

APPLICATION OF NONPARAMETRIC STABILITY METHODS IN CHICKPEA  
(*CICER ARIETINUM L.*) CROP UNDER DIVERSE ENVIRONMENTS

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## SUMMARY

*Apply different nonparametric tests for genotype x environment interactions (GEI) on 27 chickpea genotypes evaluated for Fusarium wilt across 10 environments. Results of nonparametric tests of Bredenkamp and Van der de kroon and parametric test of combined analysis of variance across environments indicated the presence of both crossover and non-crossover interactions of GEI. The results of the Principal Component Analysis and rank correlation of nonparametric stability statistics would be indicated to selection of static and dynamic stability genotypes which had low wilt. Rank Sum Method (RSM) and mean wilt had significant positive correlation and indicated that RSM was the best parameter to identify low wilt and high stability genotypes. Among the non-parametric stability, RSM would be useful for simultaneous selection for low wilt and stability and G6, G11, G14, G15, G16, G23, G25, G26 and G27 as of dynamic stability and wide adaptation, G11, G25 and G26 had lowest wilt and high stability and which becomes statistic stability. The objectives of this investigation were (i) Apply nonparametric tests to investigate the crossover and non-crossover GE interaction in multi-environment trials, (ii) Study the relationships among different nonparametric stability statistics on selection of stable chickpea genotypes.*

*Key words: Analysis of variance, RSM-Rank Sum Method, TOP, nonparametric stability, GEI-Genotype X Environment Interaction.*

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## 1. INTRODUCTION

Usually different stability statistics will be used for selection of favourable genotypes in multi-environment trials. To study genotype by environment (GXE) interaction and stability analysis, several parametric statistics and non-parametric statistics have been described by Annicchiarico (2002).

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Several non-parametric stability statistics have been expanded by biometricians to define and interpret the responses of genotypes to environmental variation. First time non-parametric stability statistics was discussed by Huehn (1979). Selection of genotypes based on high mean yield and stability was proposed by Kang (1988) using rank-sum method.

Another nonparametric adaptation procedure was discussed by Fox, Skovmand, Thompson, Braun and Cormier (1990) which consists of ranking of genotypes in each environment, by which one derives on the proportion of environments in which a genotype occurred in the Top, Middle and Lower third of the ranks. Thennarasu (1995) proposed some improved nonparametric stability indices that are free from all the aforesaid drawbacks. The important characteristics of these indices are that the levels of achievement of genotypes and their stability are quantified by expressing the individual achievements relative to the mean performance in the set of genotypes evaluated (Bajpai and Prabhakaran, 2000). According to Huehn (1996), the nonparametric stability statistics have some advantages over the other conventional methods. These statistics reduce the bias caused by outliers, no stringent assumptions are needed about the distribution of the dataset, they are easy to use and interpret, and additions or deletions of one or few genotypes do not cause much variation of results (Huehn, 1990a).

Although conventional (parametric) statistical method of the analysis of variance (ANOVA) been used to investigate GEI (Crossa, 1990; Ceccarelli, Grando, Tutwiler, Baha, Martini, Salahieh, Goodchild and Michael, 2000), most of the times it fails to distinguish between significant crossover and non-crossover interactions (Baker, 1990) due to stringent assumptions of ANOVA. As an alternative strategy, nonparametric methods for the test of crossover interactions have been proposed to test of GE interactions in multi-environment trials (Truberg and Huehn, 2000). Bredekamp (1974), Hildebrand (1980), and Kubinger (1986) proposed nonparametric tests based on the usual linear model for interactions or non-crossover interactions. De Kroon and van der Laan (1981), and Azzalini and Cox (1984) introduced nonparametric tests for evaluation of crossover GE interactions. If some of the necessary assumptions are violated, the validity of the inferences obtained from the conventional procedures such as ANOVA may be questionable or lost and so the results of nonparametric procedures can be more reliable (Truberg and Huaehm, 2000).

## 2. MATERIALS AND METHODS

### 2.1 *Data used in the study*

Data sets from previously published study (Sharma, Talluri, Gaur, Ghosh, Telangre, Chaudhary, Upadhyay, Gupta, Saxena, Kaur, Dubey, Anandani, Harer, Rathore and Pande, 2012) were used in order to evaluate phenotypic stability and comparison among non-parametric stability parameters. Data consisted of 27 chickpea genotypes that were evaluated for Fusarium wilt at 10 different environments in India (Berhampore, Dholi, Jabalpur, Junagadh, Kanpur, Ludhiana, New Delhi, Patancheru, Rahuri and Sehore) during 2007/2008 (Sharma *et al.*, 2012) with RCBD design. The names of genotypic codes of these genotypes are given in Table 1.

TABLE 1. - Chickpea genotypes used in the experiment during 2007/2008 in India

Genotype code	Genotype	Genotype code	Genotype	Genotype code	Genotype
G1	ICC 95	G10	ICCV 96851	G19	ICCV 05110
G2	ICC 2072	G11	ICCV 04104	G20	ICCV 05112
G3	ICC 11322	G12	ICCV 04107	G21	ICCV 05309
G4	ICC 11324	G13	ICCV 04108	G22	ICCV 05310
G5	ICC 14364	G14	ICCV 04113	G23	ICCV 05527
G6	ICC 14386	G15	ICCV 04311	G24	ICCV 05528
G7	ICC 15996	G16	ICCV 04312	G25	ICCV 05529
G8	ICCV 93217	G17	ICCV 04314	G26	ICCV 06106
G9	ICCV 96818	G18	ICCV 05107	G27	ICC 4951

## 3. STATISTICAL ANALYSIS

3.1 Statistical approaches for measuring of *gei*

A parametric combined ANOVA (F-test) procedure is the most common method used to identify the existence of GE Interactions from replicated multi-environment trials along with two non-parametric statistical procedures Bredeenkamp (1974) and De Kroon and Van der Laan (1981) were used to test the significance of GEI, G and E (Huehn and Leon, 1995). The test statistics for rank-change interactions, genotypes and environments are approximately  $\chi^2$  distributed with  $(l-1) \times (m-1)$ ,  $(l-1)$  and  $(m-1)$  degrees of freedom, respectively, where  $l$  is the number of genotypes, and  $m$  the number of environments (Huehn *et al.*, 1995). For a two-way dataset with  $k$  genotypes and  $n$  environments, it was denoted the phenotypic value of  $i^{\text{th}}$  genotype in  $j^{\text{th}}$  environment as  $X_{ij}$ , where  $i=1,2,\dots,k$ ,  $j=1,2,\dots,n$ ,  $r_{ij}$  as the rank of the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment, and  $\bar{r}_i$  as the mean rank across all environments for the  $i^{\text{th}}$  genotype. The analysis of variance of the combined data expresses the observed ( $X_{ij}$ ) mean yield of the  $i^{\text{th}}$  genotype at the  $j^{\text{th}}$  environment as

$$X_{ij} = \mu + G_i + E_j + GE_{ij} + \varepsilon_{ij} \quad (1)$$

$\mu$  is the general mean;  $G_i$ ,  $E_j$ , and  $GE_{ij}$  represent the effect of the genotype, environment, and the GEI, respectively; and  $\varepsilon_{ij}$  is the average of the random errors associated with the  $i^{\text{th}}$  plot that receives the  $i^{\text{th}}$  genotype in the  $j^{\text{th}}$  environment.

Testing the significance of GXE, Bredeenkamp (1974) and Van der Laan methods (De Kroon *et al.*, 1981; Huehn *et al.*, 1995) which are tested by  $\chi^2$  test under non-parametric test by using rank data.

## 3.2 Bredeenkamp method

Bredeenkamp method Interactions detected by this method correspond to usual cross-over interactions of parametric methods. In this method the value of genotype in environment  $j$  and replication  $k$  is denoted by  $X_{ijk}$  ( $i=1, 2, \dots, l$ ;  $j= 1, 2, \dots, m$ ;  $k=1, 2, \dots, n$ ) values for all environments and for all genotypes are transformed into ranks  $r_{ijk}$  of one single rank order (Huehn *et al.*, 1995).

### 3.2.1 Test of genotypes

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

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

$\chi^2_{(G)}$  is approximately  $\chi^2$  distributed, with  $l-1$  degrees of freedom and  $N=lmn$ .

### 3.2.2 Test of environments

The test statistics for a test of environmental differences as follow is approximately  $\chi^2$ -distributed with  $m-1$  degrees of freedom.

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

### 3.2.3 Test of interaction effects (non-crossover interaction)

The statistic for a test of G X E interaction differences is approximately  $\chi^2$ -distributed, with  $(l-1)(m-1)$  degrees of freedom.

$$\chi^2_{(GxE)} = \frac{12lm}{N^2(N+1)} \sum_{i=1}^l \sum_{j=1}^m \left( R^2_{ij} - \frac{1}{m^2} R^2_{i..} - \frac{1}{l^2} R^2_{.j} \right) + 3(N+1) \quad (4)$$

## 3.3 De Kroon-Van der Laan method

Interactions detected by this method correspond to crossover interactions of parametric methods (Baker, 1988). That means that interactions are used only in so far 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 (Huehn *et al.*, 1995).

### 3.3.1 Test of genotypes

The  $X_{ijk}$ -values are ranked for each environment separately into the ranks  $r_{ijk}$ . The test statistic for a test of genotypes differences is approximately  $\chi^2$ -distributed, with  $l-1$  degrees of freedom.

$$\chi^2_{(G)} = \frac{12}{lmn^2(ln+1)} \sum_{i=1}^l R^2_{i..} - 3m(ln+1) \quad (5)$$

### 3.3.2 Test of environments

The  $X_{ijk}$ -values are ranked for each genotype separately into the ranks  $r_{ijk}$ . The test statistic for a test of environmental differences is approximately  $\chi^2$ -distributed, with  $m-1$  degrees of freedom.

$$\chi^2_{(E)} = \frac{12}{lmn^2(mn+1)} \sum_{j=1}^m R^2_{.j} - 3l(mn+1) \quad (6)$$

### 3.3.3 Test of interaction effects (crossover interactions)

The  $X_{ijk}$ -values are ranked for each environment separately into ranks  $r_{ijk}$ . The test statistic for the hypothesis of no rank changes of genotypes between environments (crossover interaction) is approximately  $\chi^2$ -distributed, with  $(l-1)(m-1)$  degrees of freedom.

$$\chi^2_{(G \times E)} = \frac{12}{\ln^2(\ln+1)} \left( \sum_{i=1}^l \sum_{j=1}^m R^2_{ij} - \frac{1}{m^2} R^2_{i..} \right) \quad (7)$$

The hypothesis of no environmentally caused changes in rank orders (within genotypes) can also be tested using this method (De Kroon *et al.*, 1981).

### 3.3.4 Non-parametric measures of stability analysis

Huehn (1979) and Nassar and Huehn (1987) proposed four non-parametric stability statistics that combine mean yield and stability. Four parameters based on yield ranks of genotypes in each environment are derived as follows:

Mean of the absolute rank differences ( $S_i^{(1)}$ ) of a genotype over environments

$$S_i^{(1)} = 2 \sum_{j=1}^{q-1} \sum_{j'=j+1}^q |r_{ij} - r_{ij'}| / q(q-1) \quad (8)$$

Variance among the ranks over the  $q$  environments ( $S_i^{(2)}$ )

$$S_i^{(2)} = \sum_{j=1}^q (r_{ij} - \bar{r}_i)^2 / (q-1) \quad (9)$$

### 3.3.5 Testing of significance

The statistical properties of  $S_i^{(1)}$  and  $S_i^{(2)}$  have been investigated by Nassar and Huehn (1987). Approximate tests of significance based on the normal distribution are developed for these two nonparametric measures. One computes the "statistic"

$$S^{(m)} = \sum_{i=1}^k Z_i^{(m)} = \sum_{i=1}^k \frac{\left| (S_i^m - E(S_i^m))^2 \right|}{Var(S_i^m)} \quad (10)$$

Where  $m = 1, 2$

$$E(S_i^{(1)}) = (p^2 - 1) / 3p \quad \text{and} \quad E(S_i^{(2)}) = (p^2 - 1) / 12$$

$$Var(S_i^{(1)}) = (p^2 - 1)[(p^2 - 4)(q + 3) + 30] / 45p^2q(q - 1)$$

$$Var(S_i^{(2)}) = (p^2 - 1)[2(p^2 - 4)(q - 3) + 5(p^2 - 1)] / 360q(q - 1)$$

The statistic may be approximated by a chi-square distribution with  $p$  degree of freedom with  $E(S_i^{(m)})$  expectation mean and variance  $Var(S_i^{(m)})$ . Under null hypothesis all genotypes are equally stable. The mean  $E(S_i^{(m)})$  and variances  $Var(S_i^{(m)})$  may be computed from the discrete uniform distribution  $(1, 2, \dots, p)$ . Additionally, Parmar, Patel, Mehta, Makwana and Patel (2012) described the adoptability to high yield environments using Nassar and Huehn (1987) first two measures.

Sum of square deviations in observed units of each classification relative to the mean classification

$$S_i^{(3)} = \sum_{j=1}^q (r_{ij} - \bar{r}_i)^2 / \bar{r}_i \quad (11)$$

Sum of absolute deviations in observed units of each classification relative to the mean classification

$$S_i^{(6)} = \sum_{j=1}^q |r_{ij} - \bar{r}_i| / \bar{r}_i \quad (12)$$

Where,  $r_{ij}$  = rank of genotypes in each environment based on  $(X_{ij} - \bar{X}_i + \bar{X}_..)$ ,  $\bar{r}_i$  = mean of ranks over environments,  $p$  = number of genotypes,  $q$  = number of environments

### 3.4 Thennarasu's measure

Thennarasu (1995) proposed the four following non-parametric stability measure:

$$NP_i^{(1)} = \frac{1}{q} \sum_{j=1}^q |\hat{r}_{ij} - \hat{M}_{di}| \quad (13)$$

$$NP_i^{(2)} = \frac{1}{q} \left( \frac{\sum_{j=1}^q |\hat{r}_{ij} - \hat{M}_{di}|}{\hat{M}_{di}} \right) \quad (14)$$

$$NP_i^{(3)} = \frac{\sqrt{\sum (\hat{r}_{ij} - \hat{r}_i)^2 / q}}{\bar{r}_i} \quad (15)$$

$$NP_i^{(4)} = \frac{2}{q(q-1)} \left( \sum_{j=1}^{q-1} \sum_{j=j+1}^q |\hat{r}_{ij} - \hat{r}_{ij}| / \bar{r}_i \right) \quad (16)$$

The adjusted rank,  $r_{ij}^*$ , is determined on the basis of the adjusted phenotype values ( $x_{ij}^* = x_{ij} - \bar{x}_i$ ), where  $\bar{x}_i$  is the mean of  $i$ th genotype across all environments. The ranks, obtained from these adjusted values ( $x_{ij}^*$ ), depend only on GXE interaction and error effects. In the above formulas,  $r_{ij}^*$  is the rank of  $x_{ij}^*$ ,  $\bar{r}_i$  and  $M_{di}^*$  are the mean and median ranks for adjusted values, while  $\bar{r}_i$  and  $M_{di}$  are the same parameters computed from the original (unadjusted) data.

### 3.5 Kang's rank-sum method

Rank-sum method proposed by Kang (1988) and it was another nonparametric stability procedure where both ranks of wilt mean and Shukla's (1972) stability variance were used as selection criteria. This index assigns a weight of one to both wilt and stability statistics to identify low wilt and stable genotypes. The genotype with the lowest wilt mean was given a rank of 1 and a genotype with the lowest stability variance was assigned a rank of 1. All genotypes were ranked in this manner and the ranks by wilt and by stability variance were added for each genotype. The genotype with the lowest rank-sum was the most desirable one. This method assumed equal weight for wilt and stability variance.

### 3.6 Fox's non-parametric superiority measure

Fox *et al.* (1990) suggested non-parametric superiority measure for general adaptability. They used stratified ranking of the genotypes. Ranking (low wilt was given a rank of 1) was done at each environment separately and the number of environments at which the genotype occurred in the top, middle and bottom third of the ranks was computed. A genotype that occurred mostly in the top third was considered as a widely adapted one. TOP procedure was associated with mean wilt and the dynamic concept of stability, therefore these parameters could be used to recommend cultivars adapted to favourable conditions.

All statistical analysis has been done by using SAS v9.4 (SAS Institute Inc., 2018).

## 4. RESULTS AND DISCUSSION

### 4.1 Non-parametric methods to test $ge_i$

Results of different statistical methods for testing the presence of Genotype (G), Environment (E) and GEI in wilt of 27 genotypes (Table 1) evaluated at 10 environments. Null hypothesis for ANOVA and Bredeknamp is no non-crossover GE interaction and De Kroon-Van der Laan is no crossover GEI. From Table 2, combined ANOVA indicated that main and interaction effects of G, E and GEI are highly significant (Prob < 0.001) respectively. Significant GEI means non-crossover or usual interaction. Non-parametric statistical procedures showed that the rank-interaction effects had a

TABLE 2. – Results of the different statistical methods for testing the presence of GE interaction in wilt of 27 genotypes evaluated at ten environments during 2007-2008

		Anova	Bredenkamp	De Kroon-Van der Laan
Source	df	F-Statistic	$\chi^2$ – Statistic	$\chi^2$ – Statistic
Environment (E)	9	246.29**	168.40**	163.26**
Genotype (G)	26	8.34**	51.84**	64.17**
Genotype X Environment (GE)	234	7.46**	255.32 <sup>NS</sup>	339.46**

Note: \* and \*\*: significant at the 0.05 and 0.01 level of probability, respectively.

different pattern, while the Breadenkamp (1974) and De Kroon-Van der Laan (1981) methods revealed the same level of significance, Bredenkamp and De Kroon-Van der Laan methods clearly showed no non-crossover interaction and cross over interaction respectively.

The results of non-parametric methods (Bredenkamp, Hildibrand and De Kroon-Van der Laan) was in agreement with those from ANOVA, but provided more specific information about the nature of GEI. Both E and G showed non cross over (Bredenkamp) and cross over (De Kroon-Van der Laan) types of GEI.

#### 4.2 Non-parametric stability analysis

Non-parametric stability methods are based on ranks of the genotypes across environments. They give equal weight to each environment. 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  $S_i^{(1)}$ . The  $S_i^{(1)}$  may lose power when genotypes are similar in their interactions with the environments. Huehn (1979) proposed two rank stability measures and which were expressed as  $S_i^{(1)}$  and  $S_i^{(2)}$  are presented in Table 3. The genotypes G10, G11, G17, G23, G25 and G26 had the lowest value of  $S_i^{(1)}$  and ranked 18<sup>th</sup>, 3<sup>rd</sup>, 27<sup>th</sup>, 20<sup>th</sup>, 1<sup>st</sup> and 4<sup>th</sup> respectively for wilt. G11, G25 and G26 had lower wilt as compared to overall mean wilt and lowest  $S_i^{(1)}$  values then we treated them as stable (static stability). The highest  $S_i^{(1)}$  mean absolute rank was observed for G7, G12, G20, G21 and G22 indicating to be highly unstable genotypes. For each genotype,  $Z_i^{(1)}$  and  $Z_i^{(2)}$  values were calculated based on ranks of the corrected data and summed over genotypes to obtain Z values (Table 3).  $\sum Z_i^{(1)}$  (31.54) and  $\sum Z_i^{(2)}$  (26.73) are distributed as  $\chi^2$  and were less than the critical value of  $\chi^2_{(0.05, 26)}$  (38.89) which indicated the non-significant differences among the ranks of stability of 27 genotypes. Among the individual Z values, G23 was significantly stable relative to other for  $Z_i^{(1)}$  and G23 are significantly stable relative to other for  $Z_i^{(2)}$  values and which has greater than  $\chi^2_{(0.05, 1)}$  (3.84) and identified G23 as stable genotype from both  $Z_i^{(1)}$  and  $Z_i^{(2)}$  statistic.

Huehn (1979) proposed another two non-parametric statistics for the simultaneous estimation of performance and stability which are  $S_i^{(3)}$  and  $S_i^{(6)}$ . These parameters measure stability in units of the mean rank of each genotype on the basis of original



TABLE 3. – Non-parametric stability statistics for wilt and tests of non-parametric stability measures ( $Z_i^{(1)}$  and  $Z_i^{(2)}$ ) for 27 chickpea genotypes across 10 environments during 2007-2008

Genotype	Mean	$S_f^{(1)}$	$Z_i^{(1)}$	$S_f^{(2)}$	$Z_i^{(2)}$	$S_f^{(3)}$	$S_f^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	RSM	LOW	MID	TOP
G1	29.27	9.13	0.01	59.21	0.01	41.31	4.56	5.90	0.49	0.56	0.70	29	20	60	20
G2	28.72	9.78	0.27	67.38	0.15	48.13	5.24	6.60	0.53	0.61	0.77	27	10	60	30
G3	27.36	9.11	0.01	59.51	0.00	41.84	4.84	6.20	0.56	0.56	0.69	25	10	60	30
G4	27.61	9.01	0.00	60.07	0.00	44.13	5.06	6.20	0.44	0.62	0.77	37	10	40	50
G5	28.51	10.00	0.44	69.78	0.27	43.31	4.69	6.70	0.48	0.55	0.69	31	30	50	20
G6	22.56	8.07	0.36	45.34	0.76	34.88	4.53	5.00	0.43	0.57	0.67	14	10	60	30
G7	35.79	11.84	3.50	98.28	4.57*	57.06	5.48	8.50	0.52	0.62	0.78	48	30	40	30
G8	34.13	8.47	0.12	54.28	0.13	29.61	3.58	5.60	0.29	0.41	0.52	28	30	30	40
G9	29.03	7.76	0.65	43.12	0.99	29.18	3.68	5.20	0.39	0.50	0.62	27	10	50	40
G10	31.43	6.27	3.18	30.49	2.94	17.59	2.59	4.30	0.30	0.37	0.44	28	20	30	50
G11	21.87	7.68	0.74	42.51	1.06	39.24	5.49	6.20	0.71	0.70	0.88	11	10	70	20
G12	29.02	10.33	0.78	75.66	0.73	56.27	6.05	6.90	0.66	0.68	0.84	30	20	60	20
G13	31.32	8.67	0.04	53.16	0.18	31.06	3.84	6.40	0.39	0.50	0.63	22	30	40	30
G14	26.50	9.99	0.43	70.45	0.31	46.45	5.31	6.90	0.58	0.53	0.66	18	30	50	20
G15	26.14	9.19	0.02	61.58	0.00	42.80	5.13	6.90	0.67	0.59	0.74	18	30	60	10
G16	27.22	8.03	0.39	46.85	0.62	30.66	4.00	5.60	0.45	0.46	0.58	12	20	60	20
G17	43.66	7.71	0.70	54.40	0.13	24.12	2.41	8.70	0.42	0.47	0.58	51	40	10	50
G18	38.69	9.14	0.01	63.58	0.03	32.79	3.87	7.90	0.39	0.49	0.62	43	40	40	20
G19	39.23	9.12	0.01	60.80	0.00	32.28	3.69	7.60	0.40	0.54	0.67	51	20	30	50
G20	35.87	10.06	0.49	72.36	0.44	39.35	4.20	8.20	0.44	0.54	0.66	42	30	30	40
G21	30.53	10.13	0.56	78.40	1.02	53.45	5.52	7.70	0.73	0.71	0.84	39	30	70	0
G22	32.68	10.44	0.91	77.16	0.88	45.99	5.10	7.60	0.47	0.59	0.73	41	30	50	20
G23	33.55	3.92	11.01**	10.89	8.00**	5.82	1.63	4.70	0.28	0.30	0.37	21	0	20	80
G24	36.93	8.22	0.25	58.49	0.02	27.13	3.15	6.70	0.29	0.42	0.51	45	60	10	30
G25	15.22	6.29	3.12	40.23	1.35	63.53	8.28	6.10	2.03	1.20	1.50	4	0	80	20
G26	22.31	6.11	3.55	35.39	2.06	30.33	3.81	3.10	0.33	0.51	0.54	6	10	80	10
G27	20.74	8.86	0.01	54.96	0.11	46.01	5.91	6.00	0.63	0.71	0.87	8	0	60	40
Average			31.54		26.73										

Note: \* and \*\*; significant at the 0.05 and 0.01 level of probability, respectively.

mean data within environment and presented in Table 3. Genotypes G6, G9, G11, G16 and G26 are having lowest  $S_i^{(3)}$  and  $S_i^{(6)}$  values as well lower wilt as compared to mean wilt then we treated them as stable across all environments and G7 and G22 are most unstable ones.

Thennarasu (1995) non-parametric stability statistics are calculated from ranks of adjusted wilt means and genotypes with lowest value are considered as stable. According to the first method  $NP_i^{(1)}$ , G26 was stable in comparison with other genotypes, followed by G10 and G23. Based on the values of  $NP_i^{(2)}$  genotypes G8, G10, G23, G24 and G26 had the lowest values and were considered as highly stable. Stability parameters  $NP_i^{(3)}$  and  $NP_i^{(4)}$  identified G8, G10, G16, G23, G24 and G26 are most stable ones. According to 4 non-parametric stability measure genotypes G7 and G21 are most unstable and rank of mean wilt also very high.

According to TOP superiority index (Fox *et al.*, 1990), G23 was an adopted genotype, because it ranked in the top third of genotypes in a high percentage of environments followed by G10. The undesirable genotype identified by this method was G21.

According to Rank Sum Method (RSM) statistic (Kang, 1988), genotypes with a low rank sum are regarded as more desirable ones. This parameter revealed that G11, G25, G26 and G27 had the lowest values, and were stable genotypes, whereas G7, G17 and G19 had the highest values and which were undesirable (Table 3).

#### 4.3 Rank correlation among stability statistics and wilt

The results of the Spearman's coefficients of rank correlation among mean wilt and the ten non-parametric stability statistics are shown in Table 4. Mean wilt had a significant (Prob < 0.01) positive ( $NP_i^{(1)}$ , RSM and TOP) and negative ( $S_i^{(3)}$ ,  $S_i^{(6)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$ ) correlation with non-parametric stability measures except  $S_i^{(1)}$ ,  $S_i^{(2)}$ . TOP measure is positively correlated with  $S_i^{(3)}$ ,  $S_i^{(6)}$ ,  $NP_i^{(2)}$  and  $NP_i^{(3)}$ . Kang's rank-sum is significantly (prob<0.01) positively correlated with Nasar Huehn's ( $S_i^{(1)}$ ,  $S_i^{(2)}$ ) and Thennarasu's ( $NP_i^{(1)}$ ) non-parametric measures. According to Nasar huehn's measures,

TABLE 4. – Spearman's rank correlation between mean wilt and non-parametric stability measures for 27 chickpea genotypes across 10 environments

Statistic	$S_i^{(1)}$	$S_i^{(2)}$	$S_i^{(3)}$	$S_i^{(6)}$	$NP_i^{(1)}$	$NP_i^{(2)}$	$NP_i^{(3)}$	$NP_i^{(4)}$	RSM	TOP
$S_i^{(2)}$	0.98**									
$S_i^{(3)}$	0.68**	0.65**								
$S_i^{(6)}$	0.52**	0.48*	0.94**							
$NP_i^{(1)}$	0.72**	0.81**	0.40*	0.27						
$NP_i^{(2)}$	0.45*	0.43*	0.84**	0.93**	0.32					
$NP_i^{(3)}$	0.43*	0.41*	0.87**	0.92**	0.25	0.86**				
$NP_i^{(4)}$	0.47*	0.43*	0.88**	0.93**	0.30	0.89**	0.98**			
RSM	0.49**	0.58**	-0.05	-0.27	0.69**	-0.26	-0.17	-0.13		
TOP	0.32	0.29	0.46*	0.54**	0.14	0.55**	0.39*	0.38	-0.28	
WILT	0.21	0.28	-0.39*	-0.58**	0.49**	-0.56**	-0.52**	-0.47*	0.87**	-0.44*

Note: \* and \*\*: significant at the 0.05 and 0.01 level of probability, respectively.

all of them are significantly positively correlated with each other and range from 0.48 to 0.98. According to Thennarasu's measures, all parameters are significantly positively correlated with each other (except  $NP_i^{(1)}$ ) with range from 0.86 to 0.98.

From Table 2, Bredekamp method was proved that non cross over interactions of GEI and Van der Laan de kroon test was proved that cross over interactions was existed for GEI and this method is recommended if the crossover interaction concept is intended and non-parametric methods must be applied because the assumptions for the parametric methods cannot be accepted. Huehn and Leon (Huehn *et al.*, 1995) and Mohammadi, Abdulahi, Haghparast and Amioon (2007), who recommended the Bredekamp test for non-cross over interaction and Van der Laan de Kroon test is for cross over interaction.

From Figure 1, to better understand the relationship among non-parametric stability statistics, PCA (Principle Component Analysis) was performed based on ranks of 10 stability statics and wilt. The first two PCs explained 84% of variance explained (50.97 and 33.07 by PC1 and PC2 respectively). Four classes of stability statistics were identified. Class1 comprising  $S_i^{(1)}$ ,  $S_i^{(2)}$  and  $NP_i^{(1)}$  and under class2  $S_i^{(3)}$ ,  $S_i^{(6)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$ ,  $NP_i^{(4)}$  parameters are together and concluded stability parameters are positively and significantly correlated, indicating that these parameters were similar under different environmental conditions. Mohammadi *et al.*, (2007) had been found significant positive correlation among these parameters in durum wheat. Scapim, Oliveria, Braccinil, Cruz, Andrade and Vidigal (2000) had reported significant positive correlated between  $S_i^{(1)}$  and  $S_i^{(2)}$  in maize. Flores, Moreno and Cubero (1998) also reported high positive rank correlations between  $S_i^{(1)}$  and  $S_i^{(2)}$  in faba bean and pea. In the concept of homeostasis, these parameters are useful to identify static stability.

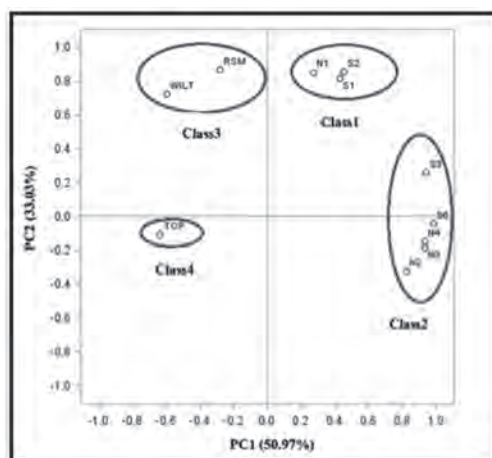


FIGURE. 1 – Plot of first two PCs (PC1 vs PC2) of ranks of 10 non-parametric stability methods and wilt from 27 chickpea genotypes across 10 environments  
Note:  $NP_i^{(1)}$ ,  $NP_i^{(2)}$ ,  $NP_i^{(3)}$  and  $NP_i^{(4)}$  are termed as N1, N2, N3 and N4 respectively;  
 $S_i^{(1)}$ ,  $S_i^{(2)}$ ,  $S_i^{(3)}$  and  $S_i^{(4)}$  are termed as S1, S2, S3 and S4 respectively

## 5. CONCLUSION

These stability statistics might be used for selection of genotypes with moderate wilt and high stability. In view of these 8 parameters, G23 and G26 can be selected with high stability. From the correlation, RSM and mean wilt had significant positive correlation and indicated that RSM was the best parameter to identify low wilt and high stability genotypes. According to RSM, G11, G25, G26 were the best genotypes. From this study, we recommend RSM is best stability parameter for selection of genotypes.

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