

## ORIGINAL ARTICLE

## Response of soybean (*Glycine max* L.) genotypes to levels of phosphorus for rooting and nodulation characteristics on acidic soils of Western Ethiopia

<sup>1</sup>Abush Tesfaye, <sup>2</sup>Mwangi Githiri, <sup>3</sup>John Derera and <sup>4</sup>Tolessa Debele

<sup>1</sup>Jimma Agricultural Research Center, P.O.Box 192, Jimma, Ethiopia, <sup>2</sup>Jomo Kenyatta University of Agriculture and Technology, Department of Horticulture, Nairobi, Kenya, <sup>3</sup>Seed Co. Ltd., Global Research and Development, Zimbabwe, Harare <sup>4</sup>Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia. Corresponding author e-mail: [abushtesfaye@yahoo.com](mailto:abushtesfaye@yahoo.com)

### Abstract

Dense and deep root systems are desirable traits in maintaining the tolerance of soybean to adverse edaphic factors; while high and effective nodulation are important in improving soil fertility. The study was conducted to assess the response of soybean genotypes to varying phosphorus (P) levels for important root and nodulation characteristics across three locations of Western Ethiopia (Jimma, Assossa, and Mettu experimental sites), which are soil acidity prone areas. Treatments were laid out in split-plot design, where levels of P and genotypes (G) were main plots and sub-plots, respectively. The study comprised of 36 soybean genotypes and three levels of P (0, 100, and 200 kg ha<sup>-1</sup> of P in the form of TSP). The results revealed that G X P interactions were significant for number of nodules and total nodule weight at Jimma, and Assossa; while root weight and root volume were significant at Mettu. Genotypes showed significant difference for all the parameters, except for number of nodules and total nodule weight. Significant and positive correlations were found between root traits, such as root volume and tap root length with grain yield at low P, reflecting the importance of these traits to improve productivity of soybean on P starved soil. Total nodule weight showed highly significant correlations with grain yield at 100 kg ha<sup>-1</sup>. Both the mean separation and cluster analysis indicated that genotype PR-142 (26) was the best genotype, and AGS-3-1, SCS-1, AGS 234, and H3 performed well for most of the studied traits

**Key words:** acid soil, nodulation, rooting, soybean

## INTRODUCTION

Soybean is a crop of diverse uses; especially for subsistence farmers in developing countries. It is considered as a strategic crop in fighting world hunger and malnutrition (Thoenes, 2004). Its role for crop rotation and improving the fertility of the soil is most appreciated by farmers (Tesfaye *et al.*, 2010). This soil fertility improvement and crop rotation role of soybean can be enhanced through breeding for high nitrogen fixation and desirable root characteristics. The desirable root characteristics can help the crop to tolerate adverse soil conditions. One of such adverse soil conditions is low soil fertility due to soil acidity.

Soil acidity is a worldwide problem (Foy, 1988) and occurs on more than 50% of the world's potentially arable land (Liao *et al.*, 2006). The major problem of acidic soils is the abundance of Al, Mn and Fe, which have toxic effects on plants, and limited availability of essential plant nutrients, such as phosphorus, nitrogen and potassium (Liao *et al.*, 2006). Such problematic soils require careful soil fertility management practices to enhance soybean production and productivity. These include: the

application of lime to neutralize soil acidity and developing varieties with desirable root attributes to overcome the acidity related problems.

Nian *et al.* (2003) reported that root system on acidic soil need to have, not only Al tolerance, but also the capacity to supply the optimum phosphorus nutrient required for good growth and productivity of the crop. Lynch *et al.* (2007) reported the remarkable role of improving root characteristics in enhancing the productivity of crops on low fertility soils. The author's reason for emphasizing in improving root characteristics was the low level of fertility of the soil, and inadequate use of fertility improving inputs in most developing countries. According to Lynch *et al.* (2007), genetic variation in the length and density of root hairs is essential for the absorption of immobile nutrients, such as P and K, and such traits contribute to considerable yield improvement on low fertility soils.

Nodulation and nitrogen fixation are also very important attributes to improve the fertility of the soil by supplying plant usable nitrogen for the soybean crop itself, and crops succeeding it. The nodulation characteristics of soybean is dependent on the nutrient availability in the soil, such as Ca and P fertilization (Waluyo

*et al.*, 2004) and the types of soybean genotypes (Moharram *et al.*, 1994). According to Waluyo *et al.* (2004), P is important in the initiation of nodule formation and the development and functioning of the produced nodules. Olufajo (1990) also reported that P fertilization enhanced the nodulation of promiscuous soybean. Moharram *et al.* (1994) reported improved nodulation and nitrogen fixation of soybean as a result of P application. The author's also reported varietal difference in the nodulation and N-fixation character in which variety Clark gave better response than Crawford. However, since this study used only two varieties, the evidence was not sufficient to conclude the existence of varietal

differences for the attributes. Therefore, the objectives of this study were to assess the response of soybean genotypes to different levels of P, locations, and their interaction for the nodulation and root characteristics of soybean on acid soils of Western Ethiopia.

## MATERIALS AND METHODS

### Experimental sites

The field experiments were conducted at Jimma Agricultural Research Center, Mettu Agricultural Research sub-station, and Assosa Agricultural Research Centers, in Ethiopia (Table 1), which are characterized by strong to moderate acidic soil and low soil P content (see Table 2).

Table 1: Agro-ecological characteristics of the experimental sites

Testing Location	AEZ	Altitude (masl)	Location	Annual mean RF	Annual mean Temperature		Soil type
					Min	Max	
Jimma	H <sub>2</sub>	1750	7°46'N 36°E	1754	11	26	Reddish brown
Mettu	H <sub>2</sub>	1550	8°3' N 30°E	1835	12	27	Dark red brown
Assosa	Hot to warm sub-humid lowlands	1550	NA	1056.2	12.4	27.8	Reddish brown

H<sub>2</sub>: Tepid to cool humid mid highlands, RF=rainfall, and AEZ=agro-ecological zone according to EIAR classification; NA=Not available and

## Experimental design and treatments

A split plot design, where levels of P (low, medium, and high i.e., 0, 100, and 200 kg ha<sup>-1</sup> P, respectively) and genotypes (36 genetically diverse soybean genotypes) were assigned to the main plots and subplots, respectively. The soybean genotypes within each of the main plots were laid-out in a 6X6 lattice design in two replications. Each experimental unit was planted in four rows with only two harvestable middle rows. Planting was done in rows of 4m long and 60 cm wide, and recommended five centimeters spacing was maintained between plants. The distance between two plots was one meter, while 1.5 meter was maintained between blocks. Three times hand weeding was done to create a weed free experimental plot till maturity. The size of one block (main plot) was 29m X 19.4 m; while the size of the total experimental plot was 59.5m X 61.2m. The experiment was conducted in the main season (June-October) of 2012. The seeds of all the soybean genotypes used in the experiments were uniformly dressed with *Bradyrhizobium* bacteria inoculum, and only starter application of 18 kg ha<sup>-1</sup> N fertilizer was applied in

the form of Urea. The P fertilization was made using TSP fertilizer.

## Laboratory analysis

Soils from all the experimental sites were analyzed for P content before the experiments were conducted. The procedure described by Sahlemedhin and Taye (2000) was used to analyze soil P using Bray II method, N using Kjeldhal method, K using flame photometry, organic carbon (OC) and organic matter (OM) using Walkley and Black method. In addition, the procedures described by Sahlemedhin and Taye (2000) were followed to analyze soil pH, exchangeable acidity, Al and H.

## Data collection

Important root and nodulation characters were measured in all the experiments. These traits were measured by carefully uprooting five random plants along with the soil from each plot. Then, the soil was removed by washing the root and nodules gently in a plastic container taking care not to damage the root and not to lose any nodule. Total number of nodules, which is the count of all the nodules formed by the root; total nodule fresh weight, which is the weight of all the

nodules produced, effective nodules, which is the weight of actively N-fixing nodules (nodules that are pinkish in color upon splitting using knives) were measured on randomly selected five plants from each plot. In addition, root characteristics, such as root fresh weight, which is 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 five randomly selected plants from each treatment.

**Table 2:** Results of soil analyses conducted on three samples collected from each of the experimental sites (Jimma, Assosa and Mettu) before the experiment in June 2012

No	Location	K (ppm)	N%	OC %	OM %	P (ppm)	pH (H <sub>2</sub> O)	Exchangeable		
								Acidity (meq/ 100g soil)	Al (meq/ 100g soil)	H (meq/ 100g soil)
1	Assosa	10	0.13	2.19	3.77	4.90	4.92	0.24	0	0.24
2	Assosa	5	0.12	2.33	4.02	5.28	5.50	0.24	0	0.24
3	Assosa	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

### Statistical analysis

Analysis of variance for the experiment was computed using Genstat Statistical Software. Test of homogeneity of error variance for the levels of P and locations was made before combined analysis using Bartlett's test (Gomez and Gomez, 1984) which was non-

significant indicating homogeneity of error variances (Gomez and Gomez, 1984). Similarly, the normality of each data was checked for the analysis using Genstat residual plot technique and the result revealed that all the traits showed normality; except total nodule weight at Assosa. The combined

analysis of G X L, G X P, and G X L X P was analyzed using Genstat, split plot analysis program. Square root transformation was performed for number of nodules. Other parameters which failed to satisfy the normality assumption were also transformed using log transformation (Gomez and Gomez, 1984). The Pearson's

correlation analysis was done using Genstat statistical software to understand the interrelationship of the rooting and nodulation traits with grain yield and other yield related traits. The linear statistical model for split plot design experiment conducted across locations is given by:

$$y_{ijk} = \mu + \alpha_i + \beta_j + \tau_k + (\alpha\beta)_{ij} + (\alpha\tau)_{ik} + (\beta\tau)_{jk} + (\tau\alpha\beta)_{ijk} + \varepsilon_{ijk}$$

Where,  $i = 1, 2, \dots, r, j = 1, 2, \dots, a, k = 1, 2, \dots, b$ ;  $\alpha_i$ , and  $\beta_j$  represent the main plot and subplot, respectively;  $\tau_k$  represents the location;  $(\alpha\beta)_{ij} + (\alpha\tau)_{ik} + (\beta\tau)_{jk} + (\tau\alpha\beta)_{ijk}$  represents main plot X subplot, main plot X location, subplot X location, and main plot X subplot X location interactions, respectively and  $\varepsilon_{ijk}$  is the residual term.

## RESULTS AND DISCUSSION

### Response of genotypes and Genotype X P interactions in each location

There were highly significant differences among genotypes for all the root and nodulation parameters i.e., total nodule weight, weight of effective nodule, root weight, root volume and tap root length, except for number of nodules that was significant at Jimma

(Table 3). The interaction of G X P was highly significant for number of nodules and total nodule weight at Jimma; while weight of effective nodules, root weight, root volume, and tap root length were not significantly different. The presence of significant G X P interaction for number of nodules and total nodule weight at Jimma and Assosa, and root weight and volume at Mettu (Table 3) indicated the differential response of genotypes for high and low P conditions, thus implying the possibility of selecting genotypes that perform exceptionally to low and high P conditions. At Assosa, the genotypes were significantly different for number of nodules, and differ highly significantly for root weight, root volume, and tap root length; while there was no significant difference for total nodule

weight and weight of effective nodules. The fact that genotypic difference existed for the entire root and nodulation characteristic in Jimma and Assosa, except for total nodule weight and weight of effective nodules in Assosa is in-line with the finding of Moharram *et al.* (1994), where varietal difference was found for nodulation and N-fixation characters, though their result was based on only two varieties. It was only root weight and tap root length that showed significant difference among the P levels at Assosa. The G X P interaction was highly significant and significant for number of nodules and total nodule weight, respectively. There were highly significant differences among genotypes for root volume and tap root

length; while the rest of the parameters were non-significant at Mettu. There was significant difference among the P levels for number of nodules, and total nodule weight, and highly significant difference for root weight. The significance of P levels for number of nodules, total nodule weight, and weight of effective nodules across locations (Table 4) is in agreement with the report of Olufajo (1990) and Moharram *et al.* (1994) that P fertilization enhances nodulation and nitrogen fixation. The value of coefficient of variation for most of the nodule characters was very high indicating that nodule formation lacks consistency from plot to plot.

Table 3: Mean squares of genotypes, and genotype X phosphorus (GXP) interaction for each of the three locations i.e., Jimma, Assosa and Mettu

Traits	Jimma		Assosa		Mettu	
	G	G X P	G	GXP	G	G X P
Number of nodules	7.23*	10.39**	13.63*	16.73**	10.10ns	6.97ns
Total nodule weight (gm)	46.33**	26.69**	19.77ns	21.10*	14.48ns	18.99ns
Weight of effective nodule (gm)	2.36**	1.46ns	2.68ns	2.49ns	0.865ns	0.7231ns
Root weight (gm)	222.47**	50.88ns	180.42**	56.66ns	1303.40ns	18.13*
Root volume (lt)	256.67**	83.90ns	40.15**	8.80ns	148.07**	46.68*
Tap root length (cm)	20.67**	5.08ns	266.42**	85.51ns	32.95**	9.16ns

Mean squares are based on square root transformation, \* = significant at ( $P < 0.05$ ), and \*\* = significant at ( $P < 0.01$ )

### Response of Genotypes and Genotype X P interactions over locations

The across locations combined analysis of variance revealed that the genotypes displayed highly significant difference for all the parameters, except for number of nodules and significant differences for weight of effective nodules (Table 4). Locations x P levels

interactions were highly significant for all the nodulation and root characteristics; while location X genotypes interaction was highly significant for number of nodules, root volume and tap root length. Total nodule weight showed significant G X P interaction. None of the traits showed significant Location X P-Levels X Genotypes (L X P X G) interactions.

Table 4: Mean squares for locations, genotypes, and P levels and their interactions across three locations i.e., Jimma, Mettu and Assossa

Factors	¥Number of nodules	¥Total nodule weight (gm)	¥Weight of effective nodule (gm)	Root weight (gm)	Root volume (lt)	Tap root length (cm)
Location (L)	295.35**	70.9**	117.26**	1043.74**	2742.16**	5090.94**
P levels (P)	26.8**	18.79**	14.6**	9054.43**	3465.33**	4108.75**
Genotypes (G)	1.16ns	0.61ns	1.71*	344.52**	246.19**	154.19**
L X P	5.77**	5.23**	14.88**	811.93**	708.93**	2853.61**
L X G	0.75ns	0.34ns	0.13ns	67.82ns	75.81**	69.51**
P X G	1.07ns	0.35ns	0.14ns	50.35ns	58.09ns	34.78ns
L X P X G	8.9ns	0.31ns)	(0.14ns)	38.29ns	38.04ns	32.11ns

¥ mean squares are based on square root transformations, \*= significant at (P<0.05), and \*\* = significant at (P<0.01)

### Performance of genotypes in each location

Genotypes PR-142 (26), AA-42-52, AGS-3-1, H-7, and SR-4-1 produced significantly higher weight of effective nodules at Jimma (Table 5). Three of these genotypes (PR-142 (26), AA-42-52, and H7) produced the highest fresh

root weight. Significantly higher root volume was produced by genotypes AA-42-52, PR-142 (26), H7, IAC 6, PR-143 (14), and IAC 11. The genotypes which produced the highest tap root length at Jimma were IAC 6, H6, SCS-1, and Bossire-2. At Assosa, PR 142(26), H6, AGS-3-1, SR-4-3, AA 42-52, and



both AGS-217 and G 9945, produced the highest root weight. Genotype H6 exceptionally produced the highest root volume, followed by H7, SCS-1, IAC 6, PR-142 (26), SR -4-3, AA-42-52, H 16, Bossire-2, Essex-1, HS 82-2136, AGS 217, and Clark 63 K. The genotypes which produced the longest tap root length at Assosa were PR 142 (26), AGS 217, H 16, SR-4-3, Essex-1, AA-42-52, AGS-3-1, G 9945, PR-143 (14), Ocepara-4, Clark 63 K, JSL-1, H7, SCS-1 and HS 82-2136. At Mettu, the highest tap root length was produced by genotypes IAC-6, PR 142 (26), IAC 11, H 6, SR-4-3, SCS-1, AA-42-52, AGS 7-1, Bossire-2, Ocepara 4, H 7, and G 9945.

At Jimma, the highest number of nodules was produced at 200 Kg ha<sup>-1</sup> level of P by two genotypes (H3 and PR-142 (26)) and at 100 Kg ha<sup>-1</sup>, SCS-1 was among the genotypes that produced the highest number of nodules (Table 6). The number of nodules at 0 level of P was generally low and H 16, AA 7138, Davis and Hardee-1 produced relatively higher number of nodules at this level of P. The highest nodule weight was produced by genotype AA-7138 followed by FB1-7636 at 100 Kg ha<sup>-1</sup> P rate. The highest nodule weight at the 200 Kg ha<sup>-1</sup> P was produced by FB1-7636, followed by PR 142 (26) and H3.

Similar to the number of nodules, the total nodule weight was generally low at 0 level of P and the highest nodule weight at this P level was produced by genotype PR-143 (14).

At Mettu, the highest root weight was produced at 200 Kg ha<sup>-1</sup> P rate by genotypes PR-142 (26) and AGS-3-1, and at 100 Kg ha<sup>-1</sup> P by genotype PR-142 (26) (Table 7). Genotypes PR-142 (26), Essex-1, G-9945, SCS-1, H7, IAC-6, IAC 11, H 16, Ocepara-4 and SR-4-3 produced highest root weights at 0 level of P; while genotypes AGS-3-1, PR-142 (16), and Essex-1 produced the highest root volume.

The highest number of nodules at Assosa was produced by genotypes SCS-1, H3 and PR-142 (26) at 200 Kg ha<sup>-1</sup> applied P (Table 8). The nodule formation was relatively lower in both the control and 100 kg ha<sup>-1</sup> levels of P. Genotypes that produced the highest number of nodule at 200 kg ha<sup>-1</sup> applied P, produced relatively low number of nodule at 100 kg ha<sup>-1</sup>. Three genotypes i.e., PR-143 (14), Hardee-1 and IAC 6 were relatively the better nodule forming genotypes at zero P. The highest total nodule weight at Assosa was produced by genotype H 3 at 200 kg ha<sup>-1</sup> applied P. The total nodule weight produced was generally low for

the control and 100 kg ha<sup>-1</sup> P level. Some of the genotypes which produced relatively higher nodule weight at zero level of P were PR-143 (14), AGS 234, IAC 6, AGS-217, and Coker 240. The high performance of genotype PR-142 (16) for almost all of the nodulation and root characteristics is shown in Tables five, six, seven, eight and nine. The unique and high performance of this

genotype was verified by cluster analysis, as it was grouped alone in cluster IV (Table 10). However, the performance of this genotype under zero level of P was low relative to other genotypes (Table 6 and 8). This implied that the genotype is more responsive to P application, but not efficient at low levels of soil P.

Table 5: Weight of effective nodules and root characters measured at Jimma, Assossa, and Mettu

Genotypes	Jimma				Assossa			Mettu
	WEN (g)	Root Weight (g)	Root Volume (ml)	TRL (cm)	Root Weight (g)	Root Volume (ml)	TRL (cm)	TRL (cm)
1. Davis	1.993	10.55	18.13	14.82	15.17	18.64	17.18	16.80
2. Tunia	1.257	19.07	21.73	13.52	20.45	19.85	25.33	22.54
3. PR-142 (26)	3.765	33.55	41.80	17.63	33.43	22.22	37.50	26.18
4. IAC 11	2.415	22.8	32.53	16.37	21.18	19.24	25.67	25.74
5. Alamo	1.907	15.72	24.00	15.68	20.33	18.13	22.17	18.76
6. FB1-7636	1.46	11.82	24.50	17.39	16.77	16.81	22.03	20.22
7. PR-143 (14)	2.272	19.55	33.17	17.80	24.08	18.90	31.67	21.91
8. AGS 217	2.353	19.53	30.30	17.69	26.45	19.95	34.37	17.98
9. HS 82-2136	1.323	12.25	21.83	16.40	23.93	20.05	28.67	21.29
10. AA-7138	2.272	11.88	23.87	16.46	22.92	19.42	26.73	21.11
11. IAC 73-5115	1.645	10.13	19.97	16.75	20.35	17.91	21.83	21.31
12. AA-42-52	3.013	32.57	42.00	16.97	27.30	21.84	32.83	24.13
13. AGS 234	1.83	11.75	19.62	15.30	11.00	18.77	17.33	20.12
14. Coker 240	1.32	8.55	20.40	13.74	13.97	15.54	13.83	21.62
15. AGS-3-1	2.842	16.97	26.33	14.91	28.28	19.85	32.33	21.44
16. Essex-1	0.995	17.57	29.37	18.39	23.45	20.06	33.67	22.54
17. Hardee-1	2.368	9.02	15.25	15.31	11.75	17.10	17.83	20.68
18. Bossire-2	1.727	17.55	28.00	18.76	22.35	20.09	28.00	23.47

19. AGS-7-1	1.747	13.07	18.20	15.76	21.58	19.17	24.17	23.55
20. TGX-297-6E-1	0.858	14.2	23.60	16.88	20.77	18.89	23.92	20.97
21. AGS-62	1.28	7.57	12.67	11.80	9.10	13.69	10.33	19.40
22. Protana 2	2.442	13.75	19.37	13.51	13.10	17.05	17.67	18.50
23. H 16	2.185	20.58	29.17	17.18	22.67	20.96	34.33	22.26
24. H 3	2.167	13.58	22.93	16.13	13.78	17.59	20.23	20.49
25. H 6	1.822	20.15	29.83	19.82	28.43	28.53	33.07	25.16
26. Ocepara 4	2.145	20.72	31.83	16.62	25.15	19.31	31.53	23.26
27. SCS-1	1.945	19.92	28.50	18.82	20.65	23.59	29.33	24.40
28. Clark 63-K	2.292	16.13	27.50	16.36	21.63	19.89	31.33	20.69
29. G 9945	1.787	15.98	32.25	15.87	26.45	20.52	31.75	22.83
30. JSL 1	1.493	17.13	25.47	16.53	23.23	18.59	30.42	19.11
31. SR-4-3	1.738	18.17	29.08	14.30	27.33	22.07	33.83	24.52
32. IAC 6	1.783	24.17	33.17	21.35	16.77	23.00	19.52	26.22
33. H 7	3.207	29.02	33.83	18.03	21.48	23.74	29.50	22.96
34. PR-162-11	1.322	13.35	25.67	16.49	18.52	18.76	24.05	19.11
35. OC-78503	1.428	16.62	28.27	17.56	20.93	18.93	27.93	20.13
36. SR-4-1	2.613	20.1	28.7	16.67	15.8	18.19	20.83	20.56
Mean	1.97	17.08	26.47	16.49	20.85	19.63	20.19	21.72
CV %	54.20	45.30	31.80	14.20	31.00	17.20	30.30	14.10
Significance level	**	**	**	**	**	**	**	**
LSD (5%)	1.22	8.85	9.65	2.67	7.40	3.88	9.08	3.51

NB. WEN= weight of effective nodules, TRL= tap root length, \*= significant at ( $P<0.05$ ), and \*\* = significant at ( $P<0.01$ )

Table 6: Mean number of nodules and total nodule weight obtained at 0, 100 and 200 kg ha<sup>-1</sup> P under Jimma condition

Genotypes	Number of nodules						Total nodule weight (g)		
	0 P	¥0 P	100 P	¥100 P	200 P	¥200 P	0 P	100 P	200 P
1. Davis	107.5	10.3	69.5	8.1	134.0	11.5	1.63	2.39	2.95
2. Tunia	39.0	6.2	134.6	11.2	81.0	8.8	1.24	3.25	2.64
3. PR-142 (26)	39.0	6.2	80.5	8.8	390.0	19.6	1.15	4.82	10.03
4. IAC 11	41.0	6.2	210.0	14.1	160.0	12.4	0.92	6.41	3.22
5. Alamo	46.5	6.7	129.9	11.3	143.5	12.0	0.77	3.76	2.67
6. FB1-7636	71.5	8.3	165.0	12.8	177.0	13.2	0.81	24.00	18.50
7. PR-143 (14)	83.0	8.9	83.5	8.8	135.0	11.5	8.92	6.33	3.23
8. AGS 217	72.0	8.3	91.0	9.5	220.0	14.8	2.19	4.38	4.50
9. HS 82-2136	64.5	8.0	96.5	9.3	172.0	13.1	1.16	1.66	2.47
10. AA-7138	124.0	11.1	151.5	12.3	200.0	11.1	2.68	33.50	3.96
11. IAC 73-5115	80.5	9.0	157.5	11.8	133.5	11.5	1.51	3.40	3.01
12. AA-42-52	76.0	8.7	170.5	12.2	239.5	15.4	1.75	5.66	6.52
13. AGS 234	60.0	7.5	230.0	15.0	127.0	11.3	1.06	4.70	1.72
14. Coker 240	98.5	9.8	105.5	10.0	120.0	10.9	1.07	1.81	2.24
15. AGS-3-1	93.5	9.7	238.0	14.9	203.5	14.2	1.44	10.25	3.38
16. Essex-1	34.5	5.8	125.0	11.1	135.5	11.6	0.50	2.32	1.56
17. Hardee-1	101.5	9.8	115.0	10.7	156.5	12.5	1.87	2.61	4.53
18. Bossire-2	87.5	9.3	130.5	11.2	74.5	8.4	1.19	4.08	1.29
19. AGS-7-1	62.5	7.9	126.0	11.2	86.0	9.2	0.92	4.04	1.65
20. TGX-297-6E-1	73.0	8.5	61.0	7.5	100.5	10.0	1.14	0.95	1.56
21. AGS-62	72.0	8.3	283.0	16.4	90.5	9.4	1.02	2.70	1.31
22. Protana 2	72.5	8.5	130.0	11.2	199.0	14.1	2.64	3.80	5.23
23. H 16	125.0	11.1	111.0	10.1	188.5	13.7	1.14	3.71	4.63
24. H 3	59.0	7.4	107.5	10.3	410.0	19.5	0.87	1.78	9.11
25. H 6	65.0	7.7	82.0	8.5	252.0	15.8	1.04	1.87	4.57
26. Ocepara 4	86.0	9.2	138.0	11.5	135.5	11.6	1.90	4.41	3.01
27. SCS-1	89.0	9.4	329.5	18.1	89.0	9.4	0.94	6.05	1.34
28. Clark 63-K	81.5	8.7	180.5	13.0	138.5	11.7	1.15	5.29	3.25
29. G 9945	66.0	8.1	117.5	10.7	231.0	15.2	1.60	2.53	4.80

30. JSL 1	85.5	9.2	119.5	10.8	132.0	11.4	1.26	2.33	2.56	
31. SR-4-3	59.0	7.7	136.0	11.0	73.0	7.8	1.17	4.50	2.51	
32. IAC 6	98.5	9.9	158.5	12.2	175.5	13.1	1.32	3.46	2.93	
33. H 7	84.5	9.1	158.5	11.9	180.0	13.3	1.44	5.68	5.60	
34. PR-162-11	59.0	7.5	116.5	9.4	174.0	13.2	0.88	2.46	2.56	
35. OC-78503	73.0	8.5	138.0	10.5	116.5	10.5	0.92	3.54	1.84	
36. SR-4-1	73.0	9.8	138.0	13.3	116.5	13.0	2.27	4.84	4.04	
Mean	75.8	8.5	143.1	11.4	165.1	12.5	1.54	5.26	3.91	
CV %	19.9						52.4			
Significance level	**						**			
LSD (5%)	4.26						3.7			

¥ Values are based on square root transformation, \*= significant at (P<0.05), and \*\* = significant at (P<0.01)

Table 7: Mean root weight and root volume of soybean genotypes obtained at 0, 100 and 200 kg ha<sup>-1</sup> P at Mettu

Genotypes	Root weight (g)			Root volume (ml)		
	0	100	200	0	100	200
1. Davis	5.0	12.0	13.5	4.0	14.1	22.5
2. Tunia	8.0	13.0	15.5	13.5	20.0	25.0
3. PR-142 (26)	20.5	30.5	35.0	21.5	34.0	44.0
4. IAC 11	16.5	31.0	22.0	26.5	25.25	24.0
5. Alamo	9.5	15.0	15.0	13.5	22.5	17.0
6. FB1-7636	9.5	19.0	23.5	19.0	20.85	22.0
7. PR-143 (14)	10.5	18.0	20.5	17.5	24.0	29.5
8. AGS 217	10.5	13.0	16.0	13.9	15.2	23.5
9. HS 82-2136	11.0	13.5	21.0	18.0	20.1	34.0
10. AA-7138	9.5	18.5	16.5	29.0	20.2	19.0
11. IAC 73-5115	11.0	18.5	18.5	20.5	21.0	18.0
12. AA-42-52	13.5	28.0	25.5	17.0	22.6	30.0
13. AGS 234	8.0	17.5	11.0	17.6	17.8	15.0
14. Coker 240	11.5	14.0	14.5	21.5	19.05	16.0
15. AGS-3-1	12.0	18.5	33.5	17.5	19.95	46.0
16. Essex-1	18.5	26.0	31.0	34.0	30.0	35.5
17. Hardee-1	6.5	13.5	10.0	12.5	15.5	12.5
18. Bossire-2	13.5	15.5	19.5	18.5	20.0	22.0
19. AGS-7-1	11.5	24.5	26.0	19.1	33.0	31.5
20. TGX-297-6E-1	9.0	17.0	19.5	12.5	20.0	14.5
21. AGS-62	12.5	15.5	15.0	17.0	18.0	17.5
22. Protana 2	10.5	16.5	16.5	13.5	17.7	19.0
23. H 16	15.5	15.0	13.5	20.0	15.5	15.0
24. H 3	11.5	19.0	17.0	19.0	21.1	21.0
25. H 6	12.0	23.5	26.5	17.5	25.5	34.0
26. Ocepara 4	14.5	13.5	20.0	26.0	19.0	24.5
27. SCS-1	18.0	20.5	23.5	22.0	24.2	16.5
28. Clark 63-K	13.0	20.5	19.5	22.5	25.4	24.0
29. G 9945	18.5	21.0	26.5	25.0	26.0	25.0

30. JSL 1	7.5	18.0	14.5	11.0	21.3	22.0
31. SR-4-3	14.5	23.5	26.5	20.0	25.0	24.0
32. IAC 6	17.0	21.5	29.5	28.5	27.0	30.0
33. H 7	18.0	20.5	19.5	23.6	23.0	20.0
34. PR-162-11	12.0	16.5	19.0	19.0	17.6	22.5
35. OC-78503	6.5	13.0	16.0	12.5	14.1	15.5
36. SR-4-1	11.5	14.5	18.0	15.0	19.0	15.0
Mean	12.18	18.58	20.24	18.86	21.51	23.53
CV %	20.30			26		
Significance level	*			*		
LSD (5%)	6.80			10.97		

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

Table 8: Mean numbers of nodules and total nodule weight obtained at 0, 100 and 200 kg ha<sup>-1</sup> applied P, at Assossa

Genotypes	Number of nodules						Total nodule weight (g)		
	0 P	¥0 P	100 P	¥100 P	200 P	¥200 P	0	100	200
1. Davis	140.5	10.69	45.0	6.64	157.0	12.06	3.8	3.6	5.7
2. Tunia	95.5	9.77	142.5	11.10	98.5	9.88	3.2	4.3	3.8
3. PR-142 (26)	100.0	9.58	84.5	9.18	360.5	18.96	3.2	4.7	12.9
4. IAC 11	42.0	6.48	113.5	9.76	96.0	9.78	2.3	2.7	3.3
5. Alamo	104.5	9.40	74.5	8.59	97.5	9.85	2.3	1.3	4.2
6. FBI-7636	65.0	7.76	85.0	9.18	46.0	6.77	2.8	2.6	1.7
7. PR-143 (14)	256.5	15.93	78.0	8.82	127.5	11.09	11.	2.7	8.3
8. AGS 217	107.5	10.36	106.5	9.58	193.5	13.36	9.1	6.0	6.0
9. HS 82-2136	50.5	6.90	92.0	9.58	79.0	8.68	2.2	1.2	3.1
10. AA-7138	75.0	8.66	146.0	12.08	316.0	17.71	2.1	2.6	12.9
11. IAC 73-5115	56.0	7.48	55.0	7.35	167.0	12.59	3.6	1.8	6.7
12. AA-42-52	83.0	9.03	184.0	12.65	107.0	9.85	3.4	2.9	3.2
13. AGS 234	193.0	13.79	152.5	12.25	282.5	14.76	11.2	3.3	7.8
14. Coker 240	193.0	13.63	140.0	11.82	46.5	6.81	7.5	4.4	1.5
15. AGS-3-1	145.0	12.04	80.0	8.55	236.5	14.54	5.8	2.7	11.3
16. Essex-1	90.0	8.56	79.5	8.87	210.5	13.14	2.2	2.5	5.7
17. Hardee-1	220.5	14.59	81.0	8.85	205.5	14.26	5.8	3.4	5.2
18. Bossire-2	162.5	12.64	40.0	6.31	101.0	9.24	5.2	1.1	2.0
19. AGS-7-1	153.0	12.10	119.5	10.84	167.5	11.87	3.5	2.9	16.8
20. TGX-297-6E-1	107.0	10.34	127.5	10.94	147.5	11.77	3.8	2.7	3.8
21. AGS-62	70.0	8.28	175.5	13.08	130.5	11.30	1.9	3.7	4.2
22. Protana 2	143.5	10.95	142.5	11.79	185.0	13.19	4.8	2.3	4.9
23. H 16	46.0	6.78	142.0	11.60	149.0	12.18	1.4	3.2	5.1
24. H 3	91.5	9.50	58.5	7.51	500.0	20.58	4.3	1.3	24.5
25. H 6	128.5	11.08	89.5	9.32	194.0	13.58	3.2	2.8	6.7
26. Ocepara 4	45.0	6.61	177.5	13.03	74.5	8.22	3.8	9.1	2.0
27. SCS-1	123.5	10.93	47.0	6.54	505.0	22.46	3.2	0.7	10.4
28. Clark 63-K	125.0	11.16	102.0	10.00	72.5	8.35	6.3	3.1	2.5
29. G 9945	165.0	12.25	68.5	7.95	122.0	10.30	4.0	2.8	6.5



30. JSL 1	54.0	7.12	55.5	6.61	107.0	9.82	2.9	1.5	4.0
31. SR-4-3	85.0	9.18	163.5	12.45	103.5	9.87	2.6	2.1	3.7
32. IAC 6	205.0	14.32	29.5	5.34	79.5	8.85	9.2	0.3	2.3
33. H 7	96.0	9.24	177.0	13.23	146.5	11.77	3.5	5.8	4.2
34. PR-162-11	186.0	13.17	163.0	12.75	195.5	12.24	6.3	4.1	7.7
35. OC-78503	125.0	10.83	95.0	9.74	244.0	14.57	4.7	2.7	5.3
36. SR-4-1	134.0	11.48	72.0	8.46	106.0	9.70	3.1	2.5	3.1
Mean	118.4	10.35	105.1	9.79	171.0	12.06	4.41	2.95	6.17
CV%	27.6						82.6		
Significance level	**						*		
LSD (5%)	5.86						7.39		

¥ Values are based on square root transformation, \*= significant at ( $P<0.05$ ), and \*\* =significant ( $P<0.01$ )

#### Performance of genotypes over P levels and locations

The genotypes that produced the overall longest tap root includes: PR-142 (26), H-6, Essex-1, PR-143 (14), G-9945, AA-42-52, H-16, AGS-217, Ocepara-4, SCS-1, H-7, Bossire-2, and IAC-11 (Table 9). Two genotypes VIZ., AA-7138, and AGS-7-1 produced the

highest total nodule weight. PR-142 (26), IAC-6 (28.23), G-9945 (26.17), H-6 (29.62), Essex-1 (28.18), AA-42-52 (29.07), and PR-143 (14) were the genotypes with the highest root volume. The highest weight of effective nodules was produced by genotypes AGS-3-1, AGS-217, Protana-2, IAC 73-5115, and Cocker 240.

**Table 9:** Mean values of the root and nodulation parameters measured over P levels and locations

Genotypes	Number of nodules	Root weight (g)	Tap root length (cm)	Total nodule weight (g)	Root volume (ml)	Weight of effective nodule (g)	¥Weight of effective nodule (g)
1. Davis	73.22	10.61	15.72	2.50	16.13	1.52	0.81
2. Tunia	75.20	18.21	20.25	2.98	20.98	1.06	0.63
3. PR-142 (26)	123.15	32.04	26.54	3.95	31.06	2.21	0.91
4. IAC 11	84.16	21.92	22.55	2.42	25.59	1.52	0.77
5. Alamo	80.75	16.53	19.46	2.00	20.72	1.58	0.81
6. FB1-7636	81.07	15.55	18.86	5.85	19.71	1.06	0.66
7. PR-143 (14)	82.01	21.29	24.60	3.73	26.75	1.37	0.74
8. AGS 217	105.46	20.62	24.17	4.97	22.82	2.19	1.11
9. HS 82-2136	70.46	17.36	21.95	2.28	22.66	1.28	0.75
10. AA-7138	113.16	16.40	21.07	9.22	22.22	1.44	0.75
11. IAC 73-5115	82.48	15.82	19.90	2.80	20.56	1.69	0.95
12. AA-42-52	94.38	27.04	24.37	2.98	29.07	1.74	0.87
13. AGS 234	127.71	12.13	18.49	3.46	18.83	1.52	0.84
14. Coker 240	92.13	11.47	16.59	2.92	18.35	1.91	0.94
15. AGS-3-1	129.53	21.51	21.76	4.89	24.47	3.27	1.26
16. Essex-1	72.06	22.02	25.36	1.68	28.18	0.83	0.58
17. Hardee-1	94.56	9.86	16.64	3.30	13.33	1.68	0.88
18. Bossire-2	64.96	19.98	23.49	1.17	23.22	0.84	0.54
19. AGS-7-1	89.89	18.29	21.68	6.11	21.52	1.52	0.77
20. TGX-297-6E-1	89.14	17.48	21.15	3.18	19.64	1.11	0.70
21. AGS-62	108.07	11.03	14.72	2.62	15.96	1.48	0.78
22. Protana 2	105.23	13.10	17.34	3.62	16.82	2.13	1.07
23. H 16	96.41	19.48	24.19	2.72	22.27	1.86	0.87
24. H 3	142.27	13.20	17.79	4.78	19.93	2.20	0.88
25. H 6	105.01	24.39	26.33	3.46	29.62	1.50	0.79
26. Ocepara 4	77.33	20.46	23.83	3.11	24.09	1.36	0.77
27. SCS-1	131.32	19.78	23.67	3.46	23.85	1.35	0.66
28. Clark 63-K	80.80	18.14	22.34	2.05	22.98	1.34	0.67
29. G 9945	97.00	20.97	24.46	2.78	26.17	1.36	0.80
30. JSL-1	65.68	17.10	21.41	2.07	19.30	1.09	0.64

31. SR-4-3	67.58	21.56	23.62	2.50	24.80	1.45	0.83
32. IAC 6	90.94	21.55	21.74	2.67	28.23	1.47	0.73
33. H 7	94.14	21.70	23.55	3.17	25.57	1.85	0.87
34. PR-162-11	92.48	16.15	19.90	2.74	20.59	1.33	0.69
35. OC-78503	100.61	16.82	22.37	3.01	20.75	1.30	0.70
36. SR-4-1	98.11	17.61	20.91	3.22	22.09	1.78	0.90
Mean	93.8	18.3	21.5	3.3	22.5	1.6	0.80
Significance level	Ns	Ns	**	**	**	**	*
CV %	38.5	20.7	25.48	125.69	30.79	91.92	53.76
LSD 5%	---	---	4.01	3.13	5.16	1.07	0.32

¥=values are based on log transformation, ns=non-significant, \*=significant at 5%, and \*\*=significant at 1%

### Clustering of the genotypes

Based on root and nodulation characteristics, genotypes were grouped into four clusters (Table 10). Genotype PR-142 (26), which was the top performing genotype for most of the studied traits across the three

locations and levels of P stand alone in cluster IV. Cluster III also included some of the well performing genotypes namely: AGS-3-1, SCS-1, AGS 234, and H3 for the root and nodulation characteristics, suggesting that these genotypes are potentially suitable for low levels soil P conditions.

**Table 10:** Summary of cluster groups of soybean accessions grown across three locations i.e., Jimma, Mettu and Assossa

Cluster group	Entries	Number of genotypes
I	Alamo, IAC 73-5115, IAC 11, PR-143 (14), Bossire-2, SR-4-3, FB1-7636, Ocepara-4, Clark 63-K, Tunia, HS 82-2136, JSL-1, Essex-1, Davis	14
II	G-9945, H-7, OC-78503, SR-4-1, AGS-7-1, TGX-297-6E-1, H-16, PR-162-11, AGS-62, Protana-2, Coker-240, Hardee-1, IAC-6, AA-42-52, AGS 217, AA-7138, H-6	17
III	AGS-3-1, SCS-1, AGS 234, H-3	4
IV	PR-142 (26)	1

### Pearson's correlation of root and nodulation traits with grain yield and yield component traits

Grain yield was significantly and positively correlated with 100-seed weight, plant fresh weight, pod number, root volume and tap root length at 0 P (Table 11). Similarly, pod number which is one of the most important yield components was positively and significantly associated with plant fresh weight, root fresh weight and root volume, which indicates the importance of the root traits in selecting and improving soybean genotypes for low P tolerance. There was highly significant and positive associations of grain yield with plant fresh weight, root fresh weight, tap root length, and total nodule weight at 100 kg ha<sup>-1</sup> applied P (Table 12). Significant and negative associations were found for grain yield with 100-seed weight, and root volume. Similarly, there was highly significant

and negative correlation of nodulation characters viz., number of nodules, total nodule weight and weight effective nodule with 100-seed weight under low P (Table 11), which indicates the competitiveness of these traits. Pod number has also established significant and positive associations with number of nodules, plant fresh weight, root fresh weight, root volume, tap root length and total nodule weight. On the other hand, grain yield was not significantly associated with all of these nodulation traits under low P (Table 11) indicating that nodule formation has little effect on yield. The fact that total nodule weight was significant at high P; while non-significant at low P indicates the importance of P availability in the soil to enhance nodule formation. This finding is in-line with the finding of Waluyo *et al.* (2004) who reported that nodulation character of soybean is dependent on P availability in the soil.

Table 11: Pearson correlations of root and nodulation traits with some of yield and yield related traits at zero P

Traits	1	2	3	4	5	6	7	8	9	10
1. 100-seed weight (g)	X									
2. Grain yield (kg ha <sup>-1</sup> )	0.21**	X								
3. Number of nodules	-0.35**	0.01	X							
4. Plant fresh weight (g)	0.32**	0.38**	-0.21**	X						
5. Pod number	-0.18*	0.58**	0.12	0.59**	X					

6. Root fresh weight (g)	0.42**	0.04	-0.24**	0.70**	0.18*	X				
7. Root volume (ml)	0.29**	0.20**	-0.11	0.69**	0.32**	0.75**	X			
8. Tap root length (cm)	0.52**	0.15*	-0.46**	0.47**	-0.12	0.53**	0.47**	X		
9. Total nodule weight (g)	-0.23**	-0.12	0.60**	-0.10	-0.04	-0.08	-0.02	-0.24**	X	
10. Weight of effective nodules (gm)	-0.25**	-0.13n	0.66**	-0.12	0.001	-0.12	-0.09	-0.38**	0.75**	X

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

Table 12 Pearson correlations of root and nodulation traits with some of yield and yield related traits at 100 kg ha<sup>-1</sup> applied P

Traits	1	2	3	4	5	6	7	8	9	10
1. 100-seed weight (g)	X									
2. Grain yield (kg ha <sup>-1</sup> )	-0.21**	X								
3. Number of nodules	-0.14	0.2	X							
4. Plant fresh weight (g)	-0.41**	0.66**	0.55**	X						
5. Pod number	-0.01	-0.03	0.77**	0.23**	X					
6. Root fresh weight (g)	0.02	0.31**	0.60**	0.50**	0.59**	X				
7. Root volume (ml)	-0.09	-0.32**	0.29**	-0.20**	0.41**	-0.14*	X			
8. Tap root length (cm)	-0.22**	0.23**	0.38**	0.38**	0.35**	0.35**	-0.11	X		
9. Total nodule weight (g)	-0.35**	0.36**	0.43**	0.49**	0.35**	0.33**	0.01	0.70**	X	
10. Weight of effective nodules (gm)	-0.11	0.10	0.10	0.10	0.04	0.15*	-0.03	0.30**	0.29**	X

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

## REFERENCES

- Foy, CD. 1988. Plant adaptation to acid, aluminum-toxic soils. Communication in soil science and plant analysis 19: 959-987.
- Gomez, KA and Gomez, AA. 1984. Statistical procedure for agricultural research. 2<sup>nd</sup> Edn. An International Rice Research Institute Book. John Wiley and Sons.
- Liao, H, Wan, H, Shaff, J, Wang, X, Yan, X, and Kochian, LV. 2006. Phosphorus and Aluminum Interactions in Soybean in Relation to Aluminum Tolerance. Exudation of Specific Organic Acids from Different Regions of the Intact Root System [W]. Plant physiology 141: 674-684.
- Lynch, JP. 2007. Roots of the second green revolution. Turner review no. 14. Australian Journal of Botany 55: 493-512. URL: [www.publish.csiro.au/journals/ajb](http://www.publish.csiro.au/journals/ajb)

- Mead, R. 1997. Design of plant breeding trials. In: R. A. Kempton, and P. N. Fox (Eds.) Statistical methods for plant variety evaluation. Chapman and Hall, 2-6 Boundary Row, London SE1 8HN, UK.
- Moharram, TMM.; Safwat, MSA; Farghaly, MM, 1994. Effect of inoculation rate and phosphorus fertilization on Nitrogen fixation in soybean. African Crop Science Journal 2: 125-129.
- Nian, H, Ahn, S J, Yang, ZM, and Matsumoto, H. 2003. Effect of phosphorus deficiency on aluminium-induced citrate exudation in soybean (*Glycine max*) Physiologia Plantarum 117: 229-236.
- Olufajo, OO. 1990. Response of promiscuously nodulating soybean to N and P fertilization and *Bradyrhizobium* inoculation in a ferruginous tropical soil (Haplustalf). *Fertilizer Research* 25: 93-100, 1990.
- Tesfaye, A, Githiri, M, Derera, J and Debele, T. 2010. Smallholder Farmers' perception and experience on the importance, consumption and market of soybean in Western Ethiopia. *Asia-Pacific Journal of Rural Development* 20: 125-139.
- Thoenes, P. 2004. The role of soybean in urehting world hunger. FAO Commodities and Trade Division, Basic Foodstuffs Service. A paper presented at the V<sup>th</sup> World Soybean Research Conference held in Foz do Iguassu, Brazil, 1-5 March, 2004.
- Waluyo, SH, Lie, TA, and Manneje, L. 2004. Effect of phosphate on nodule primordia of soybean (*Glycine max* L. Merrill) in acid soils in Rhizotron Experiments. *Indonesian Journal of Agricultural Sciences* 5: 37-44.