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APPLICATION OF AMMI ANALYSIS FOR MULTI-ENVIRONMENT TRIALS OF PIGEON PEA (*CAJANUS CAJAN. (L.) MILLSP.*) CROP IN KENYA

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Abstract: The present study aimed to use MET data generated over three years across three locations to identify most stable pigeonpea genotypes and common test environments based on representativeness. AMMI analysis showed that there were significant effects for genotypes, environments and G x E interaction for grain yield. However, greater variation was attributed to sum squares (SS) due to environment effects and less to due to genotypes and G x E interactions. Further, multiplicative effects through IPCA1 and IPCA2 explained major portion of the G x E interaction SS there by AMMI2 model (G+E+IPCA1 and IPCA2) contained major portion of the total SS, indicating that the AMMI model fits the data well, and validates the use of AMMI2. Among the test genotypes ICEAP 00040, recorded highest grain yield (1.93 t/ha) and formed distinctly in first significant group. AMMI stability values for all the traits under inquiry indicated that G2 (ICEAP 00040) as the most stable genotype (ASV of ~1 and top most performer and selection index value is 8 (which is low). AMMI1 biplot showed G2 (ICEAP 00040), G6 (ICEAP 00932), G7 (ICEAP 00933), and G8 (ICEAP 00936) are showing high performing and AMMI2 biplot showed G3 (ICEAP 00053) had high stable and among all the genotypes G2 (ICEAP 00040) as a highly dominant genotype. The superior performance and adaptability of ICEAP 00040 was rightly recognized by its release in Kenya.

Index terms: Genotype x Environment Interaction, AMMI analysis, AMMI Stability Value, Pigeon pea, Selection Index.

1. INTRODUCTION

Pigeonpea (*Cajanus Cajan* (L.) Millsp.) is one of the major grain legumes grown in semi-arid areas of Eastern Africa in about comprising of Kenya 156,200 ha. Pigeonpea is a traditional crop in Kenya; however, farmers, traders and consumers are looking for specific genotypes with compatible growth habit in cereal-based cropping systems, resistant to predominant races of *Fusarium* wilt, round, cream coloured bigger seeds with fast cookability along with maize/sorghum.

Several advance statistical models are available to detect the significance of Genotype x Environment Interaction (GEI), and how genotype performances or ranks impacted by the responses to environmental changes. Among the most common methods are conventional analysis of variance of fixed, random, and mixed models and also multivariate, regression approached analysis. One of the advance statistical methods of Principal Component Analysis (PCA) was performed to determine the quantification of GEI and yield stability.

The Additive Main effects and Multiplicative Interaction (AMMI) analysis (Gauch, 1992) was used to detect the significance of genotype x environment interaction in addition to the conventional approach of combined analysis of variance (ANOVA) for additive and interaction effects of genotypes and environments. AMMI stability value will give the information about stability of the genotypes across the environments. The objective of the current study is to use Multi-Environment Trial (MET) data generated over three years across three locations to identify most stable genotypes and mega-environment evaluations for the test environments.

2. MATERIAL AND METHODS

2.1 DATA SOURCE AND STRUCTURE

Data from 2007-08 to 2009-10 Pigeon pea trials across three locations in Kenya were used in this study. 10 genotypes were evaluated (Table 1) at 3 locations and forming 8 environments (year x location combinations, 2009-10-Kebete location was missing). An experimental trial was laid out in Randomized Complete Block Design (RCBD) with 3 replications in eight environments.

Table 1: Details of environments and genotypes

| Environment code | Year | Location | Country | Genotype code | Genotype |
|------------------|---------|---------------|---------|---------------|---------------|
| E1 | 2007-08 | Kiboko | Kenya | G1 | ICEAP 00020 |
| E2 | 2007-08 | Kampi ya Mawe | Kenya | G2 | ICEAP 00040 |
| E3 | 2007-08 | Kabete | Kenya | G3 | ICEAP 00053 |
| E4 | 2008-09 | Kiboko | Kenya | G4 | ICEAP 00576-1 |
| E5 | 2008-09 | Kampi ya Mawe | Kenya | G5 | ICEAP 00926 |
| E6 | 2008-09 | Karatu | Kenya | G6 | ICEAP 00932 |
| E7 | 2009-10 | Kiboko | Kenya | G7 | ICEAP 00933 |
| E8 | 2009-10 | Kampi ya Mawe | Kenya | G8 | ICEAP 00936 |
| | | | | G9 | ICP 13076 |
| | | | | G10 | ICP 9145 |

2.2. STATISTICAL ANALYSIS

2.2.1. AMMI analysis of variance

The Additive Main effects and Multiplicative Interaction (AMMI) analysis (Gauch, 1992) applies singular value decomposition method to the residuals of linear model then decompose genotype x environments interactions into interactive principal component axis (min of (g-2, E-2; g is number of genotypes and E is number of environments)) (), which can effectively explain G x E interaction by using Principal Component Analysis (PCA).

The linear model for Additive Main effects and Multiplicative Interaction (AMMI) model is,

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^n \lambda_k \alpha_{ik} \gamma_{jk} + \epsilon_{ij} \quad (1)$$

Where, Y_{ij} is the mean grain yield of i^{th} genotype in j^{th} environment, g_i and e_j are mean deviation of i^{th} genotype and j^{th} environment from μ , respectively, λ_k is the square root of eigen value of the k^{th} IPC axis and ϵ_{ij} is residual, α_{ik} and γ_{jk} are the IPC scores for i^{th} genotype and j^{th} environment, respectively.

AMMI 1 biplot display of PCA 1 score versus mean yield visualize the overall pattern of MET data, and AMMI 2 biplot display of PCA 1 score versus PCA2 to visualize the stable and adaptable genotypes across the environments.

2.2.2. AMMI Stability Value (ASV)

Purchase et al. (2000) developed a quantitative stability value to rank genotypes through the AMMI model,

$$ASV = \sqrt{\left[\left(\frac{SS_{IPCA1}}{SS_{IPCA2}} \right) (IPCA1SCORE) \right]^2 + (IPCA2SCORE)^2}$$

IPCA1 and IPCA2 are first and second interactive Principal Component Axis respectively.

AMMI stability values for genotypes and test environments (ASV_i) is in effect the distance from the coordinate point to the origin in a two dimensional scatter diagram of IPCA1 scores against IPCA2 scores. The larger the IPCA scores, either negative or positive, the more specifically adapted a genotype is to some certain environments; the smaller the IPCA scores, the more stable the genotype is over all environments studied.

2.2.3. Stability Index (SI)

SI assists in simultaneous selection of genotypes with desired yield performance coupled with stability across test environment (Mahmodi, N. et.al., 2011),

$$SI = RASV + RY$$

Where RASV is the rank of genotype based on ASV and RY is rank of genotype based on mean grain yield.

Lower the magnitude of SI, higher is the mean grain yield and stability and selection of genotypes with low value of SI are always preferred.

2.2.4. Combined Analysis of Variance

An another conventional approach of combined analysis of variance (ANOVA) for additive and interaction effects of genotypes and environments by using mixed model analysis. Considered environment and replication as random and genotype as fixed effect. Individual environmental variance are modelled to error distribution using REML (Restricted Maximum Likelihood) procedure using mixed procedure in SASv9.4 (SAS Institute Inc., 2018).

The linear statistical model for multi-environmental trial is,

$$Y_{ijk} = \mu + \tau_i + r(\beta)_{k(i)} + \beta_j + \phi_{ij} + \epsilon_{ijk} \quad (2)$$

Where, Y_{ijk} is the observed value of i^{th} genotype in j^{th} environment in k^{th} replication; μ is the grand mean; τ_i is the main effect of i^{th} genotype; β_j is the main effect of j^{th} environment; ϕ_{ij} is interaction between i^{th} genotype and j^{th} environment and ϵ_{ijk} is random term of error with mean '0' and variance ' σ^2 '.

The objective of the current study is to use Multi-Environment Trial (MET) data generated over three years across three locations to detect significant GEI and to identify most stable genotypes and mega-environment evaluations for the test environments using AMMI1 and AMMI2 biplots and to identify most stable genotypes across the environments by using AMMI stability value (ASV).

3. RESULTS

3.1. Genotype x Environment analysis

Results from AMMI analysis showed that there were significant effects for genotypes, environments, and G x E interaction for grain yield (Table 2). However, greater variation was attributed to sum squares (SS) due to environmental effects (~63%) and less due to genotypes (~13%) and G x E interactions (~24%). The first two Interactive Principal Components explain ~75% of total variation i.e., in total, the AMMI2 model (IPCA1 and IPCA2) contained a major portion of the total SS, indicating that the AMMI model fits the data well, and validates the use of AMMI2 biplot as well. Results from combined analysis of variance (Table 3) showed that random effects of environment and genotype x environments (GXE) variance components are the significant and fixed effect of genotype means also significant Prob<0.0001. from both AMMI and combined analysis of variance results are identical.

Table 2: AMMI analysis of variance for grain yield trait of 10 Pigeon pea genotypes in 8 environments.

| Source | d.f. | SS | MSS | F-value | ProbF | % of SS explained |
|-------------------|------|-------|-------|---------|--------|-------------------|
| Genotypes (G) | 9 | 12.51 | 1.39 | 18.38 | <0.001 | 12.61 |
| Environments (E) | 7 | 62.64 | 8.95 | 72.90 | <0.001 | 63.16 |
| Rep (Environment) | 16 | 1.96 | 0.12 | 1.62 | 0.0708 | |
| G X E | 63 | 24.03 | 0.38 | 5.04 | <0.001 | 24.23 |
| IPCA 1 | 15 | 12.51 | 0.83 | 11.03 | <0.001 | 52.06 |
| IPCA 2 | 13 | 5.56 | 0.43 | 5.65 | <0.001 | 23.14 |
| IPCA 3 | 11 | 3.33 | 0.30 | 4.00 | <0.001 | 13.86 |
| IPCA 4 | 9 | 1.09 | 0.12 | 1.61 | 0.1189 | 4.54 |
| IPCA 5 | 7 | 0.67 | 0.096 | 1.27 | 0.2702 | 2.79 |
| IPCA 6 | 5 | 0.58 | 0.12 | 1.54 | 0.1814 | 2.41 |
| Residuals | 3 | 0.29 | 0.096 | 1.27 | 0.2865 | |
| Error | 133 | 10.06 | 0.08 | | | |
| Total | 239 | 111.2 | 0.47 | | | |

Note: MSS- Mean sum of squares; SS-Sum of squares; IPCA-Interactive Principal Component Analysis; ProbF<0.0001 indicates effects are significant at <1% l.o.s

Table 3: Combined analysis of variance (conventional method) for grain yield trait of 10 pigeonpea genotypes in 8 environments.

| Random effects | | | | |
|---------------------|-----------|--------|-------------|-----------|
| Variance components | | | | |
| Random term | component | s.e. | Z-statistic | ProbChisq |
| Environment (E) | 0.285 | 0.160 | 1.785 | 0.0001 |
| Rep (Environment) | 0.004 | 0.004 | 0.885 | 0.2942 |
| GXE | 0.097 | 0.023 | 4.310 | 0.0001 |
| Error | 0.075 | 0.026 | 2.921 | 0.0014 |
| Fixed Effects | | | | |
| Effect | n.d.f. | d.d.f. | F statistic | F pr |
| Genotype (G) | 9 | 60.8 | 3.83 | 0.001 |

3.2. Performance of genotype and environments in MET trial

3.2.1. Performance of environments

Mean performance of ten genotypes and eight environments (Table 4) showed that, regarding the performance of the environment, E5 (2.67), E1 (1.72), E4 (1.61), and E2 (1.52) are top-performing environments across all the genotypes. Kampi ya Mawe location in 2007-08 and 2009-10 showed below-average performing across the genotypes. The average performance of Kiboko location across the 3 years is 1.60t/ha, Kampi ya Mawe location across three years is 1.64 t/ha, and Kebete location across 2 years is, 1.36 t/ha.

3.2.2. Performance of test genotypes

From table 4, Mean performance of 10 pigeon pea genotypes under evaluation across test environments (Table 4) revealed that the range from 1.17 to 1.93 t/ha. All the genotypes tested recorded grain yield more than 1 t/ha which shows the potential yield improvements in ESA countries. Among the test genotypes G2 (ICEAP 00040), recorded the highest grain yield 1.93, and its superior production potential was well-proven through release in Kenya. Next best performing genotypes are G4 (ICEAP 00576-1) with 1.75 t/ha, G6 (ICEAP 00932) with 1.72 t/ha, G7 (ICEAP 00933) with 1.67 t/ha, and G8 (ICEAP 00936) with 1.65 t/ha.

Table 4: Mean performance of main and interaction effects of genotypes and environments for grain yield

| Genotype\Environment | E1 | E2 | E3 | E4 | E5 | E6 | E7 | E8 | Average |
|----------------------|------|------|------|------|------|------|------|------|--------------------|
| G1 | 1.56 | 1.81 | 1.37 | 1.83 | 2.99 | 1.15 | 1.29 | 0.91 | 1.61 ^{ab} |
| G2 | 2.09 | 1.81 | 1.39 | 1.80 | 3.16 | 1.73 | 2.27 | 1.23 | 1.93 ^{bc} |
| G3 | 1.59 | 1.52 | 1.27 | 1.19 | 2.29 | 0.89 | 0.86 | 0.33 | 1.24 ^a |
| G4 | 1.50 | 1.74 | 2.07 | 1.84 | 2.60 | 1.49 | 1.48 | 1.25 | 1.75 ^{ab} |
| G5 | 1.61 | 1.29 | 1.69 | 1.57 | 2.13 | 0.96 | 1.12 | 0.83 | 1.40 ^a |
| G6 | 2.36 | 1.51 | 1.67 | 1.63 | 3.06 | 1.14 | 1.95 | 0.47 | 1.72 ^{ab} |
| G7 | 1.98 | 1.34 | 1.41 | 1.76 | 2.48 | 1.38 | 2.43 | 0.59 | 1.67 ^{ab} |
| G8 | 1.74 | 1.38 | 1.40 | 1.55 | 2.88 | 1.60 | 1.84 | 0.79 | 1.65 ^{ab} |
| G9 | 1.49 | 1.52 | 1.14 | 1.54 | 2.71 | 1.37 | 0.78 | 0.62 | 1.40 ^a |
| G10 | 1.32 | 1.24 | 1.14 | 1.46 | 2.37 | 1.01 | 0.58 | 0.25 | 1.17 ^a |
| Average | 1.72 | 1.52 | 1.46 | 1.61 | 2.67 | 1.27 | 1.46 | 0.73 | 1.55 |

AMMI 1 and AMMI 2 biplots

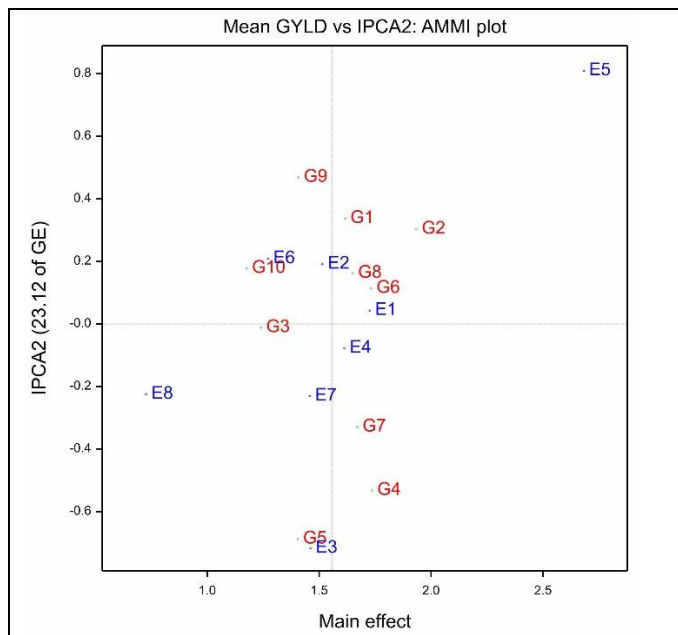


Fig 1: Graphical visualization of Mean yield performance vs IPCA2 scores

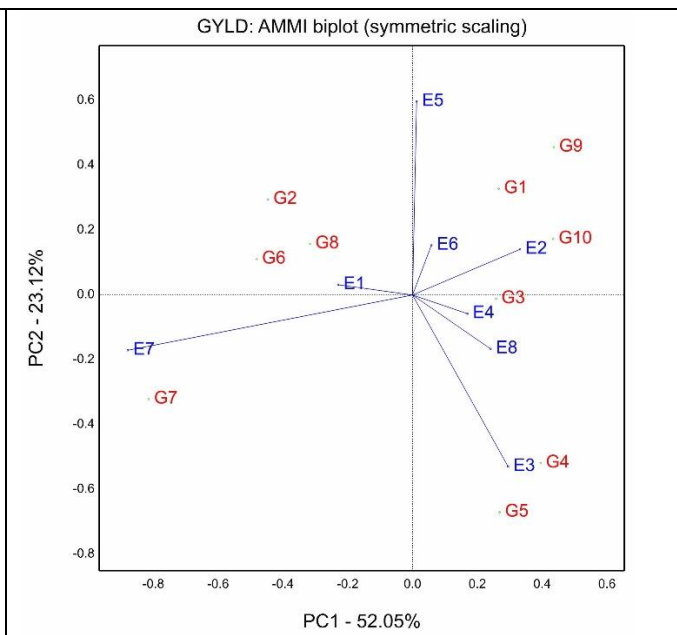


Fig 2: Graphical Visualization of IPCA1 vs IPCA2 visualize

3.2.3. AMMI biplots:

AMMI 1 and AMMI 2 biplot visualize the performance of both genotypes and environments as well stability of genotypes and mega environment evaluation among the test environments. The sign of IPCA indicates the pattern of environments across genotypes and vice versa. Environments and genotypes which have showed positive sign of IPCA 2 score (from 1st coordinate of Fig 1) indicated that respective genotypes are well interacted with the respective environments i.e., G1, G2, G6, and G8 are having above average grain yield and which are positive with E1 and E5 environments which we considered as adaptable genotypes for the specific environments. E3, E7 and E8 environments are different from the other environments which are having negative PCA scores and below average mean performance. E2 and E6 are having positive PCA score and below average mean performance. E4 has negative PCA score and above average mean performance. From Fig 2, consider IPCA1 scores alone irrespective of the sign, genotypes with high PCA score having high interaction with environments i.e., G7 is hugely effected by the environmental changes then considered it as unstable one. Whereas, genotypes with small PCA scores and which are nearer to the origin and are having small interactions with environments and are considered as stable i.e., G3, G6 and G8 are stable ones but G3 is consistently low performing across the environments and the G6 and G8 are having stable and above average performance. Similarly, environments with high PCA scores indicates genotypes explained more variation in that particular environment.

From AMMI1 biplot, G2, G6, G8 and G7 are showing high performing and G3 and G10 are low performing ones and E5, E1, and E4 are high performing ones and from AMMI2 biplot, G3, is having good stability (which are nearer to origin) but low performing one. According to the adaptability, G1, G3, G9 and G10 are good adaptable for E2, E4, and E6 environments and G4 and G5 are good for E3 environment, G2, G6, and G8 are good adaptable for E1, and G7 is good adaptable for G7.

3.2.4. AMMI stability value (ASV)

Superior yield and wider adaptability are the basic concepts of genotype development; however, it is not very easy to accomplish high yield coupled with general adaptability. AMMI stability values (Table 5) for grain yield trait under ASV indicated that ICEAP 00053 (G3) as the most stable genotype (ASV of < 1 and rank of grain yield is 9 and overall selection index is 10), which indicates that genotype consistently poor performing across the environments and which will not be recommendable for further studies. Genotype G1 have stable genotype (ASV<1) and rank of grain yield is 6 and above average performance, G2 has ASV near to 1 and top most performing genotype, G8s ASV is <1 and showed above average performance, G4s ASV is on par the value 1 and 2nd top most grain yield performer then these genotypes can be recommendable for the selection.

Table 5: Mean performance AMMI Stability value and Selection Index (SI) for 10 genotypes across the environments

| Genotype | ASV | Rank of ASV | Grain yield | Rank of yield | SI |
|----------|-------|-------------|-------------|---------------|----|
| 1 | 0.701 | 2 | 1.616 | 6 | 8 |
| 2 | 1.074 | 7 | 1.935 | 1 | 8 |
| 3 | 0.596 | 1 | 1.24 | 9 | 10 |
| 4 | 1.057 | 6 | 1.736 | 2 | 8 |
| 5 | 0.927 | 4 | 1.404 | 8 | 12 |
| 6 | 1.117 | 9 | 1.732 | 3 | 12 |
| 7 | 1.91 | 10 | 1.67 | 4 | 14 |
| 8 | 0.749 | 3 | 1.65 | 5 | 8 |
| 9 | 1.111 | 8 | 1.408 | 7 | 15 |
| 10 | 1.019 | 5 | 1.176 | 10 | 15 |

4. CONCLUSION:

Combined analysis of variance across eight environments showed significant differences among genotypes, environments, and genotypes \times environments interaction (GEI) for grain yield. The significant genotypes \times environments interaction effects indicated the performance of genotypes are affected by the tested environments.

Among the tested environments, the highest mean grain yield (2.67 t/ha) was observed at Kampi ya Mawe in 2008-09 followed by Kiboko-2007-08 (1.72), Kiboko-2008-09 (1.61) while Kampi ya Mawe in 2009-10 was the least yielding environments. The highest grain yields were obtained from G2 (ICEAP 00040) (1.93 t/ha) followed by G4 (ICEAP 00576-1) with 1.75 t/ha. The significance of GEI suggested that genotypes are not having clear information about the potentiality and stability of the genotypes then need to conduct the trial in further years also to understand the grouping of the environments for the selection of adaptable genotypes.

AMMI analysis revealed a significant ($\text{prob} \leq .0001$) effect of environment, genotype, and their interaction on grain yield. The effects of environment, genotype, and interaction accounted for 63%, 13%, and 24% of the total sum of squares, respectively. The first three PCA scores of AMMI were significant and explained 89% of the GEI. The first and second principal component axis (IPCA) of the interaction explained 52.06% and 23.14% of GEI sum of squares respectively. Both AMMI biplots selected G2 as top most and stable across eight environments. This genotype was selected both at good and poor-performing environments, recommended that it is desirable for cultivation in both kinds of environments.

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