Current Journal of Applied Science and Technology

41(29): 8-15, 2022; Article no.CJAST.87907
ISSN: 2457-1024
(Past name: British Journal of Applied Science & Technology, Past ISSN: 2231-0843, NLM ID: 101664541)

AMMI Analysis for Stability and Genotype by Environment Interaction on Common Bean (*Phaseolus vulgaris* L.) Genotypes in Mbeya Region, Tanzania

George Muhamba Tryphone [a*] and Atugonza Luta Bilaro [b]

[a] Department of Crop Science and Horticulture, Sokoine University of Agriculture, P.O.Box 3005, Chuo Kikuu, Morogoro, Tanzania.
[b] Tanzania Agricultural Research Institute, IFAKARA Centre, Private Bag, Ifakara, Morogoro Tanzania.

Authors' contributions

This work was carried out in collaboration between the authors. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/CJAST/2022/v41i2931798

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/87907

Original Research Article

Received 10 May 2022
Accepted 17 July 2022
Published 13 August 2022

ABSTRACT

A significant Genotype by Environment Interaction (GEI) makes selection of stable genotypes difficult. This study was conducted to establish the effect of GEI on yield of Common bean genotypes and reduce complaints on the under performances. Eighteen (18) Common bean genotypes were assessed for variation in gene expression linked to yield and yield predictors on three different districts in Mbeya region (Mbarali, Mbozi and Mbeya districts). Regression, pooled ANOVA and AMMI biplot models were used to evaluate the data. Variety performance showed significant variations in yield between the districts. A similar scenario was observed in regard to yield predictors. Regression analysis showed that in Mbarali 50% was the significant yield predictor (P = 0.027) while pods/ plant was the trait mostly linked to yield in Mbozi. (GEI) analysis using the AMMI model revealed that best variety performance by location based on yield. Interaction principle component (IPC1) was highly significant (P = 0.0001) and contributed about 69.1% of GEI variation. The genotypes SER 83 and RCB 266 where highly adaptable in Mbarali site. The genotypes SER 45 and KG 521 showed specific interaction with the environment of Mbozi district. A total of five

**Corresponding author: E-mail: muhamba@sua.ac.tz;*

genotypes proved to be superior in Mbeya district. The most adapted stable variety with highest grand mean yield across all three mega environments was RCB233 (IPC1= 0.07, yield = 1073 t/ha). The environment in Mbarali was found to be most predictable for evaluation of Common bean genotypes.

Keywords: Variety stability; yield predictors; environmental variation; GEI; AMMI.

1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a major source of protein globally and one of the most economically important pulse [1]. Common bean in Africa is an income earner crop where fresh pod and dry seeds attracts a higher price, with more share produced in the sub-Saharan Africa [2]. However, biotic and abiotic constraints pose a problem to common bean production [3]. Bacteria, fungi and viruses cause diseases in Common beans such as common necrosis, angular leaf spot, anthracnose and many more [4]. The physiological stress resulting from infection impair plant reproduction consequently reducing crop yield [5]. Climate change has caused rejuvenation of pathogenesis through shifting towards environmental conditions that pathogens find favorable for infection [6]. It has further proved detrimental to crop production due to changes in rainfall patterns which makes seasons unpredictable [7]. Counter measures in dealing with yield constraints in Common beans include breeding of tolerant and resistant varieties (Dennis et al., 2003).

The process of gene introgression by breeding involves gene mapping and it requires observation of inheritance patterns of genes of traits linked to the gene of interest [8]. However, in different environments, due to uneven distribution of pathogens, soil types and climatic differences, gene expression of the same Common bean varieties may differ [9]. This makes selection and evaluation of varieties difficult. Parameters such as pathogen diversity, temperature variation, soil fertility, soil pH and precipitation impact enzymology processes in molecular reactions responsible for gene expression [10]. This sets a basis for studying GEI of varieties in different locations. The presence of the (GEI) indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment [11]. There is need for understanding the nature of (GEI), quantifying its magnitude and identifying stable and widely adaptable Common bean genotypes [12]. Therefore, this study was conducted to establish the effect of GEI on yield of Common bean varieties and reduce complaints on the under performances in Mbeya region.

2. MATERIALS AND METHODS

2.1 Location of the Study

The study experiment was conducted in Mbeya region in 3 districts namely Mbarali, Mbeya and Mbozi. The locations and soil type of these studied areas are summarized in Table 1. The locations coordinate for each location were collected using the Geographical Positioning System (GPS).

2.2 Experimental Design and Treatment

The experiment was laid out in the Complete Randomized Block Design (CRBD) with 18 treatments (SER125, MR13905-6,41-EX- VAM, BFS20, RCB233, CZ109-22, CZ104-61, KG25-21, SER82, SER83, KG104-72, SER16, KG4-30, SER45 SER124, BFS60, RCB266 and PASS) collected from TARI-Uyole. The treatments were replicated three (3) times and an experimental plots with 4 m by 2 m dimensions was used. Isolation distance of 2 m was left between the plots within single replicate and 2 m between replicates/blocks. As bordering, 2 m space was measured to each side of the experimental site.

Table 1. The geographical positioning of the studied location and their respective weather characteristics

Location	Longitude	Latitude	Altitude (m)	Soil type
Mbarali	E 0330 06’	S 080 56’	1795	Sandy loam
Mbeya	E 0330 38’	S 080 51’	1505	Clay
Mbozi	E 0330 13’	S 80 57’	1241	Clay loam

2.3 Sowing and Management

Common bean seeds singly were sown at a spacing of 0.5 m × 0.1 m and there were 8 rows per plot and 20 planting holes per row making total of 160 plants per plot. Weed management was conducted using hand-hoe to reduce competition of a crop.

2.4 Data Collection

The crop yield response predictor collected from each studied location included the seeds per pod, pods per plant, seed weight per pod, weight per 100 seeds, weight of seeds per plant, plant height, 50% flowering and 85 % maturity. Common bean genotypes were defined as the categorical data and the yield response parameters were defined and continuous predictors.

2.5 Statistical Analysis

The collected data were subjected to analysis of variance (ANOVA) at (P≤0.05). Treatment means were separated using Tukey's significant test at 5% level. For a simple ANOVA of a randomized complete block design, the model was:

$$Y_{ijk} = \mu + G_i + E_j + GE_{ij} + R_{ij} + \varepsilon_{ijk}$$

Where μ is the overall mean of the grain yield in the population, G_i is the effect of the ith genotype, E_j is the efficacy of the jth environment, GE_{ij} is the Interaction of the ith genotype with the jth environment, R_{ij} is the effect of the kth replication in the jth environment, and $\varepsilon\varepsilon_{ijk}$ is the random error.

Principal component analysis was carried out on the pooled ANOVA terms and G by E biplot was generated using the best principal component which was selected by Gollobs' test. Genotype by Environment interaction (GEI) and stability were estimated using the additive main effects multiplicative interaction model (AMMI). In the AMMI model, the data was first subjected to Bartlets test for homogeneity of variance. All data analysis was performed using R software under the package "agricolae" by Mendiburu, [13]. The base on the mathematical formula of AMMI was as follows:

$$Y_{ij}^{N} = \mu + G_i + E_j + \sum \beta_k \alpha_{ik} \delta_{jk} + \varepsilon_{ij}$$

Where Y_{ij}^{N} is the yield of the ith genotype in the jth environment, N is the number of principal components in the AMMI model, μ is the overall mean of genotypes, G_i and E_j are the genotype and environment deflections from the overall mean, β_k is the eigenvalue of the PCA axis k, α_{ik} and δ_{jk} are the genotype and environment principal components scores for axis k and ε_{ij} is the remaining value.

3. RESULTS

3.1 Yield and Yield Predictors

Regression analysis revealed that each district had different set of significant continuous yield predictors (Table 2). The categorical predictor (variety) was insignificant in Mbeya district alone. Performance of the genotypes differed significantly in each location except Mbeya district (Fig. 1). Model terms (yield predictors) fit the computed regression model significantly (Table 2).

Table 2. Regression analysis of yield predictors of Common bean genotypes across three districts of Mbeya region

	Mbalai		Mbeya		Mbozi	
	F-value	**P-value**	**F-value**	**P-value**	**F-value**	**P-value**
Regression	3.21	0.003**	2.99	0.0024**	3.72	0.001**
Seeds/Pod	1.43	0.24	1.3	0.265	0.56	0.462
Pods/Plant	0.67	0.421	0.12	0.73	6.28	0.019*
100 SW	1.27	0.272	0.28	0.604	0.45	0.51
Seed weight/Plant	0.94	0.343	1.67	0.207	0.88	0.358
Plant height	0.03	0.87	0.38	0.542	0	0.973
50% Flowering	5.57	0.027*	3.8	0.062	0.01	0.918
85% Maturity	3.16	0.088	1.58	0.22	2.34	0.763
Variety	2.02	0.05*	0.99	0.498	2.44	0.019*
R-Sq	77.60%		74.23%		78.19%	

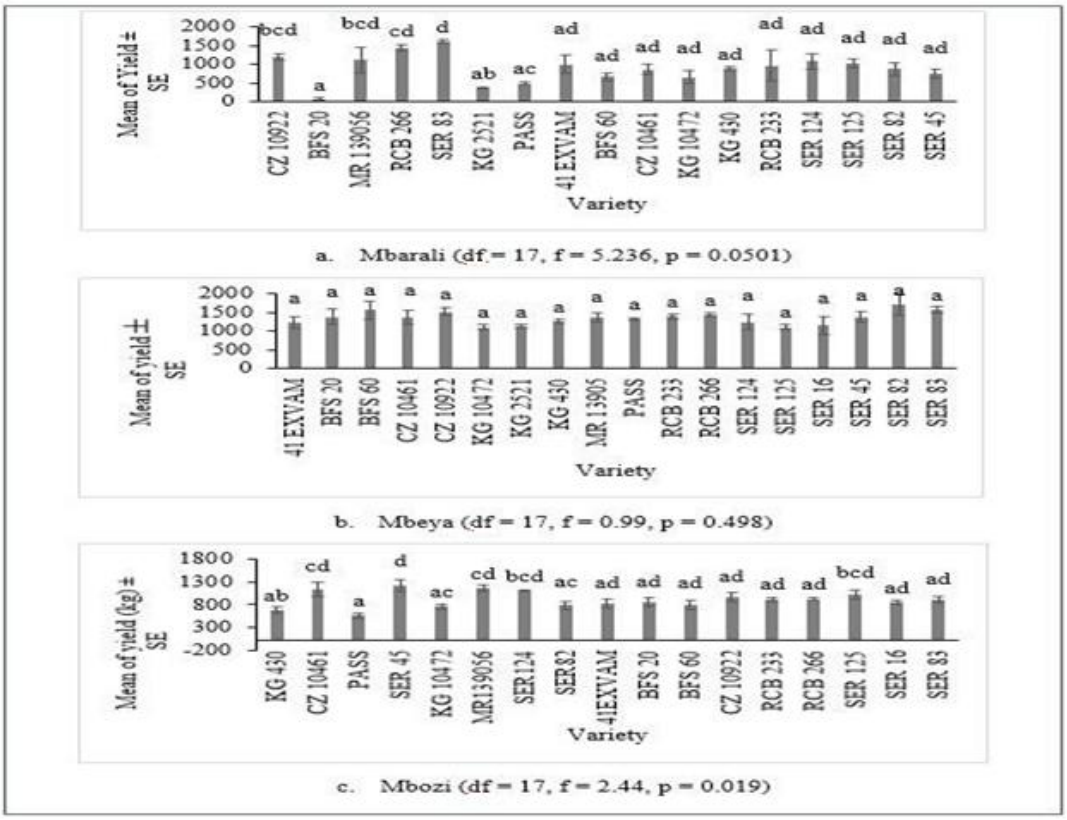

Fig. 1. Yield mean of Common bean genotype in the three Mbeya region districts

Note: Bars that do not share a letter as their data label represent means that are significantly different as per Tukey's HSD

3.2 Stability and GEI Analysis

3.2.1 AMMI and PCA analysis

The Bartlett's test for homogeneity of variance showed that group variances were equal and data qualified for principal component analysis (PCA) **(**K-squared = 23.326, df = 17, p-value = 0.1389). Based on the pooled ANOVA, the difference of yield between locations (environment) was highly significant (P = 2.2e-16). Yield also differed significantly between genotype (P = 2.86e-06). The pooled ANOVA revealed that the GEI was also significant for variation in yield (P <0.0001) as shown in Table 3. IPCIPC Three interaction principal components were generated from the PCA in terms of the pooled ANOVA. Based on Gollob's test, IPC1 covered most of the data variation (Table 3).

Table 3. Combined yield variance analysis for common bean genotypes of the three environments and Gollob's test for selection of terms

Source of variation	df	F value		P value	TSS (%)	GEI Explained (%)	Cumulative (%)
Environment	2	57.73	***	0.0000	43.2		
Genotypes	17	4.12	***	0.0000	26.2		
GEI	34	2.40	***	0.0003	30.6		
IPC1	18	3.28	***	0.0001		69.17	69.17
IPC2	16	1.64	Ns	0.0697		30.83	30.83
IPC3	14	0.00	Ns	1.0000		0	0
Residuals	108		Ns			0	100

*KEY: ns: non-significant; asterisks indicate significant differences. ***p<0.001. TSS-Total sum square*

The scatterplot of grain yield vs. IPC1 (Fig. 2) illustrates that the superior genotype had a higher agricultural yield (horizontal axis) and in terms of the first interaction item (IIPC1), which is shown on the vertical axis, had a minimum value and was near zero. “It is important to take into account both stable genotypes and excellent grain performance. The right-side genotypes outperformed the average in terms of grain yield, which is shown by the vertical line dividing the horizontal axis into two portions. On the other hand, the horizontal line that divided the vertical axis into parts is the zero line for IPC1. The stable genotypes are near to this line and have a minimum GEI” [Movahedi et al 2020]. The genotypes that are recommended in poor and weak locations have low grain yield performance (below average) with a positive value of IPC1. These included G5 (RCB 233) [IPC1 =0.07], G1 (SER 125) [IPC1=0.3] and G3 (41-EX-VAM) [0.032]. Genotypes with higher IPC1 scores showed strong GEI effects. The genotypes G4 (BFS 20) and G8 (KG 2521) were highly adapted to E3 (Mbozi).

On the other hand, genotypes G 11(SER 83) and G18 (RCB 266) were less adapted to E3 (Mbozi) but were adapted to E1 (Mbarali) and E2 (Mbeya). Also, the Interaction pattern of the 18 common bean genotypes Within the three (03) locations was cross validated by analysis of AMMI biplot of the two principal components (IPC1 and IPC2) as shown in Figure 3. Deviation of genotypes and environments from the origin indicated the degree of GEI. Based on the plot, the genotypes G9, G10, G11, G17, G4, G8, G15, G1 and G18 expressed highly interactive behavior while the environment E1 had lower interaction (Fig. 3). The genotypes G10 and G17 were plotted in pairs indicating that they had similar response patterns.

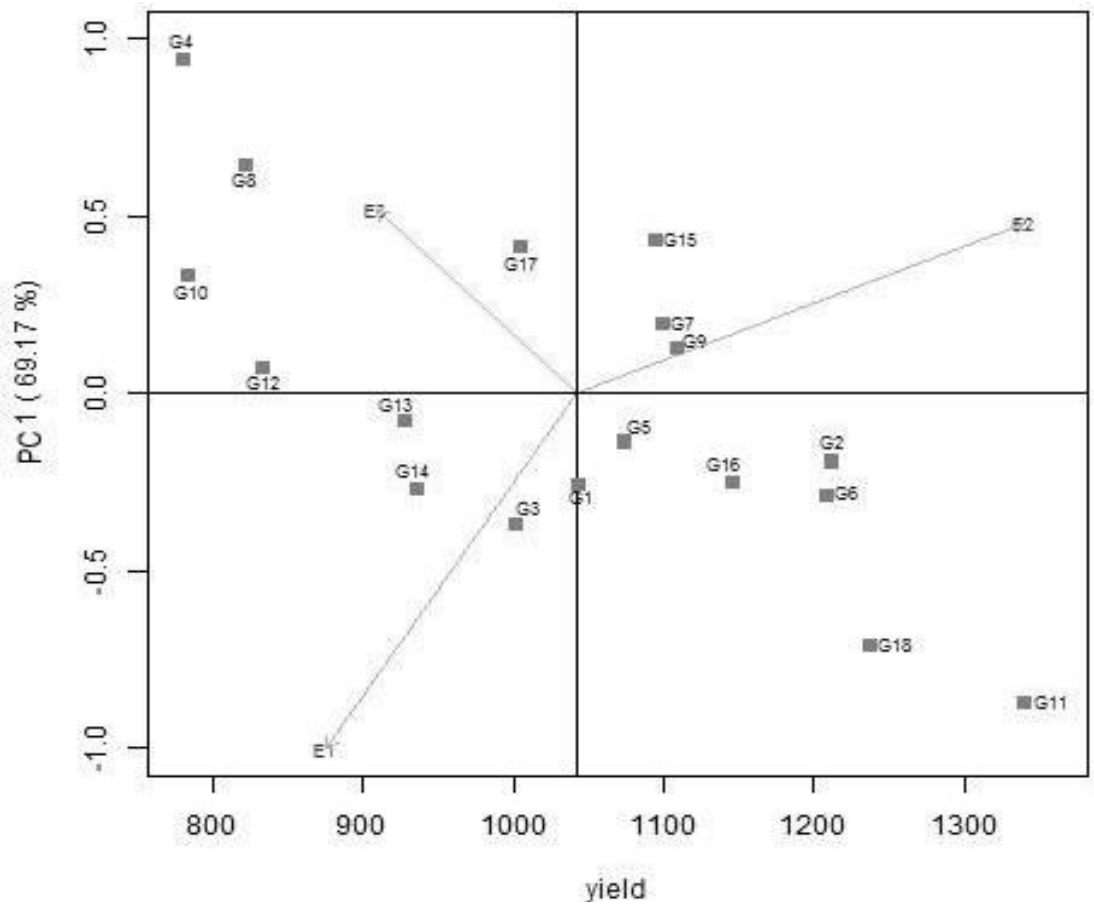

Fig. 2. Scatterplot of IPC1 vs. grain yield in AMMI analysis IPC

KEY: E-represents location and G-represents genotypes. E1 = Mbarali, E2 = Mbeya, E3 = Mbozi, G1 = SER125, G2 = MR139056, G3 = 41EX-VAM, G4 = BFS20, G5 = RCB233, G6 = CZ10922, G7 = CZ102461, G8 = KG2521, G9 = SER82, G10 =PASS, G11 = SER83, G12 = KG10472, G13 = SER16, G14 = KG430, G15 = SER45, G16 = SER124, G17 = BFS60, G18 = RCB266

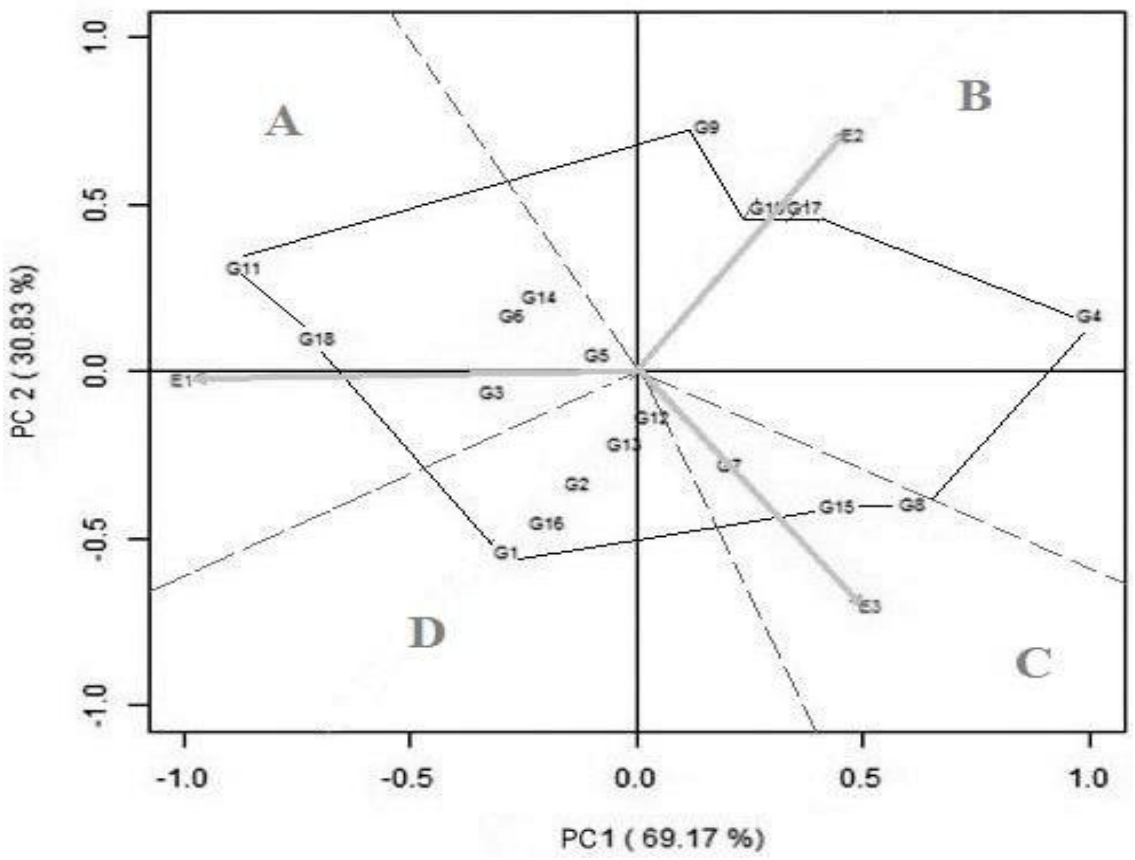

Fig. 3. Scatterplot of IPC1 vs. IPC2 in AMMI Analysis of grain yield

A polygon is formed when extreme genotypes are connected with straight lines. Perpendiculars to the sides of the polygon form sectors of genotype and environment. Genotypes at the vertex of the polygon are more adapted to the environment with which it shares a sector (Hernadez and Crossa, 2000). In figure 3, the perpendiculars of the sides of the polygon divide the biplot into four sectors where three of them harbor environments. Sector A contained the environment E1 with two genotypes at its vertexes (G11 and G18). Sector B contained environment E2. This sector had four vertexes which contained the genotypes G9, G16, G17 and G4. Environment 3 (E3) was plotted in sector C which had genotypes G15 and G8. Hence based on the AMMI biplot analysis, those are the superior genotypes for each environment (GEI). Also, environments E2 and E3 are closer in terms of characteristics that shape genotype performance compared to E1.

4. DISCUSSION

According to the results shown in Table 4, when genotypes are examined in multi-location yield experiments, a cross over GEI most often happens [14]. The cumulative percentage of the GEI that was justified by IIPC1 and IIPC2 was 100%. Also, the contributions of IPC1 and IPC2 were 69.17% and 30.83%, respectively. These results are similar to the observations reported by Baraki and Gebremariam [15]. From results as presented on scatterplot of grain vs. IPC1 (Fig. 3), the superior genotypes were G5 > G1 and G, and where located on the right side of the graph and close to zero in terms of the IPC1 axis. These results are similar to the observation reported by Movahedi et al. [16].

“AMMI is one of the best analyses for testing genotype stability. In this study, the analysis of 18 Common bean genotypes on three test locations in the grain yield trait gave similar F-test results to the AMMI analysis performed” by Movahedi et al. [17]. Yan et al., [18] pointed out that genotypes with IIPC scores near zero are more representative of an average environment. Therefore, those genotypes can be recommended for adaptation to specific environment. In this study, genotypes G4 (BFS 20) and G8 (KG 2521) were highly adapted

to E3 (Mbozi). On the other hand, genotypes G11 (SER 83) and G18 (RCB 266) were less adapted to E3 (Mbozi) but were adapted to E1 (Mbarali) and E2 (Mbeya). "Each of the AMMI stability parameters relates to a different concept of yield stability and can be useful to plant breeders attempting to select genotypes with high, stable and predictable yield across environments" [19]. Due to the low environmental impact and the proximity of the IPC value of Mbarali, Mbozi and Mbeya environments, Mbarali is being suggested for future primary breeding plans as the environment [20].

5. CONCLUSION

The significant differences in genotypes, environments, and their interactions indicated that genotype responses were highly variable, and these occurrences clearly stated the existence of GEI. The majority of the genotypes generally differed significantly from one another in terms of grain production, which may be a result of the genotypes' underlying genetic potential for variation, the conditions in which they were tested, or a combination of all three. With regard to the evironments,, Mbarali was a favorable environment for Common bean compared to Mbozi and Mbeya district. According to the AMMI 1 bi-plot genotypes G5, G1 and G3 having low contribution for the G x E interaction and are stable genotypes in most of the environments. Generally, based on the investigations of this study the grain yield of Common bean varies highly on locations which needs a due attention and further investigation.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Fetahu S, Aliu S, Rusinovci I, Behluli A, Kelmendi B. Genetic diversity for micronutrients contents in some common bean landraces (*Phaseolus vulgaris* L.). In: Marić S, Lončarić Z, editors. Proceedings of the 49th Croatian and 9th international symposium on agriculture. Dubrovnik, Croatia, 16-21 February 2015. Osijek, Croatia: Faculty of Agriculture, University of Josip Juraj Strossmayer in Osijek; 2014. DOI: 10.13140/RG.2.1.1126.8568.
2. Broughton WJ, Hernández G, Blair M, Beebe S, Gepts P, Vanderleyden J. Common beans (*Phaseolus vulgaris* L.) Model food legumes. Plant Soil. 2003;252(1):55-128. Doi: 10.1023/A:1024146710611.
3. Dita MA, Rispail N, Prats E, Rubiales D, Singh KB. Biotechnology approaches to overcome biotic and abiotic stress constraints in grain legumes. Euphytica. 2006;147:1-24. DOI: 10.1007/s10681-006-6156-9.
4. Terán H, Jara C, Mahuku G, Beebe S, Singh SP. Simultaneous selection for resistance to five bacterial, fungal, and viral diseases in three Andean 3 Middle American inter-gene pool common bean populations. Euphytica. 2013;189(2):283-92. DOI: 10.1007/s10681-012-0803-0.
5. Pandey P, Irulappan V, Bagavathiannan MV, Senthil-Kumar M. Impact of combined abiotic and biotic stresses on plant growth and avenues for crop improvement by exploiting physio-morphological traits. Front Plant Sci. 2017;8:537. DOI: 10.3389/fpls.2017.00537, PMID 28458674.
6. La Porta N, Capretti P, Thomsen IM, Kasanen R, Hietala AM, Von Weissenberg K. Forest pathogens with higher damage potential due to climate change in Europe. Can J Plant Pathol. 2008;30(2):177-95. DOI: 10.1080/07060661.2008.10540534.
7. Ali S, Liu Y, Ishaq M, Shah T, Abdullah, Ilyas A et al. Climate change and Its Impact on the Yield of Major Food Crops: evidence from Pakistan. Foods. 2017;6(6):39. DOI: 10.3390/foods6060039, PMID 28538704.
8. Pérez-de-Castro AM, Vilanova S, Cañizares J, Pascual L, Blanca JM, Díez MJ et al. Application of genomic tools in plant breeding. Curr Genomics. 2012;13(3):179-95. DOI: 10.2174/138920212800543084, PMID 23115520.
9. Pregitzer CC, Bailey JK, Schweitzer JA. Genetic by environment interactions affect plant–soil linkages. Ecol Evol. 2013;3(7):2322-33. DOI: 10.1002/ece3.618, PMID 23919173.
10. Santoyo G, Hernández-Pacheco C, Hernández-Salmerón J, Hernández-León R. The role of abiotic factors modulating the plant-microbe-soil interactions: toward sustainable agriculture. A review. Span J Agric Res. 2017;15(1):e03R01.

DOI: 10.5424/sjar/2017151-9990.
11. Falconer DS, Mackay TFC. 4th Ed. Harlow: Addison Wesley Longman. Introduction to Quantitative Genetics; 1996.
12. Gurmu F, Hussein S, Laing M. Genotype-by-environment interaction and stability of sweet potato genotypes for root dry matter, β-carotene and fresh root yield. Open Agric. 2017;2(1):473-85.
DOI: 10.1515/opag-2017-0052.
13. Mendiburu FD. Agricolae: statistical procedures for agricultural research. R package version 1.2-3; 2015.
Availablehttp://CRAN.Rproject.org/package=agricolae retrieved on 13rd July, 2022.
14. Ceccarelli S, Grando S, Booth RH. International breeding programmes and resource-poor farmers: crop improvement in difficult environments. Workshop on Participatory Plant Breeding. Netherlands: Wageningen. Rome: International plant genetics resources institute; 1996.
15. Baraki F, Gebremariam G. Genotype x environment interaction and stability of oil content of sesame (*Sesamum indicum* L.) genotypes in Northern Ethiopia. J Plant Breed Genet. 2018;6(2):57-65.
DOI: 10.33687/pbg.006.02.2452.
16. Movahedi H, Mostafavi K, Shams M, Golparvar AR. AMMI analysis of genotype×environment interaction on grain yield of sesame (*Sesamum indicum* L.) genotypes in Iran. Biotechnol Biotechnol Equip. 2020;34(1):1013-8.
DOI: 10.1080/13102818.2020.1816216.
17. Movahedi H, Mostafavi K, Shams M, Golparvar AR. AMMI analysis of genotype× environment interaction on grain yield of sesame (*Sesamum indicum* L.) genotypes in Iran. Biotechnol Biotechnol Equip. 2020;34(1):1013-8.
DOI: 10.1080/13102818.2020.1816216.
18. Yan W, Hunt LA, Sheng O, Szlavnics Z. Cultivar evaluation and mega-environment investigation based on the GGE biplot. Crop Sci. 2020;40(3):602-603.
DOI:10.2135/cropsci2000.403597x.
19. Mohammadi M, Sharifi P, Karimizadeh R. Stability of grain yield of durum wheat genotypes by AMMI model. Agric Forest/Poljopriv Sumars. 2015;61(3):181-93.
20. Hermandez MV, Crossa J. The AMMI analysis and graphing the biplot. CIMMYT. Mexico: INT [online]; 2000.
Available:http://www.cimmyt.org/biometrics/biplots.exe; verified 8 November 2007.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/87907