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Genetic Variability in Soybean (*Glycine max L.*) for Low Soil Phosphorus Tolerance

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ዝቅተኛ የፎስፈረስ መጠን ባላቸው የአፈር ዓይነቶች ላይ የአኩሪ አተር ዝርያዎችን ብዝሃነት ማጥናት በቂ የፎስፈረስ መጠን ካለመኖር ጋር ተያይዞ ያለውን የአፈር ለምነት ችግር የመቋቋም አቅም ያላቸውንና የተሻለ ምርት መስጠት የሚችሉትን ዝርያዎች ለመለየት ዕድል ይፈጥራል። በመሆኑም ይህ ጥናት የተከናወነው ከተለያዩ ምንጮች የተሰባሰቡ የአኩሪ አተር ዝርያዎች ከአሲዳማነት ጋር በተያያዘ የፎስፈረስ እጥረት ያለባቸውን የአፈር ዓይነቶች መቋቋም የሚችሉ ዝርያዎችን ለመምረጥ የሚያስችል ብዝሃነት ስለመኖሩ ለማረጋገጥ ነው። በጥናቱ ውስጥም 36 የሚሆኑ የአኩሪአተር ብዝሃዘሮች በሲምፕል ላቲስ ዲዛይን (simple lattice design) በሁለት ድግግሞሽና የፎስፈረስ እጥረት ባለባቸው በአሲዳማ አፈርነታቸው በታወቁ በሶስት የደቡብ ምዕራብ ኢትዮጵያ አካባቢዎች የተካሄደ ነው። በጥናቱም ተለያይነትን ለማጥናት የሚያስችሉ የተለያዩ ቴክኒኮች ማለትም phenotypic እና genotypic variance እና covariance, cluster analysis, heritability እና genetic advance as percent of mean, ክላስተር እና ፕሪንሲፓል ኮምፖኔንት የተባሉ የመረጃ ትንተና ዘዴዎች በመጠቀም የተሰራ ነው። የተሰራው የመረጃ ትንተና እንደሚያሳየው በዘርያዎቹ ውስጥ ዝቅተኛ የፎስፈረስ ይዘት ላላቸው አሲዳማ አፈር የተሻለ ምርታማነት መስጠት የሚያስችል ተለያይነት ጥናቱ በተካሄደባቸው ብዝሃዘሮች ውስጥ መኖሩን ለማረጋገጥ ተችሏል።

Abstract

Assessment of the genetic variability of soybean genotypes under low soil phosphorus (P) conditions provides an understanding of the genetic potential of the genotypes to improve the crop for low P tolerance. The study was designed objectively to estimate the extent of genetic variability of soybean genotypes for low P tolerance. Thirty six soybean genotypes that were introduced from various sources were grown in simple lattice design with three replications at three locations in Western Ethiopia characterized by P-deficient-acidic soils. It was revealed that weight of 100 seeds; plant height, root and biomass fresh weight exhibited relatively high heritability and genetic advance on low P soils. Principal component analysis also revealed that the first five principal components (PCs) accounted for more than 85% of the total variation. The first principal component that contributed for 37.7% of the total variation was influenced by root fresh weight, tap root length, root volume, fresh biomass weight, days to maturity and days to flowering in the order of importance; indicating the significance of these traits for low P tolerance screening. Cluster analysis grouped the genotypes into four clusters. Observation of large variation and relatively high heritability indicates that selection would be effective to improve soybean varieties for performance on P stressed soils and identify low P tolerant varieties that helps smallholder farmers optimize soybean productivity on P deficient soils.

Introduction

Soybean (*Glycine max* L.) is one of the very important leguminous and oil crops with worldwide importance as food and market crop. This is mainly because of its high grain nutritional value with 40% protein and 20% oil (Fekadu *et al*., 2009) that makes it an important raw material for food and oil processing industries. It is also a very important crop for rotation with cereals like maize and sorghum because of biological nitrogen fixation that is important in improving soil fertility. In addition, soybean provides health benefits in consumption, and is as such also considered as a strategic crop in fighting the worlds' food shortage and malnutrition problems, and most food aids to displaced and malnourished people are fortified with soybean (Thoenes, 2004).

Despite the wide range of benefits that soybean could provide to subsistence farmers of sub-Saharan Africa, its productivity is very low (below 2.0 t ha^{-1}) in many of these countries as compared to more than 2.7 t ha^{-1} productivity obtained in some other countries (FAO, 2013). Several production constraints account for the low productivity of the crop, and of these poor soil fertility that is mainly associated with soil acidity is a very important one. Soybean performs well between pH range of 6 and 7, while the optimum pH range is 6.3 and 6.5 for maximum nutrient availability and nitrogen fixation (Staton, 2012).

Soil acidity limits crop production on more than 50% of the world's potentially arable land and on 12% of the land that is currently under production (von Uexkull and Mutert, 1995). An estimated 40.9% of Ethiopian soil is acidic (Mesfin, 2007) while most of the medium to strong acid soils of the country are found in the Western and Southwestern parts of Ethiopia (van Straaten, 2002, Mesfin, 2007). The effect of soil acidity on crop production arises from a combination of several factors such as: toxic levels of iron (Fe), aluminum (Al) and manganese (Mn); low availability of P; and deficiency of K, Ca and Mg (Andrade *et al*., 2002; Kochian *et al*., 2004; Uexkull and Bosshart, 1982). Batjes (1997) reported that the availability of P is limited to plant roots on two third of the world's cultivated soil. Sample *et al* (1980) and Stevenson and Cole (1999) attributed the low P in most soils to intensive erosion, weathering and P fixation by free Fe and Al oxides in acidic soils.

The application of inorganic P fertilizers is one of the possibilities for addressing the problem of low P availability. However, most farmers of Sub-Saharan African countries have limited capacity to purchase and apply inorganic fertilizers, mainly because of high price, limited availability at the right planting time, and problem of distribution systems (Abush *et al*., 2011). Besides, the non-renewable P reserve is estimated to be exhausted from the soil in the coming few decades (Runge-Metzger, 1995; Vance *et al*., 2003). Lime treatment is commonly used approach in ameliorating soil acidity, to amend the acidity of the soil, and thereby, increasing the availability of applied P. However, due to the large quantities of lime required for such purpose, the approach is highly labor intensive and expensive (Rao *et al*., 1993).

Selection and development of crop varieties that can efficiently utilize the soil P and perform well under low soil P conditions are considered as a sustainable and economical

approach (Wang *et al*., 2010) to withstand the low P availability problem. The availability of genetic variability in a gene pool is a prerequisite for a breeding program (Aditya *et al*., 2011), and is an important factor in obtaining the expected genetic progress from selection. Further, the effectiveness of selection depends on the availability of heritable differences (Dabholkar, 1992). The presence of high genetic variability in soybean that provides good potential to improve several economically important attributes was reported by Verma *et al.* (1993).

Previous studies have also reported high genetic variability in soybean for performance under low P conditions for various economically important attributes (Ding and Li, 1998; Tong *et al*., 1999; Tang *et al*., 2007; Xiang Wen *et al*., 2008). According to Ma *et al.* (2001), root characteristics such as root hair length, density, and other root hair parameters are significantly affected P acquisition efficiency in plants. Wang *et al.* (2004) also studied the genetic variability of two contrasting genotypes of soybean and 88 F_9-derived recombinant inbred lines on moderately low P soil, and reported low heritability for root hair density estimates of basal roots (27.3%), tap roots (31.0%), and total roots (34.0%); while relatively higher genetic variance resulting in higher heritability was reported for the average root hair length estimates of basal roots (53.8), tap roots (59.2%), and total roots (61.0%). This indicated that root hair density characteristics are influenced more by environmental factors than average root length estimates.

Multivariate techniques such as cluster and principal components analyses have been used to assess the genetic variation of genotypes for P efficiency as they provide combined effects of several traits for P efficiency (Xiang Wen *et al*., 2008). Uguru *et al.* (2012) reported the effectiveness of the combination of crop performance and principal component analysis in the identification and characterization of differential genotype responses across diverse environments.

The present study was, therefore, designed to examine the genetic variability of soybean germplasm obtained from various sources and estimate the extent of genetic progress that can be made using these germplasm through selection for soil acidity tolerance.

Materials and Methods

Plant materials

Thirty six soybean germplasm were used in the study. They were obtained from various sources, and 27 of the genotypes were obtained from Hawassa and Pawe Research Centers in Ethiopia (Table 1). These genotypes were introduced into the country from various sources including the International Institute of Tropical Agriculture (IITA) and INTSOY (former International Soybean Research Program coordinated by University of Illinois). Four released varieties *viz*., Davis, Cocker 240, AGS-7-1, and Clark 63 K were included in the study as checks. Five of the genotypes (i.e., H 16, H 3, H 6, IAC 6, and H 7) were obtained from Mozambique Agricultural Research Institute. These materials were originally introduced from Southern China Agricultural University in a collaborative research with Mozambique Agricultural Research Institute on evaluating soybean for P use efficiency on acidic soils with major emphasis on rooting traits.

Table 1. List and source of 36 soybean germplasm used in the low-P tolerance evaluation study across three locations (Jimma, Mettu and Assosa) characterized by low pH, acidic and low phosphorus (P) availability of soils

No.	Germplasm	Source of materials	Description
1	H 3, H 7, H 16, IAC 6, H 6,	Obtained from Mozambique Agricultural Research Institute	These materials were under evaluation for low-P tolerance in Mozambique
2	SCS-1, SR-4-1, Tunia, AGS 234, AGS-3-1, Alamo, HS 82-2136, Bossire-2, AA 7138, Ocepara 4, PR-143 (14), AGS-62, Protana-2, G 9945, IAC 11, AGS-217, PR-162-11, Essex-1, SR-4-3, FB1-7636, OC-78503, TGX-297-6E-1, PR-142 (26), IAC 73-5115, AA-42-52, JSL-1	Materials obtained from the local sources i.e., Hawassa and Pawe Agricultural Research Centers	Materials that were at the hand of local breeding programs which were also introduced from other countries (IITA, Nigeria and Intsoy, USA) at different periods.
3	AGS-7-1, Coker 240, Davis, Hardee-1, Clark 63	Cultivars that are either released or recommended for production in Ethiopia	Included in the study as checks

Experimental sites, design and management

The field experiments were conducted at three locations in Western Ethiopia, namely Jimma, Mettu, and Assosa. These sites were characterized by strong to moderate soil acidity and low P availability (Table 2). The 36 soybean genotypes were evaluated in a simple lattice design with two replications. All the genotypes were evaluated under zero applied P conditions to be able to evaluate the genetic variation of the genotypes for low-P tolerance. The seeds of all the genotypes were uniformly dressed with Rhizobium bacteria to help us understand the N-fixing genetic potential of the genotypes.

There were four rows in each plot of 4 m x 2.4 m with a total plot size of 9.6m^2, and the middle two rows were harvested for collection of post-harvest data such as grain yield and 100-seed weight. Planting was done in rows of four meter long and 60 cm wide, and the recommended 5 cm spacing was maintained between plants. The distance between two plots was 1 m, while 1.5 m was maintained between blocks. Three times hand weeding was done to create a weed-free experimental plot till maturity.

Data collection

The traits studied included: days to 50% flowering, days to maturity, fresh biomass weight taken as the average weight of above ground biomass of five freshly harvested plants at late pod filling stage, pod number as the average of the total number of pods counted on each of the five randomly selected plants, pod length that was the average length of five randomly selected pods from five plants, number of seeds per pod as the average number of seeds of five randomly selected pods from five different plants, plant height, 100-seeds weight, and grain yield. In addition, root characteristics such as root fresh weight, which was the weight of the roots; root volume that is the volume of water displaced from the measuring cylinder by the root, and taproot length, which is the length of the central taproot were measured on randomly selected five plants from each treatment.

Laboratory analysis

Soils from all the experimental sites were analyzed for P content and soil acidity indicators before the experiments were conducted. Soil P was analyzed using Bray II method, N using Kjeldhal method, K using flame photometry, organic carbon (OC) and organic matter (OM) using Walkley and Black's method. In addition, the procedures described by Sahlemedhin and Taye (2000) were followed to analyze soil pH and exchangeable acidity, Al and H. The results of soil analyses are presented on Table 2.

Statistical analysis

Analysis of variances for the individual locations was computed using SAS Statistical Software package (SAS Institute, 2008). Test of homogeneity of error variances for the locations was made using F max test before combined analysis, and error variances of each location were found homogenous. The combined analysis for genotype X location (GXL) interaction was done using SAS software. Phenotypic and genotypic variances and coefficient of variations, broad sense heritability, genetic advance were analyzed using Genes, Quantitative Genetics and Experimental Statistics Software (Cruz, 2009). Square

root transformation was performed for the count data such as number of seeds per pod, and pod number as suggested by Gomez and Gomez (1984).

The formula for phenotypic variance in a single location is:

$\sigma_p^2=\sigma_g^2 + \sigma_{ge}^2 + \sigma_e^2$

where σ_p^2 =phenotypic variance, σ_g^2=genotypic variance, σ_{ge}^2=variance of genotype X environment interaction, and σ_e^2=environmental variance.

However, the phenotypic variance for the combined analysis across locations was estimated as per the formula provided by Hallauer and Miranda (1988):

$\sigma_{ph}^2=\sigma_g^2 + \sigma_{ge}^2/e + \sigma_e^2/re$.

Where: σ_p^2=phenotypic variance, σ_g^2=genotypic variance, σ_{ge}^2=variance of genotype X environment interaction, σ_e^2=environmental variance, r=number of replication and e=number of environments.

Table 2. Results of soil analyses conducted on three samples collected from each of the two experimental sites (Assossa and Mettu) before the experiment

No.	Location	(ppm)	% N	OC	OM	P ppm)	pH H_2O)	Exchangeable		
								idity (meq/ 00 g soil)	l (meq/ 0 g soil)	H (meq/ 100g soil
1	Assossa	10	0.13	2.19	3.77	4.90	4.92	0.24	0	0.24
2	Assossa	5	0.12	2.33	4.02	5.28	5.50	0.24	0	0.24
3	Assossa	5	0.12	2.02	3.48	3.35	4.50	1.68	0.08	1.60
4	Mettu	20	0.28	2.30	3.97	1.80	5.11	1.52	0.8	0.72
5	Mettu	15	0.28	2.62	4.52	2.84	4.86	0.72	0.32	0.40
6	Mettu	20	0.26	2.82	4.87	1.16	4.50	2.48	1.28	1.20
7	Jimma	5	0.14	1.73	2.98	2.96	5.35	0.24	0	0.24
8	Jimma	55	0.13	1.99	3.43	4.77	5.34	0.24	0	0.24
9	Jimma	10	0.14	1.79	3.08	6.96	5.68	0.08	0	0.08

The principal component analysis was performed using Genstat 11.1 software (VSN International, 2008); while cluster analysis was performed using SAS Version 9.2 software (SAS Institute, 2008). Cluster mean was calculated by taking the mean value of each trait in each cluster; while cluster mean difference was calculated by subtracting the cluster mean from the grand mean of each trait. Determination of the number of clusters was performed using Pseudo F, Cubic Clustering Criterion (CCC) and Pseudo T^2 graphs analyzed by SAS Version 9.2 software (SAS Institute, 2008), based on the procedure described by SAS Institute (2009). The histograms for the mean of genotypes for grain yield at low P was also plotted in Excel.

Results and Discussion

The genotypes showed highly significant differences ($P<0.01$) for all the traits, except for pod number, which did not show significant differences (Table 3) on P deficient acidic soil with no additional applied P. This indicates the existence of genotypic difference for the traits, and that can help improve the crop for low P tolerance through selection. Highly significant genotype X location (GXL) interactions were found for grain yield, days to flowering and days to maturity.

Table 3. Mean squares of G and GXE interactions on low P environments

Traits	Genotypes	G XL interactions
Days to 50% flowering	54.58**	16.347**
Days to maturity	66.31**	19.16**
Fresh biomass weight (gm)	8911**	2866
Root fresh weight (gm)	52.53**	13.03
Root volume (lt)	84.03**	28.92
Tap root length (cm)	26.54**	14.15
Pod number	133.80	75.30
Pod length (cm)	0.587**	0.142
Number of seeds per pod	0.144**	0.081
Plant height (cm)	261.77**	60.66
100-Seeds weight (gm)	21.4**	3.02
Grain yield (kg ha^{-1})	193860**	158876**

* = significant at 5%, and ** = significant at 1 %

Mean grain yield performance of genotypes

Two genotypes (i.e., AGS-7-1 and G-9945) produced the highest grain yield followed by PR-143 (14), H-7, HS 82-2136, H-3, SCS-1, and SR-4-1 (Fig. 1).

Estimates of genotypic and phenotypic values

Grain yield ranged between 809-1748 kg ha^{-1}, while pod number and plant height ranged between 20.3-40.9 cm and 32.7-57.6 cm, respectively (Table 4). The genotypic and phenotypic variances were very high for grain yield and fresh biomass weight. Similarly, the genotypic coefficient of variation (GCV) was high for fresh biomass weight, root fresh weight, and root volume, while grain yield showed moderate GCV and PCV. Though the phenotypic variances did not show much difference for root volume, the fact that high genotypic variance were exhibited (Table 4) indicates that the low P stress triggered genetic expression for root formation in search of P. This agrees with the report of Ragothma (1990) that P starvation activates some specific genes. Higher phenotypic and genotypic variances were observed for fresh biomass weight, plant height and grain yield indicating the existence of higher genetic variability for low P tolerance.

Generally, PCV, GCV and genetic advance as percent of mean (GAM) values were classified as low, medium and high with respective values of 0-10%, 10-20% and >20%, while H^2 values are regarded as low (0-30%), moderate (30-60%) and high (60% and above) in soybean (Gadde, 2006). Based on these criteria, the percent PCV values in the current study can be regarded as high for traits such as fresh biomass weight, root fresh weight and root volume, while the GCV of only fresh biomass weight and root fresh weight can be considered as high (Table 4). High broad sense heritability ($\geq$ 70%) was found for 100-seed weight, pod length, plant height, root fresh weight, fresh biomass weight, and days to maturity, while grain yield showed the lowest broad sense heritability (27.29). Similarly, based on the classification of Gadde (2006), the GAM of plant fresh weight, root fresh weight, plant height, weight of hundred seeds and root volume can be considered high. Generally, low genetic advance as percent of mean was found for quantitative traits such as grain yield, days to maturity and days to flowering

that are highly influenced by environmental variances, and this result is in-line with the findings of Harer and Deshmukh (1992). The traits such as root fresh weight, plant height, weight of hundred seeds, plant fresh weight and root volume combined high H^2 and genetic advance as percent of mean value. According to Gohil *et al* (2006) and Aditya *et al* (2011), traits combining such high H^2 and genetic advance are predominantly controlled by additive gene action and can easily be improved by selection. The fact that most of the root related traits showed high heritability and genetic advance as percent of mean on such P-stressed acidic soils indicates the importance of such rooting traits in the screening of soybean genotypes for low-P tolerance.

Principal component analysis

The first five PCs with eigenvalues greater than one accounted for more than 84.6% of the total variation among the genotypes (Table 5). The higher total percentage variation in the first five PCs and the higher contribution of each of the first five PCs under low P conditions is also another indicator of the higher genetic variation of the genotypes for low P tolerance. These results are in agreement with the report of Ding and Li (1998), Tong *et al* (1999), Tang *et al* (2007) and Xiang Wen *et al* (2008) who reported high genetic variability in soybean for performance under low P conditions for various economically important attributes. The first PC that explained more than 37.7% of the total variation (Table 5) was influenced by the average values of the PC scores of root fresh weight, fresh biomass weight, tap root length, root volume, days to maturity, and days to flowering (Table 5). This implies that these traits are the major contributors for the total variation in the studied genotypes for low P tolerance because of the higher percentage variation contributed by the first PCs to the total variation. The second PC that accounted for 16.1% of the total variation was influenced by traits 100-seed weight and pod length.

Cluster analysis

On the basis of pseudo F, CCC and pseudo T^2 values, the appropriate number of clusters were determined to be four. However, the dendrograms (Fig. 2) identified seven cluster groups at cluster distance of 0.5, and three cluster groups at cluster distance one. The squared distance between each of the four clusters was highly significant (Table 6), and this might be due to the careful determination of the number of clusters based on the procedures described in SAS Institute (2008), which might have provided the optimum distance between each clusters. The longest cluster distance was found between clusters three and four. The smallest cluster distance was found between clusters two and three.

Cluster analysis revealed that cluster I contains 23 soybean genotypes, and included most of the released varieties standard check varieties such as Davis, Clark 63 K, Coker 240, and one pipeline variety SCS-1 (Table 8, Figure 2). The fact that the released varieties grouped in the same cluster indicates that these varieties have nearly similar response for soil acidity tolerance. This cluster is characterized by the highest cluster mean for number of seeds per pod, and produced the second highest cluster mean for all of the rest of the traits studied (Table 7), indicating the availability of some other promising genotypes in this cluster group for performance under low P condition.

Table 4 Estimates of genetic and phenotypic parameters for 36 soybean genotypes on acidic soils with no P application

Traits	Range	Mean	σ^2g	σ^2p	σ^2e	σ^2gxe	r intra class	GCV (%)	PCV (%)	H^2	GA	GAM
DF	58-70	63	5.7	9.0	8.2	5.8	29.0	3.8	4.8	63.4	3.9	6.2
DM	120-134	125.3	8.7	12.5	9.23	6.75	35.1	2.35	2.82	69.5	5.1	4.0
FBW	86.4-273.8	150.2	1190	1684	3458	-247	27.0	23.0	27.32	70.67	59.7	39.8
RFW	6.0-17.6	10.8	7.07	9.3	11.43	1.12	36.0	24.5	28.18	75.63	4.8	43.9
Rtv	10.6-25.9	17.85	9.11	14.4	24.54	3.68	24.4	16.9	21.28	63.15	4.9	27.7
TRL	12.7-21.3	16.46	1.99	4.4	12.05	1.3	13.0	8.57	12.79	44.91	1.9	11.8
PDN	20.3-40.9	28.79	10.6	22.8	116.3	-21.5	10.1	11.3	16.59	46.45	4.6	15.9
PDL	3.6-5.1	4.12	0.09	0.1	0.107	0.011	42.2	7.13	7.961	80	0.5	13.1
NSPPD	2.3-2.9	2.59	0.01	0.02	0.069	0.006	12.7	4.02	6.0	44.83	0.1	5.6
Pht	32.7-57.6	46.3	37.7	47.8	55.71	2.52	39.3	13.3	14.93	78.82	11.2	24.3
100-SW	9.5-17.24	13.24	3.3	3.8	2.32	0.334	55.2	13.6	14.66	86.78	3.5	26.2
Gyld	809-1748	1234	10184	37316	81881	40458	7.68	8.18	15.66	27.29	108.6	8.8

DF=days to 50% flowering, DM=days to maturity, FBW=fresh biomass weight, RFW=root fresh weight, RTV=root volume, TRL=tap root length, PDN=pod number, PDL=pod number, NSPPD=number of seeds per pod, Pht=plant height, 100-SW=100-seed weight, Gyld=grain yield, σ^2g=genotypic variance, σ^2p=phenotypic variance, σ^2e=environmental variance, σ^2gxe=variance of genotype x environment interaction, r intra class=intra class correlation, GCV (%)=percent genotypic coefficient of variation, PCV (%)=percent phenotypic coefficient of variation, H^2= broad sense heritability, GA=genetic advance, GAM=genetic advance as percent of mean

NB: the values of some environmental variances are greater than phenotypic variances. The reason is the phenotypic variance is calculated based on an adjusted environmental variance for the number of replication and location i.e., $\sigma_{ph}^2=\sigma_g^2 + \sigma_{ge}^2/e + \sigma_e^2/re$ (see more details of the formula in the materials and methods)

Table 5. Principal component score values, egenvalues and per cent of variation explained by the first five PCs of soybean genotypes evaluated across three locations on acidic soils of Western Ethiopia under no applied P conditions

Traits	PC 1	PC 2	PC 3	PC 4	PC 5
100-seed weight	0.1956	-0.3702	-0.3301	0.0452	-0.36085
Days to flowering	0.32	0.07079	-0.03616	0.24776	0.21289
Days to maturity	0.33386	0.00773	0.17818	0.24624	0.1794
Grain yield	-0.01066	-0.26884	-0.51037	-0.40282	0.07255
Number of seeds per pod	0.01545	-0.14891	0.41728	-0.59247	-0.04212
Fresh biomass weight	0.39493	0.02272	-0.1044	-0.11771	0.07283
Plant height	0.28656	-0.10921	-0.37211	0.05626	0.07866
Pod length	0.19249	-0.32964	0.20449	-0.14938	-0.48125
Pod number	0.11665	0.21409	-0.24319	-0.42907	0.45895
Root fresh weight	0.39853	-0.01016	0.09329	0.02908	-0.02743
Root volume	0.36191	0.00059	0.15709	-0.07829	0.03784
Tap root length	0.37341	-0.03486	0.17222	-0.05127	0.00687
Latent roots (λ)	5.65	2.41	1.76	1.47	1.38
Variation explained (%)	37.7	16.1	11.8	9.8	9.2
Cumulative variation explained (%)	37.7	53.2	75.0	84.8	94.0

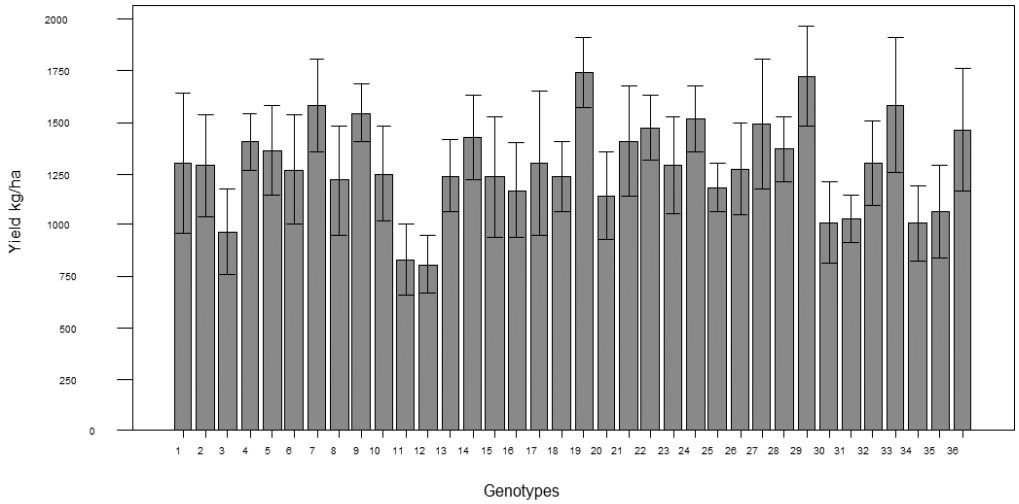

Figure 1. Mean grain yield of soybean genotypes on P deficient soil (numbers and corresponding genotypes are: 1. Davis, 2. Tunia, 3. PR-142 (26), 4. IAC 11, 5. Alamo, 6. FB1-7636, 7. PR-143 (14), 8. AGS 217, 9. HS 82-2136, 10. AA-7138, 11. IAC 73-5115, 12. AA-42-52, 13. AGS 234, 14. Coker 240, 15. AGS-3-1, 16. Essex-1, 17. Hardee-1, 18. Bossire-2, 19. AGS-7-1, 20. TGX-297-6E-1, 21. AGS-62, 22. Protana 2, 23. H 16, 24. H 3, 25. H 6, 26. Ocepara 4, 27. SCS-1, 28. Clark 63-K, 29. G 9945, 30. JSL-1, 31. SR-4-3, 32. IAC 6, 33. H 7, 34. PR-162-11, 35. OC-78503, 36. SR-4-1)

Table 6. Generalized squared distance between clusters 1-4 on acidic and low P soils of Western Ethiopia

Cluster	1	2	3	4
1	0	37.6**	79.7**	101.5**
2		0	18.0**	252.3**
3			0	343.4**
4				0

*= significant at (P<0.05), and ** = significant at (P<0.01)

Table 7. Cluster mean and cluster mean difference of clusters 1-4 for each of the studied traits on acidic soils of Western Ethiopia, with no applied P

Traits	Cluster I	Cluster mean diff	Cluster II	Clsuter mean diff	Cluster III	Clsuter mean diff	Cluster IV	Clsuter mean diff	Mean of the traits
DF	62.6	-0.1	63.1**	0.44	41.8*	-15.6	60.8	-1.8	62.65
DM	124.8	-0.5	126.3**	1	83.5*	-31.3	124.7	-0.6	125.3
GYLD	1323.7	89.7	1075.3	-158.7	829.5*	-303.3	1743.0**	509	1234
100-SW	13.5	0.3	12.7	-0.52	8.8*	-3.3	15.6**	2.3	13.24
NSPPD	2.61**	0.01	2.61**	0.01	1.7*	-0.6	2.6**	0	2.6
FBW	154.3	4.1	141.9	-8.28	100.1*	-37.6	178.2**	28	150.2
PHT	46.7	0.4	42.7	-3.57	29.9*	-12.3	55.9**	9.6	46.3
PDL	4.1	0	4.2**	0.07	2.8*	-1	4.2**	0.1	4.12
PDN	30.2	1.4	26.7	-2.09	19.4*	-7	30.6**	1.8	28.79
RFW	10.8	-0.1	11.2**	0.33	7.3*	-2.7	10.2	-0.6	10.84
RTV	17.7	-0.1	18.7**	0.87	12.1*	-4.3	15.5	-2.4	17.85
TRL	16.2	-0.3	17.4**	0.91	11.1*	-4	15.9	-0.6	16.46

* the lowest cluster mean, ** the highest cluster mean, DF=days to 50% flowering, DM=days to maturity, Gyld=grain yield (kg ha^{-1}), 100-SW=100-seed weight (gm), NSPPD=number of seeds per pod, FBW=fresh biomass weight (gm), Pht=plant height (cm), PDL=pod length (cm), PDN=pod number, RFW=root fresh weight (gm), RTV=root volume (lt), TRL=tap root length (cm)

Table 8. Distribution of the 36 soybean genotypes in four cluster groups tested on acidic soils of Western Ethiopia with no applied P

Cluster	Number of genotypes	Name of genotypes
Cluster I	23	H 3, H 7, SCS-1, SR-4-1, Tunia, H 16, AGS 234, AGS-3-1, Alamo, HS 82-2136, Bossire-2, Davis, Hardee-1, Clark 63 K, AA 7138, Ocepara 4, PR-143 (14), Coker 240, AGS-62, Protana-2, G 9945, IAC 6, IAC 11
Cluster II	9	AGS-217, PR-162-11, Essex-1, H 6, SR-4-3, FB1-7636, OC-78503, TGX-297-6E-1, PR-142 (26)
Cluster III	3	IAC 73-5115, AA-42-52, JSL-1
Cluster IV	1	AGS-7-1

Cluster II, which contained nine genotypes was characterized by the highest cluster mean for days to flowering, days to maturity, number of seeds per pod, pod length, root biomass, root volume and tap root length. This cluster produced the third highest cluster mean for grain yield, pod number, weight of 100 seeds, plant biomass, and plant height. Cluster III, which contained only three genotypes was characterized by the lowest cluster mean for all of the studied traits. Cluster IV that was characterized by the highest cluster mean for most of the productivity traits such as grain yield, pod number, hundred seed weight, number of seeds per pod, plant biomass, plant height, and pod length contained only one genotype (i.e., AGS-7-1), which indicates that this genotype is the best genotype for performance on P-stressed acidic soil. This genotype was also uniquely grouped as a single cluster group in the dendrogram (Fig. 2).

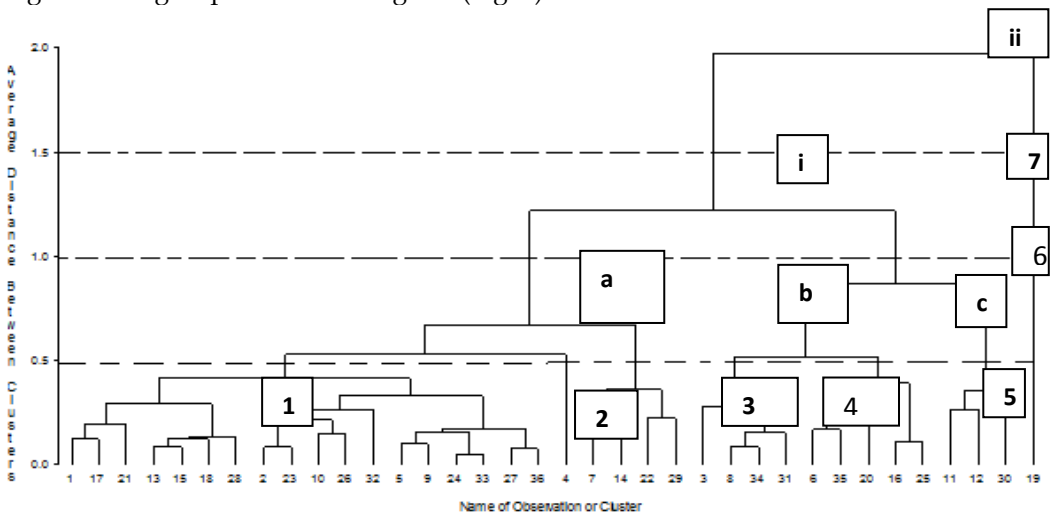

Figure 2. Dendrogram of 36 soybean genotypes evaluated across three locations on acidic soils of western Ethiopia under low-P conditions (numbers and corresponding genotypes are: 1. Davis, 2. Tunia, 3. PR-142 (26), 4. IAC 11, 5. Alamo, 6. FB1-7636, 7. PR-143 (14), 8. AGS 217, 9. HS 82-2136, 10. AA-7138, 11. IAC 73-5115, 12. AA-42-52, 13. AGS 234, 14. Coker 240, 15. AGS-3-1, 16. Essex-1, 17. Hardee-1, 18. Bossire-2, 19. AGS-7-1, 20. TGX-297-6E-1, 21. AGS-62, 22. Protana 2, 23. H 16, 24. H 3, 25. H 6, 26. Ocepara 4, 27. SCS-1, 28. Clark 63-K, 29. G 9945, 30. JSL-1, 31. SR-4-3, 32. IAC 6, 33. H 7, 34. PR-162-11, 35. OC-78503, 36. SR-4-1)

Conclusions and Recommendations

Overall, the study reveals the availability of sufficient genetic variation among soybean genotypes under both low P conditions on acidic soils. The results also demonstrated that reasonably high heritability genetic advances can be obtained with implications for breeding. Our findings suggest that selection for low P tolerance would be effective to improve grain yield and the essential agronomic traits of soybean varieties under low soil fertility and acidic soils in the smallholder sector. Future studies would be necessary to investigate the variation of these genotypes for qualitative traits such as protein and oil content under both conditions using molecular marker technologies.

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