

Research Article

AMMI and GGE Biplot for Stability Analysis of Grain Yield of Faba Bean (*Vicia faba* L.) Genotypes in the Highland to Midland Parts of Southern Oromia, Ethiopia

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Abstract

Growing in diverse agro-ecological conditions and the performance of quantitative traits often varies due to significant Genotype × Environment Interaction (GEI) therefore, the integration of yield and stability is one of the common objective of crop breeding. This investigation was carried out to study genotype × environment interaction and to identify promising genotypes for yield and stability performances. A total of 14 faba bean genotypes including the standard and local checks were evaluated at eight environments during 2022/23 and 2023/24 of main cropping season. The genotypes were arranged in Randomized Complete Block Design and replicated three times. The analysis of variance revealed that environments (E), genotypes (G) and Genotype × Environment Interactions (GEI) accounted about 12.12%, 12.54% and 38.74% of the total variation, respectively. GGE biplot graphically displayed interrelationships between test locations as well as genotypes and facilitated visual comparisons through two-dimensional biplot between the first two principal components (PCA1 and PCA2) which explained 70.98% variation for grain yield. The GGE biplot identified suitability of all the four test locations to be used for multi-location trials on the basis of discrimination ability and representativeness. Both AMMI and GGE biplot analyses result identified that genotype G11(G-25114) was confirmed as widely adapted genotype with likewise recorded higher grain yield of 4.303 tons/ha. The genotype was superior to the standard checks with grain yield advantage of 11% to 36%, and it was recommended as candidate variety for further evaluation and possible release.

Introduction

Faba bean (*Vicia faba* L.) popularly known as the poor's meat plays an important role in the world agriculture; owing to its high protein content, ability to fix atmospheric nitrogen, and capacity to grow and yield well even on marginal lands and at high altitudes [15].

Genetic-Environment Interactions (GEIs) are great interest when evaluating the stability of breeding plants under different environmental conditions. The reliability of genotype performance across different environmental conditions can be an important consideration in plant breeding. Breeders are primarily concerned with high yielding and stable cultivars as much possible as since cultivar development is a time-consuming endeavor. A successfully developed new cultivar should have a stable performance and broad adaptation over a wide range of environments in addition to high yielding potential. Evaluating stability of performance and range of adaptation has become increasingly important for breeding programs. Hence, if cultivars are being selected for a large group of environments, stability and mean yield across all environments are important than yield for specific environments [23]. Knowledge of the presence and magnitude of Genotype x Environment Interactions (GEI) is very important to plant breeders in making decisions regarding the development and

release of new cultivars [9]. Genotype x environment interactions have been defined as the failure of genotypes to achieve the same relative performance in different environments [7]. Moldovan *et al.* (2000) indicated that genotype-environment interactions are of major importance; because they provide information about the effects of different environments on cultivar performance and play a key role for the assessment of performance stability of the breeding materials germplasm. Plant breeders perform Multi-Environment Trials (MET) to evaluate new improved genotypes across test environments (several locations), before a specific genotype is released for production to supply growers. Crop improvement programs usually tests the performance of genotypes across a wide range of environments to partition the effect of genotype (G), environment (E) and their interaction (G x E) and to ensure that the released varieties have a high yield and stable performance across several environments or to the specific environments. Therefore the objective of the present study were to estimate genotypes by environment interactions and to determine the stable and high yielder faba bean genotypes fitting for optimum environments of Guji and West Guji zones as well as similar agro-ecologies in Ethiopia.

Materials and Methods

Plant Materials and Field Management

Field experiments were conducted during the 2022/23 and 2023/24 main cropping seasons for consecutive two years from July to January at eight potential faba bean producing areas of Guji zones of Southern Oromia. A total of 14 faba bean genotypes including two released varieties and one local cultivar were evaluated at four locations for two years constituting eight environments. Randomized Complete Block Design (RCBD) with three replications was used across all locations. Each variety were sown in 4 rows; 4m length with 40cm inter-row spacing and 10cm between plants. Fertilizer rates of 121 NPS Kg ha⁻¹ was applied at planting time. All pertinent management practices were carried out at all sites following standard recommendation. Harvesting was done by hand. The central two rows were used as net plot for data collection including yield.

Statistical Analysis

The homogeneity of error variance was tested using the F-max test method of Hartley (1950) prior to pooled analysis over locations. Different statistical software packages were used to analyze the data. The analysis of variance for each location and combined analysis of variance over locations were computed using the SAS program (SAS institute, 2011) versions 9.3. AMMI biplots were analyzed using GEA-R version 2.0 [28]. GenStat 18th edition (2012) was used to draw GGE biplots.

AMMI Analysis

Grain yield data was analyzed using AMMI model so as to partitions the interaction sum of squares into IPC axes. The AMMI model is:

$$Y_{ij} = \mu + G_i + E_j + \sum_{k=1}^N \lambda_k \alpha_{ik} \gamma_{jk} + \theta_{ij} + \epsilon_{ij}$$

where, Y_{ij} = the yield of the i^{th} genotype in the j^{th} environment, μ = the grand mean, G_i and E_j = the genotype and environment deviations from the grand mean respectively, λ_k = the eigen value for IPCA analysis axis k , α_{ik} and γ_{jk} = the genotype and environment principal component scores for axis k , the summation handles N number of principal components retained in the model, θ_{ij} = the AMMI residual and ϵ_{ij} = the error [23]. The degrees of freedom (DF) for the IPCA axes were calculated according to Zobel *et al.* (1988) with the following formula.

DF = G + E - 1 - 2n where, G = the number of genotypes E = the number of environments n = the n^{th} axis of IPCA.

In order to show a clear insight of the interaction and the general pattern of adaptation of varieties, a biplot of varieties and environments (Kempton, 1984) were done. In the biplots the first IPCA was used as the ordinate (Y-axis) and the main effects (mean of the genotype and environment) represent abscissa (X-axis). Similarly, the IPCA1 as abscissa and IPCA2 as ordinate was used to further explore stability.

AMMI Stability Value

AMMI stability value was calculated in the excel spread sheet using the formula developed by Purchase *et al.* (1997).

$$ASV = \sqrt{\frac{SSIPCA1}{SSIPCA2} (\text{IPCA1 Score})^2 + (\text{IPCA2 Score})^2}$$

where, $\frac{SSIPCA1}{SSIPCA2}$ is the weight given to the IPCA value by dividing the IPCA1 sum of squares by the IPCA2 sum of square.

Genotype Selection Index

Genotype selection index was also calculated by the formula suggested by Farshadfar *et al.* (2008). Here it is calculated by taking the rank of mean grain yield of genotypes (RY_i) across environments and rank of AMMI Stability Value ($RASV_i$) a selection index GSI was calculated for each genotype which incorporate both mean grain yield and stability index in a single criterion (GSI) as:

$$GSI_i = RASV_i + RY_i$$

where, RASV is the rank value of genotypes for AMMI stability value and RY is the rank value of genotypes for grain yield. A genotype with the least GSI is considered as the most stable [12].

GGE Biplot Analysis

The most recent method, GGE biplot model, provides breeders a more complete and visual evaluation of all aspects of the data by creating a biplot that simultaneously represents mean performance and stability, as well as identifying mega-environments [33] (Ding *et al.*, 2007).

To analysis stability and identify superior genotype across environment, GGE bi-plot analysis were conducted. GGE biplot best identifies Gx E interaction pattern of data and clearly shows which variety performs best in which environment. The GGE biplot model of t principal components is given as follows:

$$\bar{Y}_{ij} - \mu_i - \beta_j = \sum_{k=1}^t \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij}$$

where; \bar{Y}_{ij} = the performance of genotype i in environment j , μ = the grand mean, G_i and E_j = the main effect of environment j , k = the number of principal components (PC); λ_k = singular value of the k^{th} PC; and α_{ik} and γ_{jk} = the scores of i^{th} genotype and j^{th} environment, respectively for PC k ; ϵ_{ij} = the residual associated with genotype i in the environment j . Usually only the first two PCs are used especially if they account for the major portion of the G x E interaction.

Result and Discussion

Analysis of Variance and Mean Performance

The analysis of variance over environments revealed the relative magnitude of genotypes (G), environments (E), Genotype x environment interactions (G x E) interaction which clearly exhibited effects are significant for all of the traits under study (Table 1). The mean comparison among genotypes, the highest grain yield was recorded for G11(4.302 tons/ha) followed by G3(4.029 tons/ha) while the lowest yield was obtained from the standard check, Tosha (2.985 tons/ha).

Evaluation of Genotypes to Diseases

In terms of disease reaction, the severity scores of genotype (G11) was ranged from (3 to 4), which showed being characterized as moderately resistant to chocolate spot, ascochyta blight and faba bean rust diseases. Similar results were reported by [21,22,28], improved varieties were moderately resistant to moderately susceptible for most faba bean fungal diseases.

Table 1: Combined ANOVA for grain yield of 14 genotypes tested across 8 environments over two years.

Source of variation	Degree of freedom	Sum of Square	Mean Square	P-value
Total	335	331.126		
Locations (L)	3	11.176	3.725***	<.0002
Genotypes (G)	13	41.539	3.195***	<.0001
Years(Y)	1	8.233	8.233***	.0001
G x L	39	39.342	1.009**	0.0027
G x Y	13	32.089	2.468***	<.0001
L x Y	3	20.745	6.915***	<.0001
G x L x Y	39	56.857	1.458***	<.0001
Error	224	121.154	0.541	
CV(%)	20.4			

Mean Performances of Agronomic Traits

The genotypes revealed highly significant difference ($p < 0.001$) for days to flowering, days to maturity, plant height, number of pods, number of seeds and thousand seed weight across the tested environments except number of primary branches per plant, which showed insignificant response.

AMMI Analysis of Variance

AMMI ANOVA is an additive model that effectively describes the main effects and determines if genotype \times environment interaction is a significant source of variation [26]. As per AMMI analysis, environments (E), genotypes (G) and genotype \times environment interactions accounted about 12.12%, 12.54% and 38.74% of the total variation, respectively and genotype \times environment interactions is more than the genotypic and environment. However, the significant G \times E interaction effect was decomposed into the first IPCA explained 45.99% and the second IPCA additionally explained 24.99%, the first two IPCA totally 70.98% of the G \times E interaction variation. The genotype \times environment interactions refers to differential ranking of genotypes across environments and only genotype (G) and genotype \times environment interactions are relevant to cultivar evaluation particularly, when genotype \times environment interaction is determined as repeatable [14]. The genotype \times environment interactions may complicate the process of selecting superior genotypes, recommendation of a genotype for a target environment and reduces the selection efficiency in different breeding programs [11,13]. The large G \times E effects depicted genotypic differences in the performance, different wining genotypes at different locations as well as possibility of different mega environments in testing locations [19,24]. However, multiyear data is required for the confirmation of the observed pattern of mega environments [32].

AMMI Stability Value (ASV)

In ASV method, a genotype with high pooled mean, small IPCA1 score and least ASV score is the most stable. Accordingly, the genotype G11(G-25114) was considered as the most stable across all environments (Table). In contrast, G2 and Tosha found to have large ASV these genotypes were generally unstable.

Genotype Selection Index (GSI)

As stability per se is not a desirable selection criterion, because the most stable genotypes would not necessarily give the best yield performance [18], hence, simultaneous consideration of grain yield and ASV in single non-parametric index needed. Therefore, the rank of ASV and mean grain yield (RYi) are incorporated in single selection index namely Genotype Selection Index (GSI). The least

GSI is considered as the most stable with high grain yield. Thus GSI indicates G11, G5 and Matti have the most stability with high grain yield. Generally, based on ASV and GSI value genotype G11 was found to be the most stable.

Stability Analysis Based on GGE Biplot

'Which-Won-Where' and Mega-Environment Identification

The most attractive feature of GGE biplot is 'Which-won-where' analysis, in which crossover genotype \times environment interactions, mega-environment differentiation, specific adaptation of genotypes etc. are graphically addressed [25]. GGE biplot was the best way to visualize the interaction patterns between genotypes and environments to effectively interpret a biplot [33]. In this study, the 'which won where' feature of the biplot identified the winning genotypes. The application of the biplot for partitioning through GGE biplot analysis showed that PC1 and PC2 accounted for 35.73.% and 23.70% of GGE sum of squares, respectively (Figure 1). This biplot presents a polygon view of 14 faba bean genotypes tested at eight environments. The genotypes located at the vertex of the polygon performed either best-performance or poorest performance in the Mega-Environments (MGE). Thus, genotypes G11 and G3 were the vertex (winning genotypes) in the sector where environments located in the MGE sector. The biplot analysis presented three mega-environments. The first mega-environment contains Dama 2023 and Ana sora environments. Environments Abayi kulture 2024, Bore-songo 2024 and Dama 2024 were grouped in the second mega-environment. Finally the third mega-environment includes Bore-songo and Abayi kulture 2023.

Evaluation of Genotypes Relative to Ideal Genotype

In genotype focusing scaled comparison of GGE biplot, a genotype located nearest to the central concentric circles is both high

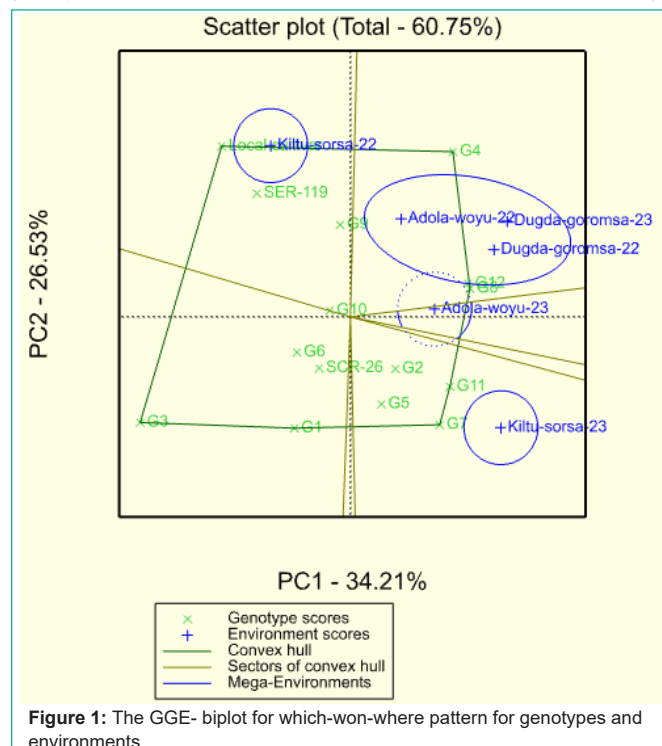


Figure 1: The GGE- biplot for which-won-where pattern for genotypes and environments.

Table 2: Mean grain yield (tons/ha) and diseases severity of Faba bean genotypes evaluated across locations for two years.

Code	Genotypes	Test locations								Overall Mean	Yield adv. (%)	Diseases severity (1-9 scale)		
		2022/23				2023/24						Ch.spot	A.Blight	Rust
		Bore-songo	Abayi-kulture	Dama	Ana-sorra	Bore-songo	Abayi-Kulture	Dama	Ana-sora					
G1	26869	3.753a-c	5.483	3.609	3.236 a-c	2.891	3.521a-c	4.417	3.875	3.848a-c		5	5	3
G2	25421	3.007bc	4.149	3.484	2.510bc	3.054	2.646de	4.389	3.391	3.329b-d		5	4	3
G3	28107	3.385a-c	3.507	3.786	3.757ab	5.714	4.259a	4.981	2.844	4.029ab		4	4	2
G4	28774	3.090bc	4.017	2.948	3.125a-c	4.312	3.444b-d	3.051	2.922	3.364b-d		5	6	4
G5	26412	2.649c	4.274	5.495	3.615ab	3.568	3.493b-d	3.384	3.901	3.797a-c		4	4	4
G6	26862	3.205a-c	3.535	3.328	2.507bc	3.120	3.586a-c	4.681	3.578	3.442a-c		3	4	2
G7	26415	4.566a	4.285	3.958	3.479a-c	2.688	3.394b-d	2.250	3.099	3.465b-d		4	3	3
G8	26884	3.167a-c	5.045	3.839	3.625ab	4.448	4.257a	2.917	3.271	3.821a-c		3	4	2
G9	25149	4.156ab	4.073	3.661	3.361a-c	3.427	2.535de	2.505	3.005	3.340b-d		5	5	4
G10	202281	3.420a-c	3.698	4.495	3.576ab	3.359	3.674ab	2.829	3.766	3.602a-d		4	6	3
G11	25114	3.931a-c	4.160	5.055	4.108a	5.115	3.891ab	3.651	4.510	4.303a	11	3	4	2
	Matti	4.292ab	4.688	4.290	3.472a-c	4.073	3.627ab	3.057	3.635	3.892ab		4	4	3
	Tosha	4.010a-c	4.576	4.344	2.014c	2.089	2.426e	1.009	3.411	2.985d		5	5	3
	L.Cultivar	3.642a-c	3.997	3.276	2.528bc	4.349	2.917cd	1.634	2.875	3.152cd		5	6	4
	Env.Means	3.591	4.249	3.969	3.208	3.729	3.405	3.241	3.435	3.598		4	5	3
	LSD(5%)	1.229	1.739	2.374	1.278	3.126	1.347	3.415	1.719	1.179				
	CV(%)	20.4	24.4	25.6	23.7	29.9	23.6	32.8	29.8	20.4				

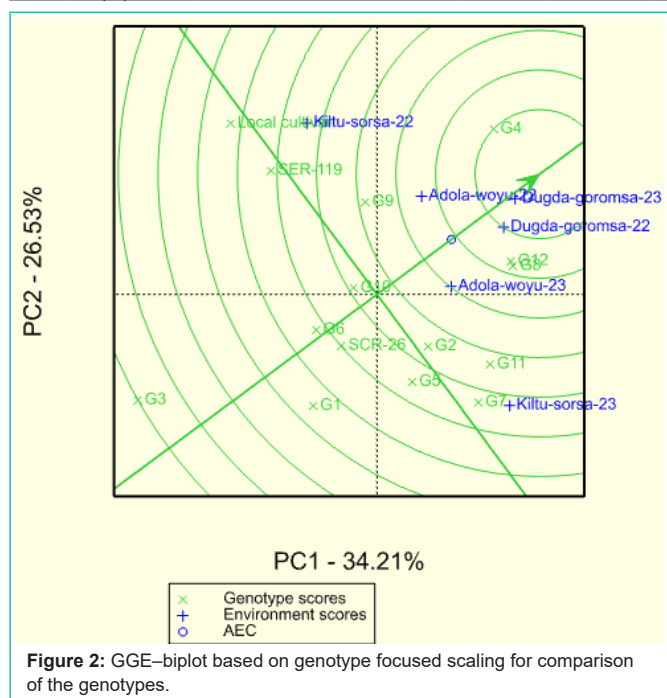


Figure 2: GGE–biplot based on genotype focused scaling for comparison of the genotypes.

yielding and most stable. The GGE bi-plot analysis for grain yield of faba bean genotypes based on genotype-focused scaling comparison is presented in Figure 2.

An ideal genotype is defined as the genotype having the greatest PC1 score (high mean performance) and with zero G x E interaction, as represented by an arrow pointing to it. Figure 2 depicts that genotype G11(G-25114), which fell in the first concentric circle, was the ideal genotype in terms of higher yielding ability and stable. Genotype G5(G-26412) was located closer to the ideal genotype, it becomes more desirable.

Mean Performance and Stability of Genotypes

In biplot, mean performance of genotype is measured by the Average Environment Coordination (AEC) abscissa which represents average environment and points towards higher mean values [12]. Whereas, stability is represented by AEC ordinate which points towards greater genotype × environment interactions effect i.e. poor stability in either direction of genotypes i.e. greater the absolute length of the projection in either direction shows greater variability or less stability [34]. Accordingly, G11 (G-25114) was the best performing genotypes in terms of grain yield of 4.303 tons/ha followed by G5(G-

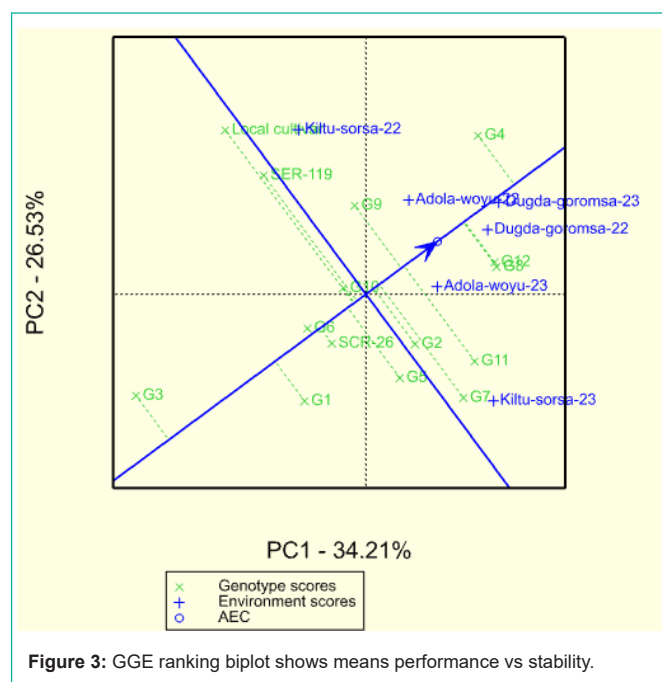


Figure 3: GGE ranking biplot shows means performance vs stability.

Table 3: Combined means of agronomic traits of FB genotypes evaluated during 2022/23 to 2023/24.

Genotype	DF	DM	PH(cm)	NPB	NPO	NS	TSW(g)
26869	55.04b-d	154.4bc	139.0ab	0.8240	19.33ab	2.979a-c	561.0d
25421	54.25cd	151.5f	130.6b	0.6796	20.70ab	2.833c	460.2f
28107	55.17a-d	155.3b	137.9ab	0.8565	20.13ab	3.025ab	555.9d
28774	53.96	151.2f	133.5b	0.7485	18.41ab	2.965a-c	538.0de
26412	54.67b-d	151.2f	137.0ab	0.6771	22.32a	2.871bc	410.0g
26862	54.96b-d	151.8f	140.8ab	0.8844	20.68ab	2.882bc	527.1de
26415	55.04b-d	152.1ef	137.6ab	0.8035	20.81ab	2.951a-c	522.7de
26884	56.00ab	153.2c-e	138.5ab	0.9446	19.35ab	3.091a	608.0c
25149	55.79ab	153.1de	137.8ab	0.7902	17.80b	2.910a-c	507.3e
202281	55.62ab	153.4cd	138.4ab	0.8002	20.68ab	2.867bc	509.6e
25114	55.25a-d	154.8b	145.3a	0.8040	19.46ab	2.984a-c	653.4b
Matti	56.42a	156.7a	137.7ab	0.9365	17.14b	2.919a-c	706.3a
Tosha	55.29a-c	153.1de	137.4ab	0.6458	19.45ab	2.854bc	525.5de
Local Cultivar	56.37a	157.7a	137.3ab	0.7619	20.84ab	2.811c	541.5de
Means	55.27	153.53	137.77	0.80	19.79	2.92	544.74
LSD(5%)	2.250	2.261	18.679	0.404	6.806	0.314	73.290
CV(%)	3.6	1.3	11.9	34.6	30.3	9.4	11.8

Keys: DF = Days to flowering, DM = Days to maturity, PH = Plant height, NPB = Number of primary branches, NPO = Number of pods, NS = Number of seeds and TSW = Thousand seed weight

Table 4: AMMI ANOVA for grain yield of 14 faba bean genotypes evaluated at 8 environments over two years.

Source of variation	Df	SS	MS	% Explained		P-value
				Total variation	G x E	
Total	335	331.13				
Blocks (Envts)	16	11.22	0.702			0.1827
Environments (E)	7	40.15	5.735**	12.12		<0.001
Genotypes (G)	13	41.54	3.195**	12.54		<0.001
G x E Interaction	91	128.28	1.410**	38.74		<0.001
IPCA1	19	58.99	3.105**		45.99	<0.001
IPCA2	17	32.06	1.886**		24.99	<0.001
IPCA3	15	18.12	1.208**		14.13	0.0052
Residuals	40	19.12	0.478		14.90	0.6371
Error	208	109.93	0.529			

Table 5: The grain yield, AMMI Stability Value (ASV), Genotype Selection Index (GSI) and Principal Component Axis (IPCA).

Genotypes	Yield (tons ha ⁻¹)	Rank	IPCA1 Score	IPCA2 Score	ASV	Rank	GSI	Rank	Overall Rank
G1	3.848	4	0.05395	-0.90997	0.91537	9	13	5	5
G2	3.329	12	0.41902	-0.75162	1.07674	10	22	11	11
G3	4.029	2	1.20724	0.51107	2.27934	13	15	6	6
G4	3.364	11	0.37405	0.37349	0.78306	7	18	8	8
G5	3.797	6	-0.0463	-0.17463	0.19431	1	7	2	2
G6	3.442	9	0.64752	-0.70137	1.38254	12	21	10	10
G7	3.465	8	-0.6500	-0.03080	1.19641	11	19	9	9
G8	3.821	5	0.07739	0.39232	0.41736	3	8	3	3
G9	3.340	10	-0.3312	0.15017	0.62771	6	16	7	7
G10	3.602	7	-0.1537	0.03888	0.28539	2	9	4	4
G11	4.302	1	0.12975	0.39220	0.45915	5	6	1	1
Matti	3.892	3	-0.2307	0.14951	0.45011	4	7	2	2
Tosha	2.985	14	-1.2408	-0.18892	2.29082	14	28	12	12
Local cultivar	3.152	13	-0.2562	0.74968	0.88556	8	21	10	10

26412 tons/ha) with 3.797kg/ha and they were more stable whereas, Tosha was poor yielder.

Conclusion and Recommendation

Development of new variety is a time consuming, resource and labour-intensive task and in the existing procedure of varietal release, mean performance of a genotype over years and locations, and its superiority over the checks is only considered and Multi-Environment Trial (MET) data is not utilized to its full potential. In the present investigation, effort was made to identify high yielding and stable genotypes by analyzing multi environment data to take the stability

of the genotypes into consideration and graphical visualization has expediently aided in identification of stable and superior faba bean genotypes across testing environments. Accordingly, analysis of AMMI Stability Value, Genotype Selection Index and GGE-biplot are primarily confirmed G11 as the most stable genotype. As a result, the promising genotype G11(G-25114) was identified for its stable high yielding and tolerant to major diseases recommended to be for further variety verification evaluation and final release.

Author Statements

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