Stability Analysis of Soybean (*Glycine Max* L. Merrill) Genotypes Across North West of Ethiopia

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Abstract: *Yield stability is an interesting feature of today's soybean breeding programs, due to the high annual variation in mean yield, particularly in the areas across North West of Ethiopia. Nineteen soybean (Glycine max. L Merrill) genotypes sourced from Pawe Agricultural Research Center were tested for yield stability and performance in four environments between 2014 and 2016 using various stability statistics. The experiment of each environment was laid out in a randomized complete block design with four replications. Combined analysis of variance of grain yield showed highly significant differences among genotypes and environments. Significant GEI indicated differential performance of genotypes across environments. Considering coefficient of several linear regression models, including conventional, adjusted independent and Tai models as well as deviation variance from these models, genotype G18 was the most stable genotype. Stability analysis in basis of parameters like environmental variance, coefficient of variation, stability variance, genotypic stability and Superiority index, genotypes G10 and G18 were the most stable genotypes. The result of principal component analysis of stability statistics and mean yield indicated that slope of linear regression of both conventional and independent models were useful for simultaneously selecting for high yield and stability. The plot of the first two principal components also showed that the stability statistics could be grouped as two distinct classes that corresponded to different static and dynamic concepts of stability. Finally, regarding both mean yield and most of stability characteristics, genotypes G10 and G18 were found to be the most stable genotypes. Such an outcome could be employed in the future to delineate rigorous recommendation strategies as well as to help define stability concepts for other crops.*

Keywords: *Adaptation, Linear regression model, Multi-environment trials, Principal component analysis*

1. INTRODUCTION

Soybean, being a source of protein and oil, is an important crop in Ethiopia. However, its production fluctuates mainly because of the use of environment-sensitive genotypes and fluctuating environmental conditions. High grain yield has been the main aim in soybean improvement and the soybean breeders are concentrating to improve the yield potential of soybean by developing new genotypes [1]. A crop genotype is considered to be the most favorable one if it has a high mean yield and a consistent performance when grow across diverse locations and years [2]. Plant breeders usually evaluate a series of genotypes across environments before a new improved genotype is released for production to farmers [3]. Therefore, indication of genotype(s) that perform consistently across environments should be emphasized [4]. In most of the genotype evaluation trials, genotype x environment (GE) interaction is observed as a common phenomenon [5]. The GE interaction complicates selection of truly superior genotypes in breeding and performance testing programs.

Several statistical procedures can be used for measuring crop yield stability. These statistical methods can be divided into two major groups, univariate and multivariate stability parameters [6]. Among univariate procedures, the most popular and most widely used is the joint linear regression analysis as proposed by several [7], [8], [9] and [10]. The nature of yield stability in terms of statistical parameters should follow the confirmatory analysis of GE interaction. It has been demonstrated that relatively a linear relationship exists between phenotype and environment when the environment is measured by its effect on the genotype yield performance. Although there are some statistical and biological limitations in the linear regression model (Crossa [11] and Flores [12]), it provides useful information when numbers of studied genotypes and test environments are relatively large.

The joint linear regression procedure provides conceptual model for genotypic stability and is simple in calculation and application [13].This modeling provides two parameters of stability including the

regression coefficient (linear sensitivity) and the deviation from linearity (non linear sensitivity (which use as the basis for understanding of the nature of GE interaction in multi-environment trial [14]. Also, the ability of the linear regression model for description of the observed variation could be determined using the coefficient of determination (R2) Pinthus [15], which is computed by individual linear regression analysis. Therefore, the linear regression model provides useful estimates for yield stability parameters when there are no extreme environments that bias regression slopes [16]. Another stability measures is the genotypic stability which is established on regression analysis since it uses the minimum slope from the conventional regression model.

Since Zobel [17] yield stability was measured by the amount of the variance of a genotype across test environments. Wricke [18] proposed the use of ecovalence, the contribution of genotype a genotype to the GE interaction as a criterion of yield stability. Also, yield stability can be measured across all interaction effects, as devised by Shukla's [19] stability of variance (SV) and the environmental variances. Lin and Binns [20] defined the superiority Index (PI) as the genotype general superiority and defined it as the distance mean square between the genotype's response and the maximum response over locations. Some plant breeders indicated that the above mentioned stability parameters follow a static concept of stability. Peterson [21] reported that the concept of optimal genotype differ somewhat from the conventionally used to describe yield stability. For breeders, stability is important in terms of changing ranks of genotypes across test environments and influences selection efficiency during improvement programs. For farmers, high yielding characteristics of genotypes is very important, regardless of changing genotypes' ranks. However, the genotypes yield usually reacts to favorable or unfavorable environmental conditions. A genotype is therefore considered to be stable if its contribution to the GE interaction is low. The objective of this study was to determine the stability of grain yield in different soybean genotypes with various univariate parametric stability models and to identify soybean genotypes that have both high mean yield and stable yield performance for North West Ethiopian areas.

2. MATERIAL AND METHODS

Planting Materials and Testing Locations

Nineteen soybean genotypes were tested in years (2012-2013, 2013-2014 and 2015-2016) at four different locations Asossa, Dibate, Mankush and Pawe. The locations are representatives of the low land of the country were soybean is widely cultivated as major rotation crop with cereals. Each year at each location was considered as a separate environment, making four test environments for the study. The descriptions of the four test locations and the nineteen test cultivars are given in table1 and 2, respectively.

Table 1. *Description of the test environments*

Environment	Geographical Position				
	Longitude	Latitude	Altitude m)	Soil Texture	Rainfall (mm)
Pawe	$36^o 03^' E$	$11^o 09^' N$	1050	Silt clay Loam	1000- 1500
Asossa	$37^0 04^' E$	$12^0 60^' N$	1155	Silt clay Loam	1200-1500
Dibate	$36^o 26^' E$	$10^O 77^' N$	1000	Silt-Loam	900-1400
Mankush	$35^o 29^' E$	$10^o 272^' N$	860	Sandy-Loam	500-1000

Table 2. *Description of the 19 soybean genotypes used in the experiment.*

No	Genotype	Source	Year		No	Genotype	Source	Year
G1	Clark 63k	USA	2005		G11	Belessa-95 (PR-149)	IITA/Nigeria	2005
G2	williams	USA	2007		G12	Wello	IITA/Nigeria	2005
G3	Gizo	IITA/Nigeria	2005		G13	Gozilla	IITA/Nigeria	2007
G4	Nyala	TURKEY	2005		G14	Wogayen	IITA/Nigeria	2005
G5	AGS-7-1	USA	2005		G15	Davis	USA	2005
G6	Afgat (TGX-1892-10F)	IITA/Nigeria	2007		G16	Ethio-yugoslavia	USA	2005
G7	crowford	IITA/Nigeria	2007		G17	Boshe	IITA/Nigeria	2007
G8	Cocker-240	IITA/Nigeria	2007		G18	Gishama	IITA/Nigeria	2005
G9	Jalele	IITA/Nigeria	2007		G19	Nova	USA	2005
G10	Awassa-95 (G2261)	USA	2005					

Source: Pawe Agricultural Research Center 2011

Experimental Layout and Design

The treatments were laid out in randomized complete block design with four replications. Each plot was four rows and 5m long with spacing of 40 cm between rows. Fertilizer was applied to each plot at the rate of 100 kg diammonium phosphate at planting. Other agronomic practices were kept as none experimental variables and applied uniformly to the entire experimental area. For data analysis, grain yield measured from net plot of $4m^2$ was converted into kg/ha at 10% standard grain moisture content.

Data Analysis

The statistics used to assess the stability and adaptability of genotypic mean yield was genotype mean square across test environments or environmental variance (EV). Coefficient of variation (CV) for each genotype as used by Francis and Kannenberg [22], the genotypic ecovalence as proposed by Wricke [18], the GEI variance or stability variance as suggested by Shukla [19]), Genotypic stability (GS) of Hanson [23], Superiority Index (PI) measure and its mean squares of GE (MSGE) as used by Lin and Binns [20], Conventional linear regression coefficient as suggested by Finlay and Wilkinson [7], deviation from conventional regression mean square [8], Coefficient of determination for conventional linear regression model [15], Adjusted linear regression coefficient and deviation as proposed by Perkins and Jink [9], independent linear regression coefficient and deviation suggested by Freeman and Perkins [10], and the regression model of Tai [24] which uses alpha and lambda measures. A comprehensive SAS based program has become available, which calculates the most parametric stability statistics [27] which is used to calculate stability statistics.

3. RESULT

Combined analysis of variance was performed to determine the effects of environment, genotype and GEI on grain yield of soybean genotypes regarding to result of Bartlett's homogeneity test. The main effects of genotype and environments were highly significant ($p<0.01$), and the GEI was also highly significant ($p>0.01$) (Table 3).

Table 3. *ANOVA of 19 soybean genotypes grown in 4 different environments*

Source of variation	Degree of freedom	Sum of square	Mean Squares	% of G+E+GE
Environment (E)	3	3777614488.6	1259204830**	88.71725
Replication/E	12	15259028.4	1271585.7[ns]	
Genotype (G)	18	12809695.9	711649.77**	3.008356
GE	54	35232713.4	652457.66**	8.274399
Error	824	28161700	34176.82	
**,* and ns, significant at 0.01, 0.05 probability level and non-significant respectively				

The high significance of GEIs for grain yield of 19 soybean genotypes tested across four locations during three years is indicating the studied genotypes exhibited both crossover and non-crossover types of genotype by environment interactions. Complexity of grain yield as a quantitative trait is a result of diverse processes that occur during development. The larger degrees of genotype by environment interaction cause to the more dissimilar the genetic system controlling the physiological processes confirming adaptation to the different environments. The relative contribution of genotype by environment interaction effects for grain yield found in this study are similar to those found in other crop adaptation studies in rain fed environments [28][32]. Therefore, genotype by environment interaction that makes it difficult to select the best performing and most stable genotypes is an important consideration in plant breeding programs [29].

According to environmental variance [20] and coefficient of variation (CV) which represent Type I stability concept (Table 4), Genotypes G10 and G18 were the most stable genotypes (Table 4). Both of these stable genotypes had low mean yield and so static concept of stability. Traditionally, the term stability is used to characterize a genotype which indicates a relatively constant yield performance, independent environmental variations. This concept may be considered as static concept of stability [2]. In contrast, a genotype showing a constant yield in all environments does not necessarily respond to improved growing conditions and usually the most stable genotypes based on this idea had low mean yield. Genotypes G10, G18 and G19 were the most stable genotypes based on the ecovalance [18], genotypic stability [28] and the stability variance [19] which genotype G19 had relatively high

mean yield (Table 4). The stability concept nature of W and GS stability statistics were as the same of static concept of stability.

Table 4. *Stability parameters based on various univariate parametric methods, for the 19 soybean genotypes grown in 4 environments.*

Gen	MY	EV	CV	W	SV	GS	PI	MSGE
G1	2497	1800695.7	55.3	1058772.6	81340.2	1486789.8	2427.5	39150.6
G2	2547.667	1674975.3	58.2	554764.3	41339.5	850693.0	2225.3	125700.3
G3	2488.333	1682988.2	58.1	634434.1	47662.5	933781.5	2233.1	119654.4
G4	2443.5	1669050.7	56.0	1282838.5	99123.2	1493480.7	2307.9	109273.3
G5	2386.083	1800695.7	55.3	1058772.6	81340.2	1486789.8	2127.5	130150.6
G6	2699.583	1672646.9	59.7	728623.2	55137.8	1002841.0	2165.7	153316.4
G7	2562.167	1913555.4	61.9	1027633.9	78668.8	1625081.8	2234.6	139680.6
G8	2421.167	1587082.9	60.7	557241.0	41536.1	723511.1	2076.2	202405.9
G9	2492.75	1656013.8	58.0	683374.6	51546.7	937863.0	2220.0	120073.7
G10	1931.833	1433041.7	54.7	408176.3	29705.5	363337.0	2189.7	131723.4
G11	2879.5	163861.3	58.3	571353.6	42656.1	811633.3	2194.2	142557.8
G12	2237.583	1636226.9	57.9	497752.2	36814.7	742629.4	2210.4	119422.5
G13	2453.417	1657283.9	59.4	604922.0	45320.3	869530.2	2165.9	145299.5
G14	2302.25	1578199.9	58.7	270753.7	18799.0	454072.7	2138.7	169192.1
G15	2546.083	1435356.1	58.7	940914.1	71986.3	843459.7	2040.3	259388.6
G16	2199.083	2166899.5	64.1	1145708.6	88239.9	2103721.8	2297.0	86859.4
G17	2649.583	1727549.4	58.8	683055.6	51521.4	1042894.6	2234.9	103890.5
G18	1940.417	1326107.4	53.3	844553.7	64338.7	596392.7	2161.9	179135.6
G19	2020.833	1516007.3	54.8	382012.4	27629.0	462069.4	2248.1	111145.3

Mean yield (MY), environmental variance (EV), Coefficient of variance (CV), Ecovalance (W), Stability variance (SV), genotypic stability (GS), Priority index (PI) and Mean squares of genotype by environment interaction (MSGE).

According to superiority index (PI) measure, genotypes G8, G14 and G15 were the most stable genotypes while based on mean squares of GE (MSGE) of PI, G1, G16 and G17 were the most stable genotypes (Table 4). Considering PI and MSGE simultaneously G10, G17 and G12 were the most stable genotypes. It is interesting that genotypes G17 had relatively high mean yield and so could be regarded as the most favorable genotype. The stability procedure of Lin and Binns [20] reflects type IV stability concept which is distinct from static or dynamic concept of stability [30]. The static type of stability is not acceptable to most plant breeders, who could prefer a dynamic concept of stability [2]. In this type of stability, it is not need that the genotypic response to environmental variations should be equal for all studied genotypes [12]. According to conventional linear regression coefficient [7], Genotypes G1, G7 and G16 were the most stable genotypes while based on deviation from conventional regression mean square [8], genotypes G10, G18 and G15 had the lowest amounts and where the most stable genotypes (Table 5). Also most of the studied genotypes had the high coefficient of determination for conventional linear regression model [15] and therefore the linear regression model could describe GEI as well as possible. Considering FW, ER, R2 and mean yield simultaneously genotypes G13 and G17 were the most favorable genotypes. According to adjusted linear regression coefficient [9], Genotypes G1, G7 and G16 were the most stable genotypes while based on deviation from this regression mean square, genotypes G10, G5 and G14 had the lowest amounts and were the most stable genotypes (Table 5). Considering adjusted linear regression parameters and mean yield simultaneously genotypes G7 and G16 were the most favorable genotypes.

According to slopes of independent linear regression coefficient [10], genotypes G6, G7 and G16 were the most stable genotypes while based on its deviation from regression mean square, genotypes G5, G8 and G15the lowest amounts and were the most stable genotypes (Table 5). Considering both regression coefficient and deviation mean square simultaneously, genotypes G7, G15 and G16 were the most stable genotypes. It is interesting genotypes G7 and G16 had relatively high mean yield and so it seems that this regression model could identified high mean yield performance genotypes as the most stable ones. According to Tai's [24] regression coefficient (Alpha), genotypes G7, G18 and G16 were the most stable genotypes while based on its deviation from regression mean square (Lambda), genotypes G10, G14 and G16 with the lowest amounts, were the most stable genotypes (Table 5).

Simultaneous regarding Alpha and Lambda, genotypes G10, G18 and G16 were the most stable genotypes. Among these stable genotypes, only G16 had the high mean yield.

Table 5. *Stability parameters based on various regression models, for the 19 soybean genotypes grown in 4 environments.*

Gen	FW	ER	R2	PJ	RPD	FP	RFD	alpha	lambda
G1	1.038	2797461.3	95.93	0.03811	114020.5	0.861	257846.1	0.0647	2.932
G2	1.010	2605261.9	97.64	0.01012	61385.1	0.848	187323.4	0.0172	1.610
G3	1.011	2617688.5	97.32	0.01085	70199.4	0.850	240295.2	0.0184	1.841
G4	0.992	25936143.5	94.52	-0.00795	142380.0	0.774	298422.0	-0.0135	3.741
G5	0.964	2355070.4	98.33	-0.03562	39282.7	0.820	52944.3	-0.0605	0.975
G6	1.006	2601819.3	96.89	0.00552	80882.1	0.895	256494.0	0.0094	2.126
G7	1.074	2962985.9	96.62	0.07401	100525.4	0.947	119388.4	0.1256	2.393
G8	0.983	2468045.1	97.52	-0.01735	61165.0	0.816	91861.8	-0.0295	1.595
G9	1.001	2576017.3	97.05	0.00134	75926.0	0.867	263532.9	0.0023	1.997
G10	0.938	2219566.7	98.40	-0.06208	35743.4	0.825	125018.9	-0.1054	0.764
G11	0.998	2548554.8	97.51	-0.00167	63476.8	0.825	339878.0	-0.0028	1.669
G12	0.999	2545240.6	97.83	-0.00070	55304.6	0.827	266240.0	-0.0012	1.454
G13	1.003	2577966.8	97.39	0.00348	67183.3	0.828	384825.0	0.0059	1.766
G14	0.986	2454506.5	98.79	-0.01374	29613.1	0.768	178521.2	-0.0233	0.770
G15	0.927	2219405.6	95.92	-0.07323	91175.4	0.878	104156.6	-0.1243	2.152
G16	1.150	3314330.2	97.90	0.15040	70898.3	1.041	122956.1	0.2553	0.830
G17	1.024	2685903.3	97.23	0.02366	74499.0	0.886	306111.5	0.0402	1.934
G18	0.895	2035260.3	96.76	-0.10516	66265.8	0.711	208239.1	-0.1785	1.237
G19	0.938	2697461.3	93.93	0.01811	304020.5	0.828	387846.1	0.0657	2.632

Slope of conventional regression coefficient (FW), Deviation from conventional regression (ER). Coefficient of determination (R2), Slope of adjusted regression model of Perkins and Jinks (PJ), Residual mean squares from the regression of Perkins and Jinks model (RPD), Slope of independent regression model of Freeman and Perkins (FP), Residual mean squares from the regression of Freeman and Perkins's model (RFD), α of tai procedure (1971) and λ of Tai

4. DISCUSSION

In this study several regression models are used for interpreting GEI. For using regression slopes as stability parameters, regression model need that heterogeneity for genotype regressions account relatively a high portion of the GEI variations [25]. Also, the most favorable genotype is the one that combines both high mean yield and stability performance together and so it is acceptable over a wide range of environmental conditions [26]. This idea for identifying favorable genotypes reflects dynamic concept of stability. Adie [31] reported that the regression coefficients of the most of the regression models benefits from dynamic concepts of stability and could be useful for detecting the most stable genotypes. Anyhow, each statistic reflects different aspects of yield stability concepts and no single method can adequately explain genotype performance across different environments [12] [31]. Therefore it seems that the reliable decision about GEI and effective selection of favorable genotypes, it is better multi-environment trails dataset is evaluated through different aspects of stability concepts.

To better show associations among genotypes based on different stability statistics, the two-way dataset of genotypes was analyzed further using a clustering procedure. The Ward's hierarchical clustering procedure indicated that the nineteen soybean genotypes could be classified into three major groups (Table 6). Cluster I include genotypes G1, G9, G3, G2, G15, G7, G4, G13, G8, G5, G6, G17,G12, G16 and 14 which were moderate or low mean yielding genotypes and low or moderate stability characteristics. Cluster II include genotypes G10, G18 and G19 which have low mean yielding and high stability characteristics. Cluster III have solitary genotype G11 which have high mean yielding genotype and low stability characteristics. Regarding almost the most of the stability statistics results as well as mean yield, genotypes G10, G18 and G19 could be introduced as the most favorable genotypes.

Table 6. *Hierarchical cluster analysis of the 19 soybean genotypes based on Ward's method using GXE matrix of mean yield.*
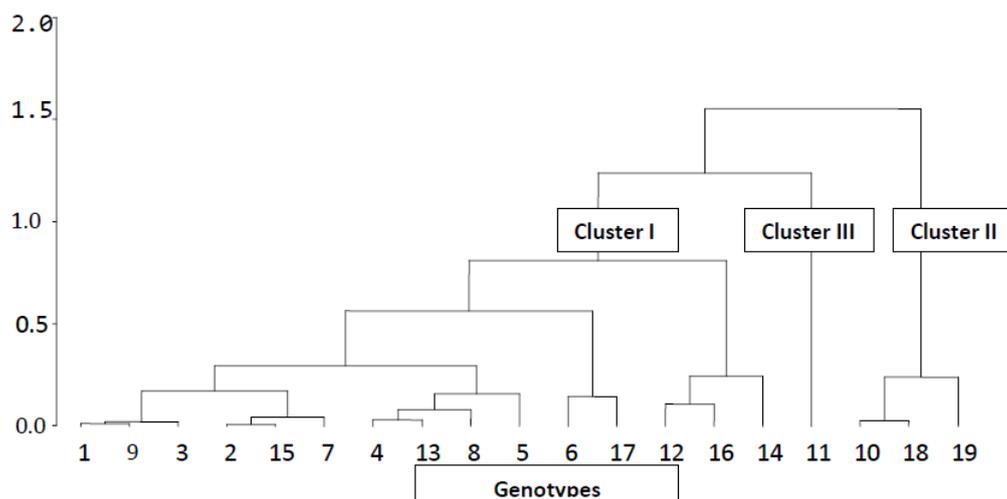
Yield stability should be considered as an important aspect of multi-environment trails and so plant breeders need some stability statistics which provide a reliable measure of yield stability. Anyhow for a successful breeding program or new genotypes evaluation trials, both stability and yield must be regarded simultaneously. Kang and Pham (1991) discussed several methods of simultaneous selection for yield and stability and relationships among them. This consideration may be reflects static or dynamic nature of different stability statistics. Also it is possible the crop nature or genetically differences among studied genotypes cause to various conclusions. However, our clustering results indicated there are three distinct groups based on stability performance and mean yield properties. Adie [13] evaluated the usefulness of several stability statistics for simultaneously selecting for high yield and stability of performance and reported relatively similar results.

Table 7. *PCA plot of ranks of stability of yield, estimated by different methods using yield data from 19 soybean genotypes grown in four environments and showing interrelationships among these parameters.*
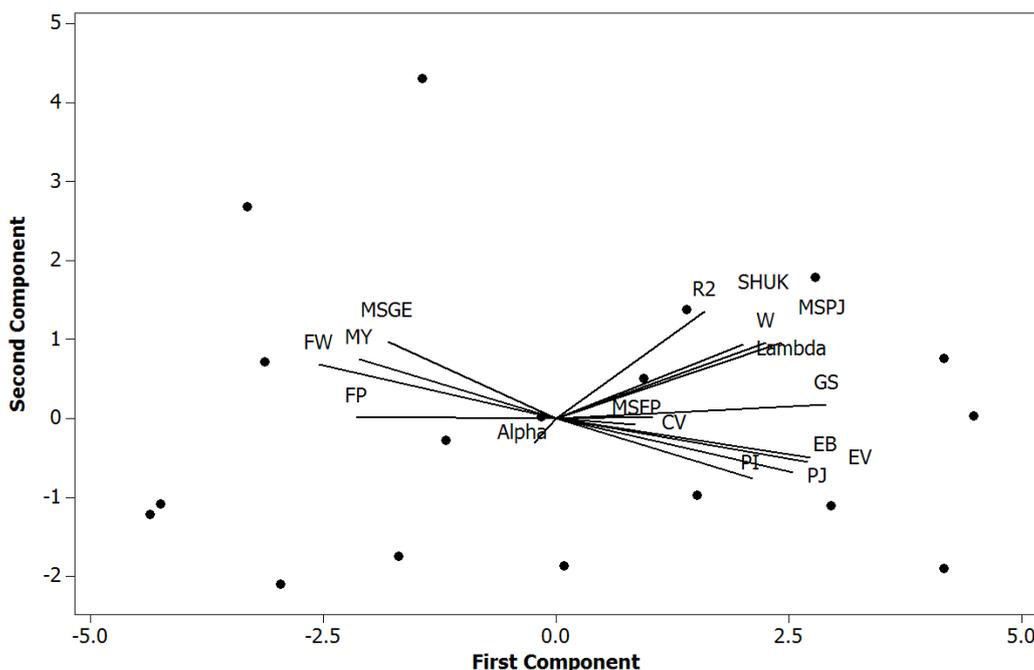
Each of the stability methods produced a unique genotype ranking and to better understand the relationships among these methods, a principal component analysis (PCA) based on the rank correlation matrix was performed. The first two principal components explained 68.77% (47.1% and 21.67% by PC1 and PC2, respectively) of the variance of the original variables. The relationships among the stability statistics were graphically displayed in a plot of PC1 and PC2 (Table 7). In this

plot, the PC1 axis mainly distinguishes the methods of FW (coefficient of conventional linear regression of Finlay and Wilkinson [7], FP (Coefficient of independent linear regression of Freeman and Perkins [10]) and MSGE (mean squares of GE of Superiority Index measure of Lin and Binns [20]) from the other methods which mean yield (MY) also is grouped near these statistics, and I refer to these as class 1 (C1) stability statistics versus the other remained stability statistics as Class 2 (C2). It could be concluded that the studied stability statistics are classified into two major groups which reflects dynamic versus static stability concepts. Therefore, it seems that considering high amounts of coefficient of determination of regression model in this investigation, the coefficient of linear regression models were suitable for interpretation GEI.

The following findings can be summarized from the present investigation: (1) genotypes G10 and G18 were found to be the most stable genotypes and (2) the linear regression model and its slope as stability statistics was found to be useful in detecting the phenotypic stability of the studied genotypes when the coefficient of determination are high; and (3)the significant GEIs and the changes in ranks of genotypes across environments suggest a breeding strategy of specially adapted genotypes in homogeneously grouped environments.

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