ASSESSING YIELD STABILITY OF WHEAT GENOTYPES THROUGH VARIOUS STABILITY ANALYSES MODELS GROWN UNDER DIFFERENT AGRO-ECOLOGICAL ZONES OF SINDH

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Abstract

Eleven stability models including parametric and non-parametric were assessed for grain yield stability. Twelve advanced wheat genotypes along with two commercial check varieties, Kiran-95 and NIA-Amber were evaluated at seven different locations viz Umerkot, Badin, Sakrand, Shahadadpur, Sanghar, Khairpur and Nausheroferoz during 2014-15 wheat growing season. The experimental layout was RCBD with three replication. Mean grain yield data showed that genotypes G4 (NIA-EST-28/11), G3, (AS-3) G5 (NIA-EST-92/9), G1 (AS-1) and G13 (Kiran-95) produced higher yield than other contesting genotypes across seven ecological zones. Results of stability analyses revealed that out 11 models studied G2, G6 were declared as stable by 8 models and G11 and G14 by 7 models. Thus, these genotypes could be more stable. Results of coefficeint of variation (CV%), deviation from regression(S^2di), coefficients of determination (R^2), stability variance (σ_i^2) ,desirabiltiy index (DJi), wricke's ecovalence (Wi) stability models, genotypic absolute rank $S_i^{(1)}$ and genotypic variance $S_i^{(2)}$ were closely similar in declaring genotypes as stable. However, the regression coefficient (bi) and superiority index (Pi) models picked high yielding genotypes as stable, which indicated that models for high yielding and low yielding genotypes may be assessed seprately for further confirmation of the results.

Key words: Yield stability, Genotype x Environmental interaction, Stability models, Wide adaptable, High yielding genotypes.

Introduction

Every breeding program targets to produce high productive genotypes with other desirable traits. Multi-environmental trials help to identify and select stable genotypes by evaluting elite lines in different environments over many years (Sajid & Mohammd, 2018). These agro-ecological trials are the key to successsfully evaluate and identify highly productive, wide adaptable, specific adaptable and stable genotypes. However, climatic conditions, soil properties, temperature, percipitation, light intensity and other major weather and micro climatic conditions vary from site to site (Kukal & Irmak, 2018). The same genotype grown in different environments often shows significant variation regarding production and performance (Conde *et al*., 2010; Devita *et al*., 2010). This fluctuation is the result of the environmental component and refers to the genotype(G) × environment (E) interaction (GEI). Various stability models have been proposed by different scientists with the passage of time to study genotype x environmental interaction. Some of which are based on univariate analysis, while other use multivariate approaches. These stability models are often categorized into parametric and non-parmetrics models. Among those methods, joint regression and deviation from regression of Finlay & Wilkinson, (1963), Eberhart &Russel, (1966) are widely used models. Other models proposed by Perkins & Jinks, (1968), stability variance by Shukla, (1972), coefficient of determination by Pinthus, (1973), coefficient of variability by Francis & Kanneberg (1978) are also used to analyze multi-environmental data. However, most of these models use univariate approaches. Single model using univariate approaches may not provide an exact stability remarks because of the genotype's multivariate response to different environments (Lin *& Binns*., 1988; Crossa *et al*., 1990 and Gauch, 1992). It has been reported that non-parametric stability methods possess some advantages over parametric methods. As, these are bias free, because they do not require assumption about the distribution of observed values. They are easy to use, understand and interpret. Moreever, additions or deletions of one or a few genotypes do not have any significant effect on the results (Huehn, 1990a). However, integrated approaches can be expoloited by using both parametric and non parmetric methods of stability for selection of genotypes. It would further strengthen in selecting best possible stable genotypes.Those genotypes which are common in more number of models during stability analyses. In literature, a lot of publications have been generated for the levels of association between different stability models. Methodologies to evaluate adaptability and stability using different models clearly indicated that more than one method should be used for reliable prediction of genotypic performance (Silva & Duarte, 2006; Roostaei *et al*., 2014). There is a need to conduct studies to compare traditional methods and recent statistical models. Hence, integrated model approach can be the best approach to select genotypes for wider adaptability. It can indicate the methodologies that can increase the accuracy of the selection process of genotypes, which can result in greater genetic gain (Bornhofen *et al*., 2017; Sabghnia *et al*., 2015). As, alarge number of models have been developed to study stability but in most of the cases all different models produce different results. Some models have close resemblance while others vary largely. Studies comparing the methods to assess wheat adaptability and stability parameters are scarce, and there is no consensus on which stability model is the appropriate in given condition (Mohammadi *et al*., 2010; Tadege *et al*., 2014). Hence, the present study was carried out with the objectives to integrate all the commonly used parametric and non-parmetric stability methods using same data of multi-environment trials (MET) and to select superior high yielding stable genotypes using these models in an integrated way.

Materials and Methods

Multi-environmental trials under field conditions were conducted during rabi season 2014-15 at seven differen zones *viz.,* Umerkot, Badin, Sakrand, Shahadadpur, Sanghar, Khairpur and Nausheroferoz in Sindh province of Pakistan.

Twelve elite spring wheat genotypes along with two commercial check varieties Kiran-95 and NIA-Amber were evaluated in a randomized complete block design (RCBD) with three replications at each site. All genotypes at all the seven locations were sown by seed drill in 1.2 m x 5 m plots, consisting of 6 rows spaced 30cm apart.List of environments and genotypes are presented in Table 1. Agronomic practices regarding irrigation, fertilizer, weeding were carried out with these experiments as per requirements of farmers to provide genotypes wih best possible local conditions. At crop maturity, four central rows of each genotype was harvested from all three replications to record grain yield data. Data recorded in grams per plot were converted into kg ha^{-1} and then subjected to various stability analyses models.

Data analysis

Parametric and non-parametric stability parameters for grain yield were performed using CIMMYT software GEA-R (2015) Version 2.0 by Angela *et al*., 2015.

These different stability models like parametric which included coefficient of variation (CV%) by Francis & Kannenberg's (1978), the regression coefficient (bi) by Finlay & Wilkinson (1963), deviation from regression (S^{2}di) by Eberhart & Russel's (1966), coefficients of determination (R^2) was estimated according to Pinthus (1973), stability variance (σi^2) by Shukla (1972), (Bi) by Perkin & Jink (1968), Desirabiltiy index (DJi) by Hernandez *et al*., (1993), ecovalence (Wi) by Wricks's (1962), Superiority index (Pi) by Lin & Binn (1988) and non-parametric such as genotype absolute rank difference mean over "n"environments and between ranks variance over "n"environments S$_i^{(1)}$ and S$_i^{(2)}$ by Nassar and Huehn (1987).

Results and Discussion

Mean grain yield data, showed that genotypes G4 (NIA-EST-28/11), G3$_\mp$ (AS-3) G5 (NIA-EST-92/9), G1 (AS-1) and G13 (check variety Kiran-95) produced higher mean grain yield than other contesting entries across seven zones (Table 2). These genotypes along with their grain yield data were assessed for their stability analyses by diffrent models. According to Francis & Kannenberg's (1978) stability model, those genotypes which had low CV% in all environments were considered stable. G11, G6, G4, G14 and G8 (DANI-15, KDJ-V2-10-12, NIA-EST-28/11, NIA-Amber and NIA-MN-6 respectively) had shown low CV% values than other entries. Hence, these genotypes can be categorized as stable genotypes by this model. Genotype NIA-EST-28/11was the only high yielding genotype with low

CV% values and could be potential selection provided most of other models gave it same ranking. Based on Eberhart & Russel (1966) that genotype having (bi) values near 1.0 is categorized as stable. Genotypes G5, G2, G14, G4, G6 and G13 (NIA-EST-29/9, AS-2, NIA-Amber, NIA-EST-28/11, KDJV2-10-12 and Kiran-95 respectively) had values around 1.0, hence were declared stable and less responsive to environmental changes. Based on S^{2}di values of Eberhert & Russel (1966), lower the deviation from regression, more stable will be the genotypes, therefore, G11, G2, G6, G14 and G7 (DANI-15, AS-2, KDJV2-10-12, NIA-AMBER and KDJV2-10-13) showed lower S^{2}di values and were kept in category of stable genotypes by this model. The value of coefficient of determination suggested by Pinthus (1973) that higher the R^2 values more stable the genotype would be considered. Therfore, G2, G7, G11, G14, G1, G6 and G10 (AS-2, KDJ-V2-10-13, DANI-15, NIA-AMBER, AS-1, KDJV2-10-12 and DANI-14) were confirmed stable according to the criterion of Pinthus (1973). According to Shukla (1962) lower the stability variance, more stable are the genotypes. Genotypes G2, G14, G6 (AS-2, NIA-AMBER and KDJV2-1012 respectively) showed desirable stability variance. According to Bi model by Perkin & Jink (1968) that genotypes showing values close to unity (1.0) are desirable. Genotype G10, G3 and G7 (DANI-14, AS-3, KDJV2-1013) showed values close to 1.0. Therefore, these were considered stable. According to Desirabiltiy index (DJi) by Hernandez *et al*., (1993) model that the lower Dji values are required to declare genotype as stable. Hence, G11, G2 and G6 have been confirmed as stable genotypes by this model. According to Wricke'secovalence model that the lower the Wi value the more stable is that genotype (Wricke, 1962). Genotypes G2, G14, and G6 (AS-2, NIA-Amber, KDJ-V2-10-12) had low Wricke'secovalence values and hence were stable. When we assessed superiority index (Pi) model given by Lin & Binn's (1988), it described that genotypes showing lower superiority index (Pi) values were considered stable genotypes. Hence, G4, G3, G8 G13 and G6 (NIA-EST-28/11, AS-3, NIA-MN-6. KDJV-2-10-13 and KIRAN-95 respectivley) were declared as stable. According to non-parametric stability models such as S$_i^{(1)}$ and S$_i^{(2)}$ values by Nassar & Huehn's (1987) that genotypes showing low variance are more adaptable. According to S$_i^{(1)}$, G11, G2, G6 (DANI-15, AS-2, KDJV2-10-12) showed low values hence were stable. Whereas, S$_i^{(2)}$ values declared G2, G11, G14 (AS-2, DANI-13, and NIA-AMBER) as stable genotypes. Abate *et al.*, (2015) found that stability models, Wricke'ecovalence and Shukla's stability variance could produce similar results. The two non-parametric models given by Nassar&Huehn's mean absolute rank difference S$_i^{(1)}$ and variance of ranks S$_i^{(2)}$ were also reported significantly correlated with AMMI stability value, Shukla'stability variance and Wricke' ecovalence stability models hence any one of them could produce equally effective results.

Table 1. List of genotypes and environments included in this study.

S. No.	Genotype name	Parentage/ Pedigree	Environments	Site name
G1	AS-1	TJ-83/VASCO//INQILAB-91	E1	Umerkot
G2	AS-2	TJ-83/4085-3//INQILAB-91	E2	Badin
G3	AS-3	TJ-83 /4085-3	E3	Sakrand
G4	NIA-EST-28/11	CIMMYT selection	E4	Shahdadpur
G5	NIA-EST-29/9	CIMMYT selecion	E5	Sanghar
G6	KDJ V2-10-12	Mutant of Bhittai	E6	Khairpur
G7	KDJ V2-10-13	Mutant of Bhittai	E7	Nausheroferoz
G8	NIA-MN-6	Sarsabz /Khirman		
G9	NIA-MN-7	Khirman / Kiran-95		
G10	DANI-14	Kiran-95/Nayab/Sarsabz//Sunco		
G11	DANI-15	Kiran-95/Nayab//Sunco		
G12	DANI-16	Sonalika / Bhittai		
G13	KIRAN-95	Mutant of WL711/Crow ''S''		
G14	NIA-AMBER	Vee #5 ''S'/Sara//Soghat-90		

Table 3 described ranking of genotypes according to various models. It could be observed that G1 ranked on 8th postions by most of models such as CV%, S^2di, Dji, Wi, Pi, and $S_i^{(2)}$. G2 were declared on number 1 or 2 by most of the models. Stability models R^2, σ_i^2, Wi, $S_i^{(2)}$ ranked it number 1, whereas, bi, S^2di, DJi, $S_i^{(1)}$ ranked it number 2. Hence, almost 8 models have decalared it as stable (Table 3). Genotype G3 was ranked number 14th or on number 13th by most of models by its stability points of view. Models S^2di, DJi, Wi, ranked it on number 14th whearas CV%, $S_i^{(2)}$ placed it on number 13th. G4 was kept on number 7 due to its stability. Models S^2di, σ_i^2, DJi, Wi, $S_i^{(2)}$ declared G4 on 7th ranking. Genotype G5 exhibited variabile positions and fell on 12th, 14th and 11th rank according to stability models S^2di and DJi, $S_i^{(1)}$ and $S_i^{(2)}$, Wi and σ_i^2 respectively. Hence, it can be assumed that in case of genotype G5, its response to various environments is highly variable which indicates that some time more Gx E interactions exist and patterns or partition of variation is higher in one genotype as compared with other genotypes. It showed presence of some other source of variation even at the same site. Genotype G6 has been ranked uniformly on number 3 or 4 by most of models. Models Bi, S^2di, σ_i^2, DJi, Wi, $S_i^{(1)}$ have ranked it on number 3 whereas, Pi and $S_i^{(2)}$ ranked it on number 4. G7 has been ranked as on 5th postion by S^2di, R^2, DJi and Wi. G8 has been ranked on number 6 due to its stability by S^2di, R2, σ_i^2, Dji, Wi, $S_i^{(2)}$ models. G9 has been categorized number 13th by S^2di, σ_i^2, Bi, DJi, Wi, $S_i^{(1)}$ models. G10 has been placed on number 12 by σ_i^2, Wi, $S_i^{(1)}$ and $S_i^{(2)}$ stability models. G11 has been ranked as on number 1 by CV%, S^2di, DJi and $S_i^{(1)}$. G12 has been ranked by different models differently. S^2di, σ_i^2, Wi models ranked it on number 9 where as DJi and Pi ranked it as number 11 and $S_i^{(1)}$ and $S_i^{(2)}$ on number 10. G13 has been ranked on number 9,10 and 11 by most of models under study. G14 has been declared on number 4

by CV%, S^2di, DJi , $S_i^{(1)}$ and Bi, R2, σ_i^2, Wi ranked it on number 2. By observing closely, it can be assessed that Wi, Pi, $S_i^{(1)}$, $S_i^{(2)}$ R2, σ_i^2, S^2di, DJi models have close simliarities in ranking genotypes whearas, bi, Pi models have pointed high yielding genotypes and confirmed them among stable genotypes. This shows that high yielding and low yielding lines may be sepratley analysed for stability parmeters which may possibly generate still a better identification and ranking of genotypes. Table 4 showed that how many models had declared genotypes as stable or not. Plus (+) sign declared that genotype had been ranked as stable and (–) sign represented unstable genotypes declared by the respective models. Out of 11 models, 7 models clearly indicated that genotypes 2, 6, 11 and 14 were stable. Hence, these can be effectivley used in breeding programme to produce high yielding and wide adaptable genotypes. Rharrabti *et al*., (2003) used five stability models to assess G x E interaction of various genotypes for quality and other traits. They placed genotypes among the category of stable genotypes if 3 models out of 5 models had declared as stable in stability analyses. The close view of results showed that coeffiecient of variability (CV%,), deviation from regression(S^2di), coefficients of determination (R^2), stability variance (σ_i^2) ,desirabiltiy index (DJi), Wricke'secovalence (Wi) stability models and parametric models such as genotypic absolute rank $S_i^{(1)}$ and genotypic variance $S_i^{(2)}$ were very closely similar in declaring genotypes as stable. However, the regression coefficient (bi) and superiority index (Pi) modle picked high yielding genotypes as stable, this indicates that model for high yielding and low yielding genotypes may be assessed seprately to further confirm these findings. Sabaghnia *et al*., (2012) in their yield stability studies identified the desirability index (DJi), superiority index (Pi) models were found to be useful in detecting the stability as well as high yielding of the genotypes.

Table 2. Various stability analyses models of 14 elite wheat genotypes grown in seven different ecological zones in Sindh Province of Pakistan.

GEN	Mean	Sd	CV (%)	bi	S^2_{di}	R^2	σ_i^2	Bi	DJi	Wi	Pi	$S_i^{(1)}$	$S_i^{(2)}$
G1	5037.2	972.2	19.3	1.3	233580.4	0.7	352844.3	0.3	344370	1967049	666161.0	1.0	11.5
G2	4627.0	733.0	15.8	1.1	-54788.7	0.9	34535.39	0.1	56000.85	330032	794867.0	0.6	2.4
G3	5234.2	1198.5	22.9	1.4	742779.5	0.5	868723.6	0.4	853569.1	4620142	403335.2	0.8	20.7
G4	5336.5	640.3	12.0	0.7	159865.6	0.4	271180.1	-0.3	270655.2	1547062	212846.8	1.1	10.0
G5	5039.5	890.3	17.7	0.9	489161.7	0.4	559068.9	-0.1	599951.3	3027633	502663.1	2.0	22.5
G6	4834.1	468.9	9.7	0.7	-35405.9	0.7	96526.16	-0.3	75383.68	648841	499100.6	0.6	6.3
G7	4301.5	910.0	21.2	1.4	6765.909	0.9	154877.5	0.4	117555.5	948934	1240208.7	0.9	7.4
G8	4069.1	558.6	13.7	0.6	110802.1	0.4	260070.6	-0.4	221591.7	1489927	1735312.3	1.0	9.6
G9	4067.5	805.7	19.8	0.6	509621.5	0.2	643968.2	-0.4	620411.1	3464258	1920988.3	1.7	18.2
G10	4547.7	1130.6	24.9	1.5	404375.7	0.7	584984.1	0.5	515165.3	3160911	1045977.4	1.5	20.5
G11	4177.7	312.6	7.5	0.5	-83796.5	0.8	127426.2	-0.5	26993.11	807756	1458666.1	0.5	2.6
G12	4502.3	993.5	22.1	1.3	312419.3	0.6	422726.5	0.3	423208.9	2326443	1257096.9	1.4	17.4
G13	5008.7	1002.0	20.0	1.2	452666	0.5	535519	0.2	563455.6	2906519	476041.9	1.4	13.9
G14	4461.2	566.4	12.7	0.8	-26012.1	0.8	66641.09	-0.2	84777.51	495147	1066023.3	0.6	3.5

Mean= Mean grain yield (kg ha⁻¹), Sd=Standard deviation, CV% = Coefficient of variation, bi = Regression coefficient, S^2_{di} =Deviation from regression, R^2= Coefficients of determination, σ_i^2 = Shukla's stability variance, Bi= Perkin and Jink, Dji=Desirability index Pi = Superiority index, Wi = Wricke's ecovalence, $S_i^{(1)}$ = Genotype absolute rank difference mean over 'n'environments and $S_i^{(2)}$ = Ranks variance over 'n'environments

Table 3. Rank order of fourteen advanced wheat genotypes according to different stability models grown in seven different ecolgical zones in Sindh Province of Pakistan.

GEN	Mean	Sd	CV(%)	Bi	S^2_{di}	R^2	σ_i^2	Bi	DJi	Wi	Pi	$S_i^{(1)}$	$S_i^{(2)}$
G1	4	10	8	5	8	3	14	4	8	8	8	7	8
G2	7	6	6	2	2	1	1	7	2	1	7	2	1
G3	2	14	13	6	14	5	12	2	14	14	2	5	13
G4	1	5	3	3	7	6	7	10	7	7	1	9	7
G5	3	8	7	1	12	6	11	8	12	11	5	14	14
G6	6	2	2	3	3	3	3	11	3	3	4	3	4
G7	11	9	11	6	5	1	5	3	5	5	10	6	5
G8	13	3	5	4	6	6	6	12	6	6	3	8	6
G9	14	7	9	4	13	7	13	13	13	13	4	13	11
G10	8	13	14	7	10	3	12	1	10	12	8	12	12
G11	12	1	1	5	1	2	4	14	1	11	12	1	2
G12	9	11	12	4	9	4	9	5	11	9	11	10	10
G13	5	12	10	3	11	5	10	6	9	10	3	11	9
G14	10	4	4	2	4	2	2	9	4	2	9	4	3

Mean= Rank according to mean grain yield (kg ha⁻¹), Sd=Standard deviation, CV% = Coefficient of variability, b i = Regression coefficient, S^2_{di} =Deviation from regression, R^2= Coefficients of determination, σ_i^2 = Shukla's stability variance, Bi= Perkin and Jink, Dji=Desirability index Pi = Superiority index, W i = Wricke's ecovalence, $S_i^{(1)}$ = Genotype absolute rank difference mean over 'n'environments and $S_i^{(2)}$ = Ranks variance over 'n'environments

Table 4. Summary of stability analyses seprating genotypes as stable or unstable genotypes according to different models.

Genotype	Mean	Sd	CV (%)	bi	S^2_{di}	R^2	σ^2_i	Bi	DJi	Wi	Pi	$S_i^{(1)}$	$S_i^{(2)}$	Total models	No of model declared genotypes as stable
G1	4	10	-	-	-	+	-	-	-	-	-	-	-	11	1
G2	7	6	-	+	+	+	+	-	+	+	-	+	+	11	8
G3	2	14	-	-	-	-	-	+	-	-	+	-	-	11	2
G4	1	5	+	+	-	-	-	-	-	-	+	-	-	11	3
G5	3	8	-	+	-	-	-	-	-	-	-	-	-	11	1
G6	6	2	+	+	+	+	+	+	+	+	+	+	-	11	8
G7	11	9	-	-	-	+	-	-	-	-	-	-	-	11	2
G8	13	3	-	-	-	-	-	+	-	-	+	-	-	11	1
G9	14	7	-	-	-	-	-	-	-	-	-	-	-	11	0
G10	8	13	-	-	-	+	-	-	-	-	-	-	-	11	2
G11	12	1	+	-	+	+	+	-	+	-	-	+	+	11	7
G12	9	11	-	-	-	-	-	-	-	-	+	-	-	11	0
G13	5	12	-	+	-	-	-	-	-	-	-	-	-	11	2
G14	10	4	+	-	+	+	+	-	-	+	-	+	+	11	7

Note (+) Indicates that respective model has declared genotypes stable and (-) as unstable

Conclusion

Based on the present results, out of 11 stability models studied, G2, G6 were decalred as stable by 8 models and G11 and G14 by 7 models. Results of coefficient of variability (CV%,), deviation from regression(S^2di), coefficients of determination (R^2), stability variance (σ_i^2),desirabiltiy index (DJi), Wricke'secovalence (Wi) and stability models such genotypic absolute rank $S_i^{(1)}$ and genotypic variance $S_i^{(2)}$ were very closely similar in declaring genotypes as stable. However, the regression coefficient (bi) and superiority index (Pi) model picked high yielding genotypes as stable. This indicates that model for high yielding and low yielding genotypes may be assessed seprately to further confirm these findings.

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