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Adaptation and Yield Stability of Small Red Bean Elite Lines in Ethiopia

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Abstract: Different stability analyses ranging from univariate nonparametric to multivariate parametric methods were employed in this study for the assessment of stability and adaptability of genotypes and evaluation of test locations for their discriminativeness and representativeness. Replicated grain yield data of 16 elite small red bean genotypes tested in national variety trials at nine locations representing major bean production environments in Ethiopia for two years were used for the analysis. The results from the analysis revealed presence of cross over genotype x location interactions. The magnitude of location x year interaction indicated considerable intra-location variation in genotypic response pattern over years. The observed inter and intra-locations variation in genotypic response complicated the identification of high yielding stable genotypes across locations with both parametric and nonparametric stability estimates. However, with genotype plus genotype×location interaction (GGL) biplots of the site regression (SREG) model analysis, the overall picture of the genotypes at different locations and testing ability of the locations were assessed.

Key words: Common bean, genotype×location interaction, *Phaseolus vulgaris*, yield stability

INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is one of the key grain legumes in Ethiopia. It is occupying unique position in both production and social space in the country. The crop is best produced in areas falling in altitude ranges of 1400-2200 m above sea level with mean maximum temperature of less than 32°C and 350-500 mm of rain through the growing season. It is often cultivated by small-scale farmers in small plots of land in association with other crops or as a sole crop with low external input. It is rapidly evolving as an important export earnings of the country in recent years. The crop also is playing significant role in smallholder economy being an important source of proteins and income as cash.

The demand for a variety with high productivity and high performance for agronomic traits over a range of production environments is very high among growers and development practitioners. Breeding programs often conduct a range of multi-location and multi-year trials in order to identify the superior cultivar for target set of production environments (Yan *et al.*, 2000). Apparently, variation in target production environments complicates cultivar recommendation and minimizes the selection efficiency in breeding programs. Targeting of cultivars that win in a range of bean production space is

difficult when genotype x environment (GE) interaction is present. In presence of GE interaction, yield is less predictable and unlikely interpreted based on genotype (G) and environment (E) means alone (Ebdon and Gauch, 2002). The measured yield of each cultivar in each test environment is a mixture of environment main effect (E), genotype main effect (G) and GE interaction (Yan, 2002).

Biotic and abiotic factors such as the incidence of disease or pests, low soil fertility, distribution and intensity of annual precipitation, photoperiod, etc are the main contributors of GE interaction and yield instability in crops. However, the most of GE interactions cannot be explained by these known factors alone (Ferreira *et al.*, 2006).

Several biometrical methods have been developed to explain GE interaction and facilitate cultivar recommendation in breeding programs (Flores *et al.*, 1998; Hussein *et al.*, 2000; Ferreira *et al.*, 2006). The methods are broadly categorized as univariate parametric-nonparametric and multivariate parametric methods. The univariate parametric includes simple and bi-segmented linear regression, variance components with mixed models, descriptive statistics and non-linear regression models whereas the non-parametric univariate methods include the variance of genotype rank values. The multivariate methods include principal component (PCA), additive main effects and multiplicative interactions (AMMI) and genotype plus genotype×environment interaction (GGE) analysis (Zoble *et al.*, 1988; Ferreira *et al.*, 2006).

The use of different methods for explaining GE interaction and analyzing performance stability have been reported in many crops including common beans in the world. Although both national and regional variety trials of different bean market classes have been part of the bean breeding program in national research system for many years in Ethiopia, the relative magnitude of GE interaction and use of stability statistics in common beans in general and small red Mesoamerican gene pools in particular have not been very much documented. This text discussed the importance of GE interaction and utilization of different stability statistics in selection and recommendation of small red bean genotypes for different environments as well as characterization of variety testing locations.

MATERIALS AND METHODS

Experimental Data

Fifteen elite genotypes and one check variety grown in national variety trials during 2002 to 2003 cropping season in Ethiopia were used for this analysis. The trials were executed at nine locations representing the major bean production ecologies of the country (Table 1). The experimental genotypes were XAN-311, XAN-310, DICTA-109, DOR-811, XAN-307, EMP-388, XAN-316, DOR-564, SEQ-35, RAZ-54, DOR-364, DOR-548, DOR-526, DOR-527 and EMP-376. Red wolyta was used as a check cultivar in the trial. The test genotypes were obtained from International Center for Tropical Agriculture (CIAT), Cali, Colombia. A four-by-four triple lattice treatment design was used in all the locations and years. The plots were six rows of four meter long with between row and plant spacing of 40 and 10 cm, respectively. The central four rows were harvested for grain yield measurement. Recommended agronomic practices to raise good crop were used at each location. The grain yield was adjusted for 12% seed moisture before conversion to tons per hectare for the analysis.

Data Analysis

Analysis of Variance

The grain yield ($t\ ha^{-1}$) data per location/year were analyzed first separately and then combined after Bartlett's test of homogeneity for error variance. The classical fixed effect three-way analysis of variance (ANOVA) model that includes additive terms for the main effects of replications, blocks,

Table 1: Description of the test locations

Locations	Coordinates	Altitude (m a.s.l.)	Soil type ^a	Total seasonal ^b rainfall in mm		Mean seasonal temperature in °C	
				2002	2003	Min	Max
Bako	9° 06'N 37° 09' E	1650	Nitosol	780.0	967.1	12.1	27.9
Alemaya	9° 26' N 42° E	1980	Fluvisol	502.1	622.2	10.2	22.8
Melkasa	8° 24' N 39° 21' E	1550	Cambisol/Vertisol	320.1	577.8	13.8	28.6
Awassa	7° 05' N 38° 29' E	1700	Fluvisol	499.0	522.4	12.2	26.9
Ziway	7° 09' N 38° 7' E	1650	Sandy	301.9	520.2	12.1	27.4
Asasa	7° 12' N 39° 19' E	2300	Vertisol	410.3	684.6	5.6	24.2
Pawe	11° 12' N 36° 25' E	1100	Oxisol/Vertisol	1980.6	1200.8	15.0	32.4
Ambo	8° 57' N 37° 57' E	2225	Vertisol	618.9	812.8	11.2	25.6
Areka	7° 09' N 37° 47' E	1830	Nitosol	810.0	1045.7	15.3	28.1

^aAccording to FAO system of soil classification, ^bGrowing season includes months from June to November

genotypes, locations and years together with an extra additive terms that account for all possible interaction effects of genotype, location and year were used. The ANOVA model used for the data is

$$X_{ijk} = \mu + G_i + L_j + Y_k + (GL)_{ij} + (GY)_{ik} + (LY)_{jk} + (GLY)_{ijk} + \varepsilon_{ijk}$$

where, X_{ijk} is the mean yield over r replications of the i th genotype in the j th location in year k and the right hand side of the equation gives grand mean yield μ and respective main and interaction effects of genotypes, locations and years. ε_{ijk} is mean error related to the observed X_{ijk} which is assumed to be normal with a mean 0 and a variance σ^2/r . The magnitude of variance components was computed as the percentage of total variation in order to understand how the main and interaction effects explain the yield variation in small red bean multi-location trials.

Stability Analysis

The parametric and non-parametric univariate stability statistics for grain yield were computed by SAS GLM procedures using a program written by Hussein *et al.* (2000) available on-line (<http://www.nlh.no/ipt/publikasjoner/hussein/stability>). The parametric stability estimates computed were ecovalency (W_i) of Wricke (1964), regression coefficients (b_i) of Eberhart and Russell (1966), coefficient of determination (r^2) of Pinthus (1973), unbiased variance estimator (σ_i^2) of Shukla (1972), coefficient of variance (CV_i) of Francis and Kannenberg (1978), cultivar superiority measure (P_i) of Lin and Binns (1988a) and α and λ statistics of Tai (1971). Ecovalency (W_i) is referred as genotype ability to respond to environmental changes. The genotypes are considered stable and unstable when their W_i values are equal to zero and greater than zero, respectively. The Shukla's stability variance is the variance component of each genotype throughout the environments and its small value is an indicator of genotype stability. The linear regression coefficient (b_i) is most frequently used parameter among plant breeder communities. It is referred as a measure for genotype response pattern across test environments. Based on b_i values, genotypes are broadly classed as responsive to improvements in environmental conditions ($b_i > 1$), less responsive to improvements in environmental conditions ($b_i < 1$) and average in response ($b_i = 1$). Genotypes with less values of coefficient of variation (CV_i) are considered stable. Coefficient of determination (r^2) values of 1.0 is an indication of maximum stability. P_i associates stability and productivity and defines a superior genotype as the one with near the maximum in various environments. The smaller the P_i estimate, the more superior the new genotype is. The Tai's α and λ statistics indicate the linear response of genotypes to environmental effects and deviation from linear response, respectively. Genotypes with $(\alpha, \lambda) = (-1, 1)$ are considered perfectly stable and those with $(\alpha, \lambda) = (0, 1)$ are represented as expressing average stability.

The univariate non-parametric stability statistics including the rank-based stability parameters S_i^2 , S_i^3 and S_i^6 of Nassar and Huhn (1987), stratified rank analysis of Fox *et al.* (1990) and modified rank sum (Kang and Pham, 1991) were computed. Nonparametric measures for stability are handy for breeders because they are rank based on absolute data and free from stringent statistical assumptions. The non-parametric $S_i^{(2)}$ statistics measures the variance among the ranks over environments. $S_i^{(3)}$ and $S_i^{(6)}$ represents mean rank of each genotype. The lowest value for each of the statistics represents high stability (Flores *et al.*, 1998). A stratified rank analysis of Fox *et al.* (1990) is another nonparametric superiority measure for genotype general adaptability. With this method, the ranking of genotypes at each location was done based on yield performance and the percentage proportion of each genotype's ranking in the top, middle and bottom one third of the ranks was calculated. A genotype that occurred mostly in the top third was considered widely adapted. Kang and Pham's (1991) rank-sum is another non-parametric stability statistics which is calculated based on the ranks of the genotype's yield and Shukla's stability variance. With this statistics, genotypes were ranked by yield (highest yield ranked 1) and by stability variance (lowest stability variance ranked 1). The ranks by yield and by stability variance were summed for each genotype. The genotype with the lowest rank-sum was considered as the most desirable.

Clustering and Correlation Analysis

The genotypes were clustered based on distance measures as proposed by Abou-El-Fittouh *et al.* (1969) and Fox and Rosielle (1982). Accordingly, GL interaction weighted by the square root of Wricke's ecovalency as per Abou-El-Fittouh *et al.* (1969) and yields adjusted for genotype means and weighted by standard deviation as per Fox and Rosielle (1982) were used for the clustering. Computation of distances measures and clustering of genotypes was done using the average linkage algorithm of a SAS program written by Hussein *et al.* (2000) available on-line (<http://www.nlh.no/ipt/publikasjoner/hussein/stability>). Furthermore, the interrelationship among the test locations in determining grain yield performance of genotypes was assessed using simple correlation coefficients.

Genotype Plus Genotype x Location Interaction (GGL) Biplot Analysis

The GGL biplot method as of Yan *et al.* (2000) was employed to visualize the results of Site Regression (SREG) Model analysis for grain yield data performed by a SAS program written by Hernandez and Crossa (<http://www.cimmyt.org/biometrics/biplots.exe>). The GGE biplot was constructed by plotting the first principal component (PC1) scores of the genotypes and the environments against their respective scores for the second principal component (PC2) derived from subjecting environment-centered yield data (yield variation due to genotype plus genotype x environment interaction) to singular value decomposition (Yan *et al.*, 2007). In this analysis GGE biplots were used to understand the existence of mega-environments (defined as a group of locations that consistently share the best set of genotypes over years (Yan and Rajcan, 2002)) and to characterize the test locations in terms of representativeness and discriminating power of genotypes for small red bean national variety evaluation. Biplot for PC1 vs. PC2 scores obtained from yield data of 16 genotypes across nine locations was also used to compare the genotypes at different locations and identify the highest yielding genotypes at the different locations.

RESULTS

Analysis of Variance

The classical fixed effect three-way ANOVA model for grain yield expressed significant differences ($p < 0.01$) for genotype (G), location (L) and year (Y) main effects as well as GL, GY, LY

Table 2: Analysis of variance of grain yield (t ha⁻¹) for 16 red bean genotypes evaluated at nine location in 2002 and 2003

Source	df	SS	MS	Variance proportion (% of total SS)
Replication (L*Y)	36.00	9.503	0.264	0.85
Block (R*L*Y)	162.00	22.304	0.137**	2.00
Genotypes (G)	15.00	10.795	0.720**	0.97
Location (L)	8.00	563.787	70.473**	50.66
Year (Y)	1.00	102.098	102.09**	9.17
GL	120.00	28.541	0.238**	2.56
GY	15.00	3.653	0.244**	0.33
LY	8.00	343.721	42.965**	30.89
GLY	120.00	25.599	0.213**	2.30
Error	378.00	32.829	0.087	
CV%	15.78			
R ²	97.20			
Mean grain yield	1.87			

**Significant at p<0.01 with classical fixed effect ANOVA

Table 3: Genotype mean grain yield (t ha⁻¹) and parametric stability estimates of regression coefficients (b_i), ecovalence (W_i), coefficient of determination (r²), coefficient of variance (CV_i), stability variance (σ²), cultivar superiority measure (P_i) and Tai's α and λ for 16 genotypes

Genotypes	Mean	b _i	W _i	r ²	CV _i	σ ²	P _i	α _i	λ _i
XAN-311	1.84	0.98	6.29**	0.64	40.23	0.80**	2.13	-0.04	1.34
XAN-310	2.18	0.95	14.68**	0.42	40.84	1.99**	1.89	-0.09	3.10**
DICTA-109	2.02	0.89	14.28**	0.40	42.44	1.94**	2.21	-0.22	2.99**
DOR-811	2.05	1.08	11.08**	0.55	42.83	1.48**	2.05	0.16	2.34*
XAN-307	1.85	1.13	8.52**	0.64	46.05	1.11**	2.36	0.25	1.70
EMP-388	1.76	0.86	8.66**	0.51	42.12	1.13**	2.60	-0.27	1.76
XAN-316	1.72	1.00	9.95**	0.54	48.04	1.32**	2.91	0.00	2.13*
DOR-564	1.89	1.10	11.31**	0.56	47.07	1.51**	2.36	0.20	2.34*
SEQ-35	1.74	1.09	11.37**	0.55	51.25	1.52**	2.71	0.19	2.39*
RAZ-54	1.78	0.92	10.40**	0.49	44.55	1.38**	2.54	-0.17	2.39*
DOR-364	1.90	1.03	10.23**	0.55	44.32	1.36**	2.27	0.06	2.18*
DOR-548	1.74	0.90	8.93**	0.52	43.53	1.17**	2.59	-0.20	1.86
DOR-526	1.97	1.07	12.09**	0.53	45.22	1.62**	2.12	0.14	2.56**
DOR-527	1.92	1.13	14.31**	0.51	49.65	1.94**	2.41	0.25	2.98**
EMP-376	1.76	1.02	8.55**	0.59	45.95	1.12**	2.57	0.05	1.83
Redwolyata	1.77	0.85	11.39**	0.43	44.06	1.52**	2.69	-0.30	2.32*
Mean	1.86								
LSD5%	0.11								

*, **Significant at p<0.05 and p<0.01

and GLY interaction effects (Table 2). The location main effect and location by year interaction effects explained most of (up to 80%) of total yield variation. The contribution of G and Y main effects and GL, GY and GLY interaction effects appeared to be small. Location main effect by itself explained more than half of the total grain yield variation. Moreover, the significant GL effect (p<0.01) revealed the differential responses of bean genotypes to the variation in environmental conditions of the locations.

Mean Yield and Stability Statistics

Table 3 shows the mean grain yield (t ha⁻¹) and estimates of parametric statistics. The mean grain yield (t ha⁻¹) of the genotypes at each location ranged from 1.72 (XAN-316) to 2.18 (XAN-310) with overall mean of 1.86. Seven genotypes namely XAN-310, DICTA-109, DOR-811, DOR-564, DOR-364, DOR-526 and DOR-527 significantly out yielded the check variety 'Red wolyata'.

The analysis of the response pattern of the genotypes to the test locations using uni-segmented linear regression model of Eberhart and Russel (1966) indicated that all genotypes had the slope estimates (b_i) not significantly different from unity (p>0.05). Hence, all the genotypes were average in their responsiveness to improvements in the environmental conditions and their performance could

not be predicted by bi value alone. The coefficient of determination (r^2) ranged 0.40 to 0.64, which indicated that GE interaction in grain yield could not be explained by linear regression alone and the responses of genotypes were unpredictable. No genotype showed a desirable environmental response pattern i.e., low sensitivity at unfavorable environments and high response to improvements in environmental conditions. Both the Wricke's ecovalency (W_i) and Shukla's stability variance (σ_i^2) estimates of the genotypes were significantly greater than zero (Table 3). The W_i and σ_i^2 estimates revealed the less consistence in the yield performance of the genotypes in the national variety trials. The high yielding genotypes XAN-310 and DICTA-109 with larger estimates of W_i and σ_i^2 values were therefore considered suitable for locations with better environmental conditions. According to the coefficient of variance (CVi) of Francis and Kannenberg (1978), genotype XAN-311 with the least score was considered stable indicating less fluctuation in its mean yield across test locations. In an alternative measure for genotype superiority (Pi), the highest yielding genotype XAN-310 and DOR-811 had relatively least Pi estimate. However, DOR-811 that combine least Pi score and intermediate values of other parametric and non-parametric estimates could preferably be good-enough genotype for wider adaptation across the test locations. The use of α and λ statistics of Tai (1971) identified genotypes XAN-311, XAN-307, EMP-388, DOR-548 and EMP-376 as average in their relative stability (Table 3). Their respective estimates of α and λ values were not significantly deviated from $(\alpha, \lambda) = (0, 1)$. None of the genotypes expressed perfect stability $(\alpha, \lambda) = (-1, 1)$.

Table 4 shows the non-parametric estimates of stability for the genotypes. S_i^2 , S_i^3 and S_i^6 statistics were computed to assess yield stability of genotypes in response to environmental changes. According to these statistics, genotypes with lower estimates of S_i^2 , S_i^3 and S_i^6 are considered stable. The genotypes XAN-311, XAN-307, SEQ-35 and RAZ-54 had the lower values of the three statistics but none of them had mean yields higher than the grand mean for the trial and also not significantly out-yielded the check Redwolayta (Table 4). The genotypes XAN-310 and DICTA-109 with mean yields above the grand mean and also significantly better than the check had relatively high values of S_i^2 , S_i^3 and S_i^6 and hence showed low stability. Genotype DOR-811 combined significantly higher grain yield with intermediate values of S_i^2 , S_i^3 and S_i^6 estimates. In general, parallelism was observed in genotypes classification based on S_i^2 , S_i^3 and S_i^6 estimates.

Fox *et al.* (1990) proposed a stratified ranking of the genotypes as an alternative approach for measuring cultivar adaptation. In this method, the genotypes are ranked based on their mean performance at each test environment and the proportion of sites at which the genotypes occurred in the top, middle and bottom third of the ranks were used to judge the genotypes adaptation. A widely adapted genotype is the one that occurred mostly in the top third i.e., high value of top.

Table 4: Non-parametric stability estimates of S_i^2 , S_i^3 and S_i^6 (Nassar And Huhn, 1987), stratified ranksum analysis of Fox *et al.* (1990) and Kang's Rank sum (Kang and Pham, 1991) for the 16 genotypes

Variety	S_i^2	S_i^3	S_i^6	Top	Mid	Low	Ranksum
XAN-311	144.75	33.15	3.11	11	6	83	10
XAN-310	309.25	63.25	6.31	39	17	44	17
DICTA-109	234.12	62.41	6.13	33	22	45	17
DOR-811	171.75	40.94	5.15	28	28	44	11
XAN-307	139.81	31.13	3.72	6	11	83	10
EMP-388	169.62	36.30	3.83	6	22	72	17
XAN-316	177.75	41.10	3.96	11	17	72	22
DOR-564	199.12	45.20	4.52	22	11	67	17
SEQ-35	144.14	29.99	2.91	6	11	83	26
RAZ-54	156.64	32.80	3.33	6	0	94	18
DOR-364	193.31	50.74	4.80	17	17	66	13
DOR-548	165.50	32.34	3.51	0	28	72	19
DOR-526	211.45	43.99	4.54	22	22	56	17
DOR-527	259.64	64.04	5.44	22	17	61	20
EMP-376	165.25	38.38	3.78	6	17	77	15
Redwolayta	190.14	44.43	3.97	17	6	77	23

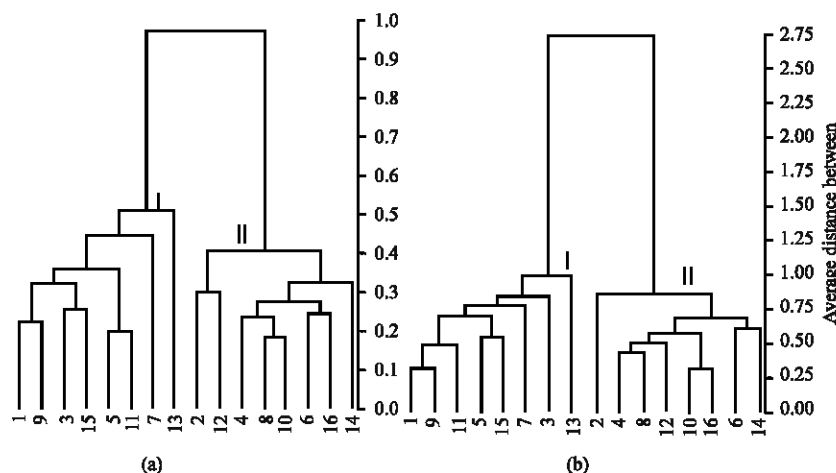


Fig. 1: Clustering of genotypes (a) using the GL interactions weighted by the square root of Wickes Ecoalence according to Abou-El-Fittouh *et al.* (1969) and (b) using yields adjusted for genotype means and weighted by the standard deviation according to Fox and Rosielle (1982). Genotypes are denoted with Arabic number 1-16: 1 = XAN-311, 2 = XAN-310, 3 = DICTA-109, 4 = DOR-811, 5 = XAN-307, 6 = EMP-388, 7 = XAN-316, 8 = DOR-564, 9 = SEQ-35, 10 = RAZ-54, 11 = DOR-364, 12 = DOR-548, 13 = DOR-526, 14 = DOR-527, 15 = EMP-376, 16 = Redwolyata

The use of this statistics in the present analysis did not identify a single genotype that fit to all the test locations. XAN-310, DICTA-109 and DOR-811 recorded relatively the highest TOP values of the trial. However, the proportion of the locations these genotypes occurred mostly in the top third is less than 50%. Hence, TOP values are not strongly enough to consider the three best yielding genotypes as widely adapted. Kang's rank sum method identified genotypes XAN-311, XAN-307, DOR-811 and DOR-364 as the most desirable combining high yield with consistent performance where as SEQ-35 as least desirable genotype not combine high yield and consistence performance (Table 4).

Interrelationship Among the Genotypes

The clustering analysis by Abou-El-Fittouh *et al.* (1969) and Fox and Rosielle (1982) methods could classify the 16 genotypes into two groups (Fig. 1). Cluster I included genotypes XAN-311, SEQ-35, DICTA-109, EMP-376, XAN-307, DOR-364, XAN-316 and DOR-526. The second cluster included genotypes XAN-310, DOR-811, DOR-564, DOR-548, RAZ-54, EMP-388, DOR-527 and Redwolyata. The clustering of genotypes could probably explain similarities in selection histories and origins. All test genotypes were from CIAT origin and hence had similar selection environments at their early and advanced stage of breeding that could lead to similarity in their adaptation pattern. The genotypes in cluster II had higher mean yield as compared to the first cluster.

Test Locations Characterization

Clustering of the locations and their testing ability were assessed with GGL biplot (Fig. 2 and 3) and correlation (Table 5) analysis. Figure 2 shows the interrelationship among the test locations with respect to their discriminativeness and representativeness. On a biplot display, the cosine angle between vectors (i.e., lines that connect the locations marker to biplot origin) of any two location approximates their correlation in ranking to the genotypes and the vector length, which is proportional to the standard deviation within the respective environments, estimates the discriminating ability of the locations (Yan and Tinker, 2006). Thus, Awassa and Ambo in year 2002 and Awassa, Areka and Melkasa in 2003 were most discriminating locations. The least discriminating locations were Ziway,

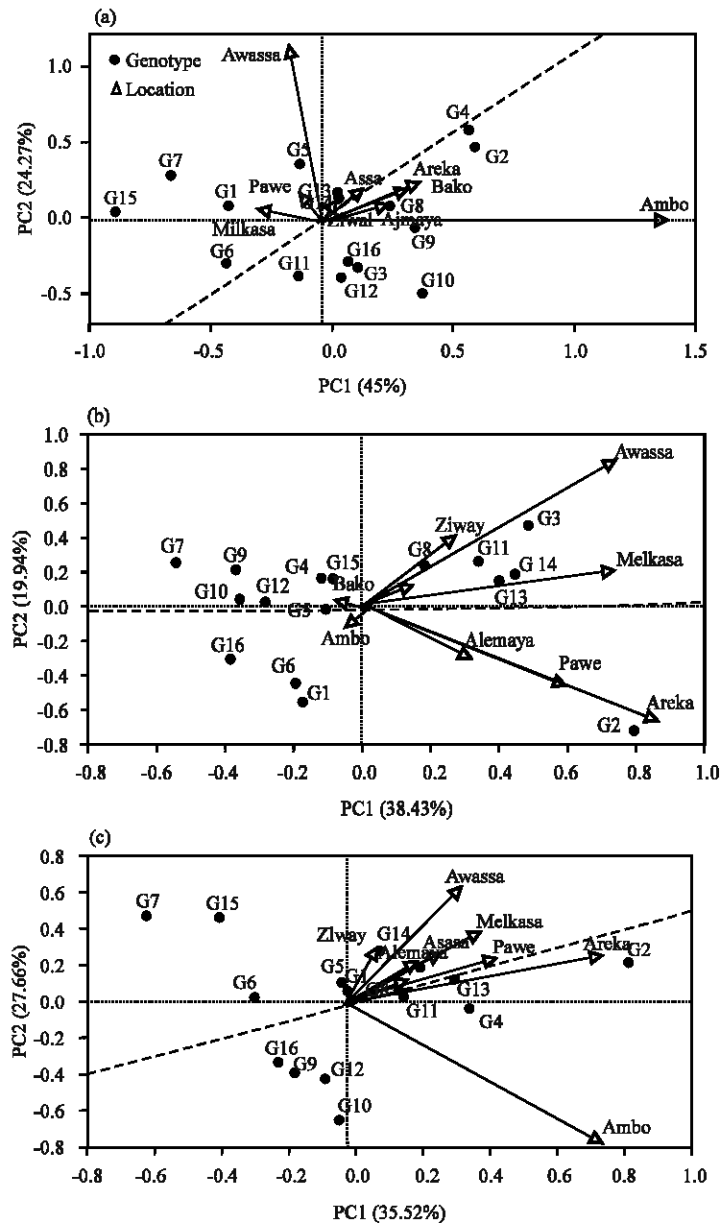


Fig. 2: Genotype plus genotype x location (GGL) biplot obtained from site regression (SREG) analysis showing interrelation among test locations in terms of discriminating power and representativeness. (a) year 2002 data, (b) 2003 and (c) location mean yield averaged over years. The locations are indicated by their name (Lower case letters). Genotypes are denoted by G1 to G16 Upper case letters: G1 = XAN-311, G2 = XAN-310, G3 = DICTA-109, G4 = DOR-811, G5 = XAN-307, G6 = EMP-388, G7 = XAN-316, G8 = DOR-564, G9 = SEQ-35, G10 = RAZ-54, G11 = DOR-364, G12 = DOR-548, G13 = DOR-526, G14 = DOR-527, G15 = EMP-37 6, G16 = Redwolyata

Table 5: Correlation coefficients between Pairs of Locations (above diagonal between location correlations in year 2003, below diagonal in year 2002 and diagonal within location over years)

Location	Alemaya	Ambo	Areka	Asasa	Awassa	Bako	Pawe	Melkassa	Ziway
Alemaya	0.19	-0.34	0.46	0.33	-0.07	-0.01	0.27	0.51*	0.20
Ambo	0.35	0.41	-0.04	-0.20	0.10	-0.06	0.26	-0.12	-0.40
Areka	0.11	0.50*	0.45	0.15	0.23	-0.20	0.68*	0.46	0.02
Asasa	0.04	0.23	0.71*	0.39	0.38	0.30	0.05	0.58*	0.43
Awassa	0.13	-0.12	0.13	0.18	-0.09	-0.18	0.18	0.58*	0.26
Bako	0.25	0.60*	0.61*	0.58*	0.17	-0.09	0.17	-0.12	0.32
Pawe	-0.04	-0.14	-0.08	0.11	0.16	0.28	0.13	0.52*	0.23
Melkassa	-0.46	-0.29	-0.16	0.15	0.06	0.05	0.45	-0.06	0.51*
Ziway	0.51*	0.17	0.38	0.48	0.51*	0.21	0.18	-0.11	0.52*
No of Corr. ^a	2	2	4	3	2	3	2	5	4

*Significant at 5% probability level, ^aNo of +ve and significant correlations with other locations

Melkassa, Pawe and Asasa in 2002 and Bako, Asasa and Ambo in 2003. The pattern of discriminating ability of the test locations was not repeatable over year except for Awassa and Asasa. Awassa and Asasa expressed most and less genotype-discriminating ability over years, respectively. Based on averaged data over years Awassa, Areka and Ambo were most informative, Melkassa and Pawe intermediate and the rest locations were least informative (Fig. 2). The wide obtuse (>90°) angles between Ambo and Awassa in both years indicated crossover genotype by location interaction and their very dissimilarity in maximizing the variance among the genotypes in the study. Among the test locations Asasa, Ziway and Bako in 2002 and Bako, Ambo, Asasa and Melkassa in 2003 were more representative of other test locations (based on the absolute difference between location markers and the mean location axis) (Fig. 2). Awassa in both years was least representative of the overall locations. The genotypes expressed the highest performance at Awassa in both years.

The polygon drawn by a straight line connecting markers of genotypes that were furthest from the GGL biplot origin and a perpendicular line to each side of the polygon starting from the biplot origin delimiting the polygon into different sectors were used for identification of mega-locations (group of locations that share the same best genotypes) for small red bean cultivar evaluation. This was done for each year separately to see its repeatability and for mean location data averaged over years. The pattern of locations in biplot in Fig. 3 suggested the existence of mega-locations for small red bean variety evaluation. In year 2002, the test locations were clustered in to four mega-locations where Awassa and Pawe in one cluster, Asasa, Ziway, Bako, Areka and Alemaya in another cluster and Ambo and Melkassa each as single independent mega-locations. Accordingly, G5 (XAN-307) at Awassa and Pawe, G4 (DOR-811) at Areka, Alemaya, Ziway, Asasa and Bako, G15 (EMP-376) at Melkassa and G10 (RAZ-54) at Ambo were winner genotypes. Year 2002 was a bad year for bean production in which the crop suffered a lot from intermittent drought occurred during the season (Table 1). In year 2003, which was good environment for bean production, the test locations were clustered in to four mega-locations. Areka, Pawe, Alemaya and Melkassa in one sector with G2 (XAN-310) as winner genotype and Awassa, Asasa and Ziway in other sector with winner genotype G3 (DICTA-109). Bako and Ambo each represented independent mega-location sector with G7 (XAN-316) and G1 (XAN-311) as winner genotypes, respectively. The pattern of location clustering varied across years. Clustering pattern of Alemaya with Areka and Asasa with Ziway repeated over years. Alemaya and Areka were intermediate and Asasa and Ziway were poor environments for the genotypes to express their full potential in the trial.

The GGL biplot analysis based on averaged data over two years delimited the test locations in two mega-locations: Ambo in one sector and the rest eight locations in other mega-locations sector (Fig. 3). Genotype XAN-310 (indicated as G2 in biplot Fig. 3) was identified as desirable genotype for all the locations except Ambo. Ambo was negatively correlated with majority of the test locations and had only one particular correlation repeated over years (Table 5). Therefore, Ambo could be considered as most different environment in relative to other test locations for small red bean evaluation. Bako, Awassa and Melkassa had positive correlations with other locations in many

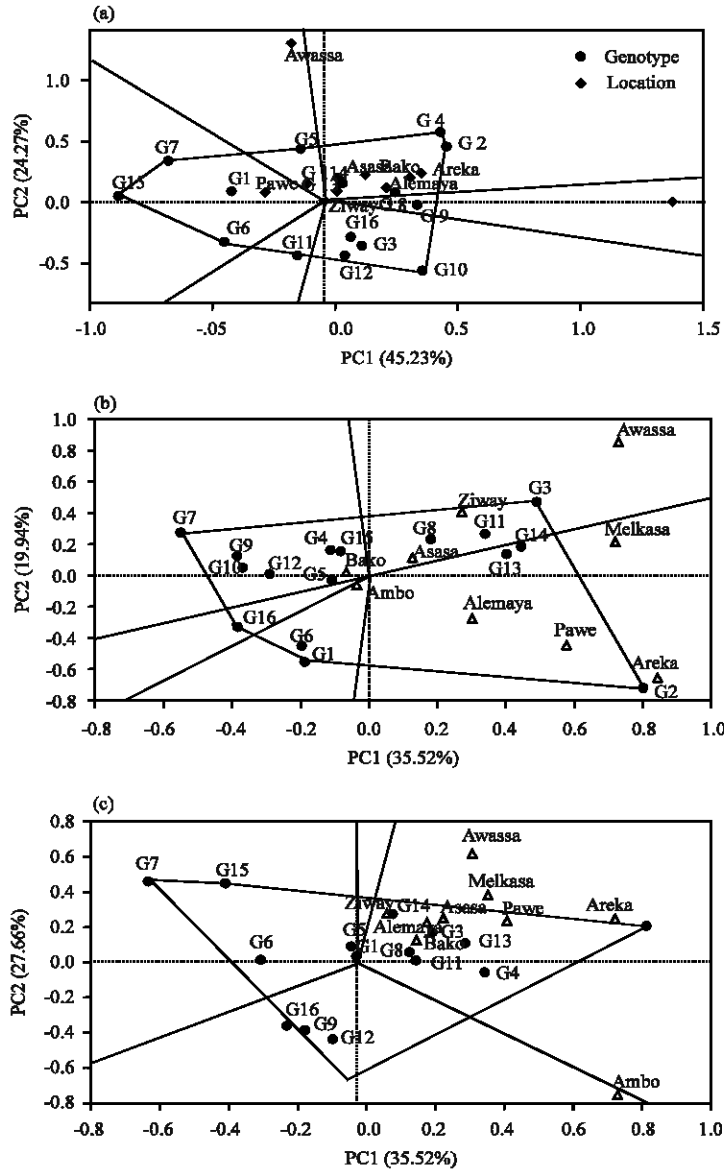


Fig. 3: Genotype plus genotype x location (GGL) biplot obtained from site regression (SREG) analysis showing mega-locations and their winning genotypes. (a) Year 2002 data; (b) year 2003 and (c) location mean yield averaged over years. Location and genotype specification as of Fig. 2

of the cases. The pattern of correlations with other locations relatively repeated over years for these three locations. However, Bako had least discriminative power over years (Fig. 2).

DISCUSSION

Understanding the performance stability and adaptability of genotypes to different production environments facilitate targeting the genotypes onto its growing environments in breeding programs.

To have this understanding, the present study employed different stability analyses ranging from univariate nonparametric to multivariate parametric using the grain yield data from nine locations repeated over two years. The measured yield of each genotype in each test location over years is a function of genotype main effect, location main effect, year main effect and the interactions (Yan, 2002). Location had a larger role to play than other sources of variation in determining yield in present study indicating it as a relevant entity in small red bean variety evaluation. Typically, environment (location) explains most (up to 80% or higher) of the total yield variation in multi-environment trials (Yan, 2002). Moreover, the LY effect was the second main contributor to yield variation in the trial (Table 2). This suggests the need to evaluate bean genotypes in national trials more than one year for more reliable inference on performance. The present result is not in agreement with the earlier report by Setegn and Habtu (2003), in navy beans who suggested the relevance of years rather than locations in cultivar evaluation. It is obvious that locations are physical entities with their own edaphic and climatic characteristic and the ultimate target for the final variety release (Lin and Binns, 1988b; Hussein *et al.*, 2000). Years within locations are unpredictable and selecting genotypes for high yielding and low yielding years could be non-sense. Hence, the present study suggests the need for evaluation of genotypes for more than one year at multiple test locations that are very representative of the target set of environments and good enough in discriminating the potential of test genotypes for reliable inference to be made on the performance.

Representativeness of the test locations in relative to target set of environments and their differentiating ability of the potential of genotypes are very crucial elements for considering locations in variety performance trials. An ideal location should be both highly discriminating of the genotypes and representative of the target production environments (Yan *et al.*, 2007). Subjecting the bean grain yield data for SREG GGE model analysis revealed non-repeatability on the pattern of representativeness and discriminating ability of the nine test locations over years except for few locations (Fig. 2, 3). The location effects on a genotype depend on its edaphic as well as climatic factors (Lin and Binns, 1988b; Hussein *et al.*, 2000). The edaphic factors are relatively consistent from year to year and could be considered as predictable whereas the climatic factors are highly variable and unpredictable (Lin and Binns, 1988b). This beckons the difficulty in identifying a genotype that performs best at all locations when evaluated over years. To this end, the result from present study surmises the existence of complex mega-locations that involved crossover GL interactions that are not repeatable over years. This requires distinct test sites to select cultivars that are superior across the whole region (Yan and Rajcan, 2002). Accordingly, Pawe, Melkassa, Areka, Alemaya and Awassa are good enough in differentiating the genotypes and moderately representative of the conditions of other locations in national variety trial (Fig. 2). These locations representing major bean production areas from eastern, rift valley and western part of the country are preferably good for reliable genotype evaluation. Moreover, these locations were clustered in one mega-location with mean data averaged over year's analysis. Genotype by location mean averaged over years is biological equivalent of genotype x predictable variation (Lin and Binns, 1988b). Asasa and Ambo represent the high altitude areas which marginal to bean production seldom provide unique information on genotype performance seems unnecessary locations for small red bean cultivar evaluation. Bako identified as the most representative and relatively less informative among the nine locations in both years preferably be good location for selection during segregating generations. On other hand, Awassa located in center of the countries bean production belt in the rift valley preferably most informative in differentiating the small red bean genotypes. This suggests Awassa as ideal location for culling genotypes based on the genetic potential in initial multi-location trials.

Needless to mention, both non-parametric and parametric models were very effective for studying the pattern of genotype by environment interaction and interpreting of small red bean grain yield data from multi-location trials. Application of different model analysis in present study aided in

determination of the relative performance of genotypes at a specific environment, comparison of the performance of genotypes at different environments and identification of genotypes suitable for group of environments. Different models interpreted the adaptation pattern of genotypes not exactly in similar manner. However, XAN-311 and XAN-307 combined average mean yield with lowest estimates of $S_i^{(2)}$, $S_i^{(3)}$ and $S_i^{(6)}$ (Table 4), W_i , CV_i and σ_i^2 values (Table 3) could be selected for target set locations ranging from less unfavorable and moderately favorable environmental conditions. The Tai's α and λ statistics classified the two genotypes in average stability. GGE biplot identified XAN 310 as desirable genotypes for majority of the test locations.

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