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RESEARCH ARTICLE

Grain yield stability analysis for food-type common bean (*Phaseolus vulgaris* L.) genotypes in Southern Oromia of Ethiopia

T. A. Beyene, D. S. Legesse, C. G. Molu, R. N. Dinagde

Bore Agricultural Research Center, Pulse Crops Research, P.O. Box21, Bore, Ethiopia

Corresponding author's email: tekafeta2009@gmail.com

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Abstract

Twelve common bean genotypes including the standard and local checks were evaluated at eight locations during 2019-20 and 2020-21, to identify high yielding and stable or specifically performed genotypes for target environments and to identify mega-environments to inform future testing strategies. The genotypes were arranged in Randomized Complete Block Design and replicated three times. A combined analysis of variance detected significant ($p<0.01$) variation among genotypes, environment and genotype-by-environment interactions for grain yield and other agronomic traits. GGE biplot analysis identified genotypes *viz.*, NSEA515-11-1 and NSEA515-11-34 as widely adapted genotypes with greater grain yield of 2.90 tons/ha and 2.823 tons/ha. So that genotype NSEA515-11-1 the most stable and high yielder across all locations and recommended to be verified for possible release. Overall, Gobicha was the most suitable environment for discriminating among genotypes and for being a representative test environment. Three mega-environments (MGE) were identified; where midland and lowland sites fell in the same mega-environments.

Key words: GGE biplot, AMMI, *Phaseolus vulgaris*, environment, yield

Introduction

Common bean (*Phaseolus vulgaris* L.) is one of the principal grain legumes of eastern and southern Africa, occupying more than 4 million hectare annually. It provides food for more than 100 million people (Wortmann *et al.*, 1998). In Ethiopia, common bean has been known as an export crop, contributing to foreign exchange earnings. In the year 2008 Ethiopia earned 36.2 million United States dollars from common bean export (Ethiopia Custom Authority, 2009, unpublished).Genetic-environment interactions (GEIs) are great interest when evaluating the stability of breeding plants under different environmental conditions.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 (Piepho, 1996). 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 (Chakroun *et al.,* 1990). The phenomenon of genotype × environment interaction refers to the differential performance of genotypes in different environments that affect the efficiency of selection in a breeding program. G × E interaction arises due to the differences in the sensitivities of genotypes to the different environmental conditions.

The phenomenon of genotype × environment interaction refers to the differential performance of genotypes in different environments that affect the efficiency of selection in a breeding program. G × E interaction arises due to the differences in the sensitivities of genotypes to the different environmental conditions. Genotype x environment interactions have been defined as the failure of genotypes to achieve the same relative performance in different environments (Baker, 1988). 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 and to ensure that the released varieties have a high yield and stable performance across several environments or to the specific environments. Thus, the objectives were to identify high yielding and stable or specifically performed genotypes for target environment (s) and to identify mega-environments to inform future testing strategies.

Materials and methods

Field experiments were conducted during the 2019/20 and 2020/21 main cropping seasons for consecutive two years at eight potential common bean producing locations of Guji zones of Southern Oromia. A total of 12 common bean genotypes including two standard checks and local cultivar were evaluated. Randomized Complete Block Design (RCBD) with three replications was used across all locations. Each variety were sown in 6 rows, 3m length with 40 cm inter-row spacing and 10cm between plants and fertilizer rates of 38:19:7 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 four 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 (CIMMYT, 2015). GenStat 18thedition (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:

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

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 eigenvalue for IPCA analysis axis k,$\alpha_{ik}$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 (Zobel *et al.*, 1988).

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).

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

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

Genotype selection index

Genotype selection index was also calculated by the formula suggested by Farshadfar *et al.*, (2008). Here it is calculated by taking therank 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 andstability index in a single criteria (GSI_i) as:

$$\text{GSI}_i = \text{RASV}_i + \text{RY}_i$$

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 (Farshadfar, 2008).

GGEBiplot 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 (Yan and Kang, 2003; Ding *et al.*, 2007).

To analysis stability and identify superior genotype across environment, GGE bi-plot analysis wereconducted. GGE biplot best identifies GxE 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:

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

where; $\bar{Y}ij$= the performance of genotype i in environment j,

μ= the grand mean, β_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 GxE interaction.

Results and discussion

Analysis of variance and mean performances

The result of pooled analysis of variance revealed statistically highly significant differences ($p<0.001$) for days to flowering, plant height, number of pods and hundred seed weight while non-significant was recorded for remaining agronomic traits. The highest pooled mean performance of grain yield was recorded for the genotypes NSEA515-11-1 (2.900 tons ha^{-1}) followed by NSEA515-11-34 (2.823 tons ha^{-1}) whereas the lowest mean was obtained from the local cultivar. In addition both genotypes showed highest number of seeds andthe manifestation of diseases on plant parts was generally low indicating the possibility of resistant to common bean diseases such as common bean blight, angular leaf spot, anthracnose and common bean rust (Table 4).

Table 1: Combined analysis of variance for grain yield of bean genotypes

Source of variation	**Df**	**SS**	**MS**	**SS(%)**	**P-value**
Total	287	121.20	0.422		
Environment	7	52.72	7.531**	43.50	<0.001
Genotype	11	8.25	0.750**	6.81	<0.001
Reps (Env.)	16	6.21	0.388**	5.12	0.0079
GxE Interaction	77	22.42	0.291**	18.50	0.008
Residual	190	35.47	0.187		

Additive main effect and Multiplicative interaction (AMMI)

AMMI analysis of variance for grain yield revealed highly significant (p<0.001) differences for genotype, environments and genotype by environment interactions (Table 2). The ANOVA using the AMMI model accounted about 6.81% of the total sum square (SS) was attributable to the genotypes (G), 43.50% to theenvironments (E), and importantly 18.50% to Gx E interaction effects (Table 2).A large total variation due to E indicated the overwhelming influence of environments on grain yield performance of common bean genotypes. Similar results were reported for various crop such as soybean (Asrat *et al*., 2009), field pea (Tamene *et al*., 2013), cowpea (Nunes *et al*., 2014) and durum wheat (Shitaye, 2015; Temesgen *et al*., 2015; Tekalign *et al*.,2019; Tekalign *et al*., 2021). Likewise, Yan and Kang (2003) in which environment showed predominant effect on varietal performance. AMMI analysis also showed that IPCA1 and IPCA2 captured 40.79% and 29.62% of the genotype by environment interaction sum of squares and this two PCA's accurately predict the AMMI model. Yan and Rajcan (2002) reported that the best accurate model of AMMI can be predicted by using the first two PCA's.

AMMI stability value (ASV)

In ASV, the genotypes with least ASV score is the most stable where as those which have highest ASV are considered as unstable (Purchase, 1997). However, stability needs to be considered in combination with yield (Farshadfar, 2008). Thus, genotype (NSEA515-11-1) was considered as the moststable and high yielder across all environments (Table 5)

Table2: The AMMI analysis of variance for grain yield for common bean genotypes tested under eight environments

Source of variation	Df	SS	MS	Total variation explained(%)	GxE explained (%)	GxE cumulative (%)	P-value
Total	287	121.2	0.4				
Genotype	11	8.2	0.7**	6.81			<0.001
Environment	7	52.7	7.5**	43.50			<0.001
Reps (Env.)	16	6.2	0.3**	5.12			0.0079
GxEInteraction	77	22.4	0.2**	18.50			0.0048
IPCA1	17	9.1	0.5**		40.79		<0.001
IPCA2	15	6.64	0.4**		29.62	70.41	0.0026
Residual	46	6.6	0.1ns				0.7785
Pooled error	176	31.6	0.18				

Table 3: Mean grain yield for common bean genotypes under eight environments during the 2019 and 2020 main cropping seasons

Code	Genotypes	Test locations								Overall Mean
		2019				2020				
		Adola-woyu	Kiltu-sorsa	Gobicha	Wodera	Adola-woyu	Kiltu-sorsa	Gobicha	Wodera	
G1	NSEA515-11-34	2.67^{a}	2.55	3.10^{ab}	2.89^{ab}	3.03^{a}	23.89	3.54	2.42	2.82^{ab}
G2	NSEA515-11-1	2.78^{a}	2.87	3.39^{a}	$2.63^{a\text{-}d}$	$2.53^{a\text{-}c}$	2.38	4.21	2.15	2.90^{a}
G3	NSEA515-11-30	2.25^{ab}	2.15	2.63^{bc}	2.11^{de}	$2.51^{a\text{-}c}$	2.44	3.80	2.24	2.52^{cd}
G4	NSEA515-11-31	2.79^{a}	2.11	2.77^{bc}	3.15^{a}	3.00^{ab}	2.63	3.62	2.28	$2.77^{a\text{-}c}$
G5	NSEA515-11-42	2.84^{a}	2.17	2.73^{bc}	$2.20^{c\text{-}e}$	$2.51^{a\text{-}c}$	2.54	3.12	1.64	2.47^{d}
G6	NSEA515-11-46	1.91^{ab}	1.83	2.55^{bc}	$2.82^{a\text{-}c}$	$2.58^{a\text{-}c}$	1.89	3.38	2.00	2.37^{d}
G7	NSEA515-11-52	2.95^{a}	2.59	2.68^{bc}	2.03^{de}	$2.63^{a\text{-}c}$	3.16	3.34	1.76	$2.64^{a\text{-}d}$
G8	NSEA515-11-63	2.43^{ab}	3.05	2.54^{bc}	$2.29^{b\text{-}e}$	2.02^{c}	2.62	3.72	2.03	$2.59^{b\text{-}d}$
G9	NSEA515-11-65	2.27^{ab}	2.40	2.58^{bc}	$2.21^{b\text{-}e}$	1.97^{c}	2.66	3.68	2.03	2.48^{d}
G10	SER-119	2.11^{ab}	2.42	2.77^{bc}	$2.63^{a\text{-}d}$	2.29^{bc}	2.80	3.54	2.19	2.50^{cd}
G11	IBADO	2.13^{ab}	1.88	2.59^{bc}	$2.36^{b\text{-}e}$	$2.52^{a\text{-}c}$	1.96	3.68	1.91	2.38^{d}
G12	LOCAL CULTIVAR	1.38^{b}	1.92	2.48^{c}	1.89^{e}	2.26^{bc}	2.18	3.56	2.09	2.36^{d}
Means		2.38	2.34	2.74	2.43	2.49	2.47	3.60	2.06	2.56
LSD (5%)		0.73	0.81	0.58	0.68	0.65	1.12	0.64	0.66	0.70
CV (%)		18.2	20.4	12.6	16.5	15.4	26.7	10.5	18.8	16.9

Table 4: Combined mean performances of agronomic traits and reaction to diseases for genotypes under eight locations during 2019 and 2020 main cropping seasons

Genotypes	**Agronomic traits**							**Diseases severity score (1-9 scale)**			
	DF	**DM**	**PH (cm)**	**NB**	**NPO**	**NS**	**100SW (g)**	**CBB**	**ALS**	**Leaf Rust**	**Anthracnose**
NSEA515-11-34	42.8^{d}	91.7	70.8^{c}	1.2	14.2	5.6^{ab}	24.3^{cd}	3	3	1	2
NSEA515-11-1	44.2^{bc}	91.1	90.6^{b}	1.5	16.5	5.4^{b-d}	23.3^{cd}	3	3	1	2
NSEA515-11-30	43.5^{b-d}	91.3	77.5^{c}	1.3	13.4	5.3^{b-d}	25.4^{c}	4	3	1	2
NSEA515-11-31	43.2^{b-d}	92.3	74.3^{c}	1.2	12.3	5.6^{bc}	31.3^{b}	3	2	1	2
NSEA515-11-42	43.3^{b-d}	90.4	50.6^{d}	1.1	13.6	5.2^{cd}	25.4^{c}	3	3	1	2
NSEA515-11-46	42.8^{d}	89.9	54.0^{d}	1.0	12.8	5.3^{b-d}	25.3^{c}	4	3	1	2
NSEA515-11-52	43.0^{cd}	87.5	78.2^{c}	1.1	11.8	5.6^{ab}	29.3^{b}	3	4	2	3
NSEA515-11-63	43.9^{b-d}	91.2	71.2^{c}	1.3	15.9	5.3^{b-d}	23.8^{cd}	3	3	2	2
NSEA515-11-65	44.5^{b}	92.1	69.0^{c}	1.3	15.5	5.2^{d}	24.6^{cd}	3	4	2	2
SER-119	46.2^{a}	92.4	69.7^{c}	1.4	15.7	5.9^{a}	22.3^{d}	3	3	1	3
Ibado	43.2^{b-d}	89.0	70.0^{c}	1.2	10.9	3.8^{e}	44.6^{a}	4	2	1	2
Local Cultivar	45.9^{a}	94.2	122.1^{a}	1.2	15.4	5.4^{b-d}	21.5^{e}	4	4	2	2
MEANS	44.0	91.1	74.8	1.2	14.0	5.3	26.6	3	3	2	2
(5%) LSD	1.1	3.9	9.2	0.3	2.11	0.3	2.80	0.5	0.5	0.4	0.4
CV(%)	4.6	7.6	21.6	47	26.5	10.	18.5	30.2	29.4	31.1	36.7

AMMI Stability value (ASV)

In ASV, the genotypes with least ASV score is the most stable where as those which have highest ASV are considered as unstable (Purchase, 1997). However, stability needs to be considered in combination with yield (Farshadfar, 2008). Thus,genotype (NSEA515-11-1) was considered as the moststable and high yielder across all environments (Table 5)

Genotype selection index (GSI)

Stable genotypes would not inevitably provide the best yield performance and hence identifying genotypes with high grain yield coupled with consistent stability across growing environments has paramount importance. In this regard, genotype selection index was utilized to further identify stable genotypes with better yield performance. Accordingly, NSEA515-11-1 and NSEA515-11-34 were considered as the two most stable genotypes with high grain yield.

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
NSEA515-11-34	2.82	2	0.3006	-0.1794	0.45	4	6	2
NSEA515-11-1	2.87	1	-0.1203	0.1383	0.23	2	3	1
NSEA515-11-30	2.52	6	0.0071	0.1048	0.11	1	7	3
NSEA515-11-31	2.77	3	0.5095	-0.4257	0.82	10	13	4
NSEA515-11-42	2.47	8	-0.2135	-0.5875	0.66	7	15	6
NSEA515-11-46	2.37	11	0.6515	0.0425	0.90	11	22	8
NSEA515-11-52	2.64	4	-0.6117	-0.4989	0.98	12	16	7
NSEA515-11-63	2.59	5	-0.5377	0.3070	0.80	9	14	5
NSEA515-11-65	2.48	9	-0.3095	0.2245	0.48	6	15	6
SER-119	2.50	7	0.1282	0.6851	0.71	8	15	6
Ibado	2.38	10	0.3392	0.0046	0.47	5	15	6
Local Cultivar	2.36	12	-0.1434	0.1844	0.27	3	15	6

Environmental mean yield and IPCA scores of the testing environments were presented in Table 6. The mean grain yield at the individual environment ranged from 2.062 tons ha^{-1} at Wodera 2020 to 3.597 tons ha^{-1}at the highest yielding potential environment of Gobicha, 2020.

Table 6: Mean grain yield response and estimates of the first two IPCA scores of AMMI for the environments used for this study

Environment	Env.code	Env.Mean	IPCA1score	IPCA2score
Adola-woyu-2019	AW-19	2.376	-0.36535	-0.88597
Adola-woyu-2020	AW-20	2.488	0.48758	-0.43028
Gobicha-2019	GO-19	2.735	0.08032	0.05884
Gobicha-2020	GO-20	3.597	0.00680	0.46881
Kiltu-sorsa-2019	KS-19	2.344	-0.67432	0.40666
Kiltu-sorsa-2020	KS-20	2.471	-0.54431	-0.02763
Wodera-2019	WO-19	2.432	0.73703	0.05566
Wodera-2020	WO-20	2.062	0.27222	0.35392

Stability analysis based on GGE biplot

GGE biplot was the best way to visualize the interaction patterns between genotypes and environments to effectively interpret a biplot (Yan and Kang, 2003). In each bi-plot, different mega-environments (MGEs) were grouped into sectors. Environments within the same MGE were assumed to have a similar effect on genotype performance and were considered a homogeneous group. Similarly, genotypes within the same MGE were assumed to have a similar response to the environmentslocated in the MGE sector. In this study, the polygon view of a GGE biplot clearly displays the which-won-where pattern, and hence it arranged the genotypes in such a way that some of them were on the vertices while the rest were inside the polygon. Accordingly, the bi-plot showed that seven vertex genotypes (Figure 1).The vertex genotypes for each quadrant (sector) are the one that gave the highest yield for the environment that fall within that quadrant. The falling of all environments into a single sector indicates that a single genotype has the highest yield in all environments which means a genotype consistently performed best in a group of environments. In this study, the biplot identified winning genotype; NSEA515-11-1 for instance was corner/vertex genotype at Adola-woyu, Kiltu-sorsa and Gobicha (Figure 1). In genotype focusing scaled comparison of GGE biplot, a genotype located nearest to the central concentric circles is both high grain yielding and most stable. Figure 2 depicts that genotype NSEA515-11-1, which fell in the first concentric circle, was the ideal genotype in terms of higher yielding ability and stable. Genotype NSEA515-11-34 was located closer to the ideal genotype, it becomes more desirable

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

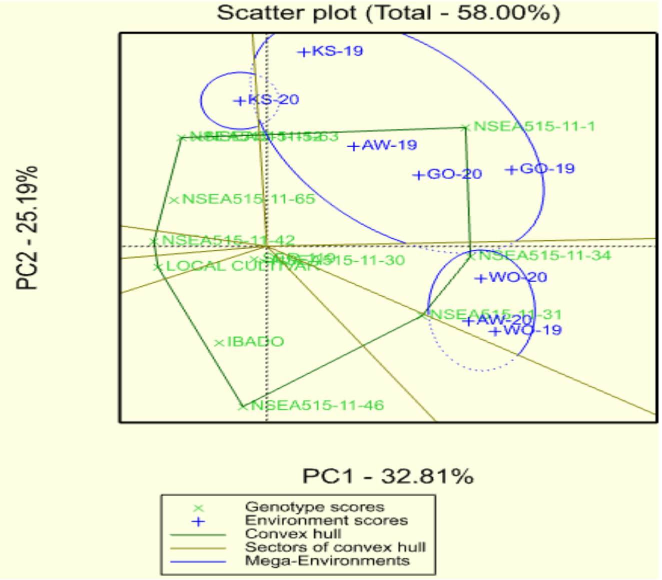
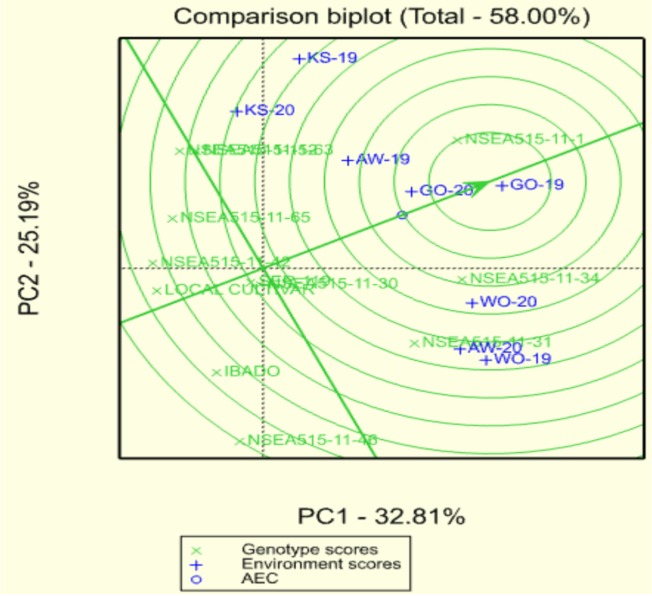


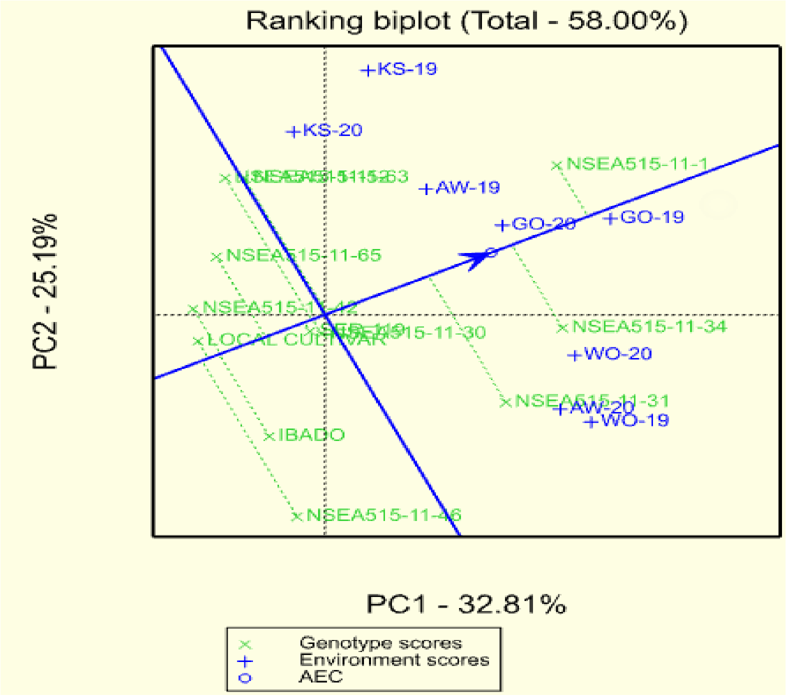
Fig.2: GGE–biplot based on genotype focused scaling for comparison of the genotypes



Mean performance and stability of genotypes

A genotype which has shorter absolute length of projection in either of the two directions of AEC ordinate (located closer to AEC abscissa), represents a smaller tendency of G x E interaction, whichmeans it is the moststable genotype across different environments. The mean performance and stability of these 12 genotypes in 8 locations shows NSEA515-11-1 was relatively high yielding and stable genotype.

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



Conclusion and recommendation

In multi-location trial, considering both the stability and mean grain yield is vital. The significant G x E interaction and the changes in the rank of genotypes across environments suggest a breeding strategy for specifically adapted genotypes in homogenously grouped environments, as well as for high yielding stable genotypes suggesting for wider adaptation.In view of that, genotype NSEA515-11-1 showed 16.00% grain yield advantage over the standard check, resistant to major bean diseases, stable and also possessed other desirable agronomic characteristics. Accordingly, genotype (NSEA515-11-1) was identified as the most stable high yielding across environments and recommended for eventual varietal release to the set of tested environments and similar agro-ecologies.

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