Yield Stability and Correlation Among Stability Parameters in Faba Bean (*Vicia faba* L.) Yield Trial in Ethiopia

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Abstract: The relationship between the adaptableness and stability estimates of different models is revealing of whether one or more estimates should be obtained for consistent forecasts of cultivar behavior, and also helps the breeder to select the best adjusted and most informative stability parameter(s). Twelve faba bean genotypes were assessed in 2018/2019 cropping season across seven environments in Ethiopia using randomized complete block design with four replications. The objectives were to identify stable faba bean genotypes across the target environments and determine the relationship among univariate stability parameters. The yield stability was estimated using various stability parameters. Using Eberhart and Russell's model the regression coefficient (bi) values ranged from 0.85 (G5) to 1.08 (G3). The regression coefficient of G1 (bi = 0.99) and G11 (bi= 1.02) indicated average adaptable across environments. In contrast G2, G3, G4, and G8 have a regression coefficient bi value significantly greater than 1; this showed that genotypes are very sensitive when the environment is changed. To see the level of association among the parameters Spearman's rank correlation was employed and the result showed highly significant positive rank correlation between cultivar mean performance Pi (r = 0.978) and mean seed yield. Shukula stability variance (σ^2) was significant positive rank correlated (r=1) with (ωi) indicating, the two stability parameters were similar for ranking purposes. Most of the univerate stability (ωi, σ2, S^2di, bi, ASV) parameters identified G8, G6 and G12 were stable and high yielder. Moreover, the experiment has to be repeated in multi locations to provide more reliable results and make recommendations for wide or specific adaptable genotypes in Ethiopia.

Keywords: Association, Environment, Faba Bean, Parameter, Rank, Stability

1. Introduction

The manipulation of genetic variability is the most significant implement in plant breeding and this has to be contingent by phenotypic expression [4]. The results of the phenotypic variation depend largely on the location or genotypes. This variation is further complex by the fact that not all genotypes respond in similar ways to change in the environment and no two environments are the same. Therefore, Genotype by Environment interaction (GEI) denotes different ranking or there is no clear dominance of a single genotype performance through environments in a multiple-environment trial (MET) [6, 19]. Genotypes grown in different environments would frequently come across substantial variations in yield performance, especially when the growing environments are different among them, and the test genotypes differentially respond to changes in the growing environments [1]. Assessing genotypes under diverse environmental conditions to recommend new varieties for release as cultivars is fundamental and it has a direct role in the adoption of a variety, productivity and total production of the crop [7]. Crop breeders have been striving to develop genotypes with superior grain yield, quality and other desirable characteristics over a wide range of environmental conditions.

In plant breeding program yield stability is an important feature to measure consistency in relative performance of genotypes across a wide range of environments. The relative performances of genotypes for quantitative traits i.e. yield and other characters were influence from one environment to another [8]. The procedure of selection and recommendation of varieties for a target set of

environments became difficult when it is a "crossover" type of G x E interaction that makes the breeder job more complicated due to the differential genotypic responses that result in rank changes of genotypes across environments. The role of understanding the level GEI and yield stability in crops serves as a decision tool at the final stage of variety development process, to generate important information on pattern of adaptation in breeding lines, new varieties for release and to determine the recommendation domains for released varieties [18]. Developing varieties being generally adaptable across diverse environments or clustering environments into homogenous groups is the solution to mitigate this problem [12].

The performance of genotypes over variable locations can be estimated using various stability models. The level of association between the adaptableness and stability estimates of different models is revealing of whether one or more

estimates should be obtained for consistent forecasts of cultivar behavior, and also helps the breeder to choose the best familiar and most informative stability parameter (s) to fit his concept of stability [16].

2. Materials and Methods

2.1. Descriptions of Experimental Area

The experiment was conducted at seven environments from June to November, 2018 in the main cropping season under rain fed condition. These locations represent the varying agro ecologies of the major faba bean growing areas of Ethiopia. The description of the test locations in terms of geographical position, altitude and climatic conditions and soil properties is given in below.

Table 1. *Description of experimental sites.*

	Geographical position	Altitude	Average	Temperature	agro-	Soil
Locations	Latitude Longitude	m.a.s.l	Rainfall	Min. Max.	Ecology	Type
Asassa	07°06′12″N 39°11′32E	2300	620	5.8 23.6	THMH	Clay
Kulumsa	08°01′00″N 39°09′32E	2200	820	10.5 22.8	TSMMH	Clay
Bekoji	07°31′22″N 39°14′46E	2780	1010	7.9 16.6	CHMH	Clay
Holeta	09°04′12″N 38°29′45E	2400	1044	6.05 22.4	TMMH	Nitosol
Kofele	07°04′27″N 38°46′45E	2660	1211	7.1 18.0	CHMH	Nitosol
Debark	130 7' N 37053'E	2900	1044	8.6 19.8	CHMH	Nitosol
Adet	110 16' N 372 29'E	2240	1119.1	11.8 25.8	THMH	Nitosol

THMH: Tepid Humid Mid-Highland; TSMMH: Tepid Sub Moist Mid-Highland; CHMH: Cool Humid Mid-Highland; TMMH: Tepid Moist Mid-Highland.

2.2. Experimental Materials and Design of Experiment

A total of twelve faba bean genotypes that comprise ten advanced breeding lines and two recently released varieties (standard checks) were used for field experiment.

Table 2. *List of experimental Materials.*

List of Genotypes (breeding lines) used for the Experiment											
G1	Gora (Sc.)	G3	EH010008-5-1	G5	EH010058-1	G7	EH09012-1	G9	EH09021-1	G11	EH09046-3
G2	EH010002-1-1	G4	EH01005-1-1	G6	EH010058-2	G8	EH09017-5	G10	EH09028-3	G12	Tumsa (Sc.)

Where, G1…G12, are Genotypes.

The research was carried out using a randomized complete block design (RCBD) with four replications. For each trial unit a plot size of 4 m length by 1.6 m width (6.4 m^2) was used with inter row spacing of 40 cm and the spacing between plants was 10 cm. The space between plots and replications were 0.6 m and 1.5 m respectively. All the agronomic practices were applied uniformly to the experimental units according to the recommendations. Fertilizer was applied to each plot at the rate of 121 kg NPS ha^{-1} at the time of sowing.

2.3. Data Collected and Stability Analysis Using Various Stability Parameters

According to descriptors developed for Faba bean, the data were recorded in plot and single plant basis [10]. All yield and yield related traits data were recorded on the two middle rows of each experimental unit (net plot size 3.2 m^2). The plot-based

data was collected from the entire rows. For individual plant based data was recorded from a total of five randomly taken plants from each plot and averaged for data analysis. All tests were judged statistically significant at $P = 0.05$.

The stability model suggested by Eberhart and Russell [5] was employed to analyze the data over seven environments. According to this model, environment and GEI component were further divided into environment (linear), G x E (linear) and pooled deviations from regression. Mean performance of genotype, regression coefficient (bi) and deviation from regression (S^2di)) were employed based on the following equation; $Y_{ij} = \mu_i + \beta_i I_j + \delta_{ij}$ Where; Y_{ij} = Mean of ith genotype in jth environment. μi = the grand mean, βi = the regression coefficient of the ith genotype on environmental index and Ij = the environmental index obtained by the difference between the mean of each environment and the grand mean, $I_j = X_j - \mu$.

δ_{ij} = the regression deviation of the ith cultivar in the jth environment. The two stability parameters, regression coefficient (bi) and variance of the regression deviations (S^2di) were estimated as: $bi = \frac{(\sum y_{ij} l_j)}{\sum I^2 j}$ Where, $\sum y_{ij} l_j$ = the sum of products of the ith observation in the jth environment and the environmental index, and $\sum I^2_j$ = the sum of squares of environmental index. Therefore, the performance of each variety could be predicted by using the estimates of the parameters, $\hat{Y}_{ij} = x_i + b_i I_i$ where x_i is the estimate of μ. The second stability parameter is the mean square deviation from linear regression and could be estimated first by squaring the deviation $\delta_{ij} = (Y_{ij} - \acute{y}_{ij})$ to provide an estimate of another stability parameter (S^2di) that could be calculated as:$S^2_{di} = \frac{1}{E-2} [\sum_{j=1}^{e} (\bar{y}_{ij} - \bar{y}_{i..} - \bar{y}_{.j.} + \bar{y}_{...})^2 - (b_i - 1)^2 \sum_{j=1}^{e} (y_{.j.} - y_{...})^2]$. Where b_i is the linear regression coefficient, $\bar{y}_{ij}$ is the mean performance of genotype i in the jth environment $\bar{y}_{i..}$ and $\bar{y}_{.j.}$ are the genotype and environment means, respectively, $\bar{y}_{...}$ is the overall mean. The deviation sums of squares are the sums of variance due to deviation from regression divided by (E -2), and subtracting pooled error mean square, where E stands for the number of environment at which each variety was [5].

The second stability parameter is the mean square deviation from linear regression and could be estimated first by squaring the deviation $\delta_{ij} = (Y_{ij.} - \acute{y}_{ij})$ to provide an estimate of another stability parameter (S^2di). The regression coefficients (bi) tested for the significance of difference from unity using t-test whereas; the significance of the S^2di from zero was tested using the F-test by comparing the deviation from regression with pooled error estimate.

Stability Variances (Sh-σ^2i) was computed to predict variance across environments after the main effects of environmental means have been removed [17]. Since the genotype main effect is constant, the stability variance is thus based on the residual (GEij+eij) matrix in a two-way classification. The stability statistics is termed "stability variance" variance" (σ^2i) and is estimated as follows [17]:

$$\delta^2_i = \frac{1}{(G-1)(G-2)(E-1)} [G(G-1) \sum_j (Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2 - \sum_i \sum_j (Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})^2]$$

Where Y_{ij} is the mean yield of the ith genotype in the jth environments, $\overline{Y}_{.j}$ is the mean of all genotypes in j^{th} environment, $\overline{Y}_{i.}$ is the mean of all environments in i^{th} genotype and $\overline{Y}_{..}$ is the mean of all genotypes in all environments.

Eco valence (W^2_i) suggested by Wricke (1962) was computed for the relative contribution of genotype "i" to the overall genotype by environment interaction and G x E interaction mean square as the criteria for stability was estimated to understand stability of each genotype for seed yield. The smaller the value of the (W^2_i) is the more stable. The ecovalence (Wi) or stability of the ith genotype is its interaction with the environments, squared and summed across environments, and expressed as; $\omega i = \sum_{j=1}^{q} (Y_{ij} - \overline{Y}_{i.} - \overline{Y}_{.j} + \overline{Y}_{..})$ Where, (Y_{ij} is the mean performance of genotype i in the jth environment. $\overline{Y}_{i.}$ is the marginal mean of the ith genotype. $\overline{Y}_{.j}$ is the marginal mean of the jth environment. $\overline{Y}_{..}$ is the overall mean.

AMMI Stability Value (ASV): The AMMI model does not make provision for a quantitative stability measure, such measure is essential in order to quantify and rank genotypes according to their stability. This stability value was calculated in the excel spread sheet using the formula developed by Purchase [14] ASV measures the distance from the genotype coordinate point to the origin in a two-dimensional scatter diagram of IPCA2 against IPCA1 scores. Genotypes with the lowest ASV values are identified by their shortest projection from the biplot origin and considered the most stable.

$$ASV \sqrt{\left[\left(\frac{SSIPCA1}{SSIPCA2} \text{ IPCA1 score}\right)^2 + (\text{IPCA2 score})^2\right]}$$ Where, ASV = AMMI's stability value, SSIPCA1 = sum square of interaction principal component axis one, SSIPCA2 = sum square of interaction principal component axis two.

3. Results and Discussion

3.1. Eberhart and Russel's Stability

In the present study the regression coefficient (bi) values ranged from 0.85 (G5) to 1.075 (G3). The genotypes (G1, G5, G6, G9, G10 and G12) were found significant when tested for bi=0. In contrast, genotypes such as G2, G3, G4 and G8 were found significant for bi=1. G11 and G6 showed bi value is equal to 1 or close to one. In general, stable genotype was defined as one, which showed high mean yield, regression coefficient bi is around unity and deviation from regression S^2di components close to zero. According to this stability model, genotypes which had the smallest S^2di values were G7, G8, and G5 can be regarded as more stable genotypes. Among these, genotype G8 can be considered as best genotypes, judging from its mean yield (3125.3kg/ha) and deviations from regression (-15301.1). In contrast, G11, G10 and G1 can be grouped as unstable genotypes (Table 3). The significant S^2di component indicates that the behavior of genotypes is highly unpredictable and they are not suitable where the environment is changing (Table 3).

This study is in covenant with [13] reported significant differences among faba bean genotypes along with G X E interaction at three locations for three consecutive years. Stability analysis further showed that, non-significant differences among regression coefficients (bi) of various varieties studied for grain yield. In contrast the deviation from regression (S^2di) was significant for eight of the genotypes showing their instability over environmental changes. When bi value is close to 1, it indicates that the genotype is stable and behaves similar to the average across all environments. A genotype with bi value is equal to one and S^2di = 0 interpreted as stable with desirable mean yield. However, usually, S^2di is considered as stability parameter rather than bi, which are more about responsiveness of genotypes [5, 2].

Table 3. Mean grain yield, various stability analysis and the ranks of 12 faba bean genotypes across seven environments.

GEN.	YLD	R	Wi	R	o^2	R	bi	R	S^2di	R	Pi	R
G1	2986.4	8	394966.3	9	60584.1	9	0.99	1	35925.7	10	125827	5
G2	2960.2	9	149304.9	3	11451.8	3	1.05	8	-18966.5	6	109536	4
G3	3081.3	4	306957.3	7	42982.3	7	1.08	10	6854	5	171680	9
G4	3052.7	6	264156.1	6	34422	6	1.05	8	4213.6	4	157074	8
G5	3030.3	7	443873.1	10	70365.5	10	0.86	11	3832.1	3	151769	6
G6	3081.4	3	91660.5	1	-77.1	1	0.97	4	-26265.2	9	155563	7
G7	2643.8	12	217111.4	5	25013.1	5	1.03	3	-1501.2	1	15553	1
G8	3125.3	2	181604.3	4	17911.7	4	1.07	9	-15301.1	2	197532	11
G9	2866.3	11	349635	8	51517.8	8	0.97	5	24704.2	7	88481	2
G10	2895.4	10	517233.1	11	85037.5	11	0.96	6	57654.4	11	99607	3
G11	3078.2	5	722113.6	12	126013.6	12	1.02	2	100796.6	12	195584	10
G12	3171.8	1	113371.1	2	4265	2	0.95	7	-24778.4	8	205220	12

Where R= rank, bi= regression coefficient, $S^2{}_{di}$ = deviation from regression, W_i= Wricke's Ecovalence Analysis, δ^2= Shukla's Stability Variance, Pi = Cultivar performance superiority measure, GEN = genotypes YLD = grain yield.

Genotypes characterized by regression coefficient (bi) close to one have average stability over all environments accordingly, G1 (bi = 0.99) and G11 (bi= 1.02) respectively and indicated as wide adaptable genotypes. In cintrast G2, G3, G4, and G8 have a regression coefficient bi value significantly greater than 1 (1.05, 1.06, 1.05 and 1.07), respectively. This showed that genotypes are very sensitive when the environment is changed (small changes in environment large variation in yield). These genotypes produced below average stability over location that means specifically adapted to high-yielding environments but poorly adapted in low-yielding environments. On the other hand genotypes with low value of regression coefficient (bi <1) for instance G5 (bi= 0.857) exhibited opposite type of adaptation very little change despite large change in environments (above average stability). This genotype produced above average yield in low-yielding environments but being insensitive to environmental change it yields relatively small grain yield in high-yielding environments.

Wrickes stability variance

This stability measure is considered as a dynamic concept and popularly known as "Eco-valence" (Wi). This parameter is estimated by the decomposition of the sum of squares of the G x E interaction in to its components. According to the eco-valence (Wi) the stability of the ith genotype is its interaction with environments squared and summed across environments. Genotypes with low Ecovalence have smaller interaction or fluctuation across environments and therefore, are stable. Accordingly, G6 and G12 are the stable genotypes according to the Wricke's Eco valence measures of stability (Table 3). Moreover, G12 is the one with high yield and more stable genotype across the tested environments. The most interactive and unstable genotypes were G11 followed by genotypes G10 and G5 with mean grain yield ranked 5th 10th and 7th respectively. In contrast, the most stable or low interactive genotypes were G6, G12, G2 and G8 with yield response ranked 3rd, 1st, 9th and 2nd respectively (Table 3).

Shukla's Stability Variance

When the stability variance ($\delta^2{}_i$) and environmental variance ($\delta^2{}_0$) have equal ($\delta^2 i=0$) the genotype is/are stable. Thus, relatively large value of ($\delta^2{}_i$) will indicate greater

genotypic instability. According to Shukula stability parameter the most stable genotypes were G6, G12 and G2. This implies genotypes showed lower differential responses to the changes in the growing environment and contributed minimally to the sum of squares of the interaction effect regarding of their high mean yield. On the other hand the most unstable genotypes were G11, G10 and G5 (Table 3). The result obtained based on Shkula and Wrick's stability measure were identical and identify similar stable genotypes across the environment.

3.2. Cultivar Superiority Measure (Pi)

The smaller the values of Pi the smaller the distance of the genotype from the maximum yield; that indicate the better the genotype. Pi values were measured on overall location mean; it represents superiority in the sense of general adaptability or wide adaptation [3]. Therefore, ideal genotype is the one, which have lowest Pi value and the small contribution for genotype by environment interactions. According to this stability model G7, G9 and G10 were considered as stable regardless mean grain yield. However, G12, G8 and G11 were considered unstable though highest in grain yield (Table 3.). The application of this stability parameter was reported in various researchers [14, 11] as cultivar superiority measure to select the stable faba bean genotypes.

3.3. AMMI Stability Value (ASV)

AMMI Stability Value (ASV), IPCA1 and IPCA2 scores for each genotype were also computed and presented in Table 4. ASV is the distance from the coordinate point to the origin in a two-dimensional scatter diagram of IPCA1 scores against IPCA2 scores. The larger the IPCA scores, either positive or negative the more specifically adapted genotype to a certain environments, whereas, the smaller the IPCA scores, the more stable the genotype in all environments. Therefore, based on ASV the genotype G6, G2, G12 (Tumsa) and G8 had the lowest AVS score thus, which were widely adapted across environments. However, the genotypes such as the standard check G1 (Gora), G3,

G5 and G11, which had the highest ASVs, were unstable genotypes over the testing environments (Table 4). Therefore, based on ASV the genotype G6, G2, G12 (Tumsa) and G8 had the lowest AVS score thus, which were widely adapted across environments. However, the genotypes such as the standard check G1 (Gora), G3, G5 and G11, which had the highest ASVs, were unstable genotypes over the testing environments (Table 4). The closer the IPCA scores near zero, the more stable or adapted genotype in overall test environments.

Table 4. Mean grain yield (GY) (kg ha^{-1}), AMMI stability value (ASV) and genotypic (IPCA 1 and IPCA 2) score for tested genotypes.

Genotypes	GY	Rank	IPCAg [1]	IPCAg [2]	ASV	Rank
G1	2986	7	17.0	1.5	24.3	11
G2	2960	8	1.9	-4.8	5.5	3
G3	3081	3	-8.3	14.1	18.4	9
G4	3053	5	-0.4	-11.3	11.3	6
G5	3030	6	12.2	7.2	18.8	10
G6	3081	3	-2.0	1.2	3.1	1
G7	2644	12	4.8	7.4	10.1	5
G8	3125	2	-2.6	3.3	4.5	2
G9	2866	10	-0.9	-16.0	16.1	8
G10	2895	9	-4.0	-12.8	14	7
G11	3078	4	-23.2	4.8	33.5	12
G12	3172	1	5.5	5.4	9.6	4

Where, IPCAg 1 and IPCAg 2 = interaction principal component axis one and two for each genotype.

3.4. Comparison of Stability Parameters and Spearman's Rank Correlation

Spearman's rank correlation was performed between seven stability parameters and the overall mean grain yield (Table 5). The results described that some stability parameters were significant ($P \leq 0.01$) and positively correlated with the mean grain yield and other stability parameters.

Table 5. The Spearman's rank correlation coefficients for six stability measures.

	Yield	Wi	σ^2	Bi	S^{2}di	Pi	ASV
Yield	1						
Wi	-0.077^{ns}	1					
σ^2	-0.077^{ns}	1**	1				
bi	-0.010^{ns}	-0.222^{ns}	-0.222^{ns}	1			
S^{2}di	-0.131^{ns}	0.953**	0.953**	-0.05^{ns}	1		
Pi	0.978**	0.043^{ns}	0.043^{ns}	0.017^{ns}	-0.010^{ns}	1	
ASV	0.026^{ns}	0.885**	0.885**	0.158^{ns}	0.854**	0.135^{ns}	1

Wricke's ecovalence, bi = regression coefficient and S^{2}di = deviation from regression, ASV = AMMI stability value *, ** significant at $P \leq 0.05$ and $P \leq 0.01$ respectively ns = non-significant.

Lin and Binn's procedure shows highly positive rank correlation Pi (r = 0.978**) with mean grain yield. This indicates that selection for yield would change yield stability leading to the development of genotypes that are specially adapted to environments with optimal growing conditions. This finding is similar with earlier reports which indicated the presence of strong positive correlation between grain yield and Pi [17]. Similarly, Pi is non-significant and positively rank correlated with other stability statistics except S^{2}di.

ASV shows positive and highly significant rank correlations with Wricke (r =0.885**), Shukula (r = 0.885**) and deviation from regression (r = 0.854**). In contrast the non-significant positive rank correlations was observed between mean yield, regression coefficient and cultivar performance (r = 0.026^{ns}, 0.158^{ns} and 0.135^{ns} respectively) and ASV. Positive and highly significant rank correlations were also observed between Shukula, Wrickes, and deviation from regression. All stability statistics were showed non-significant and negative rank correlation with mean yield except ASV and Pi.

The Wrickes procedure of stability parameter shows the highest significant positive correlation with Shukula (r = 1**) indicated that the two procedures are similar for ranking purposes. Significant positive correlation between different stability parameters revealed that these parameters would provide similar result in stability ranking of genotypes [14, 17]. The non-significant and negative significant correlation among yield and stability parameters described that stability parameters provide information that cannot be collected based on the average yield only [5].

4. Conclusions

This study demonstrates the importance of different stability parameters to assess yield stability and identifying specific applications of each stability parameters. Therefore, to predict the constant performance of the selected genotype most common stability parameters were employed and accordingly (ωi, σ2, S^{2}di, bi, ASV) showed G6, G12 and G8 were stable across seven environments. Spearman's rank

correlation showed that ASV and ωi were highly significant positive rank correlation and the wrickes (ωi) and Shukula (σ^2) were showed similar for ranking, this indicate the two parameters provide the same result for cultivar performance prediction. Cultivar superiority measure (Pi) and ASV were significant rank correlation with mean yield hence, these parameters will provide best prediction or recommendation for the stability performance of a crop.

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