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

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**Authors’ contributions**

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

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**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 genotypes performed well under all the three districts.

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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.

| 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   |

Table 1. The geographical positioning of the studied location and their respective weather
characteristics.
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, 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 \( \mu \) is the overall mean of the grain yield in the population, \( G_i \) is the effect of the \( i \)th genotype, \( E_j \) is the efficacy of the \( j \)th environment, \( GE_{ij} \) is the Interaction of the \( i \)th genotype with the \( j \)th environment, \( R_{ij} \) is the effect of the \( k \)th replication in the \( j \)th environment, and \( \varepsilon_{ijk} \) 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:

\[ Y_{ij}^N = \mu + G_i + E_j + \sum \beta_k a_{ik} s_{jk} + \varepsilon_{ij} \]

Where \( Y_{ij}^N \) is the yield of the \( i \)th genotype in the \( j \)th environment, \( N \) is the number of principal components in the AMMI model, \( \mu \) is the overall mean of genotypes, \( G_i \) and \( E_j \) are the genotype and environment deflections from the overall mean, \( \beta_k \) is the eigenvalue of the PCA axis \( k \), \( a_{ik} \) and \( s_{jk} \) are the genotype and environment principal components scores for axis \( k \) and \( \varepsilon_{ij} \) 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 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%      |
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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       | 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*
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 (Hernandez 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).

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 IIIPC1 and IIIPC2 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 IIIPC 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 environments, 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.

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