, like normal distribution of errors and interaction effects; however, they may not perform well if these hypotheses are violated and homoscedasticity is found. The nonparametric stability methods does not require any normality assumption and variance homogeneity. However, this research data may not perform well under the assumption of normality so we select the nonparametric methodology.

Main purpose of this investigation was (1) to recognize the stable and high yield best genotype across various test environments in (Southern Punjab) Pakistan (2) to investigate crossover interaction in multi environmental trials and to study relationship amongst nonparametric statistics stability by using nonparametric measures.

Literature Review

In static stability, the genotype's results are constant in each environment, but in dynamic stability the genotype's results are change in various environment. The main objective of most plant breeders is to choose stable genotypes, which mean yield performance residue high across a field of atmospheric conditions. According g to (Hussain et al., 2000) the stability analysis is applicable only in the presence of G×EI. The crossover and noncrossover interaction are two main classes of G×EI. In crossover interaction the genotype's ranking is not similar in various atmosphere. According to (Laan de Kroon, 1981) and (Truberg and Huehn, 2000) crosserover interaction is not present in the similar ranking. Biometricians implemented measures of G×EI and stability to introduced several methods of analysis as (Shukla's,1972), (Lin et al., 1986), (Leon and Becker 1988), (Flores et al, 1998) and (Mohammadi and Amri, 2008).

The various univariate and multivariate measures has been used for G×EI to achieve the best result amongst every environment. (Leon and Baker, 1988), (Kang ,1988), (Pham and Kang ,1991), (Ham and Cooper, 1996), (Scapim et al. 2000) and (Sabaghnia et, al;2006) studied the G×EI with various aspects. (kang's, 1988) proposed a nonparametric stability measure rank – sum, on the base of variance of Shukla's (1972) with mean yield. The NP_i^1 , NP_i^2 , NP_i^3 and NP_i^4 , were proposed by (Thennarasu, 1995). The S_i^1 , S_i^2 , S_i^3 and S_i^6 are also nonparametric methods proposed by (Huehn, 1979). GGE bi-plot is graphically presented the G×EI in two-way analysis of Variance (Yan, 2000). Several non-parametric measures of univariate and multivariate are applied to get the stability of variates.

Methodology

The formulae for computing the statistic, based on genotype's yield ranks in all environments are defined as follows by (Huehn, 1979).

$$S_i^1 = 2 \sum_j^{n-1} \sum_{j'=j+1}^n |r_{ij} - r_{ij'}| / [e(e-1)]$$

$$S_i^2 = \sum_{j=1}^n (r_{ij} - \bar{r}_i)^2 / (e-1)$$

$$S_i^3 = \sum_{j=1}^n (r_{ij} - \bar{r}_i)^2 / \bar{r}_i$$

$$S_i^6 = \sum_{j=1}^n |r_{ij} - \bar{r}_i| / \bar{r}_i.$$

In above formula's

(Huehn, 1979) and (Nassar and Huehn, 1987) suggested four non parametric stability methods, these statistics combine stability and mean yield. Genotypes g and n environments in a two-way data, r_{ij} is the rank of the i^{th} genotype in j^{th} environment, r_{ij} is the absolute deviation of rank r_{ij} , \bar{r}_i is the rank's mean all across environment.

The smallest value for each statistic showed maximum genotype's stability. (Huehn, 1990) preferred the use of S_i^1 to S_i^2 due to many practical contemplations reported to calculate easily, interpret and is effective to test the significance. The homogeneity of variance assumption is not essential for these statistics. The genotype's stability of in non-normal and heteroscedastic data is also determined by using these statistics. The implementation of nonparametric stability statistics is hypothetically strong for missing values. The missing value was replaced with genotype's average rank for the environments (Huehn, 1990). To tests of significance for S_i^1 and S_i^2 were suggested by (Huehn and Nassar, 1987).

The obvious formulae for means $E(S_i^k)$ and variances $var(S_i^k)$ are:

The statistic

$$Z_i^k = \{ S_i^k - E(S_i^k) \}^2 / \text{Var}(S_i^k)$$

Here Z_i^k , for $k = 1, 2$. Has an approximate χ^2 distribution with (1) degree of freedom and the statistic S_i^k , $k = 1, 2, 3, \dots, 18$ may be approximated by a χ^2 distribution with degree of freedom g and e represent the number of genotypes and environments in given equations.

$$E(S_i^1) = (g^2 - 1) / 3g$$

$$E(S_i^2) = (g^2 - 1) / 12$$

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

$$\text{Var}(S_i^2) = \{(g^2 - 1) / 36e\} [(g^2 - 4) / 5 + (g^2 - 1) / 2(e - 1)]$$

(Huehn & Nassar 1987, 1989 and 1991) developed the statistical tests of significance and characteristics of S_i^1 and S_i^2 which depends upon the normal distribution under the null hypothesis of no genotype environment interaction effects.

Rank-Sum (RS) is another nonparametric method by (Kang, 1988), where both grain mean yield and (Shukla's 1972) stability variance are used.

The genotype's adjusted rank in every environmental test is contemplated by Thennarasu's (1995) nonparametric stability analysis. The adjusted genotype's values ($Y_{ij}^* = Y_{ij} - \bar{Y}_i$) determined the adjusted rank r_{ij}^* . The ranks depend only on $G \times EI$ and error effects. (Thennarasu, 1995) suggested the four following nonparametric stability methods by applying the adjusted rank values defined :

$$NP_i^1 = \sum_{j=1}^n |r_{ij}^* - M_{di}^*| / n$$

$$NP_i^2 = \left[\sum_{j=1}^n |r_{ij}^* - M_{di}^*| / M_{di}^* \right] / e$$

$$NP_i^3 = \frac{\sqrt{\sum (r_{ij}^* - \bar{r}_i^*)^2 / e}}{\bar{r}_i}$$

$$NP_i^4 = 2 / e (e - 1) [\sum_{j=1}^{n-1} \sum_{j'=j+1}^n |r_{ij}^* - r_{ij'}^*| / \bar{r}_i]$$

In these formulae r_{ij}^* is rank of Y_{ij}^* , \bar{r}_i^* and M_{di}^* are mean and median ranks for the adjusted values, while \bar{r}_i and M_{di} is the same methods calculated from original values. In order to study the relationship amongst the above nonparametric statistics to evaluate mean yield stability of testing wheat genotypes, Spearman's rank correlation analysis and (PCA) based on the rank correlation matrix was applied.

Data Source

This research data set involved 18 wheats genotypes tested in seven environments used for yield trials: Multan, Bahawalnagar, Raheem Yar Khan, Lodhran, Muzaffargarh, Khanewal and Bahawalpur were evaluated in randomize complete block design (RCBD) with two replications in each trial. Each trial plot size was 16.5ft x 6ft =5m x 1.8 grain yield in kg/ha selected from National Uniform Wheat Yield Trial (NUWYT). All agricultural practices were applied, based on suggested conventions for all places. Grain yield of each cultivar was recorded on a plot basis. Names and codes of genotypes are mentioned in Table.1.

Table 1. Eighteen Wheat Genotype Names and their Codes.

| Code | Genotype | Code | Genotype |
|------|-------------|------|------------------|
| G1 | DN-111 | G10 | PR-115 |
| G2 | NW-1-8183-8 | G11 | IV-11 |
| G3 | NW-5-20-1 | G12 | NIBGE-CANDUM-III |
| G4 | KT-335 | G13 | CT-12176 |
| G5 | V-12066 | G14 | NRL-1123 |
| G6 | NR-443 | G15 | QS-3 |
| G7 | NR-487 | G16 | FSD-08 |
| G8 | WBG-14 | G17 | PAKISTAN-13 |
| G9 | MSH-3 | G18 | Aas-11 |

Statistical Analysis

The two statistical nonparametric methods of (Laan de Kroon ,1981) and (Bredenkamp J,1974) were applied to examine the importance of G×EI. These methods are based on the usual linear model for interaction described as "deviation from additively of main effects for environments and genotypes" (Huehn, 1979). (Huehn and Nassar 1987) , (Leon and Huehn ,1995), and (Truberg and Huehn 2000) defined these parameters in detail and suggested the four nonparametric stability statistics S_i^1 , S_i^2 , S_i^3 and S_i^6 which measure collective mean yield and stability. (Thennarasu ,1995) stability of non-parametric procedures NP_i^1 , NP_i^2 , NP_i^3 and NP_i^4 and Kang (1998) R Statistic were also calculated.

To evaluate nonparametric measures in order to study the yield stability we examined wheat genotypes, rank correlation method by Spearman's and PCA which was applied on the based rank

correlation matrix. The nonparametric methods were applied to yield data by using different software R,3.1.3, Minitab 16 and Excel 2016.

Results and Discussion

Analysis of the variance was used to ascertain the effects of atmosphere, genotype and environment interactions amongst these components on grain production of the wheat genotypes in Table.2. The environmental effects E and G×E interaction were very highly significant at ($P < 0.01$) and genotype major effect was significant at ($P < 0.05$). G×E interaction and environmental effects were computed for sum of the squares Table.2.

Table 2. The Variance Analysis for Wheat *Triticum Aestivum L.* Yield of Eighteen Genotypes at Seven Environments

| Source of Variation | d. f | Sum of Square | Mean Square | F | Total % |
|---------------------|------|---------------|-------------|-------------|----------|
| ENV | 6 | 115211992 | 19201999 | 1357.345*** | 33.24155 |
| REP(ENV) | 7 | 99027 | 14146.71 | 1.0477 | |
| GEN | 17 | 34285177 | 2016775 | 149.3594*** | 9.892133 |
| ENV x GEN | 102 | 195387298 | 1915562 | 141.8637*** | 56.37413 |
| Residuals | 119 | 1606837 | 13502.83 | | 0.463613 |
| Total | 251 | 346590331 | | | |

The probability level at $P = 0.05$ is significant *; The probability level at $P = 0.01$ is significant**
The probability level at $P = 0$ is significant***

The calculated values to test statistic for various statistical nonparametric methodology are given in Table.3. The null hypothesis is significant in crossover by Laan-de Kroon but significant in non-crossover by Berdenkamp. These conclusions are related to ANOVA and provide most specific information about the nature of G×E.

Table 3. The Analysis of the G × EI applying various nonparametric tests on 18 Wheat *Triticum Aestivum L.* Genotypes Cultivated in 7 Locations.

| Methods | d.f | χ^2 statistic |
|------------------------------|-----|--------------------|
| Berdenkamp (non- crossover) | 102 | 758.23 |
| Laan - de Kroon (crossover) | 102 | 12.81 |

The probability level at ($P < 0.01$) is significant **

Analysis of Stability

The conclusion of 9 nonparametric methods and grain mean yield of 18 genotypes are extracted and are given in Table 4. The tests S_i^1 and S_i^2 are significantly derived from (Huehn and Nassar, 1987). For Z_i^1 and Z_i^2 values were based on the ranks of the summed and adjusted data over genotypes to obtain Z-values sum $Z_i^1 = 19.672$ and sum $Z_i^2 = 24.66$ as shown in Table 4. The value of Z_i^1 and Z_i^2 are less than the critical value of χ^2 ($0.05, d.f = 17$) = 27.587, so no significant difference between Z_i^1 and Z_i^2 in the rank stability were found amongst the 18 genotypes cultivated in 7 environments. However, the individual Z-values for genotypes were significant because they showed large Z-values, in comparison with the critical value of χ^2 ($0.05, d. f = 1$) = 3.84.

According to mean yield genotype G3 is the highest yielder followed by G7 and G1 although remarkable differences are evident between the studied wheat genotypes in Table .4. For the S_i^1 and

S_i^2 measures, G16 is the smallest value in the ranks and thus considered as the more stable genotype (Table 4). However, G16 is the smallest and stable value in S_i^3 measures. In S_i^6 , G16 is also the smallest value and followed by G5 and G1. According to (Huehn's, 1987) nonparametric stable genotype measures from uncorrected values demonstrate high mean yield. In other words, with maintenance of genotype effect in each cell of two-way mean yield data confounds $G \times EI$ and affects stability analysis (Farshadfar et. al., 2014). Concurrent adaptation for both grain mean yield and stability is a significant consideration as (Pham and Kang 1991) studied numerous stability methods simultaneous for yield stability. These measures give liveness for plant breeders for the concurrent selection for both stability and mean yield (Mohammadi et. al, 2007). G1 and G15 were considered stable genotypes with high yields, because of the lowest values of rank-sum (Kang, 1988) .

The nonparametric stability measured by (Thennarasu, 1995), calculated by the ranks of stability yield means is given in Table.4. Genotypes G16, G1, G5 and G14 were stable according to NP_i^1 , but G7 and G10 were not stable. Genotype G16 had the smallest and stable value in NP_i^2 , followed by G5 and G2. Genotype G3 and G10 had low stability, although according to NP_i^2 they had highly mean yield. Genotype G16 was the most stable in NP_i^3 and NP_i^4 because of the lowest value in other genotypes. The genotype G16 showed the most stable result in mean yield all nonparametric measures (Mohammadi et. al, 2008).

Table 4. Nonparametric Statistics and Grain Mean Yield Eighteen Wheat (*Triticum Aestivum* L) Genotype at Seven Locations.

| Code | Yield (Kg ha ⁻¹) | Si1 | Si2 | Si3 | Si6 | RS | NPi1 | NPi2 | NPi3 | NPi4 | Zi1 | Zi2 |
|-----------------------|---------------------------------|-------|-------------------|--------|-------|------------------|-------|-------|----------------------------|-------|-------|--------|
| G1 | 5170 | 5.238 | 18.810 | 12.344 | 2.531 | 5 | 3.286 | 0.548 | 0.618 | 0.573 | 0.324 | 0.564 |
| G2 | 4228 | 7.143 | 35.000 | 23.333 | 3.556 | 23 | 4.571 | 0.315 | 0.419 | 0.794 | 0.792 | 0.561 |
| G3 | 5717 | 7.238 | 37.143 | 22.609 | 3.536 | 12 | 4.714 | 1.571 | 1.013 | 0.734 | 0.927 | 0.897 |
| G4 | 4625 | 6.476 | 28.667 | 17.200 | 3.000 | 27 | 4.143 | 0.414 | 0.479 | 0.648 | 0.144 | 0.026 |
| G5 | 4843 | 5.619 | 24.286 | 12.593 | 2.025 | 22 | 3.286 | 0.299 | 0.394 | 0.486 | 0.077 | 0.059 |
| G6 | 4916 | 6.381 | 28.571 | 20.690 | 3.897 | 9 | 4.286 | 0.952 | 0.624 | 0.770 | 0.094 | 0.023 |
| G7 | 5293 | 8.190 | 49.905 | 26.532 | 3.873 | 19 | 5.571 | 0.557 | 0.769 | 0.726 | 2.864 | 4.535 |
| G8 | 4197 | 6.476 | 30.667 | 23.000 | 4.250 | 23 | 4.429 | 0.341 | 0.392 | 0.810 | 0.144 | 0.121 |
| G9 | 4714 | 6.476 | 30.143 | 19.781 | 3.594 | 24 | 4.286 | 0.390 | 0.560 | 0.708 | 0.144 | 0.089 |
| G10 | 4840 | 9.048 | 61.143 | 45.053 | 6.035 | 26 | 6.429 | 1.429 | 0.881 | 1.111 | 5.518 | 10.052 |
| G11 | 4463 | 5.810 | 22.476 | 14.750 | 2.969 | 23 | 3.714 | 0.354 | 0.368 | 0.635 | 0.017 | 0.169 |
| G12 | 4463 | 5.810 | 22.476 | 14.750 | 2.969 | 23 | 3.714 | 0.354 | 0.368 | 0.635 | 0.017 | 0.169 |
| G13 | 4786 | 7.048 | 34.143 | 20.783 | 3.159 | 22 | 4.429 | 0.554 | 0.592 | 0.715 | 0.667 | 0.448 |
| G14 | 4813 | 5.810 | 22.952 | 16.067 | 2.967 | 18 | 3.571 | 0.420 | 0.509 | 0.678 | 0.017 | 0.135 |
| G15 | 5111 | 6.095 | 24.905 | 14.528 | 2.750 | 5 | 4.000 | 0.571 | 0.548 | 0.593 | 0.008 | 0.035 |
| FG16 | 4675 | 2.857 | 5.810 | 3.536 | 1.304 | 16 | 1.714 | 0.191 | 0.220 | 0.290 | 5.730 | 3.823 |
| PG17 | 5054 | 5.810 | 23.476 | 14.290 | 2.754 | 15 | 3.857 | 0.643 | 0.628 | 0.589 | 0.017 | 0.102 |
| AG18 | 4524 | 7.905 | 45.143 | 30.581 | 4.645 | 30 | 5.429 | 0.418 | 0.640 | 0.892 | 2.171 | 2.851 |
| Test statistics | | | | | | | | | | | | |
| E(Si1) = 5.98 | | | E(Si2) = 26.92 | | | Sum Zi1 = 19.672 | | | $\chi^2(0.05, 17) = 27.59$ | | | |
| Var(Si1) = 1.70 | | | Var(Si2) = 116.53 | | | Sum Zi2 = 24.66 | | | $\chi^2 Zi1 Zi2 = 3.48$ | | | |
| Grand mean = 86429.28 | | | | | | | | | | | | |

(i) S_i^1 is the absolute average rank dispersion of the genotype over environments, and S_i^2 is the variance amongst the ranks over environments, S_i^3 is the sum of absolute deviations and S_i^6 and the sum of squares of ranks for every geno-

type relative to the average of ranks respectively. (ii) Z_i^1 and Z_i^2 are chi-square χ^2 test statistics for S_i^1 and S_i^2 (iii) (Kang 1988) rank-sum statistics

Table 5. The rank of grain mean yield and different nonparametric measures of eighteen Wheat (*Triticum Aestivum L*) genotype at seven environments

| Code | Y (Kg ha ⁻¹) | S _i ¹ | S _i ² | S _i ³ | S _i ⁶ | RS | NP _i ¹ | NP _i ² | NP _i ³ | NP _i ⁴ |
|------|--------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|----|------------------------------|------------------------------|------------------------------|------------------------------|
| G1 | 3 | 2 | 2 | 2 | 3 | 1 | 2 | 2 | 2 | 3 |
| G2 | 17 | 14 | 14 | 15 | 12 | 11 | 14 | 18 | 18 | 15 |
| G3 | 1 | 15 | 15 | 13 | 11 | 4 | 15 | 3 | 4 | 13 |
| G4 | 13 | 10 | 10 | 9 | 9 | 17 | 9 | 11 | 10 | 8 |
| G5 | 7 | 3 | 7 | 3 | 2 | 9 | 2 | 9 | 11 | 2 |
| G6 | 6 | 9 | 9 | 11 | 15 | 3 | 10 | 5 | 7 | 14 |
| G7 | 2 | 17 | 17 | 16 | 14 | 8 | 17 | 15 | 12 | 12 |
| G8 | 18 | 10 | 12 | 14 | 16 | 11 | 12 | 16 | 17 | 16 |
| G9 | 11 | 10 | 11 | 10 | 13 | 15 | 10 | 14 | 8 | 10 |
| G10 | 8 | 18 | 18 | 18 | 18 | 16 | 18 | 10 | 15 | 18 |
| G11 | 15 | 4 | 3 | 6 | 7 | 11 | 5 | 12 | 13 | 6 |
| G12 | 15 | 4 | 3 | 6 | 7 | 11 | 5 | 12 | 13 | 6 |
| G13 | 10 | 13 | 13 | 12 | 10 | 9 | 12 | 8 | 9 | 11 |
| G14 | 9 | 4 | 5 | 8 | 6 | 7 | 4 | 7 | 5 | 9 |
| G15 | 4 | 8 | 8 | 5 | 4 | 1 | 8 | 6 | 6 | 5 |
| G16 | 12 | 1 | 1 | 1 | 1 | 6 | 1 | 1 | 1 | 1 |
| G17 | 5 | 4 | 6 | 4 | 5 | 5 | 7 | 4 | 3 | 4 |
| G18 | 14 | 16 | 16 | 17 | 17 | 18 | 16 | 17 | 16 | 17 |

Table 6. Spearman’s rank correlation coefficient amongst various nonparametric stability methods

| Methods | Y | S _i ¹ | S _i ² | S _i ³ | S _i ⁶ | RS | NP _i ¹ | NP _i ² | NP _i ³ |
|------------------------------|---------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|---------|------------------------------|------------------------------|------------------------------|
| S _i ¹ | -0.048 | | | | | | | | |
| S _i ² | -0.073 | 0.976** | | | | | | | |
| S _i ³ | 0.150 | 0.943** | 0.925** | | | | | | |
| S _i ⁶ | 0.203 | 0.844** | 0.825** | 0.939** | | | | | |
| RS | 0.639** | 0.430 | 0.432 | 0.514* | 0.532* | | | | |
| NP _i ¹ | -0.029 | 0.983** | 0.961** | 0.951** | 0.882** | 0.403 | | | |
| NP _i ² | 0.619** | 0.505* | 0.514* | 0.628** | 0.607** | 0.731** | 0.514* | | |
| NP _i ³ | 0.627** | 0.528* | 0.533* | 0.661** | 0.633** | 0.694** | 0.540* | 0.906** | |
| NP _i ⁴ | 0.209 | 0.862 | 0.844** | 0.965** | 0.957** | 0.456 | 0.888** | 0.562* | 0.628** |

The probability level at the 0.05 is significant *; The probability level at the 0.01 is significant **

The Relationship amongst Distinct Stability Statistics

Nonparametric measures produced a distinctive genotype by ranking as mentioned in Table. 5. Rank correlation by Spearman amongst every pair of stability through nonparametric statistic was

computed in Table. 6, which demonstrated the highest significant at the ($P < 0.01$), the rank correlation amongst S_i^1 , S_i^2 , S_i^3 , NP_i^2 and NP_i^3 . Two parameters of stability NP_i^2 and NP_i^3 were correlated positively and significant in mean yield. The RS test and grain mean yield of genotype $r = 0.639^{**}$ were also significant at $P < 0.01$.

To test the relationships amongst the non- parametric measures, the PCA depends upon the correlation rank matrix in Table. 6. The showings of the two PCAs of the ranks of various nonparametric parameters are given in Table.7. The initial two PCAs explained variation of 89.722% (68.825 and 20.897) % by PCA1 and PCA2. The relationship between the various stability statistic is displayed on a biplot in Fig.3. In given biplot PCAs axis mostly differentiate the NP_i^2 , NP_i^3 , RS and grain mean yield (Y), and also these value referred to class 1 as C1 stability measures. The S_i^1 , S_i^2 , S_i^3 , S_i^6 , NP_i^1 and NP_i^4 statistic are referred in the second class, as C2 statistics.

Table 7. Initial Two (PCA) derived with Nonparametric Measures

| Statistics | PC1 | PC2 |
|------------|--------|--------|
| | 68.825 | 20.897 |
| Y | 0.115 | 0.613 |
| S_i^1 | 0.347 | -0.250 |
| S_i^2 | 0.343 | -0.249 |
| S_i^3 | 0.371 | -0.128 |
| S_i^6 | 0.356 | -0.085 |
| RS | 0.250 | 0.387 |
| NP_i^1 | 0.350 | -0.247 |
| NP_i^2 | 0.290 | 0.366 |
| NP_i^3 | 0.300 | 0.345 |
| NP_i^4 | 0.355 | -0.112 |

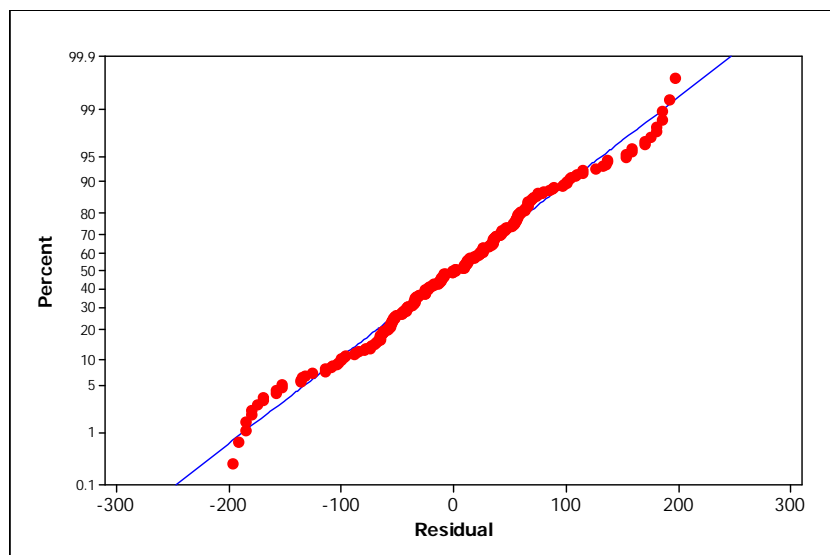


Figure 1. Representation of infringement of linearity hypothesis. Standardized residual plot indicates the violation of homogeneity along with ample outliers.

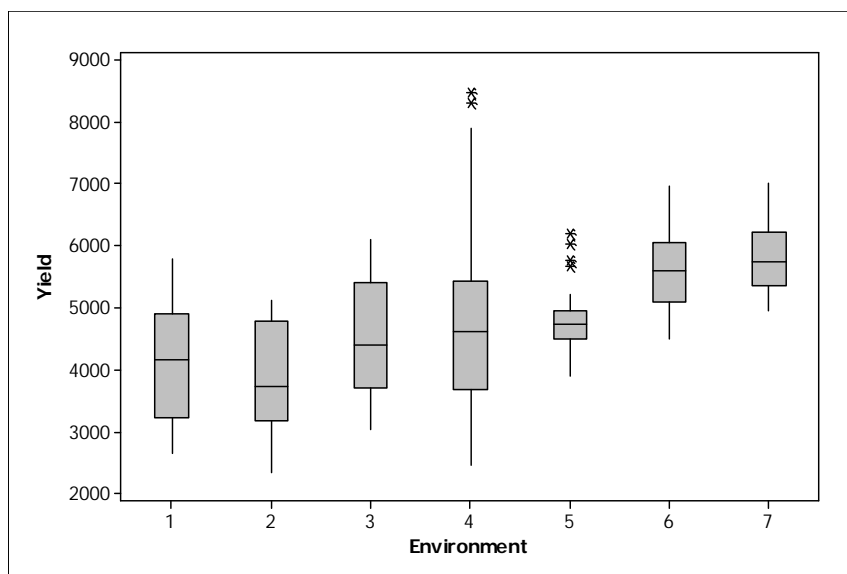


Figure 2. Yield against Environments render Heterogeneity amongst Environment with ample Outliers. This data is displaying six outliers in 4th and 5th in box plot environment.

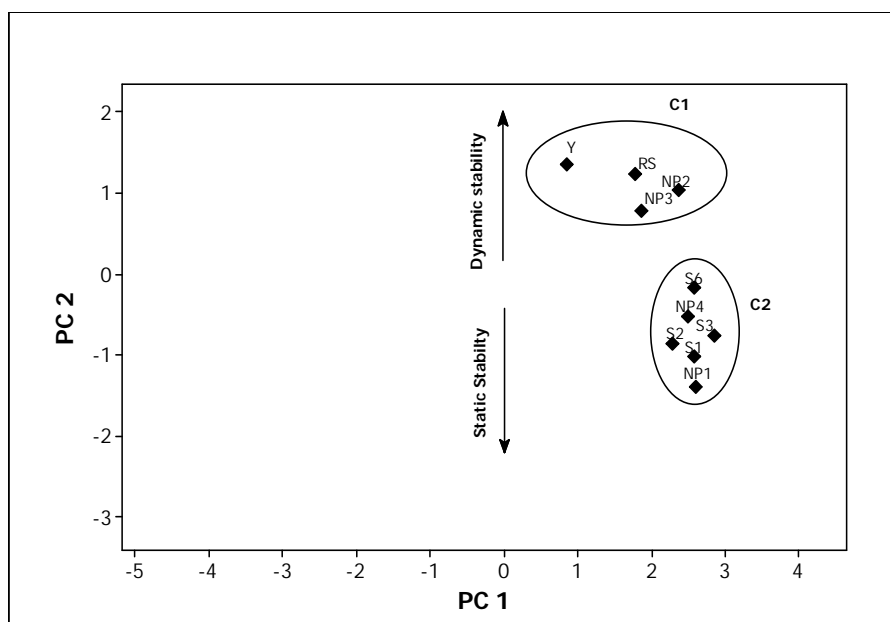


Figure 3. Principal component analysis (PC 1 and PC 2) biplot of the rank of yield stability, estimated by 9 measures using grain mean yield data consist of 18 wheat genotypes in 7 location.

The interaction of $G \times EI$ is a significant source of distinction in a crop. Sometimes a term of stability is used for the peculiarity of a genotype, which represents a comparatively stable yield, which is independent in varied environmental conditions. According to this concept lowest variance of grain yield across various environment are observed very stable.

These PCA's differentiate methods, depends upon two ideas of the stability (i) The biological or static (ii) The agronomical or dynamic concepts. These classified genotypes are measured as stable or unstable in a related way. Consequently, only one of these parameters would be adequate to choose stable genotypes in a breeding program. (Scapim et al. 2000) observed positive and significant correlation between S_i^1 , S_i^2 , and S_i^3 in maize. (Kara, 2000) and (Mut, 2004) reported same in wheat. The high correlation between S_i^1 and S_i^2 in (*Vicia faba L.*) faba bean and (*Pisum sativum L.*) pea was reported by (Flores et al; 1998). (Sabaghnia et al; 2006), (Mohammadi and Amri ;2008) and (Shah, Shah et al. 2009) reported high rank correlation amongst S_i^1 , S_i^2 , S_i^3 , and S_i^4 in lentil and wheat. (Nassar and Huehn ;1987) suggested that S_i^1 and S_i^2 were related to the static stability concept. Figure 3 represent the first two PCA axis that separates (RS), NP_i^2 , NP_i^3 and mean grain yield (Y) from other methods. Parameter of rank-sum is concerned with dynamic stability (Leon and Becker, 1988), and remaining measures are connected with biological stability. (Pham and Kang, 1991) explored that rank-sum measured is concerned with highly grain mean yield performance. Hence this parameter explains stability with agronomical concept. The stability between parameter NP_i^2 and NP_i^3 was significant at ($P < 0.01$) and correlated positively.

According to (Huehn, 1979) four nonparametric measures clustered together on plot, the parameter of (Thennarasu, 1995), NP_i^1 and NP_i^4 clustered combine on biplot, these are combined as class C2 statistics. These parameters differentiate stable or unstable genotypes in the same manner as in Table. 6. Two NPs statistics NP_i^1 and NP_i^4 of (Thennarasu, 1995) and the S_i^1 , S_i^2 , S_i^3 and S_i^6 of (Huehn, 1979) were also in class C2. These parameters indicate the static or biological concept of genotype's stability.

Conclusion

The most agronomists and breeders who prefer the highly grain mean yield do not agree to the idea of stability. G16, G1, and G5 had stable mean yield while G10 unstable performance but had lowest mean grain yield based on the method of (Huehn and Nasar, 1987) and (Thennarasu, 1995). This study recommends using these statistics for the adaption of genotypes.

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