AMMI modeling of Stability and Genotype by Environment Interaction of Common Bean Varieties (*Phaseolus vulgaris* L.) in Mbeya region, Tanzania

ABSTRACT

A significant genotype by environment (GxE) interaction makes selection of stable genotypes difficult. A total of 18 bean varieties were assessed for variation in gene expression linked to yield and yield predictors in three different districts in Mbeya region. Each of these varieties were grown in 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%f was the significant yield predictor (P = 0.027) while pods/ plant was the trait mostly linked to yield in Mbozi. G by E interaction analysis using the AMMI model revealed best variety performance by location based on yield. PCA1 was highly significant (P = 0.0001) and contributed about 69.1% of GEI variation. The varieties SER 83 and RCB 266 where highly adaptable in Mbarali site. The varieties SER 45 and KG 521 showed specific interaction with the environment of Mbozi district. A total of five varieties proved to be superior in Mbeya district. The most adaptable stable variety with highest grand mean yield across all three mega environments was RCB233 (PC1= 0.07, yield = 1073t/ha). The environment in Mbarali was found to be most predictable for evaluation of common bean genotypes.

Keywords: Variety stability; yield predictors; geographical variation; GEI; AMMI

Introduction

Bean (*Phaseolus vulgaris* L.) is a major source of protein globally and one of the most economically important pulse (Fetahu *et al.*, 2014). Smallholder farmers in Africa account for most of the 3.5 metric tons produced in the sub-Saharan Africa (Broughton *et al.*, 2003). However, biotic and abiotic constraints pose a problem to common bean production (Dita *et al.*, 2006). Bacteria, fungi and viruses cause diseases in beans such as common necrosis, angular leaf spot, anthracnose and many more (Teran *et al.*, 2012). The physiological stress resulting from infection impair plant reproduction consequently reducing crop yield (Pandey *et al.*, 2017). Climate change has caused rejuvenation of pathogenesis through shifting towards environmental conditions that pathogens find favorable for infection (La Porta *et al.*, 2008). It has further proved detrimental to crop production due to changes in rainfall patterns which makes seasons unpredictable (Ali *et al.*, 2017). Counter measures in dealing with yield constraints in 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 (Perez – De - Castro *et al.*, 2012). However, in different environments, due to uneven distribution of pathogens, soil types and climatic differences, gene expression of the same bean varieties may differ (Pregitzer et al., 2013). 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 (Santoyo et al., 2017). This sets a basis for studying G by E interaction (GEI) of varieties in different locations. The presence of the G x E interaction indicates that the phenotypic expression of one genotype might be superior to another genotype in one environment but inferior in a different environment (Falconer and Mackay, 1996). There is need for understanding the nature of G X E interaction, quantifying its magnitude and identifying stable and widely adaptable common bean genotypes (Gurmu et al., 2017). The study was conducted to established the GEI of bean varieties on yield in Mbeya region. The findings will help reduce farmer complaints which may arise due to under performance of respective locations and provide insight on which superior genotypes to be adapted. In turn it will help improve yield of common beans in the region.

MATERIALS AND METHODS

Experimental Setup

The experiment was conducted in 3 districts namely Mbarali, Mbeya and Mbozi. A total of 18 genotypes namely; 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 which were collected at TARI – Uyole were assessed. The experimental design used was a randomized complete block design (RCBD) with variety as the treatment. The plot size was 4m x 2m where each row had 20 plants with a spacing of 50x20 cm.

Data collection and analysis

Yield data was collected for each region and regression of yield against predictors was performed. Variety was defined as the categorical predictor. Continuos predictors included 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. Mean separation after analysis of variance was carried out by Tukeys' Honest Significant Difference (HSD).

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. A pooled analysis of variance (ANOVA) was carried out with location, variety and the interaction of location and variety (GEI) as the terms. 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. All data analysis was performed using R software under the package "agricolae" by Mendiburu, (2015).

RESULTS AND DISCUSSION

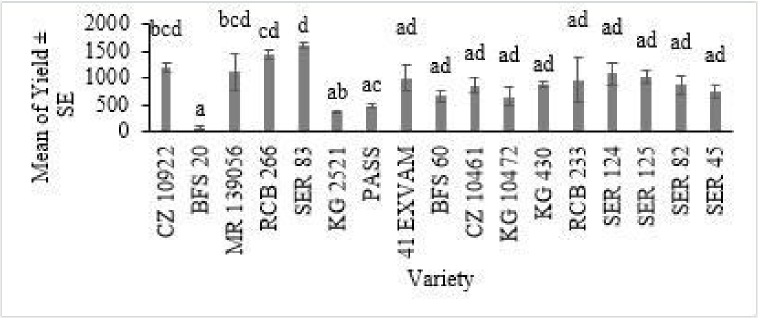
Yield and Yield Predictors

Regression analysis revealed that each district had different set of significant continuous yield predictors (Table 1). The categorical predictor (variety) was insignificant in Mbeya district alone. Performance of the varieties differed significantly in each location except Mbeya district (Figure

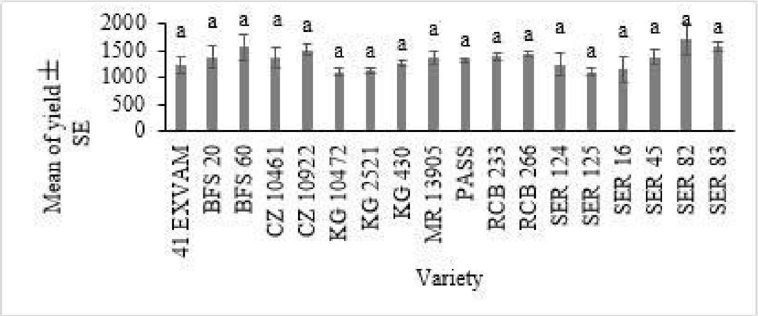
1). The model terms (yield predictors) fit the computed regression model significantly (Table 1)

Table 1: Regression analysis of yield predictors of common bean varieties across three districts

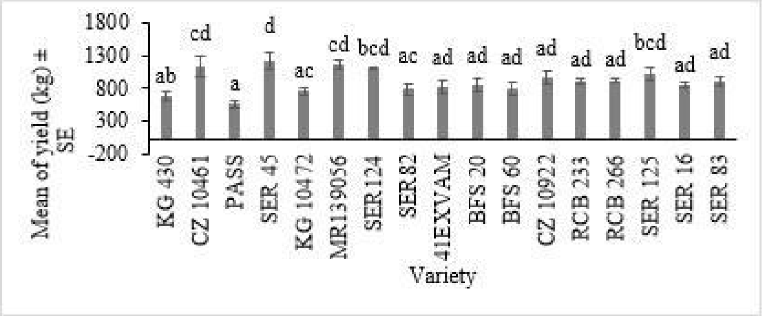
	Mbarali		**Mbeya**		**Mbozi**	
	F - value	**p value**	**F value**	**p value**	**F value**	**p value**
Regression	3.21	0.003**	2.99	0.0024**	3.72	0.001**
Seeds/ pod	1.43	0.24	1.3	0.265	0.56	0.462
Pods/ plant	0.67	0.421	0.12	0.73	6.28	0.019*
Seed weight/ pod	1.27	0.272	0.28	0.604	0.45	0.51
%Weight/100 seeds	0.94	0.343	1.67	0.207	0.88	0.358
Seed weight/ plant	0.03	0.87	0.38	0.542	0.00	0.973
Plant height	2.78	0.108	0.2	0.8814	2.72	0.058
%50f	5.57	0.027*	3.8	0.062	0.01	0.918
%85 pm	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	77.6%		74.23%		78.19%	



a. Mbarali (df = 17, f = 5.236, p = 0.0501)



b. Mbeya (df = 17, f = 0.99, p = 0.498)



c. Mbozi (df = 17, f = 2.44, p = 0.019)

Figure 1. Means of yield of bean varieties in three districts in Mbeya region. 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

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 ($F_{(2)}$ = 57.73, P = 2.2e-16). Yield also differed significantly between varieties (genotype) ($F_{(17)}$ = 4.11, P = 2.86e-06). The pooled ANOVA revealed that the interaction term variety*location (genotype*environment) was also significant for variation in yield ($F_{(34)}$ = 2.405, P = 2.86e-060.000335).

Three principal components were generated from the PCA in terms of the pooled ANOVA. Based on Gollob's test, Principal component 1 (PC1) covered most of the data variation by 69% (Table 2)

Table 2: **Combined analysis of variance of yield for common bean genotypes across three environments and Gollobs test for selection of terms**

Source of variation	**Percent**	**df**	**F value**	P value
Environment	43.20	2	57.73	0.0000
Genotypes	26.20	17	4.12	0.0000
Genotype x Environment	30.59	34	2.40	0.0003
PC1	69.17	18	3.28	0.0001
PC2	30.83	16	1.64	0.0697
PC3	0.00	14	0.00	1.0000
Residuals	0.00	108	NA	NA

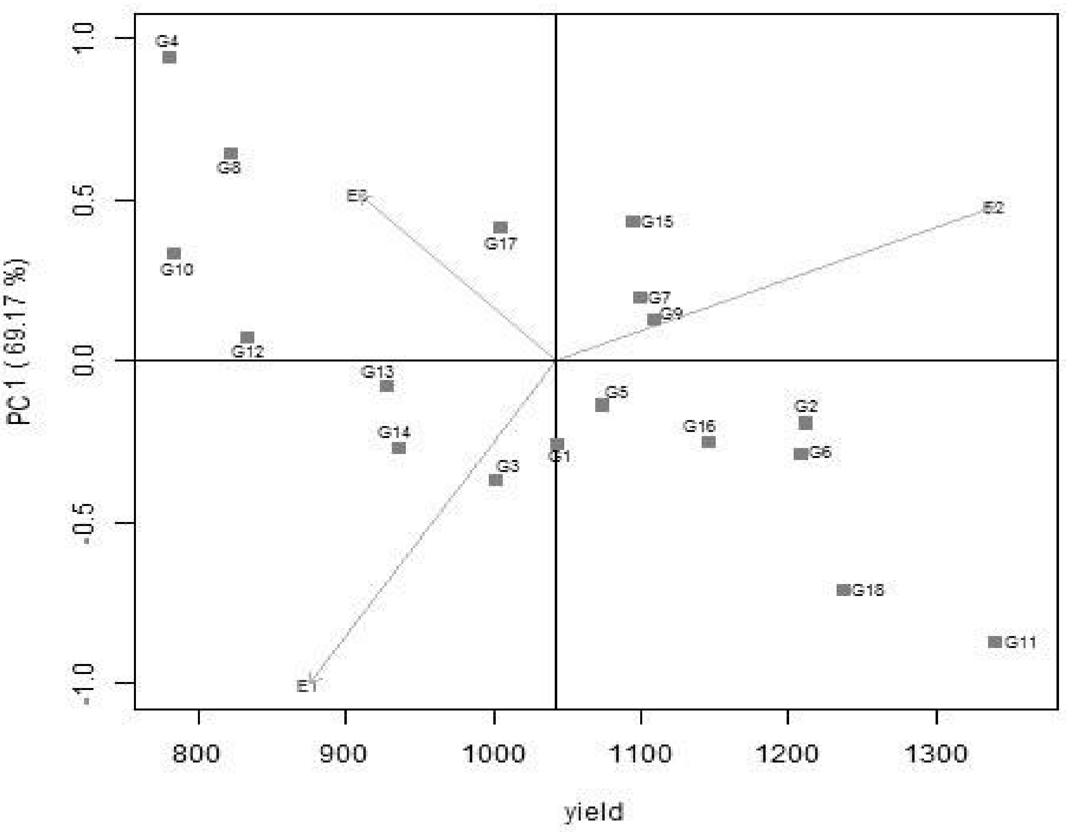


Figure 2: AMMI biplot depicting main and interaction effects of genotypes and environment on yield of Common bean (*Phaseolus vulgaris* L) in Mbeya. The GEI effect for a specific genotype in each environment is measured by its interaction PC1 scores.

KEY: E1 = Mbarali, E2 = Mbeya, E3 = Mbozi, G1 = ser125, G2 = mr139056, G3 = 41exvam, 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

In the AMMI biplot (Figure 2), genotypes are represented as points (Gx) and environments as vectors (Ex). The interaction score of zero is represented by the horizontal line drawn from the point (0, 0). The vertical line drawn from the point 1050 on the x axis represents the grand mean of yield. Deviation along the vertical axis indicated interaction differences between genotypes and environments, and deviation along the horizontal axis indicated difference in genotype and environment main effects. Genotypes with PC1 scores close to zero showed general adaptation and had higher yields. This small deviation indicates they maintain yield performance closer to the average yield in all three environments (stable genotypes). These included G5 (RCB 233) [PC1 =0.07], G1 (SER 125) [PC1=0.3] and G3 (41-EX-VAM**) [**0.032]. Genotypes with higher PC1 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 G11(ser 83) and G18(rcb 266) were less adapted to E3 (Mbozi) but were adapted to E1 (Mbarali) and E2(Mbeya). Further, Yan et al., (2000) pointed out that genotypes with PC scores near zero are more representative of an average environment. Therefore, those genotypes can be recommended for adaptation to specific environment. The Interaction pattern of the 18 common bean genotypes with 3 environments was cross validated by analysis of AMMI biplot of the two principal components (PC1 and PC2) (**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 (Figure 3). The genotypes G10 and G17 were plotted in pairs indicating that they had similar response patterns.

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.

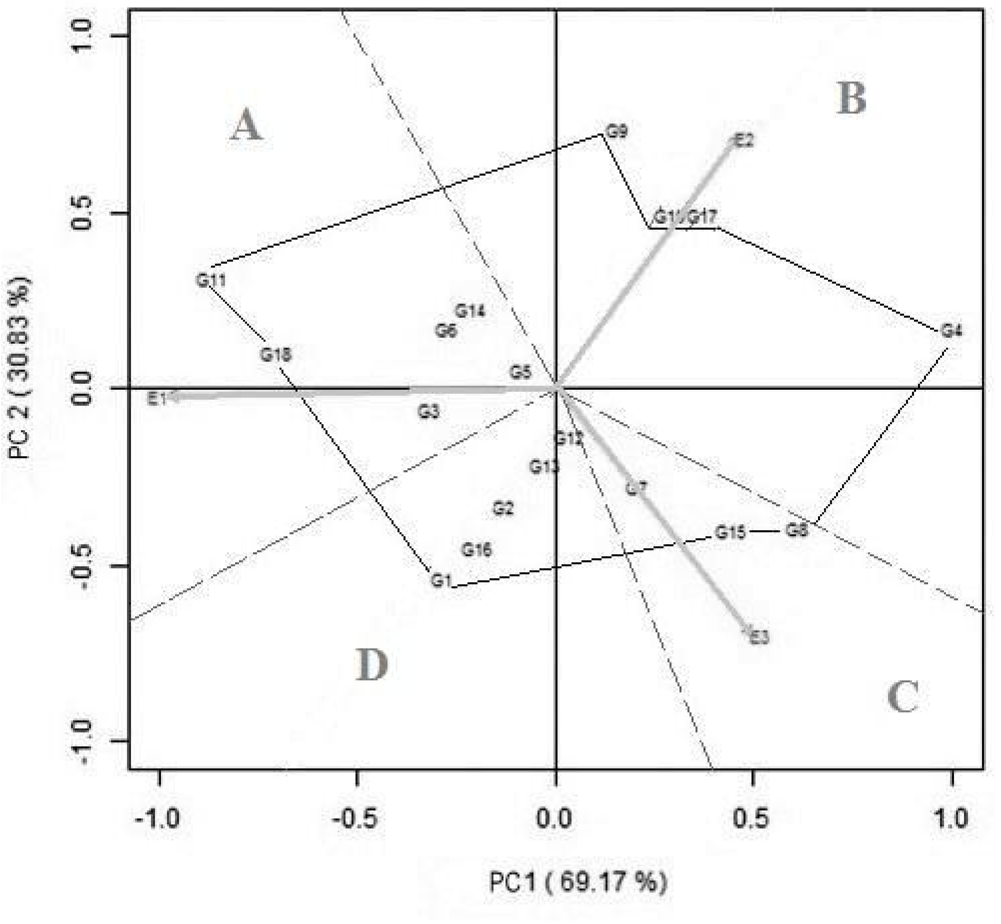


Figure 3: AMMI biplot analysis showing mega-environments and their respective high yielding varieties

4. CONCLUSION

Variety trials determine the whole selection and release process. Varying effects GEI complicate this process. The current study provided insight on indicators for early prediction of common bean variety performance in each location. The AMMI model developed in this study resolved the GEI of common bean varieties as it pertains to Mbeya region. It revealed that GEI had a significant impact in yield variation of common bean varieties and it allowed visualization of the response patterns of both the genotypes and environments. The AMMI model aided in selection of superior and stable common bean genotypes for smart release in Mbeya region.

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