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An overview on the use of stability parameters in plant breeding

Abstract

The phenotype of an individual depends upon both the genetic make-up and environmental influences. Genotype × environment interaction is considered as an important source of discrepancy in any crop, and different methods have been used to distinguish genotypes for their behavior in different environmental conditions. These constitute univariate parametric, such as environmental variance, regression slope, and deviation from regression, to multivariate methods. In this review, we summarize the priorities and limitations of different parametric stability statistics, and also their correlations which might help agronomists and crop breeders to choose the proper methods for their analysis.

Keywords: genotype by environment interaction, performance, stability

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Introduction

Yield stability has always been considered as an important topic in plant breeding but will be more concern by the continued variation in climatic condition. The phenotype of an individual is a mixture of both genotype (G) and environment (E). As a consequence of G × E interaction, crop varieties may not show uniform performance across different environments. The term genotype refers to the genetic makeup of an organism while environment refers to biophysical factors that have an effect on the growth and development of a genotype.[1] The G × E study is especially important in countries with various agro-ecologies. Significant G × E interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (called as a qualitative or rank changes) or variations in the comparative ranking of the genotypes (called as a quantitative or absolute differences between genotypes).[2-4]

Stability definition

All performance stability, phenotypic stability, and adaptation terms are usually used in total various meanings and different senses and explanations are introduced over the years.[5,6] In a static mean of stability defined by Becker and Leon,[6] a stable genotype is the one possessing a constant performance irrespective of any changes in environmental conditions. According to Peterson et al.,[7] the optimal genotype stability definition and response for quality parameters varies relatively from that conventionally used to characterize yield stability. For breeders, stability of quality properties is important from the points of changing genotypes ranks' throughout environments and influences selection efficiency. For end-users, such as millers and bakers, stability in quality properties of genotypes is more important, irrespective of genotypes rank changes. However, as pointed out by Grausgruber et al.,[8] the quality of a genotype often behaves similar to other quantitative characters to desirable and undesirable environmental conditions. As a result, a genotype is regarded stable if it has a low contribution to the G × E interaction.

Basic concepts

In the final stage of plant breeding, the new varieties are grown under different seasons of the year, environments, climatic and soil conditions.[6,9] Environments and seasons, in the role of different conditions, are specified to be a single factor for environmental conditions. The most commonly used designs in these experiments are randomized complete blocks and incomplete block designs. For the latter, owing to the large number of genotypes, lattice designs are usually used. In all experiments, plant breeders usually focus on modeling the genotype means estimated in the j[th] environment. Therefore, one may consider the linear model:

$$Y_{ij} = \mu + g_i + e_j + ge_{ij} + e_{ij} \quad (1)$$

where: Y_{ij} is the observed mean of the i^{th} genotype at the j^{th} environment, for $i = 1, 2.....,n$, and $j= 1, 2,.....,n;\mu$ is the overall mean of the i^{th} genotype; g_i is the effect of the i^{th} genotype, e_j represents the effect of the j^{th} environment, ge_{ij} is the effect of interaction between i^{th} genotype and j^{th} environment, e_{ij} is the mean error related to the observed Y_{ij} .

The $G \times E$ interaction (term ge_{ij} in equation 1) can be explained as the differential yield response of a genotype to environments. As a direct consequence of $G \times E$ interaction, the approximate performances of two genotypes vary with the environment stimuli. As a result, one of the most significant goals of the phenotype stability analysis is to distinguish the genotypes whose phenotypic performance remains constant while the environmental conditions change. In the presence of $G \times E$ interaction, these analyses make sense.[10] Radiation, water, and nutrients availability are among the factors which strongly influence crop growth and yield[11] therefore, the components of phenotypic variance may often rank as follows:[12-20]

$$\sigma^2_E > G \times E > \sigma^2_G$$

In contrast to the above ranking, in a study by Puttha et al.,[21], the genotype contributed to a large proportion of variation in inulin content and fresh tuber yield, whilst $G \times E$ and environment had a smaller contribution to discrepancies. The difference in contrast is feasibly largely because of materials used and environments' conditions. In other studies, it was observed that the G × sowing seasons (SS) interaction was less important than the $G \times E +$ year interaction.[22] These results show that the evaluation of genotypes based on several environments and years is more important than the evaluation for the two seasons.

Illustration of $G \times E$ effect

To show the environmental effect, the 2 genotypes called A and B, are tested in two environments (E_1 and E_2) in Figure 1. Figure 1a indicates the presence of an interaction effect in which genotype A is superior to genotype B in E_1 but has the lowest mean in E_2. Figure 1 b shows the absence of $G \times E$ interaction.

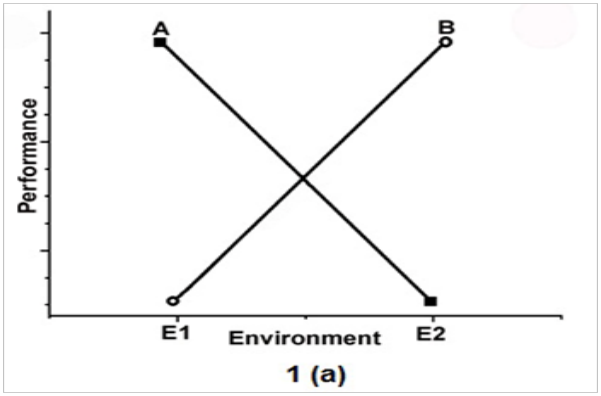

Figure 1a Indicates the presence of an interaction effect in which genotype A is superior to genotype B in E1 but has the lowest mean in E2.

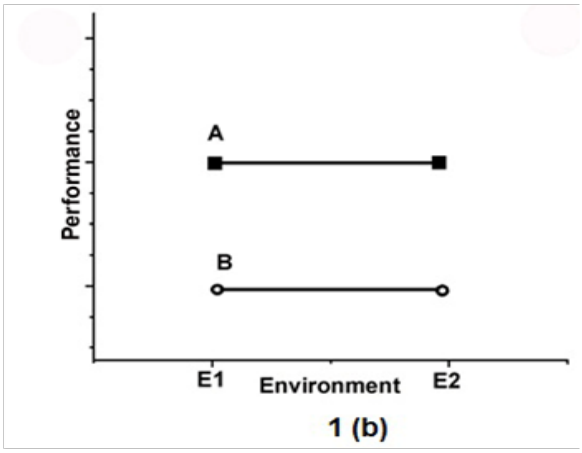

Figure 1b Shows the absence of interaction.

Methods for estimating phenotypic stability

The economic significance of stability for the cultivation of a genotype was first identified by Roemer [1917, cited in 8] who used the variance across environments as a parameter for yield stability. This stability parameter follows a biological/static sense implicating that a stable genotype is recognized as the one having small variance across the tested environments.[6] Therefore, to estimate the static phenotype stability of the genotype, the following equation can be used:

$$S^2_{xi} = \frac{\Sigma (X_{ij} - \bar{X}_{i.})^2}{E-1} \qquad (2)$$

where X_{ij} is the performance of the i^{th} genotype in the j^{th} environment, $X_{i.}$ is the mean performance of the i^{th} genotype and E is the number of environments.

If the sample estimate is not significantly different from zero, a genotype is then recognized to be stable which means that environmental changes will not influence the genotype performance. However, this type is rarely a favored feature of crop landraces, inasmuch as genotypes with high phenotypic stability obtained through the environmental change have low yield. As a result, this method does not desired by plant breeders to evaluate the phenotypic stability of the genotype performance, or other related random variables. Although, it is helpful to evaluate the phenotypic stability of the traits that should retain their levels such as stress characters like winter hardiness, qualitative traits, or disease resistance.[23] In contrast, if a genotype response to environmental changes has no deviation from the general response of all genotypes in the trial, it is called as dynamic or agronomic stability. The dynamic concept of stability is useful for quantitative traits such as yield.[23]

Using the dynamic concept of stability, Wricke's[24,25] model is the simplest method to evaluate the stability. Wricke[24,25] suggested the ecovalence (W^2_i) concept as the ratio of the interaction sum of squares contributed by each genotype to the $G \times E$ interaction sum of squares. In other words, the ecovalence of the i^{th} genotype is its interaction with the environments, squared and summed across environments, and expressed as

$$W_i^2 = \Sigma \left(X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..} \right)^2 \qquad (3)$$

Where X_{ij} is the mean performance of the i^{th} genotype in the j^{th} environment and $X_{i.}$ and $X_{.j}$ are the genotype and environment mean deviations, respectively, and $X_{..}$ is the overall mean. For this reason, genotypes with a low W^2_i value have smaller deviations from the mean across environments and are therefore more stable. Based on Becker and Leon,[6] a genotype with $W^2_i = 0$ is considered stable.

Shukla[26] proposed the variance component of each genotype across environments as another relevant measure of phenotypic stability. It measures stability rather than performance. According to Shukla's stability variance (σ^2_i), $G \times E$ sum of squares is partitioned into components, one corresponding to each genotype and estimated as

$$\sigma^2_i = \frac{1}{(G-1)(G-2)(E-1)} \left[G(G-1)\Sigma_j \ (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 - \Sigma_i \ \Sigma_j \ (X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..})^2 \right] \ldots \qquad (4)$$

Where G is number of genotypes, E is number of environments, X_{ij} is the mean yield of the i^{th} genotype in the j^{th} environment, $X_{i.}$ is the mean of the i^{th} genotype in all environments, $X_{.j}$ is the mean of all genotypes j^{th} in environments and $X_{..}$ is the overall mean.

If the stability variance of a genotype was equal to the environmental variance $(\sigma^2_i = 0)$,then genotype is identified as stable. A slightly large value of σ^2_i will therefore illustrate more instability of the i^{th} genotype. Significant σ^2_i value's also shows that a genotype's performance throughout the environments was unstable. Genotypes with a non significant or negative σ^2_i would be regarded stable throughout the environments.[26] Since σ^2_i is the difference between two sums of squares, negative σ^2_i may sometimes occur which can be considered as equal to zero in such conditions.[26] It is also important to note that σ^2_i cannot be computed from unbalanced data.[27]

The level of correlation among different stability parameters

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represents whether one or more parameters should be used for cultivar performance prediction, and also gives breeder the right to choose the best stability parameter(s) to fit the sense of stability.[28] Shukla[26] stability variance is a linear combination of deviation mean squares, in other words the Wricke[24,25] ecovalance. Significant positive correlation between W^2_i and σ^2_i was found in different studies (Table 1) which indicates that W^2_i and σ^2_i are equivalent in ranking genotypes for stability.[29-33] As a result, it is adequate and acceptable to use one of the two statistics solely.[34] However, in a study by Kang and Miller,[35] Shukla's method method was preferred to Wricke[24,25] for estimating the yield stability of sugar cane cultivars. Contrary to the results of previous studies (Table 1), Akcura et al.,[36] reported a significant negative association (-0.88, $P < 0.05$) between σ^2_i and W^2_i.

The main type of stability analysis called joint regression analysis or joint linear regression (JLR) was termed by Freeman.[37] It helps to estimate whether the genotypes have characteristic in a linear responses to environmental changes. The interaction sum of squares is partitioned into two parts: one describes the heterogeneity of linear regression coefficient (b_i) whereas the second represents a deviation (d_{ij}):

$$(G \times E)_{ij} = b_i E_j + d_{ij} \quad (5)$$

and therefore

$$Y_{ij} = \mu + G_i + E_j + \left(b_i E_j + d_{ij}\right) + e_{ij} \quad (6)$$

Whereis E_j the environmental index, b_i is the regression coefficient that measures the response of the genotype of varying environments, d_{ij} stands for the deviation from regression of the i^{th} genotype at the j^{th} environment, and the remaining stands as specified in equation 1. The joint regression analysis approach was first introduced by Yates and Cochran[38] and was later modified by Finlay and Wilkinson[39] and Eberhart & Russell[40] which is a widely used method nowadays.

The regression coefficient was introduced by Finlay and Wilkinson[39] as the regression of the mean of i^{th} genotype in j^{th} environment on the mean performance of all genotypes in that environment and is expressed as

$$b_i = 1 + \frac{\Sigma_i \left(X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..}\right)\left(\bar{X}_{.j} - \bar{X}_{..}\right)}{\Sigma_j \left(\bar{X}_{.j} - \bar{X}_{..}\right)^2} \quad (7)$$

where X_{ij} is the performance of the i^{th} genotype in the j^{th} environment, $X_{i.}$ Is the mean performance of the i^{th} genotype, and $X_{.j}$ is the mean performance of the j^{th} environment, $X_{..}$ is the overall mean and E is the number of environments. The regression coefficient (b_i) mainly indicates the adaptation of a genotype to several environments and also describes the linear response between environments. However, it does not reflect stability, crop performance, or stability extension.[40,41]

As it could be seen in Figure 2, a genotype which has a regression line above that for overall mean performance is regarded to have high performance stability and is able to adapt to all environments. As the productivity of the environment improves, the performance of such genotype would increase. A genotype is considered to have adaptation to a specific environment if its regression line crosses that for overall mean performance. A genotype is regarded to have low performance adaptability across environments if its regression line placed below that for the overall mean performance.[39] The slope of regression line showed a positive association with yield potential in different studies[16,36,42-46] which means that high yielding genotypes have larger values for bi which are particularly adapted to environments with favourable growing condition. Therefore, such genotypes, when cultivated in poor environments would show less than optimal performance but when cultivated in optimal environments, they could achieve maximum performance.

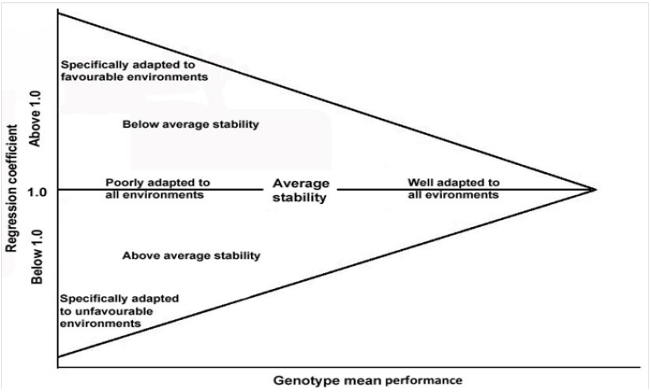

Figure 2: Genotype regression coefficients plotted against genotype performance, adapted from Finlay and Wilkinson.[39]

Altay[47] suggested that Finlay and Wilkinson[39] method is a preferable method for the assessment of specific or wide adaptation of genotypes compared with Wricke[24,25] ecovalence.

Eberhart and Russell[40] suggested using the mean of squared deviations from regressionas $\left(s^2_{di}\right)$ a measure for stability and a stable genotype is the one has a small deviation from regression mean squares (equation 8).

$$S^2_{di} = \frac{1}{E-2}\left[\Sigma_i \left(X_{ij} - \bar{X}_{i.} - \bar{X}_{.j} + \bar{X}_{..}\right)^2 - (b_i - 1)^2 \Sigma_i \left(\bar{X}_{j.} - \bar{X}_{..}\right)^2\right] \quad (8)$$

where all components have their usual meanings.

According to Eberhart and Russell[40] model, genotypes are grouped based on their variance of the regression deviation (either equal or not to zero). A genotype with variance in regression deviation equal to zero is highly predictable, whilst a genotype with regression deviation more than zero has less predictable response.[48] Although, regression model is displayed to be the most useful approach for geneticists[37,48-51] but authors have found a number of statistical and biological restrictions and criticisms.

One of the drawbacks of this analysis is that the mean of all genotypes in each environment is considered as a measure of the environmental index and is used as an independent variable in the regression. According to the regression analysis assumptions, no independence can be among the variables, particularly when the number of genotypes is less than 15.[6,52] In addition, the variation in regression coefficient result is most often so small which makes it difficult to rank the genotypes for stability and adaptability. Regression analysis should be used with caution when only a few low or high performance sites are included in the analysis;[51,52] since the genotype fit may be determined greatly by its performance in a few extreme environments, it leads to the generation of misleading results.

A strong positive relationship between S^2_{di} and σ^2_i was found in studies on durum wheat, lentil, maize, and pea (Table 1) and also between S^2_{di} and W^2_i for durum wheat, lentil, maize, pea, popcorn, sorghum, and soybean cultivars (Table 1). Jowett[53] concluded that the Eberhart and Russell[40] method, which uses an arithmetic scale, was more explicit than the Finlay and Wilkinson procedure, which uses a logarithmic scale. Stability parameters such as S^2_{di}, σ^2_i and W^2_i were found to be useful in assessing the phenotypic stability of field genotypes.[34,54-57] Marjanovic-Jeromela et al.,[45] found a negative correlation between W^2_i and S^2_{di} which indicates that either of these two methods could be used independently from each other without influencing accuracy of estimation.

Joint regression and QTL mapping

Two possible genetic mechanisms including the allelic sensitivity and gene regulation models are proposed for supporting stability.[58,59] In the first model and in direct response to the environment, the constitutive gene regulates itself through the activation of different alleles in various environments.

Regardless of how stability is expressed or measured, one of the most important questions for a stability parameter is whether it is genetic.[60] Two possible genetic mechanisms are proposed for underpinning stability;[58,59] the allelic sensitivity model, which suggests that the constitutive gene is regulated itself in direct response to the environment through the activation of different alleles in various environments. The gene regulation model implies that one or more regulatory loci are under the direct influence of the environment and the constitutive gene is switched on or off by the regulatory gene. Collocation of QTLs (a segment of DNA that influences a quantitative trait) illustrating $G \times E$ interactions and QTLs for stability parameters would support the allelic sensitivity model,[59,61] whilst QTLs for stability parameters detected in regions other than those for the trait would imply a regulatory model.[62,63] Joint regression analysis is widely used in quantitative genetics to analyze QTL × environment interaction.[59,64] Previous studies found that the deviation from regression is not under genetic control,[59,65] which is in contrary to the findings of Kraakman et al.,[61]

Perkins and Jink[66] introduced a statistical analysis to measure non linear sensitivity to the environmental variations by considering the $G \times E$ interaction component of each genotype as a linear function of the additive environmental component. In this model, the deviation from the regression line of each environment is considered as a fixed effect and a genotype with $\beta_i = 0$ and $\sigma^2_i = 0$ is regarded as stable. The b -values[38-40] have a mean of unity, while the β -values[6,26] have a mean of zero.

In a study by Annicchiarico and Mariani,[67] 9 wheat lines were grown at six Italian locations for three seasons. Positive correlation between β -values and σ^2_i indicated lines adaptability with generally low yield stability.

Lin and Binns[68] proposed the superiority measure (P_i) of the i^{th} genotype as the performance difference comparison among a set of genotypes compared with a reference genotype with the maximum performance within each environment:

$$P_i = \frac{\left[\sum_{j=1}^{n} (X_{ij} - M_j)^2\right]}{2E} \quad (9)$$

Where X_{ij} is the average performance of the i^{th} – genotype in the j^{th} environment, M_j is the genotype with maximum performance among all genotypes in the j^{th} environment, and is the number of environments.

Small P_i value's indicates less distance between the i^{th} genotype and the genotype with maximum performance and the better the genotype.[69,70] This explanation of superiority is compared to the breeder's purpose, because a superior genotype should be placed among the most productive genotypes across environments.

Although, Lin and Binns[68] method is seldom used in different studies but it does not have restrictions of the regression model. In this method, the stability statistics are on the basis of both the average genotype effects and $G \times E$ interaction effects,and each genotype is compared only with the one maximum performance at each environment.[52] It also seems to be extremely a measure of genotype performance rather than stability. P_i displayed the largest deviation from all the other procedures, including negative and significant rank correlation coefficients with b_i compared to the other procedures (Table 1). Positive correlations between yield values and P_i were found.[46,71]

Table 1 Relationship among different stability parameters

Correlation Type	Crop Species	References
Correlation between S^2_{xi} and W^2_i		
Positive correlation	Common bean, *Phaseolus vulgaris* L.	[43]
Negative correlation		
Correlation between S^2_{xi} and W^2_i		
Positive correlation	Common bean, *Phaseolus vulgaris* L.	[43]
Negative correlation		
Correlation between S^2_{xi} and b_i		
Positive correlation	Chickpea, *Cicer arietinum* L.	[83]
	Durum wheat, *Triticum durum* Desf.	[84]
	Tea, *Camellia sinensis*	[42]

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Table Continued

Correlation Type	Crop Species	References
Correlation between S^2_{xi} and CV		
Positive correlation	Durum wheat, *Triticum durum* Desf.	85
	Durum wheat, *Triticum durum* Desf.	84
	Lentil, *Lens culinaris* Medik	71
	Pea, *Pisum sativum* L.	56
Negative correlation		
Correlation between S^2_{xi} and S^2_{di}		
Positive correlation	Chickpea, *Cicer arietinum* L.	83
	Common bean, *Phaseolus vulgaris* L.	43
Negative correlation		
Correlation between S^2_{xi} and R^2_i		
Positive correlation		
Negative correlation	Common bean, *Phaseolus vulgaris* L.	43
	Lentil, *Lens culinaris* Medik	71
Correlation between W^2_i and σ^2_i		
Positive correlation	Barley, *Hordeum vulgare* L.	91
	Chenopodium spp.	92
	Chickpea, *Cicer arietinum* L.	83
	Common bean, *Phaseolus vulgaris* L.	43
	Cowpea, *Vigna unguiculata* [L.] Walp	93
	Durum wheat, *Triticum durum* Desf.	84
	Lentil, *Lens culinaris* Medik	71
	Maize, *Zea mays* L.	55
	Pea, *Pisum sativum* L.	94
	Pea, *Pisum sativum* L.	56
	Rapeseed, *Brassica napus* L.	95
Negative correlation	Durum wheat, *Triticum durum* Desf.	36
Correlation between b_i and W^2_i		
Positive correlation	Durum wheat, *Triticum durum* Desf.	36
	Sorghum, *Sorghum bicolor* (L.) Moench	96
Negative correlation		
Correlation between b_i and σ^2_i		
Positive correlation	Soybean, *Glycine max* (L.) Merr.	97
Negative correlation		
Correlation between S^2_{di} and W^2_i		

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Table Continued

Correlation Type	Crop Species	References
	Chickpea, *Cicer arietinum* L.	83
	Common bean, *Phaseolus vulgaris* L.	43
	Durum wheat, *Triticum durum* Desf.	84
	Durum wheat, *Triticum durum* Desf.	85
	Lentil, *Lens culinaris* Medik	71
	Maize, *Zea mays* L.	55
Positive correlation	Pea, *Pisum sativum* L.	57
	Pea, *Pisum sativum* L.	56
	Popcorn, *Zea mays* L.	48
	Rubber tree, *Hevea brasiliensis*	86*
	Sorghum, *Sorghum bicolor* (L.) Moench	96
	Soybean, *Glycine max* (L.) Merr.	41
	Winter Rapeseed, *Brassica napus* L.	45
Negative correlation	Durum wheat, *Triticum durum* Desf.	36
Correlation between S^2_{di} and σ^2_i		
	Common bean, *Phaseolus vulgaris* L.	43
	Durum wheat, *Triticum durum* Desf.	36
	Lentil, *Lens culinaris* Medik	71
Positive correlation	Maize, *Zea mays* L.	55
	Pea, *Pisum sativum* L.	94
	Pea, *Pisum sativum* L.	56
	Tea, *Camellia sinensis*	42
Negative correlation		
Correlation between S^2_{di} and b_i		
	Chickpea, *Cicer arietinum* L.	83
Positive correlation	Lentil, *Lens culinaris* Medik	71
	Sorghum, *Sorghum bicolor* (L.) Moench	96
Negative correlation	Winter Rapeseed, *Brassica napus* L.	45
Correlation between S^2_{di} and β_i		
Positive correlation	Lentil, *Lens culinaris* Medik	71
Negative correlation		
Correlation between S^2_{di} and R^2_i		
	Durum wheat, *Triticum durum* Desf.	36
Positive correlation	*Sorghum, Sorghum* bicolor (L.) Moench	96
	Chickpea, *Cicer arietinum* L.	83
Negative correlation	Common bean, *Phaseolus vulgaris* L.	43
	Lentil, *Lens culinaris* Medik	71
Correlation between S^2_{di} and CV		
Positive correlation	Pea, *Pisum sativum* L.	56
Negative correlation		
Correlation between β and σ^2_i		
Positive correlation	Lentil, *Lens culinaris* Medik	71
Negative correlation		

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Table Continued

Correlation Type	Crop Species	References
Correlation between b_i and P_i		
Positive correlation		
	Chickpea, *Cicer arietinum* L.	83
	Durum wheat, *Triticum durum* Desf.	85
	Popcorn, *Zea mays* L.	48
Negative correlation	Rye	69
	Maize, *Zea mays* L.	98
	Timothy, *Phleum pratense* L.	70
Correlation between R^2_i and W^2_i		
Positive correlation	Sorghum, *Sorghum bicolor* (L.) Moench	96
	Chickpea, *Cicer arietinum* L.	83
Negative correlation	Common bean, *Phaseolus vulgaris* L.	43
	Durum wheat, *Triticum durum* Desf.	36
Correlation between R^2_i and σ^2_i		
Positive correlation	Durum wheat, *Triticum durum* Desf.	36
Negative correlation	Common bean, *Phaseolus vulgaris* L.	43
Correlation between R^2_i and b_i		
Positive correlation	Sorghum, *Sorghum bicolor* (L.) Moench	96
Negative correlation		
Correlation between R^2_i and P_i		
Positive correlation	Lentil, *Lens culinaris* Medik	71
Negative correlation		
Correlation between b_i and CV		
	Durum wheat, *Triticum durum* Desf.	36
	Durum wheat, *Triticum durum* Desf.	84
	Durum wheat, *Triticum durum* Desf.	85
Positive correlation	Maize, *Zea mays* L.	55
	Soybean, *Glycine max* (L.) Merr.	41
	Sugar beet	99
Negative correlation		
Correlation between P_i and S^2_{xi}		
Positive correlation		
Negative correlation	Durum wheat, *Triticum durum* Desf.	85
Correlation between P_i and W^2_i		
Positive correlation	Rubber tree, *Hevea brasiliensis*	86*
Negative correlation		
Correlation between P_i and S^2_{di}		
Positive correlation	Rubber tree, *Hevea brasiliensis*	86*

Table Continued

Correlation Type	Crop Species	References
Negative correlation	Durum wheat, *Triticum durum* Desf.	[85]
Correlation between P_i and CV		
Positive correlation	Maize, *Zea mays* L.	[55]
Negative correlation		

*Vigor characteristic,

S^2_{xi} : Environmental Variance, W^2_i : Ecovalence σ^2_i : Shukla's Stability Variance, CV: Coefficient of Variability, R^2_i : Coefficient of Determination, b_i :Regression Coefficient, P_i :Superiority Measure, S^2_{di} :Deviation from Regression mean Squares, β_i :Perkins and Jinks's Stability Parameter.[66]

Francis and Kannenberg[72] proposed coefficient of variation (CV) as a stability measure as follows:

$$CV(\%) = \frac{\left(\sqrt{\frac{ev_i}{(E-1)}}100\right)}{\bar{X}_{i.}} \qquad (10)$$

where evi is the sum of squares of interaction effects and the remaining stands as specified in equation 3. Although CV is a simple method and repeatedly used by breeders and other workers but it has its own limitation's. While comparing genotypes across high and low yielding environments if the mean and standard deviation do not vary in a parallel way as performance increases, a bias would happen, whereby high means result in low CV and low means in high CVs.[73]

In different studies, Francis and Kannenberg[72] method was found most useful and informative compared with other stability parameters.[34,74,75] A positive correlation was also found between b_i and CV.[41] Pinthus[76] introduced coefficient of determination (R^2_i) method to estimate stability of genotypes (equation 11). He suggested R^2_i as an alternative to the deviation mean squares, since R^2_i is strongly related to S^2_{di}.[77]

$$\text{Coefficient of determination: } R^2_i = 1 - \frac{S^2_{di}}{S^2_{xi}} \qquad (11)$$

In comparison with CV, R^2_i is a more robust index and is shown to be a better platform compared with S^2_{di} since its value ranges between zero and one.[78] Higher R^2_i values are desired because illustrate favourable responses to environmental variations. In general, if the CV is below 15% and R^2_i is above 70%, the experiment is valid. Mekbib[43] found a significant positive correlation between R^2_i and yield values.

Multivariate approaches for stability analysis

There are different multivariate models for stability analysis among which the two most commonly used approaches are:

a) The additive main effects and multiplicative interaction (AMMI) method which gives information on main and interaction effects in addition to a biplot. It is specifically efficient for illustrating adaptive responses[79,80] and is recently suggested as a replacement to the joint regression analysis for most of the breeding programmes.[81] However, it needs greater number of genotypes, small number of replications, and also several years for evaluation in comparison with other models. Furthermore, the complexity of the result's interpretation compared with Eberhart and Russell[40] models should be highlighted. In addition, AMMI is incapable to found close relationship between high performance and stability.[82] In a study by Purchase,[31] joint regression, Wricke[24,25] and AMMI methods were found to be more useful in assessing the stability of durum wheat genotypes. Highly significant rank correlation was found among S^2_{di}, W_i and AMMI stability values in chickpea,[83] durum wheat,[84,85] pea,[56,57] and rubber tree.[86] Also positive correlations were found between AMMI and other stability parameters such as σ^2_i [56] and P_i.[86]

b) The biplot technique named 'GGE biplot' was developed by Yan et al.,[87] to represent genotype main effects and $G \times E$ interaction graphically. Although biplot analysis is not sensitive to the number of genotypes but it is the best predictor of genotype stability for a small number of genotypes.[88] In a study by Alwala et al.,[17] evaluating 24 maize hybrids at 24 environments across 7 Midwestern states in 2007, biplot analysis was found better than Eberhart and Russell joint regression analysis in identifying stable and high yielding genotypes.

Although AMMI and GGE are equivalent in achieving predictive accuracy, the AMMI method is considered superior to GGE for evaluating yield trial data,[89] because it shows genotype main effects, environment main effects and interaction effects, whilst the GGE biplot only displays G and $G \times E$ effects.[90]

Conclusion

The advantage of selecting superior genotypes using stability analysis instead of average performance is that stable genotypes are dependable across the environments which reduce $G \times E$ interaction. Studies showed that stability analyses according to various principles can result in better identification of stable genotypes, even when there were no interactions among the parameters. Indeed, what was sought in this review, was, investigation of the correlation among different stability parameters in different crops and also emphasizing the advantageous and disadvantageous of each parameter which would facilitate the choice of breeders to select the appropriate method. Since W^2_i and σ^2_i are equivalent and bi indicates the adaptation of a genotype than stability, it is recommended that the S^2_{di}, W^2_i / σ^2_i and CV should be used concurrently to estimate phenotypic stability effects. Further studies of the correlation between parametric and nonparametric parameters in different crops are required to answer the remained questions.

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Conflict of Interest

None.

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