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REGRESSION AND ADDITIVE MAIN EFFECTS AND MULTIPLE INTERACTIONS (AMMI) IN COMMON BEAN (*PHASEOLUS VULGARIS* L.) GENOTYPES

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ABSTRACT: Common bean (*Phaseolus vulgaris L.*) genotypes were tested over locations (Bako, Boshe and Gute) and years (2004 – 2005) with the objective of identifying high yielding, stable and adaptable varieties for western parts of Ethiopia. Regression and AMMI analysis were computed to identify stable genotypes across multi-environments (location-year combinations). Analysis of variance revealed highly significant difference among environment, genotype and genotype x environment (G x E) interactions, implying that genotypes suitable for specific conditions can be selected. Evidently, MD-23-4, A-802 and LM-93204324 were found to be stable and adapted to wide environments. Genotypes, VAX-2 and Angar were the top yielders but were sensitive to changed environmental conditions, suggesting that these genotypes produce higher yield under good management and favorable environmental conditions. Therefore, we recommend MD-23-4, A-802 and LM-93204324 for wide adaptation and VAX-2 and Angar for specific adaptation.

Key words/phrases: AMMI, Genotype x Environment, *Phaseolus vulgaris*, Regression, Stable

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the third most important food legume after soybean [*Glycine max* (L.) Merr.] and pea nut (*Arachis hypogaea* L.) (Singh *et al.*, 1999). It is nutritionally rich, especially in protein and iron, as well as a good source of dietary fiber and complex carbohydrates (CGIAR, 2005). The percentage of protein in the seeds of wheat, rice, and maize ranges from 8 to 12%, whereas it exceeds 20% in the legume seeds such as common bean.

Bean is an attractive crop for farmers, because of its adaptability to different cropping systems and short growing cycle (CGIAR, 2005). Belay Simane *et al.* (1998) studied common bean agro-ecology in Ethiopia. Their results indicated that the agro-ecology of bean growing in Ethiopia is diverse. Altitude ranged from 1200 to 2212 m, while annual rainfall varied from 580

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to 1950 mm. The length of the growing period was from as short as 80 to 220 days. Accordingly, the seasonal rainfall during the growing period ranged from 120 to 1636 mm.

Existence of genotypic differences for adaptability has long been known to geneticists and plant breeders. However, such differences could not be exploited earlier in breeding for wide adaptation because of difficulty in defining or assessing the adaptability itself and problem in measuring the complexities of environments (Sharma, 1998). Stability analysis is a step ahead of conventional analysis of variance in partitioning the interactions sums of squares into linear and non-linear components (Smithson and Gridley, 1990). In the model proposed by Eberhart and Russell (1966) sum of the mean squares attributable to environments and genotypes x environments interaction is partitioned into three components, viz., Environments (linear), Genotypes x Environments (linear) and Deviations from regression (Pooled deviation over all the genotypes). This enables us to characterize our genotypes in multi-environments. According to Eberhart and Russell (1966) a variety can be considered as stable if it meets high mean yield, coefficient of regression (b_i) = 1 and squared deviation from regression (s^2_{di}) approaching zero (Singh, 1993).

Additive Main effects and Multiple Interaction (AMMI) is another stability model, which is popular and powerful in estimating stability test. It combines analysis of variance for the genotype and environment main effects with principal components analysis of the genotype x environment interaction (Gauch and Zobel, 1996). According to the authors, AMMI is to seek a high yielding, widely adapted genotype that wins throughout the growing region of interest. Otherwise, it helps to subdivide the growing region into several relatively homogeneous macro-environments and then breed and recommend varieties for each.

Therefore, the objective of this work was to identify superior and stable genotypes of common bean that can be adopted for general and specific adaptations.

MATERIALS AND METHODS

Eleven common bean (*Phaseolus vulgaris* L.) genotypes including two standard checks (Angar and Dicta-105) were tested at Bako, Boshe and Gute for two years during 2005 and 2006 cropping seasons. The experiment was laid out in Completely Randomized Block design with four replications in which each plot comprised six rows having 4 m length. The spacings between rows and plants were 40 cm and 10 cm, respectively. Fertilizer of

100 kilogram Di ammonium phosphate (DAP) ha^{-1} was applied at planting. Seed rate and other agronomic practices were used.

Data were recorded on plot basis. The central four rows were harvested and seed yield was adjusted at 10% seed moisture content before data processing for analysis. Stability analysis was carried out using regression (Eberhart and Russel, 1966) and AMMI models in Agrobase 20 software (Agrobase, 1998).

A linear model proposed by Eberhart and Russell (1966) is:

$$Y_{ij} = \mu_i + b_i I_j + s^2 d_{ij}$$

Where Y_{ij} is the mean performance of ith variety (I = 1, 2, …, V) in jth (j = 1, 2, …., n) environment; μ_i is the mean of ith variety over all the environments; b_i is the regression coefficient which measures the response of ith variety to varying environment; $s^2 d_{ij}$ is deviation from regression of ith variety in the jth environment, and I_j is the environmental index of jth environment.

AMMI combines analysis of variance and principal component analysis (PCA) into a single model with additive and multiplicative parameters (Gauch and Zobel, 1996)

The AMMI model equation is:

$$Y_{ger} = \mu + \alpha_g + \beta_e + \sum_n \lambda_n \gamma_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger}$$

Where Yger is the observed yield of genotype g in environment e for replication r; Additive parameters: μ the grand mean; α_g the deviation of genotype g from the grand mean and β_e the deviation of environment e; the multiplicative parameters: λ_n the singular value for interaction principal component axis (IPCA) n, γ_{gn} the genotype eigenvector for axis n, and δ_{en} the environment eigenvector; ρ_{ge} PCA residuals (noise portion) and ε_{ger} error term.

Genotypes with low magnitude (score of the same sign) of interaction principal component analysis (IPCA) scores have general adaptability while those with high magnitude of IPCA scores have specific adaptability to environments. The results can be graphed in a very informative biplot that shows both main and interaction effects for both genotypes and environments (Gauch and Zobel, 1996).

RESULTS AND DISCUSSION

Data of seed yield

Data of seed yield for individual locations and years is presented in Table 1. Statistically significant differences were observed for seed yield among the genotypes for all environments except at Gute in the year 2005. This indicated the presence of genetic variability among the genotypes. Differences in deviations among genotypes were mainly due to specific responses to environments and especially due to differences in disease pressure. Similar result was reported from Uganda (Male-Kayiwa and Musaana, 1990). Across locations and years, the genotype VAX-2 (1.62 ton (ha)$^{-1}$) is the top yielder in mean seed yield, followed by Angar (1.42 ton ha^{-1}) and LM-93204324 (1.30 ton ha^{-1}). The lowest mean seed yield was 0.83 ton ha^{-1}, which was obtained for MX-9065-5-B.

Table 1. Mean seed yield (ton/ha) of common bean across years (2005 - 2006) and locations (Bako, Boshe and Gute)

		Mean seed yield in tonh^{-1}						
		Year-2005			Year-2006			
No.	Variety	Bako	Boshe	Gute	Bako	Boshe	Gute	Mean
1	A-802	1.05	0.36	0.87	2.65	0.67	1.43	1.17
2	LM-93204324	1.21	0.38	0.78	2.49	0.92	2.03	1.30
3	LP-90-15	0.75	0.25	0.85	1.72	0.47	1.07	0.85
4	VAX-2	1.31	0.58	1.03	3.1	1.17	2.51	1.62
5	MX-8754-3B	1.4	0.39	0.91	1.75	0.68	1.57	1.12
6	SEQ-1036	1.33	0.22	0.8	1.87	0.33	1.46	1.00
7	LR-93201723	1.54	0.32	0.72	1.78	0.64	1.4	1.07
8	MX-9065-5-B	0.87	0.2	0.87	1.55	0.55	0.96	0.83
9	MD-23-4	1.32	0.43	0.77	2.31	0.95	1.78	1.26
10	Angar	0.92	0.22	0.58	2.68	1.18	2.92	1.42
11	DICTA-105	1.72	0.48	0.98	2.29	0.61	1.2	1.21
	MEAN	1.22	0.35	0.83	2.199	0.742	1.658	1.168
	CV	30.01	24.29	32.03	16.22	30.58	33.17	
	LSD	0.439	0.102	0.319	0.428	0.272	0.66	
	F – test	*	**	ns	**	**	**	

CV=coefficient of variation; LSD=least significant difference; *, **= significant level at 5% and 1% probability level, respectively.

Regression analysis based on Eberhart and Russell model

Mean square due to genotype and genotypes x environments (linear) was found to be significant (Table 2). The significance of genotypes x environments (linear) indicated that variation in the performance of genotypes was due to the regression of genotypes on environments and consequently, the performance is predictable in nature. Similar results were reported in common bean (Teshome Girma, 1990; Smithson and Gridley, 1990), field pea (Chaudhary *et al.*, 1994) and maize (Mosisa Worku *et al.*, 2001; Wende Abera *et al.*, 2004; Wende Abera and Labuschagne, 2005)

Table 2 Analysis of variance for grain yield using Eberhart-Russel Regression Model

Source of variation	DF	Mean squares
Total	263	
Genotype	10	0.327**
Env. +Gen. x Env.	55	0.544
Env. in linear	1	25.075
Gen. x Env. (linear)	10	0.176*
Pooled deviation	44	0.070
Residual	198	0.039

Grand mean = 1.168; R^2 = 0.897; CV (%) = 33.68; *, ** = significant level at 5% and 1% probability level, respectively.

The mean performance, regression coefficient (b_i) and squared deviations (s^2d_i) from regression values are presented in Table 3. The regression coefficient differed significantly from unity for VAX-2, Angar and MX-9065-5-B while regression coefficients of others were close to unity. Genotypes, LM-93204324 and MD-23-4 have mean yield higher than average, (b_i), did not differ significantly from unity and (s^2d_i) approached zero. This implied that the genotypes were stable and widely adapted. Furthermore, Dicta-105 and A-802 were also adaptable varieties. On the other hand, high seed yielding genotypes, viz., VAX-2 and Angar, had regression coefficient values significantly higher than unity, showing that these genotypes were responsive to changes in environment. Accordingly, VAX-2 and Angar provide high yield under favorable environmental conditions with suitable agronomic practices. Nevertheless, MX-9065-5-B is poorly adapted to all the environments because its mean performance was lower than the average and coefficient of regression was significantly less than unity.

Table 3. Partioning of deviation from linearity of varietal responses

Genotypes	b_i	S^2d_i	Mean grain yield (ton ha^{-1})
A-802	1.152	0.022	1.17
LM-93204324	1.174	-0.019	1.30
LP-90-15	0.726	-0.009	0.85
VAX-2	1.401*	0.019	1.62
MX-8754-3B	0.765	-0.010	1.12
SEQ-1036	0.937	0.005	1.00
LR-93201723	0.805	0.018	1.07
MX-9065-5-B	0.628*	-0.010	0.83
MD-23-4	1.018	-0.029	1.26
Angar	1.486**	0.275	1.42
DICTA-105	0.906	0.086	1.21

b_i=regression coefficient; s^2d_i=squared deviations from regression; standard error of beta = 0.1755; *, **= significant level at 5% and 1% probability level, respectively.

Additive main effects and multiple interaction (AMMI) model

Analysis of variance revealed significant difference among environments, genotypes, genotypes x environments interactions and interaction principal component analysis (IPCA) 1 axis at $p \leq 1\%$ (Table 4). The percentage of G x E interaction explained by IPCA 1 was 73.98 while the remaining 30.11% was not significant. Therefore, we preferred to carry out the analysis in AMMI.

Table 4. Analysis of variance for Additive Main effects and Multiple Interaction (AMMI)

Source of variation	DF	Mean squares	% G x E interaction explained
Total	263		
Environments	5	20.060**	
Reps within Env.	18	0.548	
Genotype	10	1.306**	
Genotype x Env.	50	0.388**	
IPCA 1	14	1.024**	73.98
IPCA2	12	0.228	14.10
Residual	180	0.116	

Grand mean = 1.168; R^2 = 0.873; CV (%) = 29.09; Reps=replications; Env.= environment; **= significant level at 1% probability level.

The AMMI analysis result revealed that Angar (0.954) had the highest IPCA score followed by VAX-2 (Table 5), signifying that these genotypes were sensitive to changes in environment. The finding is in agreement with the result obtained in regression analysis based on Eberhart and Russell model. Furthermore, these varieties performed very well in the second cropping season under A and under C environmental conditions, which showed high IPCA (Fig.1). The result implies that these genotypes produce high yield under specific environments. However, A-802 and MD-23-4 had scores close to zero (Fig.1), suggesting that they were stable and well adapted. We also found similar results using regression analysis based on Eberhart and Russell model. Hence, these varieties may be recommended for wide adaptation.

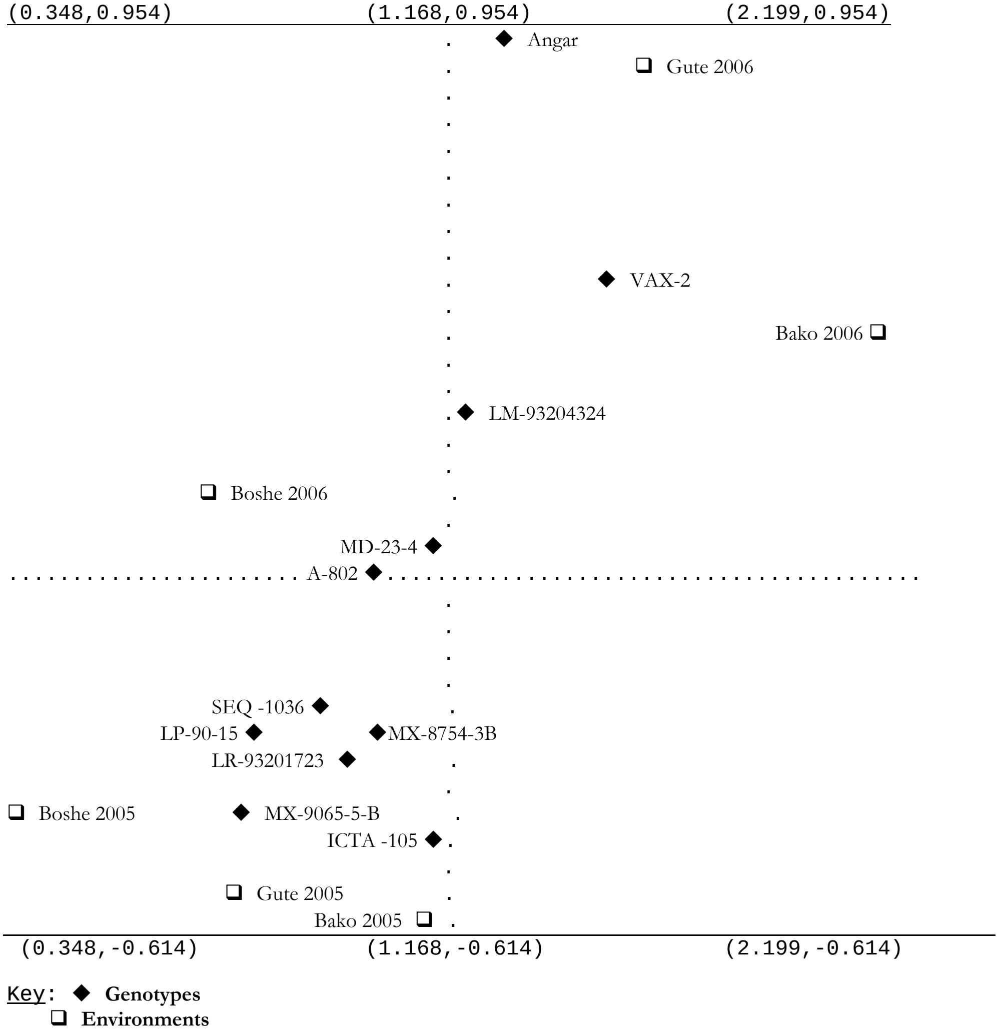

Fig 1. Biplot with abscissa (X-axis) plotting mean seed yield (ton ha^{-1}) from 0.348 to 2.199 and with ordinate (Y-axis) plotting IPCA1 from - 0.614 to 0.954. Genotypes plotted as a,b,c, ... and environments as A,B,C, ...,as cross-referenced in the IPCA1 axis scores tables shown above.

Table 5 IPCA1 Scores of genotypes and environments

Designation of	Genotype and environment	IPCA 1 Score	Mean grain yield (ton ha^{-1})
Genotypes			
a	A-802	0.036	1.17
b	LM-93204324	0.274	1.30
c	LP-90-15	-0.262	0.85
d	VAX-2	0.534	1.62
e	MX-8754-3B	-0.252	1.12
f	SEQ-1036	-0.213	1.00
g	LR-93201723	-0.308	1.07
h	MX-9065-5-B	-0.386	0.83
i	MD-23-4	0.066	1.26
j	Angar	0.954	1.42
k	DICTA-105	-0.443	1.21
Environment			
A	Bako 2006	0.475	2.20
B	Boshe 2006	0.134	0.74
C	Gute 2006	0.919	1.67
D	Bako 2005	-0.614	1.22
E	Boshe 2005	-0.383	0.35
F	Gute 2005	-0.531	0.83

CONCLUSION

Both models (regression analysis based on Eberhart and Russell and Additive main effects and Multiple Interaction (AMMI)) generated similar results. Genotypes, MD-23-4, A-802 and LM-93204324 are well stable and adapted to multi-environmental conditions. On the other hand, VAX-2 and Angar were the top yielders but more responsive to changed environments, suggesting that the genotypes produce high yield under favorable environmental conditions. Therefore, we recommend MD-23-4, A-802 and LM-93204324 for wide adaptation and VAX-2 and Angar for specific adaptation.

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