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Original Research

Multivariate Analysis as a Tool for Indirect Selection of Common Bean Genotypes (*Phaseolus vulgaris* L) for Soil Acidity Tolerance under Field Conditions

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Abstract

A field experiment was conducted to evaluate soil acidity tolerance of 25 common bean (*Phaseolus vulgaris* L.) genotypes on lime-treated and lime-untreated acid soils. The twenty-five common bean genotypes were tested in a randomized complete block design with two replications per treatment in 2009 in western Ethiopia. Morpho-agronomic parameters were recorded to evaluate the genotypes. Multivariate methods, including principal component and cluster analysis were used to assess the patterns of morpho-agronomic variation to group the genotypes into distinct categories. The genotype bi trait (GT) bi-plot was used to identify the best traits that are important to identify tolerant genotype and to know the relationships between traits and genotypes. The principal component analysis indicated that the first three principal components contributed 64.6 and 66.1% of the total variability among the 25 common bean genotypes grown on the lime-untreated and lime-treated soils, respectively. Among the measured traits, plant height, number of pods per plant, days to pod setting, grain yield, days to flowering and maturity, biomass yield, and 100 seed weight were the parameters that most significantly caused the variations among the genotypes. Genotype by trait (GT) bi-plot led to grouping of the tested genotypes into four categories based on PC1 and PC2 values and also enabled to identify traits such as number of pods per plant, plant height, pod length, 100 seed weight, and grain yield, which were found to be the most responsive characters in evaluating the genotypes for tolerance to soil acidity. The cluster analysis led to classification of the 25 common bean genotypes in to four groups, the first group (cluster) of which contained four genotypes of BILFA material (new BILFA 38, new BILFA 58, New BILFA 61, and new BILFA 60) that outperformed genotypes in the other group (clusters) when grown on lime-untreated acid soil. In conclusion, the results of this study have revealed that multivariate analysis can be used as an indirect method of selecting high-yielding common bean genotypes having the most important desirable traits that contribute to soil acidity tolerance.

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is a grain legume grown on more than four million hectares annually in Africa (Buruchara *et al*., 2011). It provides dietary protein for over 100 million people in rural and poor urban communities, with an annual per *capita* bean consumption of 50 - 60 kg in Eastern Africa, which is the highest in the world (ISAR, 2011). Acid soils may account for as much as 50% of the world's potentially arable land (Dahlgren *et al*., 2004). However, aluminium toxicity is a major problem constraining crop production in acid soils. This problem is exacerbated by the current extensive use of ammonium fertilizers and acid rain (von Uexkull and Mutert, 1995). There are two most common ways to mitigate Al toxicity: liming and use of tolerant cultivars. Detoxification of Al by liming is possible in surface soil in the field to a pH 5.5 or above. However, liming does not remedy for sub soil acidity and it may not always be practical or cost effective (Tesfaye *et al*., 2001). Under such situations, use of tolerant cultivars may be a satisfactory solution to this problem. Use of tolerant genotypes and breeding of crops for aluminium tolerance is a reliable approach to enhance production on acidic soils (Choudhary *et al*., 2011).

The genotype-by-trait (GT) biplot proposed by Yan and Kang (2003) is a powerful statistical tool for evaluating cultivars based on multiple traits and for identifying those that are superior in certain traits and hence could be used as parents in breeding programmes or directly released for commercial production. Genotype by trait analysis allows visualization of the genetic correlation among traits (Lee *et al*., 2003) and evaluation of genotypes on the basis of multiple traits (Ober *et al*., 2005). It also provides information on the usefulness of cultivars for production and also helps to detect less important (redundant) traits, and identifies those that are appropriate for indirect selection for a target trait (Badu-Apraku and Akinwale, 2011).

There are no specific varieties for cultivation in these problem areas. Available literature on Al toxicity is only a few and also not well documented. The present paper provides multivariate analysis as an indirect selection method for soil acidity tolerance in common bean genotypes under field conditions. In the present study, a set of different inbreed lines and released varieties were used to describe genotypic evaluation on the basis of multiple traits using principal component analysis, cluster analysis and the GT biplot techniques was described by Yan *et al*. (2000) to reveal the interrelationship among common bean genotypes in grain yield and traits under acid soil and to compare genotypes on the basis of multiple traits for soil acidity tolerance.

MATERIALS AND METHODS

Description of the Study Site

The field study was conducted at Nedjo TVET College, which is located in west Wollega Zone of the Oromia Regional State in Ethiopia at the latitude of 9°5'N and longitude of 35°45'E. The site has an elevation of 1735 meters above sea level with a gently undulating slope (0-5%). The rainfall distribution is mono-modal with the long rains occurring from April to October (Figure 1). The annual rainfall during the experimental period was 1386 mm with mean minimum and maximum temperatures of 12°C and 26°C, respectively. The soils are acidic (pH, 4.45), well drained, deep, and reddish brown in colour.

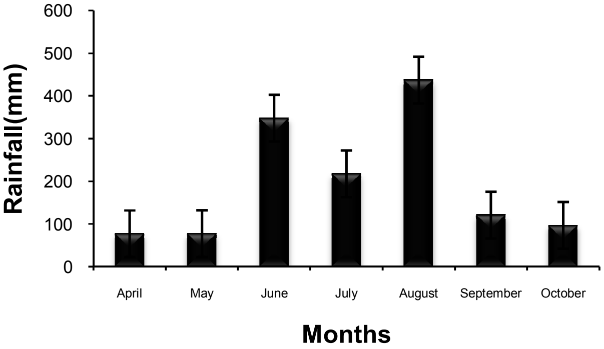


Figure 1: Rainfall distribution of the experimental area (Nedjo) during 2009 cropping season, west Wollega zone, Ethiopia.

Planting Material

Twenty-five common bean varieties and bred-lines were evaluated against soil acidity under field conditions. The improved genotypes included in the evaluation were varieties released by Melkassa and Bako Agricultural Research Centres. To have a sizable variability among the genotypes, accessions or varieties that were assumed to be sensitive, resistant, and mildly resistant to soil acidity were included. All genotypes included in the evaluation have a bushy and semi prostrate growth habit, and vary in seed colour and size. The genotypes were evaluated based on growth, yield, and yield components.

Treatments and Experimental Design

The treatments consisted of 25 genotypes (Table 1) and two types of soil amendment (lime-treated soil and lime-untreated soil). The experiment was laid out as a randomized complete block design and replicated two times per treatment. Each plot consisted of three rows of bean plants occupying a 2 m long distance and a 1.2 m width. The distance between successive plots and adjacent blocks were 1.0 m and 1.5 m, respectively. The spacing between plants and rows was 10 cm and 40 cm, respectively.

Planting

Two seeds of the common bean genotype were sown at each planting hole at the spacing of 40 x 10 cm in all plots. Two weeks after planting, the seedlings were thinned to one per hill, thereby retaining the recommended population of 250,000 common bean plants per hectare. At the time of planting, the soil was fertilized with phosphorus at the rate of 92 kg P_2O_5 per hectare. All other recommended agronomic management practices were applied uniformly to all genotypes grown in the field. The first weeding was done two weeks after germination, and then weeding was performed as required until the plants started flowering.

Table 1: Common bean genotypes screened for soil acidity tolerance on field at Nedjo during 2009.

No	Genotype	Seed Source	Provenance	Growth Habit	Adaptation Environment	Seed Colour	Type of Germplasm
1	New Bilfa 38	MARC	CIAT	III	LSF	pinto	inbred line
2	New Bilfa 57	MARC	CIAT	II	LSF	cream	inbred line
3	New Bilfa 50	MARC	CIAT	III	LSF	red	inbred line
4	New Bilfa 60	MARC	CIAT	III	LSF		inbred line
5	New Bilfa 58	MARC	CIAT	III	LSF	yellow	inbred line
6	Gabisa (Vax-2)	BARC	CIAT	II	WE	tan	released
7	New Bilfa 51	MARC	CIAT	III	LSF	black	inbred line
8	New Bilfa 61	MARC	CIAT	III	LSF	dark	inbred line
9	New Bilfa 45	MARC	CIAT	II	LSF	black	inbred line
10	New Bilfa 46	MARC	CIAT	II	LSF	red	inbred line
11	Awash 1(G4445)	MARC	CIAT	II	CRV	white	released
12	Awash Melka (PAN182)	MARC	CIAT	II	ABGR	White	released
13	Argane (AR04GY)	MARC	CIAT	II	CRV & SA	White	released
14	Nasser (Dicta-105)	MARC	CIAT	III	ABGR	Red	released
15	Dimitu (DOR-554)	MARC	CIAT	II	ABGR	Red	released
16	Dinknesh (RAB484)	MARC	CIAT	II	CRV & SA	Red	released
17	Roba 1(A176)	MARC	CIAT	II	ABGR	Cream	released
18	Beshbesh(XAN x BAT85)	MARC	CIAT	II	SE	Cream	released
19	Anger(EMP-376)	BARC	CIAT	I	WE	Dark red	released
20	Chore (STTT-165-92)	MARC	CIAT	II	ABGR	White	released
21	SER 16	MARC	CIAT	II	DS	Red	inbred line
22	SEA 5	MARC	CIAT	II	DS	cream	inbred line
23	SER78	MARC	CIAT	II	DS	Dark red	inbred line
24	SER 128	MARC	CAIT	II	DS	Dark red	inbred line
25	SER 176	MARC	CIAT	II	DS	Red	inbred line

Growth habits I determinate bush; II indeterminate bush; III indeterminate prostrate, MARC Melkassa Agricultural Research Centre; BARC Bako Agricultural Research Centre; CIAT International Centre for Tropical Agriculture; CRV-Central Rift Valley; DS drought stress; SE Southern Ethiopia; WE Western Ethiopia; ABGR all bean growing regions; LSF = low soil fertility

Data Collection and Measurements

Data were recorded on the number of days required for emergence, flowering, and physiological maturity. The number of days required for emergence was determined by counting when at least 50% of the seedlings emerged above the soil. The number of days required for flowering was determined when at least 50% of the plants in a plot had at least one open flower. The duration in days required for physiological maturity was determined when at least 75% of the plants in each plot senesced and had at least 90% of the plants had dry pods (Tesso, 2007). Plant height and leaf area were recorded from five plants taken from each plot just at flowering. LAI was calculated as the ratio of total leaf area to ground area occupied by the plant. Leaf area was determined at 50% flowering using CID-202 leaf area meter (CID, Inc., USA).

At harvest, the number of pods and primary branches per plant were recorded from five randomly selected plants from each plot. The number of seeds per pod was determined from 10 randomly selected pods from each plot. Pod length was measured from the exterior distance of a fully matured pod from the pod apex to the peduncle in centimetres. Grain yield was recorded from the entire plot after counting the number of plants harvested from each plot. Hundred seed weight was determined from 100 seeds randomly sampled from all plants harvested per plot. Harvest index (HI) was calculated as the proportion of seed weight to the above ground dry weight (stem + leaves + pod + seed) at harvest. Pod harvest index was calculated as the weight of dry pod (seed + pod shell) divided by the total above ground biomass.

Statistical Analysis

Multivariate analyses such as PCA and cluster analysis were performed on the variables collected. The PCA was based on Pearson correlation matrix and Euclidean distances. Latent roots or Eigenvalue for all principal components were shown. Eigenvectors generated by the PCA were used to identify parameters that best differentiated the genotypes for soil acidity tolerance. The first two PC scores, i.e., PC1 and PC2 that accounted for maximum variability of the parameters tested were used to group the genotypes by genotype by trait biplot. Genotypes that had +PC1 and +PC2 scores were classified as tolerant; those with +PC1 and –PC2 scores were classified as moderately tolerant; those with –PC1 and +PC2 were classified as moderately susceptible. Genotypes with –PC1 and –PC2 were classified as susceptible (Uguru *et al*., 2012). Based on the value of the PC1 and PC2 scores, biplot using PC1 as a vertical axis and PC2 as horizontal axis were constructed. Cluster analysis was performed using the SAS software (SAS, 2004).

RESULTS

Principal Component Analysis

Principal component analysis (PC) was performed to identify the major components (i.e. principal components) that could explain much of the total variations observed in the data. Fifteen measured agronomic data obtained from lime-treated as well as lime-untreated plants of each genotype were subjected to principal component analysis. Five and four principal components (80.6 and 77.7%) for both lime-untreated and lime-treated soils, respectively, which were captured for the major variations in the whole data set of the variables, were identified (Table 2 and 3). Certain parameters had high coefficients of correlation with only one principal component, but a few had lower correlation levels with more principal components (Table 2 and 3).

Table 2: Eigenvectors, Eigenvalue, individual and cumulative percentage of variation explained by the first eight principal component (PC) for 15 morpho-agronomic traits of common bean genotypes evaluated under unlimed acid soil on field at Nedjo, western Ethiopia.

Variables	Eigenvectors				
	PC1	PC2	PC3	PC4	PC5
Days to 50 % flowering	-0.18	0.46	0.02	0.14	-0.06
Days to 50 % podding	-0.28	0.65	0.16	0.11	-0.07
Days to 50 % maturity	-0.19	0.37	0.11	-0.26	0.57
Leaf area index	0.01	-0.05	-0.02	-0.09	0.05
Plant height	0.91	0.37	0.16	-0.001	-0.03
No. branches/plant	-0.01	0.01	0.01	0.001	0.03
No. pods/plant	0.04	0.02	0.48	-0.28	0.49
No. seeds/plant	-0.01	0.01	0.05	-0.04	-0.05
Pod length(cm)	-0.03	0.05	-0.07	0.17	-0.05
100- seed weight(g)	0.09	-0.05	-0.26	0.77	0.53
Grain yield(g plant^{-1})	-0.02	-0.17	0.44	0.20	0.16
Grain yield(t ha^{-1})	-0.01	-0.01	-0.04	0.11	0.05
Biomass yield(t ha^{-1})	-0.1	-0.08	0.64	0.38	-0.32
Pod harvest index	-0.01	-0.01	0.04	0.02	0.04
Harvest index	0.001	-0.01	0.01	0.002	0.012
Eigenvalue	5.54	2.38	1.769	1.321	1.07
Individual % variation explained	36.9	15.9	11.8	8.8	7.2
Cumulative % variation explained	36.9	52.8	64.6	73.4	80.6

Where- PC- Principal component

Table 3: Eigenvectors, Eigenvalue, individual and cumulative percentage of variation explained by the first eight principal component (PC) for 15 morpho-agronomic traits of common bean genotypes evaluated under limed acid soil on field at Nedjo, western Ethiopia.

Variables	Eigenvectors			
	PC1	PC2	PC3	PC4
Days to 50% flowering	-0.04	-0.05	0.23	-0.07
Days to 50% pod setting	-0.09	-0.15	0.58	-0.02
Days to 50% maturity	-0.07	-0.32	0.43	0.47
Leaf area index	-0.02	0.05	0.02	-0.01
Plant height	0.98	-0.03	0.13	-0.09
No. branches/plant	-0.01	0.01	0.09	0.001
No. pods/plant	-0.02	0.37	-0.14	-0.09
No. seeds/plant	-0.02	0.05	0.01	-0.04
Pod length(cm)	0.02	-0.01	-0.02	0.10
100 seed weight(g)	0.13	-0.12	-0.42	0.78
Grain yield(g/plant)	-0.01	0.42	-0.15	0.002
Grain yield(t/ha)	-0.01	0.11	-0.04	0.001
Biomass yield(t ha^{-1})	0.03	0.71	0.41	0.36
Pod harvest index	-0.003	0.02	-0.01	-0.004
Harvest index	-0.001	0.01	-0.01	-0.001
Eigenvalue	3.79	2.744	2.054	1.511
Individual % variation explained	29.2	21.1	15.8	11.6
Cumulative % variation explained	29.2	50.3	66.1	77.7

The first PC accounted for about 36.9 and 29.2% of the variance and could be named as components of growth since it contained parameters such as plant height, which had the greatest share of the variance that occurred under both lime-treated and lime-untreated soils (Table 2 and 3). The variable with the highest loading on this component was plant height; this parameter had the largest share in the differences observed among the 25 common bean genotypes. The second PC was associated with growth duration of the genotypes, which accounted for about 15.9 and 21.1% of the variance among the genotypes evaluated under lime-untreated and lime-treated soil conditions, respectively (Table 2 and 3). The highest correlation with this PC was days to 50% pod setting under lime-untreated acid soil (Table 2) and biomass yield (t ha^{-1}) in lime-treated soil (Table 3). In addition to this parameter, days to 50% flowering and maturity had relatively higher correlation with this component in lime-untreated soil (Table 2). The first and second PC alone accounted for about 52.8 and 50.3% of the variance observed among the common bean genotypes screened for soil acidity tolerance under lime-untreated and lime-treated soil conditions, respectively.

The third PC directly related to biomass yield in lime-untreated soil, and days to 50% pod setting, in lime-treated soil (Tables 2 and 3). This PC accounted for about 11.8 and 15.8% of the variance among the genotypes under lime-untreated and lime-treated soils, respectively. Grain yield and number of pods per plant in lime-untreated soil, and days to physiological maturity and biomass yield in lime-treated soil had strong correlations with the third PC (Table 2 and 3).

Fourth PC was named as a component related to 100 seed weight in both lime untreated and lime-treated soils. This PC contributed 8.8 and 11.6% of the total variation of the genotypes for lime-untreated and lime-treated soils, respectively. The most important parameter that had a high loading value in this component was 100 seed weight in both lime-untreated and lime-treated soils (Tables 2, 3). From this result, it could be assumed that genotypes that had heavier seeds may have the potential for soil acidity tolerance since they produced higher grain yields under lime-untreated soil (new BILFA 58 and new BILFA 38). Physiological maturity and number of pods per plant had a higher loading in the fifth PC for lime-untreated soil.

Trait Relationships

The genotype by trait (GT biplot) revealed that the largest variation explained by biplot came from grain yield, plant height, 100 seed weight, pod length, above ground biomass yield, and harvest index as indicated by the relative length of their vectors. It is the interrelationships among these traits that are most relevant to screen acid soil tolerant common bean genotypes in breeding programmes. The most prominent relations revealed by the GT biplot were a positive association among grain yield, plant height, pod length, 100 seed weight, and number of pods per plant as indicated by the acute angles. On the other hand, high values for pod shell proportion, days to flowering and maturity and seed number per pod were considered inferior in this study (Figure, 2). This is because high values for these traits were found to be undesirable for obtaining high grain yield under lime-untreated acid soil (Figure 2 and 3). The genotype by trait biplot display based on the plot of PC2 on PC1 led to classification of the genotypes in to four groups, namely, genotypes with the highest soil acidity tolerance, genotypes having mild soil acidity tolerance, genotypes with mild susceptibility to soil acidity, and genotypes that are susceptible to soil acidity (Table 4)

Table 4: Classification of 25 common bean genotypes based on the scores of the first two principal components (PC1 and PC2) (Figure 1) under lime untreated acid soil.

Tolerant (+PC1, +PC2)	Moderately tolerant (+PC1, -PC2)	Moderately susceptible (-PC1, +PC2)	Susceptible (-PC1, -PC2)
SER128	New BILFA 38	Roba 1	Nasser
Dimtu	New BILFA 58	New BILFA 45	Anger
New BILFA 51	New BILFA 51	Awash I	SEA 5
Beshbesh	New BILFA 60	Argane	New BILFA 46
SER78	SER 176	Chore, Awash Melka	SER 16
	New BILFA 57	New BILFA 50, Gabisa	

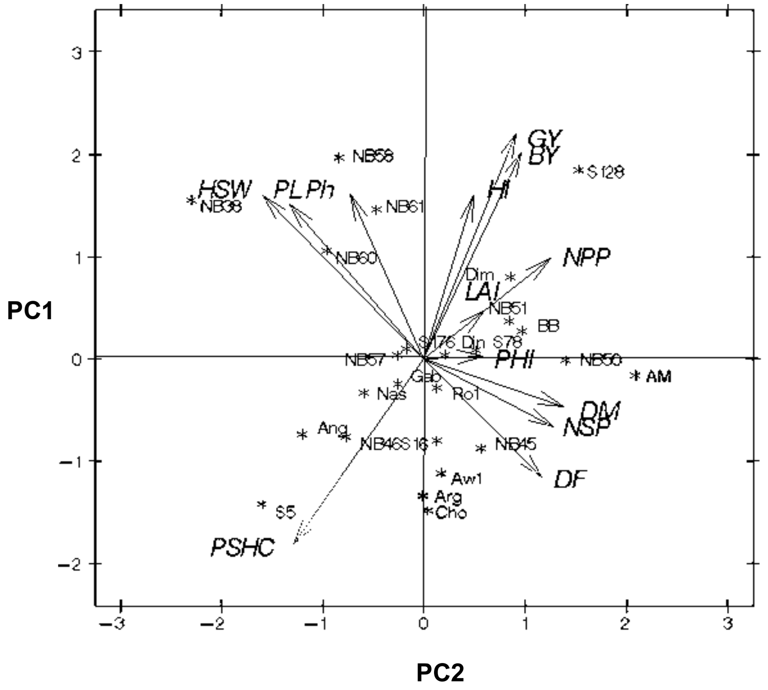


Figure 2: Genotype by trait (GT) biplot of the twenty-five common bean genotypes grown under lime-untreated acid soil at Nedjo on field, Western Ethiopia.

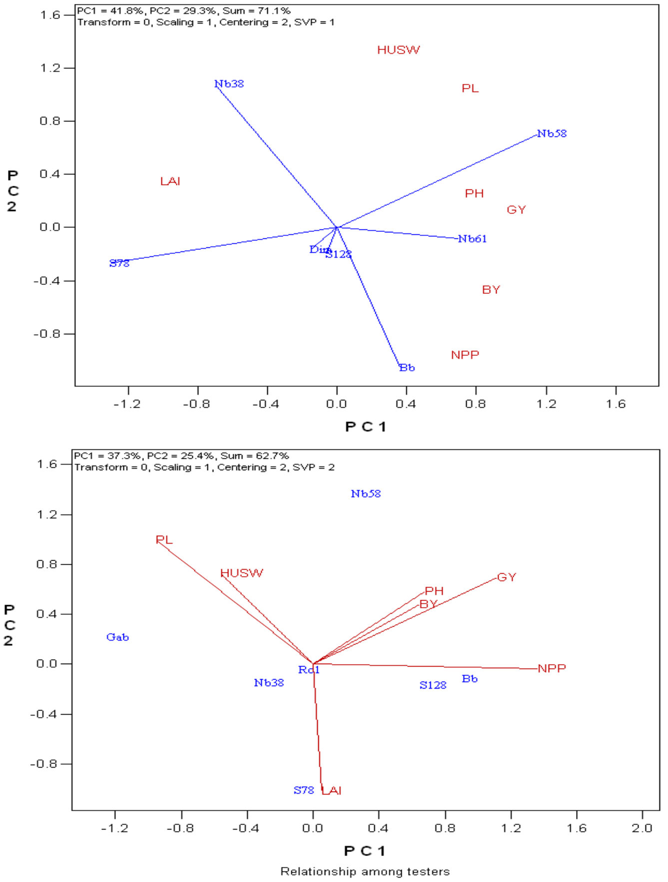
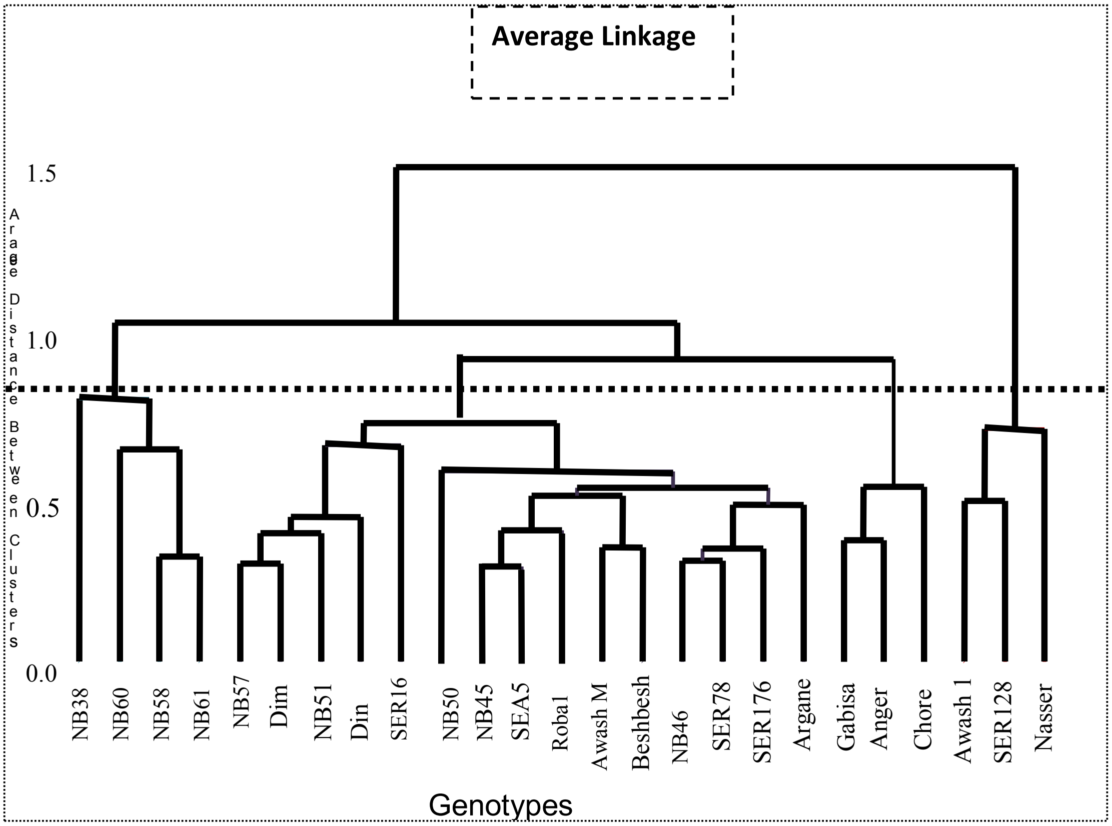


Figure 3: Relationship among entries (1st graph) and testers (2nd) for selected genotypes grown under lime untreated soil on strong acid soil.

Cluster Analysis

To determine similarities or differences among cultivars/populations, a cluster analysis was performed. The clustering obtained by SAS average method for the lime-untreated genotypes is shown in Figure 4. The dendrogram based on the morpho-agronomic traits allowed categorization of the twenty-five common bean genotypes in to four main clusters (Figure 4). Genotypes were displayed with an average distance in clusters ranging from 0 to 1.50 units (Figure 4).Clear distinctions were discerned among the genotypes, with the BILFA materials markedly dispersed in the first and second groups of the dendrogram.

Cluster 1 contained four new BILFA materials (Figure 4). These genotypes were characterized by good growth performance on the field, with indeterminate prostrate (type III growth habit), medium seed weight, relatively taller plants, and earlier days to maturity, longer pod lengths, higher harvest indices as well as grain yields (except new BILFA 60). The three genotypes had almost similar results for all the recorded data, and had a potential for soil acidity tolerance.



NB= new BILFA, Dim= dimitu, Din= Dinknesh,

Figure 4: Dendrogram of the hierarchical cluster analysis for showing similarity value between 25 common bean genotypes grown under unlimed acid soil on field.

Cluster 2 contained 15 genotypes, and was divided into two sub clusters (Figure 4). The first group contained five genotypes, two new BILFA materials, two released varieties and one drought-tolerant SER material. These genotypes had bushy growth habit and small-sized seed with different colours. The second group of cluster 2 contained 10 genotypes, namely three BILFA materials, four released varieties, two SER materials, and SEA material (Figure 4). These varieties had an upright growth habit with small-sized seeds, and are medium yielders under lime-untreated acid soil condition. The varieties that were released by Bako agricultural research centre (Gabisa and Anger) for humid western Ethiopia as well as Chore, which was released by Melkassa Agricultural Research Centre for the rift valley area clustered together in Group 3. These varieties had a bushy growth habit with low yield on lime-untreated acid soil. Cluster 4 contained three genotypes, two released varieties Awash 1 and Nassir and one SER material (SER128). These genotypes were characterized by short pod lengths, early maturity, medium yield potential, and high number of pods per plant and lower 100 seed weight.

DISCUSSION

The existence of morpho-agronomic variations among the common bean genotypes was further substantiated by the principal component analysis when the genotypes were grown under lime-untreated and lime-treated acid soils. In this study, the first three principal components captured 64.6 and 66.1% of the total variation recorded for the genotypes in lime-untreated and lime-treated soils, respectively. Consistent with the results of this study, Castineiras (1990) evaluated 60 common bean cultivars using 34 quantitative and qualitative descriptors and found that the first three components were responsible for 37% of the total variation and that 23 of the 34 descriptors were disposable.

Certain parameters such as days to flowering, days to maturity, plant height, number of pods per plant, 100 seed weight, grain yield (g/plant), and biomass yield in lime-untreated soil, days to maturity, 100 seed weight, and number of pods per plant in lime-treated soil had high coefficients of correlation with more principal components. From this result, it could be assumed that genotypes that had shorter maturity date, taller plants, and heavier seeds have the potential for soil acidity tolerance since they produced high grain yields under both lime-untreated and lime-treated soils. Therefore, the results obtained from the principal component analysis identified important traits that could explain the major variance among the common bean genotypes tested for soil acidity tolerance on strongly acidic soil under field conditions. Consistent with the results of this study, Hornakova *et al.* (2003) also reported that plant height, 1000 seed weight, and days to flowering were the major traits contributing to the diversity assessment of Western and Eastern Carpathian common bean landraces.

The results obtained from the GT biplot of the genotypes grown on the lime-untreated soil identified parameters that could be considered best in discriminating among the genotypes for soil acidity tolerance. A major advantage of the GT biplot analysis is that it provides information that helps to detect less important traits, and identify those that are appropriate for indirect selection for a target trait such as yield (Yan and Rajcan, 2002). A GT biplot is an effective tool for exploring multi-trait data. It graphically displays the genotype by trait relationship and allows the visualization of the associations among traits across the genotypes and of the trait profile of the genotypes (Yan and Kang, 2003). As observed in this study, it appears possible to improve common bean genotypes by selecting genotypes with higher grain yield, number of pods per plant, leaf area index, pod length, plant height, 100 seed weight, and biomass yield. In addition, this study demonstrated that the GT biplot is an excellent tool for visualizing genotype by trait data. First, it effectively reveals the interrelationships among the common bean traits. Second, it provides a tool for visual comparison among genotypes on the basis of multiple traits as suggested by Yan and Reid (2008). Results of the GT biplot analysis indicated that selecting for reduced days to maturity, pod shell proportion and days to flowering, and selecting for increased number of pods per plant, plant height, 100 seed weight and pod length under lime-untreated acidic soil results in genotypes that produce high grain yields under soil acidity.

The GT biplot analyses have been used to compare genotypes on the basis of multiple traits and to identify genotypes or groups of genotypes that are particularly good in certain aspects, and therefore can be candidates for soil acidity tolerance. On a GT biplot, the vector length of a genotype, which is the distance between the genotype and the biplot origin, is a measure of the genotype's peculiarity (i.e. how it differs from an "average" genotype), which is a hypothetical genotype that has an average level for all traits and is represented by the biplot origin (Akcura, 2011). Therefore, genotypes with long vectors are those that have extreme levels for one or more traits. Such genotypes may or may not be superior, but they may be useful as parents (Yan and Rajcan, 2002). As depicted in Figure 3, new BILFA 58 has a higher vector length than the other genotypes, followed by new BILFA 38. Among the important traits identified by the biplot & principal component analysis, pod length, number of pods per plant and grain yield had higher vector lengths followed by plant height and 100 seed weight (Figure 2 and 3).

The dendrogram based on the morpho-agronomic traits allowed the categorization of the twenty-five common bean genotypes in to four main clusters. Genotypes were displayed with an average distance in clusters ranging from 0 to 1.50 units. Clear distinctions were discerned among the genotypes, with the BILFA materials markedly dispersed in the first and second groups of the dendrogram. The classification of the genotypes based on cluster analysis that considered about 16 measured agronomic parameters revealed that the BILFA materials (NB 38, NB61, NB58, and NB 60) were grouped under tolerant genotypes. These classifications are sound as these genotypes did not show any deficiency or stress symptoms on field during the growth period. These genotypes are characterized by good growth performance on the field, with indeterminate prostrate (type III growth habit), medium seed weight, relatively taller plants, and earlier days to maturity, longer pod lengths, higher harvest indices as well as grain yields (except new BILFA 60). The three genotypes had almost similar results for all data recorded, and had a potential for soil acidity tolerance. Corroborating the results of this study, Stoilova *et al*. (2005) showed that the evaluation of phenotypic variability by cluster analysis led to the identification of suitable common bean genotypes and characters for inclusion in breeding programmes.

CONCLUSION

The most reliable traits to select for improved grain yield under acid soil stress were grain yield, plant height, pod length, 100 seed weight, and number of pods per plant. The cluster analysis based on the morpho-agronomic traits grouped the twenty-five genotypes into four groups. The first group contained the BILFA (new BILFA 58, new BILFA 38, new BILFA 60 and new BILFA 61) which had better performance under acid soil whereas the third and fourth groups contained released varieties in Ethiopia (except SER 128), and were poor in yielding ability under acid soil conditions. The most promising common bean genotypes identified in this study for soil acidity tolerance were SER 128, Dimtu, New BILFA 51, Beshbesh, and SER 78.In contrast, Nasser, Anger, SEA 5, new BILFA 46, and SER 16 were found to be genotypes with the highest susceptibility to soil acidity. Therefore, the results of this study revealed that it is possible to select common bean genotypes based on morpho-agronomic data for soil acidity tolerance for enhanced productivity of the crop and income of farmers cultivating the crop on soils affected by acidity. Furthermore, the genotypes selected for soil acidity tolerance in this study could also be used in breeding programmes meant to develop high-yielding varieties of the crop for cultivation under such adverse soil conditions.

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