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Association between Parametric and Non-Parametric Stability Models in Multi-Location Trials of Pakistan

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Abstract

The study was carried out on twenty wheat genotypes across ten environments during 2015-16 growing season (rain-fed) of Pakistan. To compare the various stability measures of both parametric and non-parametric type and identify the stability and adaptability of genotypes also evaluate association among them. Combined ANOVA was applied with 2 replications in each environment through NUWYT. Theimpacts of genotypes, environments and GEI were found highly significant at (P<0.01). Mean yield of genotypes had +ve and highly significant correlation along with bi, S_i ⁽³⁾ and S_i ⁽⁶⁾ while had inverse and highly significant

interrelationship with S^{2}_{i} , NP_{i} ⁽²⁾, NP_{i} ⁽³⁾. Wricke's Ecovalence and Interaction variance, Superiority index and deviation mean square had significant perfect association so therefore they can be used as alternatives. Accordingly, most of the stability parameters among all showed that G1 and G8 were the stable genotypes across environments.

Keywords: Parametric and non-parametric stability models, Association, Multi-Location Trials

INTRODUCTION

Wheat is known as the socio-political crop of Pakistan that occupies the major position in the complex farming system and it is cultivated in throughout Pakistan including all the four provinces. It is the most important crop as a dietary food that contributes approximately 60 percent of the everyday diet food of a common man. In Rabi season wheat is cultivated about 70% of the entire cultivation area in Pakistan with 14% of its contribution in agriculture while 2.1% to the Gross domestic product (GDP) in 2015-16. (PARC, 2015-16). In our country wheat, being the staple food, is consumed 124 kg per person per year on average basis which is maximum in the world.

In crop breeding programs the genotypes of wheat are examined under multi environmental experiments for assessing the stability of various genotypes as well as their performance in diverse environments. The cultivars mostly face the problems of genotype * environmental interaction (GEI) in the program of plant breeding. The importance of GEI have always been demonstrated mostly in all chief crops for cultivars evaluation and crop breeding [1, 2].

The Static or biological concept of stability that defines the genotypes are believed to be stable when they have low variation across environments whereas such stability concept may not be accepted by different plant cultivars and agronomists having interest in high yielding genotypes. Other concept of stability known as the dynamic or agronomic concept. In this stability concept that genotype is considered stable if the results of its locations are found collateral with genotypes average response among the trials.

Last concept of stability for stable genotypes is believed to be when the genotypes have low residual mean square from the regression equation in respect to the index about the environments [3].

Diverse stability models, either parametric or non-parametric, including uni-variate, multivariate and graphical techniques are suggested to evaluate the genotypes stability across environments because any individual method alone may not explain the genotypes performance in all environments. The most commonly applied stability parameters are: mean yield (\overline{Z}_i), Genotype variance(S_i^2), Coefficient of variation (CV_i) , Wrick's ecovalence (W_i^2) , Superiority index (P_i), Interaction variance (σ_i^2), Deviation of mean square (DMS), Rank correlation (r_s) , Regression slope (b_i) , Nassar and Huehn nonparametric stability parameters, Thennarasu's methods and Kang's rank sum method. The parametric stability parameters follow the of distribution while non-parametric assumptions stability parameters do not require any assumption and have advantage over parametric that they decrease the bias instigated due to the presence of outliers [4].

The major aims of the study were to use various stability measures including both parametric as well as non-parametric types to assess the genotypes*environmental interaction (GEI), to identify the genotypes which are both high yielding and stable for determining the association among various methods of stability.

Materials and Methods

Source of data

20wheat genotypes had been evaluated in field trials at 10(ten) environments that are Bars-Fatehjang (E1), Piplan (E2), Bhaun (E3), Bari-Chakwal (E4), Attock (E5), Faisalabad (E6), NARC-Islamabad (E7), Haripur (E8), Bunir (E9) and ARI-Quetta (E10) in Pakistan during (2015-2016) cropping season underneath rain-fed situations. Design of trial was RCBD having two replicates in every site in coordination of National Uniform Wheat Yield Trials (NUWYT).

Genotype	Code	Location
BWP-122557	G1	BARI -Bwp
BWP-122559	G2	BARI- Bwp
11C023	G3	AARI Fsb
V-13372	G4	AARI Fsb
V-2120	G5	AARI Fsb
V 11098	G6	AARI Fsb
NR 443	G7	NARC-Isb
NR 429	G8	NARC-Isb
NR-449	G9	NARC-Isb
NR-423	G10	NARC-Isb
012BT004	G11	AARI Fsb
PR-115	G12	CCRI Pirsabak (PS)
PR-112	G13	CCRI (PS)
PR 110	G14	CCRI (PS)
CT 12016	G15	NIFA (KPK)
CT 121716	G16	NIFA (KPK) NIFA
NRL 1139	G17	(KPK)
NRL 1123	G18	NIFA (KPK) WRI-Fsb
FSD-08	G19	Wheat-NARC-Isb
Pakistan-13	G20	

Table:1 Codes and Locations of 20 Genotypes

Statistical evaluation

Combined ANOVA has been computed for measuring the genotype effect, environmental effect and genotype environment interaction, the genotype was taken as constant variable and environment as varied.

Mean Yield

$$\bar{Z}_{i} = \Sigma_j Z_{ij} / l$$

The highest value of mean among all genotypes shows stable genotypes. Genotype Variance

$$S_i^2 = \sum_j (Z_{ij} - \bar{Z}_i)^2 / (l-1)$$

Minimum value of the Genotype Variance among all genotype shows stable genotype

$$CV_i = (\sqrt{S_i^2}/\bar{Z}_{i.})100$$

The least value of Coefficient of variation shows stable genotype

Wricke's Ecovalence

$$W_i^2 = \sum_j (Z_{ij} - \bar{Z}_{i.} - \bar{Z}_{.j} + \bar{Z}_{..})^2$$

Theminimum value of Equivalence (W_i^2) shows the higher genotype's stability. In contrary this the higher value of Ecovalence (W_i^2) shows the genotype's minimum stability. Rank Correlation

$$r_s = 1 - \frac{6\Sigma d_i^2}{k(k^2 - 1)}$$

Rank correlation measure the association b/w various measures and the value of 'r=1'shows aquite positive association and 'r=-1' shows the quite inverse relationship among methods

Superiority Index

$$P_i = \frac{\sum_{j=1}^l (X_{ij} - M_j)^2}{2l}$$

The least value of Superior Index Pi shows stable genotype

$$\sigma_i^2 = \left[\frac{k}{(k-2)(l-1)}W_i^2 - \frac{SS(GE)}{(k-1)(k-2)(l-1)}\right]$$

The least value of Interaction Variance σ_i^2 shows stable genotype.

Regression slop $b_i = \left[\Sigma_j \left(Z_{ij} - \bar{Z}_{i.}\right) \left(\bar{Z}_{.j} - \bar{\bar{Z}}\right)\right] / \Sigma (\bar{Z}_{.j} - \bar{\bar{Z}})^2$

The genotype is considered stable If regression slope b_i is equal to 1(bi = 1) and deviation mean square is zero.

$$\delta_i^2 = \left[\frac{1}{l-2}\right] [\Sigma_j (Z_{ij} - \bar{Z}_{i.})^2 - b_i^2 \Sigma_j (\bar{Z}_{.j} - \bar{\bar{Z}})^2]$$

Nassar and Hueh Method

$$\begin{split} S_{i}^{(1)} &= \frac{2\Sigma_{j}^{m-1}\Sigma_{j=j+1}^{m} \big| r_{ij} - r_{ij} \big|}{[m(m-1)]} \\ S_{i}^{(2)} &= \Sigma_{j=1}^{m} (r_{ij} - \overline{r_{i.}})^{2} / (m-1) \\ S_{i}^{(3)} &= \Sigma_{j=1}^{m} (r_{ij} - \overline{r_{i.}})^{2} / \overline{r_{i.}} \\ S_{i}^{(6)} &= \Sigma_{j=1}^{m} \big| r_{ij} - \overline{r_{i.}} \big| / \overline{r_{i.}} \end{split}$$

Thennarasu's methods

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

$$\begin{split} NP_i^{(3)} &= \sqrt{\Sigma(r_{ij}^* - \frac{\overline{r_{i.}^*})^2}{m}} \\ NP_i^{(4)} &= 2/m(m-1)[\Sigma_{j=1}^{m-1}\Sigma_{j'=j+1}^m \big| r_{ij}^* - r_{ij'}^* \big| /\overline{r_{i.}}. \end{split}$$

Kang's rank sum technique considers the maximum value of average yield and low value of Interaction variance with minimum value of R-S identifies the genotypes that are stable.

Results and Discussion

A combined ANOVA of twenty genotypes of wheat verified through ten environments displayed that sixty-six percent (66%) of the TSS was attributed because of the effects of environments although G and GEI effects elucidated 1% and 17% respectively. The large ESS displayed a great variation for environments with huge differences among their environmental means producing maximum variability for yield. The amount of the genotype environment interaction sum of squares found to be approximately eight times greater as compared to the genotypes, showing that considerable differences were present among genotypes responding in various environments (Table 2). The average yield of twenty genotypes of wheat grown in various environments differed remarkably ranging from 2169kg/ha (E2) to 5883 kg/ha (E7) with CV of 32%.

Parametric Stability Measures: -

Mean Yield and nine parametric stability measures of the current study were summarized in 'table 4', the wheat genotypes displayed significant variation for yield. Upon considering Mean Yield as 1st measure to assess the wheat genotypes, G6, G14, G3 & G10 were identified as a stable genotype but had the high mean Yield and G 16, G 19, G 18 & G15 were found as weak and unreliable genotypes. On the basis of the result of regression slope (table 4), slope ranged from 0.76 to 1.31. Wheat genotypes G6, G9, G13 & G11 with $b_i > 1$ presented the maximum average Yield and displayed higher adaptability against their environment. However, G18, G19, G2 & G4 with Regression Slope lower than one ($b_i < 1$) and minimum mean Yield depicted poor adaptation against ten locations and it is possible

that these genotypes require specific conditions for better performance. Wheat genotype G6 which showed the maximum average yield had the highest Deviation mean square(S^{2}_{di}) and G13 with the lowest Deviation mean square ranked 5th for Yield presentation. This wheat genotype demonstrated best performance both in terms of yield as well as its stability.

Based on the results of Genotype Variance (S_i^2) G8, G1 and G16 were found stable but had the lowest results through ten environments and G11, G 12 & G15 were found to be fickle and unstable. Genotype Variance (Si²) were inversely interconnected with Average Yield 'r=-0.63' and slope 'r=-0.85'. Based on stability method CV_i genotypes, G10, G6, G18 were confirmed as stable genotypes but had lowest values and G16, G11, G5 and G8 were declared as unstable genotypes through environments (Table.4). CV_i (Coefficient of Variation) were identical associated with Wi2(Wrick's method) and interaction variance (σ_i^z) measures. Both W_i² (Wricke's method) and interaction variance (σ_i^2) Stability methods ranked the genotypes G1. G8, G13 and G9 as stable genotypes and G19, G2, G11 and G5 as unstable genotypes. Wricke's and interaction variance (σ_i^2) were perfectly positive (r=1.00**) and significantly associated with each other and displayed that these procedures led to alike results. Based on the result of Superiority stability method (Pi), G8, G1, G13 and G9 were identified as stable genotypes but had the lowest values across ten environments whereas G19, G5, G3 and G11 were declared as unstable genotypes. Pi and DMS (Deviation mean square) were perfect positive (r=1.00**) and significant associated with each other and presented that these methods led to like results.

Different non-parametric methods results are given in Table: 6. Measures of the Nassar and Huehn grounded on ranks of varieties through ten locations and give equal weight to all locations [4]. First two methods of the Nassar and Huehn (S_i^1, S_i^2) identified G1, G7, G10 and G13 as stable genotypes but had the lowest numerical quantity but G12, G14 and G16, G19, G3 were identified as unstable genotypes. Last two methods of the Nassar and Huehn (S_i^3, S_i^6) identified G13, G6 and G14 as stable genotypes with the lowest numerical quantity while G19, G2 and G18 were identified as

unstable genotypes. Similar results were previously obtained by [5]. The stability methods $S_i^{(1)}$ and $S_i^{(2)}$ declared G6 as stable genotype and trailed by G8, G9 and G13. $S_i^{(3)}$ and $S_i^{(6)}$ were declared G4 as stable genotype and followed by G7,G15 and G17.

Stability measures of NP⁽¹⁾, NP⁽²⁾, $NP^{(3)}$ and NP⁽⁴⁾ (Thennarasu's Measures) that were computed from the ranks of adjusted yield averages were displayed in Table: 6. Ranks of the NP $^{(1)},\ NP$ $^{(2)},\ NP^{(3)}$ and NP $^{(4)}$ were displayed in Table7. First two measures of the Thennarasu's method identified G17, G1, G20 and G8 as stable but had the lowest numerical quantity while G16, G19, G3 and G14, G3 G6 were identified as unstable genotypes. Last two methods of the Thennarasu's identified G1, G8, G10, G17, G18 as stable genotypes but had the lowest numerical quantity whereas G14, G6 were identified as unstable genotypes. Last three measures of the Thennarasu's were negatively correlated with mean yield. First three methods declared G1 as stable though it had the lowermost average yield value and G14 as unstable genotype and these measures results were related to each other.

Based on the result of non-parametric measure RS (ranksum), G10, G6, G1, G3 were declared as stable genotypes whereas G19, G11, G9 were declared as unstable genotypes and RS were positively interconnected with average yield, NP ⁽¹⁾, NP ⁽²⁾ and measures of the Nassar and Huehn.

Association between Stability Methods

Association between Stability methods are presented in table 9. Genotype Variance (S_i²) had significant and positive association with average yield, NP ⁽²⁾ and NP ⁽³⁾. CVi had significant and positive intercorrelation with non-parametric stability method of RS (rank-sum). W_i² (Wricke's method) was significantly and perfect positively connected with interaction variance. Fentaw Abate also found Interaction variance (σ_i^2) and Wricke's Ecovalence perfect positive and significant correlated [6]. W_i² method was significantly and positively associated with σ_i^2 , DMS, P_i, S_i⁽²⁾ and S_i⁽³⁾.other researcher also found Wrick's method significant and positively correlated with S_i⁽²⁾ and S_i⁽²⁾ [4]. Regression Slope (b_i) was significantly and positively

associated with vield. Genotype Variance. $S_{i}^{(3)}$ mean and S_i⁽⁶⁾.Deviation of mean square (DMS) was significantly and positively associated with W_i² (Wricke's method), interaction variance(σ_i^z). P_i. $NP^{(1)}$, $S_i^{(2)}$ and $S_i^{(3)}$. P_i was significantly and positively associated with Wi² (Wrick's method), interaction variance (σ_i^2), NP⁽¹⁾, Si⁽²⁾ and Si⁽³⁾. Non parametric measure NP⁽¹⁾ had significant and positive association with Wi² (Wricke's method), interaction variance (σ_i^2), Si⁽¹⁾, Si⁽³⁾ and $S_{i}^{(6)}$. NP ⁽²⁾ was significantly and positively associated with Genotype Variance (Si²) and NP ⁽³⁾. Stability measure of NP ⁽³⁾ was significantly and positively associated with Genotype Variance (S_i^2), $S_i^{(1)}$ and $S_i^{(2)}$. Si⁽¹⁾ had significant and positively intercorrelation with Wi² (Wricke's method), $S_i^{(2)}$, interaction variance (σ_i^2), DMS, P_i , NP (1) and $S_i^{(3)}$. Stability measure S_i⁽³⁾ had significant and positive association with mean yield, W_{i^2} (Wricke's method), interaction variance (σ_i^z) . Regression Slope (bi), NP⁽¹⁾ and Si⁽⁶⁾. Stability method of Si⁽⁶⁾ had significant and positive intercorrelation with mean yield, Regression Slope (bi), NP (3), Si (2) and Si (3). Rank sum was significantly and positively associated with Wricke's.

Table: 2 ANOVA for 20 wheat genotypes verified through ten environments in Pakistan.

Source	DF	SS	MS	F	Р	Explained%
Genotype	19	67101762	3531672	9.84	0.000**	8
Environment	9	538941321	59882369	166.90	0.000**	66
Genotype*Environment	171	140627926	822386	2.29	0.000**	17
Replication(Genotype)	20	9734571	486729	1.36	0.000**	1
Error	180	64582598	358792			
Total	399	820988177				

"*, ** -Significant at 5% and 1% respectively" S=598.993 R-sq=92.13%, R-sq(ad)=82.56%

Table: 3 Results of various stability parameters across 10 environments.

Code	$\overline{\mathbf{Z}}_{i}$	S_i^2	cv	W_i^2	σ_i^2	b _i	DMS	Pi
G1	3640	1420945	32.7	712168.7	64226.6	0.948	84493.3	4224.666122
G2	3547	1535043.3	34.9	6585956	789386	0.866	465222	23261.11177
G3	4277	2113200.6	34	5301556	630818	1.009	662557	33127.8352
G4	4009	1601272.2	31.6	4271161	503608	0.876	508126	25406.29127
G5	3658	2110257.7	39.7	5786323	690665	0.99	723124	36156.2182
G6	4437	1878360.8	30.9	2783355	319929	1.024	346944	17347.2183
G7	4099	2105719.9	35.4	1960879	218388	1.131	216420	10820.99417
G8	3695	2047503	38.7	844834.4	80605.1	1.152	66441.4	3322.071466

G9	3994	2202884.8	37.2	1665003	181861	1.174	157164	7858.224261
G10	4248	1541614.1	29.2	2213813	249615	0.933	269104	13455.22175
G11	4082	3161278.8	43.6	6503148	779162	1.314	646311	32315.53035
G12	4140	2346222	37	3026658	349966	1.171	328917	16445.83374
G13	4232	2209040.9	35.1	1495400	160922	1.182	130954	6547.702978
G14	4364	2340364.7	35.1	3430346	399804	1.154	388667	19433.34004
G15	3442	1557741.8	36.3	3860830	452950	0.877	457121	22856.02851
G16	2791	1510234.6	44	5615801	669613	0.796	631885	31594.26194
G17	3591	1584737.2	35.1	2489246	283619	0.937	304452	15222.58181
G18	3442	1147070.1	31.1	3416722	398122	0.756	327078	16353.90317
G19	3433	1739258.4	38.4	8542423	1030925	0.764	973908	48695.40082
G20	3489	1601097.2	36.3	2428892	276168	0.945	298445	14922.22929

Table: 4 Ra	ankings of	various	Parametric	stability	measures	across	10
environment	s.						

Code	$\bar{Z}_{_{i}}$	\mathbf{S}_{i}^{2}	cv	W_i^2	σ_i^2	bi	DMS	Pi
G1	13	2	5	1	1	11	2	2
G2	15	4	7	19	19	17	14	14
G3	3	15	6	15	15	9	18	18
G4	9	9	4	14	14	16	15	15
G5	12	14	18	17	17	10	19	19
G6	1	11	2	9	9	8	11	11
G7	7	13	11	5	5	7	5	5
G8	11	12	17	2	2	6	1	1
G9	10	16	15	4	4	3	4	4
G10	4	5	1	6	6	14	6	6
G11	8	20	19	18	18	1	17	17
G12	6	19	14	10	10	4	10	10
G13	5	17	10	3	3	2	3	3
G14	2	18	9	12	12	5	12	12
G15	17	6	12	13	13	15	13	13
G16	20	3	20	16	16	18	16	16
G17	14	7	8	8	8	13	8	8
G18	18	1	3	11	11	20	9	9
G19	19	10	16	20	20	19	20	20
G20	16	8	13	7	7	12	7	7

Table: 5 Association among stability parameters.

	\overline{Z}_{i}	\mathbf{S}_{i^2}	cv	\mathbf{W}_{i^2}	σ_i^2	bi	DMS
S_i^2	-0.632						
CV	0.362	0.388					
W_{i^2}	0.277	0.015	0.244				
σ_i^2	0.277	0.015	0.244	1.000**			
bi	0.684**	-0.851**	-0.263	0.403	0.403		
DMS	0.167	0.093	0.229	0.962**	0.962**	0.340	
Pi	0.167	0.093	0.229	0.962**	0.962**	0.340	1.000**

"*, ** significant at 5% and 1% respectively.

Table: 6	Results	of	various	non-parametric	stability	parameters	across	10
environn	nents							

Gen	\overline{Z}_{i}	N1	N2	N3	N4	S 1	S2	S 3	S6	RS
G1	3640	3.3	0.275	0.3238	0.0018	0.0222	17.3444	9.5	2.9545	15
G2	3547	4.4	0.2933	0.3745	0.0104	0.1556	35.0667	33.3333	6.3333	19
G3	4277	5.7	1.425	0.9605	0.0097	0.0667	48.1	26.4329	3.9717	18
G4	4009	4.7	0.6267	0.6155	0.0173	0.1556	34.1	25.3333	3.8333	18
G5	3658	5.6	0.4	0.5081	0.0241	0.3111	47.7333	40.8519	5.8272	26
G6	4437	4.3	1.075	1.1198	0.0602	0.2889	32.1	8.2469	1.7037	12
G7	4099	3.6	0.4	0.5667	0.0056	0.0444	22.2667	8.4656	2.229	20
G8	3695	4	0.2857	0.3442	0.0152	0.2	22.9333	20.2051	4.5641	23
G9	3994	4.5	0.45	0.536	0.0109	0.1111	33.2111	22.9259	3.5556	26
G10	4248	4.2	0.7	0.6638	0.0031	0.0222	25.3778	8.8116	2.058	9
G11	4082	5.2	0.8	0.85	0.018	0.1333	43.9556	15.7647	2.7059	28
G12	4140	4.3	0.7818	0.8495	0.0547	0.3556	33.8778	14.1034	2.4828	25
G13	4232	3.8	0.608	0.7322	0.0034	0.0222	25.5556	7.8356	2.0415	22
G14	4364	5.5	1.5714	1.306	0.0773	0.3556	40.1	8.439	1.6585	20
G15	3442	5.6	0.3613	0.4716	0.0117	0.1556	44.0444	31.6373	5.634	23
G16	2791	7	0.3684	0.4111	0.0049	0.0889	60.8444	28	6.6667	23
G17	3591	3.1	0.2583	0.3489	0.0102	0.1333	23.2111	11	3.1899	21
G18	3442	5.4	0.3375	0.4362	0.0032	0.0444	40.8444	31.6761	6.0845	19
G19	3433	6.4	0.4414	0.5039	0.0143	0.2	55.2889	42.2857	6.5714	29
G20	3489	4	0.2857	0.3642	0.015	0.2	26.667	22.2255	3.5033	24

Table: 7 Association among Mean yield and Non-parametric stability parameters

		NP ⁽¹⁾	NP ⁽²⁾	NP ⁽³⁾	NP(4)	S _i ⁽¹⁾	S _i ⁽²⁾	S _i ⁽³⁾	S _i ⁽⁶⁾
	\overline{Z}_{i}								
NP (1)	0.240								
NP	-0.748**	0.386							
(2)NP	-0.795**	0.277	0.973**						
(3)NP	-0.284	0.222	0.406	0.412					
(4)	-0.061	0.267	0.199	0.192	0.926**				
$S_{i}^{(1)}$	0.299	0.964**	0.333	0.250	0.245	0.302			
S _i ⁽²⁾	0.711**	0.663**	-0.288	-0.379	0.006	0.183	0.693		
$S_{i}^{(3)}$	0.815**	0.556*	-0.468*	-0.567*	-0.168	0.039	0.579	0.938	
$S_{i}^{(6)}$	0.369	0.258	-0.081	-0.093	0.377	0.394	0.348	0.353	0.283
RS									

"*, ** Significant at 5% and 1% respectively"

Table: 8 Ranking of various non-parametric stability parameters across 10 environments

Gen	\overline{Z}_{i}	NP ⁽¹⁾	NP ⁽²⁾	NP ⁽³⁾	NP ⁽⁴⁾	$\mathbf{S}_{\mathbf{I}^{(1)}}$	$S_{I}^{(2)}$	$S_{I^{(3)}}$	$S_{I}^{(6)}$	RS
G1	13	2	2	1	1	1	1	6	8	3
G2	15	10	5	5	9	11	12	18	18	6
G3	3	18	19	18	7	6	18	14	13	4
G4	9	12	14	13	15	11	11	13	12	4
G5	12	16	9	10	17	18	17	19	16	17
G6	1	8	18	19	19	17	8	2	2	2
G7	7	3	9	12	6	4	2	4	5	8

G8	11	5	3	2	14	14	3	10	14	12
G9	10	11	12	11	10	8	9	12	11	17
G10	4	7	15	14	2	1	5	5	4	1
G11	8	13	17	17	16	9	15	9	7	19
G12	6	8	16	16	18	19	10	8	6	16
G13	5	4	13	15	4	1	6	1	3	11
G14	2	15	20	20	20	19	13	3	1	8
G15	17	16	7	8	11	11	16	16	15	12
G16	20	20	8	6	5	7	20	15	20	12
G17	14	1	1	3	8	9	4	7	9	10
G18	18	14	6	7	3	4	14	17	17	6
G19	19	19	11	9	12	14	19	20	19	20
G20	16	5	3	4	13	14	7	11	10	15

Table: 9 Association among parametric and non-parametric stability models of 20 genotypes across 10

	Y	S^{2_i}	cv	W12	a:2	bi	DMS	Pi	NPi (I)	NPi cp	NPi	NPi (4)	Si (1)	Si (2)	Si (0)	S ₁ (6)
S^{2} i	-0.63**															
cv	0.362	0.39														
Wi ²	0.277	0.015	0.24	1		1										
σ. ²	0.277	0.015	0.24	1.00**												
bi	0.684**	-0.85**	-0.26	0.40	0.40											
DMS	0.167	0.093	0.23	0.96**	0.96**	0.34										
Pi	0.17	0.09	0.23	0.96	0.96**	0.34	1.00									
NP ₁ (i)	0.24	0.04	0.30	0.78	0.78	0.33	0.81	0.81								
NPi ⁽²⁾	-0.75**	0.64**	-0.12	0.26	0.26	-0.43	0.37	0.37	0.39							
NP ₁ (1)	-0.80**	0.68	-0.16**	0.39	0.20	-0.49**	0.30	0.30	0.28	0.97						
NPi ⁽⁴⁾	-0.28	0.59	0.31**	0.33	0.33	-0.35	0.38	0.38	0.22	0.40	0.41					
Si ⁽¹⁾	-0.06	0.38	0.33	0.38	0.38	-0.12	0.40	0.40	0.27	0.20	0.19	0.93				
Si (2)	0.30	0.06	0.35	0.87**	0.87**	0.33	0.08	0.082	0.96	0.33	0.25	0.24	0.30			
Si (0)	0.71**	-0.33	0.32	0.66*	0.66**	0.62	0.60**	0.60	0.66	-0.29	-0.37	0.006	0.18	0.69		
Si (6)	0.81**	-0.47	0.35	0.53*	0.53*	0.67	0.45**	0.45**	0.56	-0.47	-0.57	-0.17	0.04	0.58	0.94	
RS	0.37	0.45	0.89**	0.27	0.27	-0.26	0.24	0.24	0.26	-0.08	-0.09	0.38	0.394	0.35	0.35	0.28

CONCLUSION

Stability parameters indicated that Wricke's ecovalence and Interaction variance also Deviation mean square and Superiority index resulted perfectly positive significant association that specified these both approaches of stability were identical for stability of genotypes and can be used as alternatives. Mean yield of genotypes had positive and highly significant association with bi, S_i ⁽³⁾ and S_i ⁽⁶⁾ while had inverse and highly significant interrelationship with S_{i}^2 , $NP_i^{(2)}$, $NP_i^{(3)}$.

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