

## ORIGINAL ARTICLE

## Response of soybean (*Glycine max* L.) genotypes to varying levels of phosphorus for yield and related traits under acid soils of Western Ethiopia

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

<sup>1</sup>International Institute of Tropical Agriculture, PMB 5320, Oyo Road 200001, Ibadan, Nigeria, <sup>2</sup>Jomo Kenyatta University of and Technology, Department of Horticulture, Nairobi, Kenya, <sup>3</sup>Seed Co. Ltd., Global Research and Development, Zimbabwe, Harare

<sup>4</sup>EIAR, Addis Ababa, Ethiopia,

Corresponding author: [at.abebe@cgiar.org](mailto:at.abebe@cgiar.org)

### ABSTRACT

Low availability of soil phosphorus (P) is one of the major limiting factors for soybean production on acidic soils of the tropics. The objectives of this study were to assess the interaction of soybean genotypes (G) with levels of P, and identify genotypes that are responsive to high P and tolerant to low P conditions. A total of 36 soybean genotypes were evaluated under three levels of P (0, 100, and 200 kg ha<sup>-1</sup>) in three locations (L) of Western Ethiopia in split plot design with P levels as main plots, and genotypes as sub plots. The individual locations analysis, revealed that the genotypes X phosphorus interaction for grain yield was significant (P<0.05) at Assosa. The genotypes showed highly significant differences for most of the studied traits in all the locations. The combined analysis revealed that there was significant G, and LXG interactions for most of the traits. Essex-1, IAC 11 and AGS-3-1 were the best performing genotypes on 200 kg ha<sup>-1</sup> P; while IAC 11, AA-7138, G 9945 and Hawassa 04 exhibited tolerance to low P. AMMI analysis for grain yield at Assosa revealed that zero and 200 kg ha<sup>-1</sup> were highly interactive with the genotypes. Genotypes: AA-7138, PR-142 (26) and H 3 were stable genotypes across the P levels with relatively high main effect; and hence, such genotypes are useful in breeding soybeans for consistent response to varying P conditions.

**Key words:** Soybean genotypes, low P tolerance, AMMI, Stable performance

## INTRODUCTION

Soybean is a crop of global importance for various purposes, mainly for oil, food and feed processing. Demand for the crop has risen tremendously in the recent past. Some of the driving forces for worldwide increase in soybean production include: its high protein and oil content, its health benefits derived from long-term consumption (Wang *et al.*, 2010), the role it plays in improving soil fertility, and for crop rotation (Tesfaye *et al.*, 2010). The crop is in high demand for oil and poultry feed in Northern Guinea Savanna zone of Nigeria (Chiezey and Odunze, 2009). However, the productivity of soybean has been low on acidic soils in the tropics (von Uexku<sup>ll</sup> and Mutert, 1995). On acidic soils that account for 50% of the world's arable land (von Uexku<sup>ll</sup> and Mutert, 1995) most of the P is found in a form that is unavailable to plants, usually, bound by free Fe and Al (Barber, 1995).

Phosphorus is one of the major nutrients that limit crop production on more than 30% of the world's arable land (Vance *et al.*, 2003). It is the most immobile in the soil, inaccessible and unavailable of all plant nutrients, and the second most crop production limiting nutrient, after nitrogen (Holford, 1997; Otani and Ae, 1996). Phosphorus is insoluble in most of its natural forms and hence, its concentration in the soil solution is usually low (2-10 mM) (Raghothama, 1999). The P recycling is very slow compared to nitrogen (Holford, 1997). Chemically, P is very reactive and found in more than 170 compounds.

The application of inorganic fertilizers has, for long, been considered as one of the best options to amend the deficiency of phosphorus in the soil. Chiezey and Odunze (2009) reported significant soybean grain yield increase in response to the application of phosphorus fertilizer. Xiang-wen *et al.* (2008) also reported that the application of P increased biomass production. Aluminum toxicity might be ameliorated through the application of phosphorus, which in-turn might improve root growth and P uptake (Tan and

Keltjens, 1990). Kapoor and Gupta (1977) reported increased fractions of protein and P compounds in soybean seed as a result of increased P supply. On the other hand, Payne *et al.* (1986) reported non-significant effect of P on grain yield of two soybean (one low P tolerant, and the other P-sensitive) varieties, though the study materials were few.

Despite the importance of the use of inorganic P fertilizers to enhance the productivity of soybean and other crops, it has several drawbacks that limits its accessibility and sustainability to subsistence farmers. High price of P fertilizers (Wang *et al.*, 2010; Tesfaye *et al.*, 2011) and unavailability of fertilizers at the right planting time and in a sufficient amount, and problem of distribution systems (Tesfaye *et al.*, 2011) are some of the most common problems of subsistence farmers in the use of commercial fertilizers. The reserve P (rock phosphate) is very limited and estimated to be exhausted within the next 60-90 years (Runge-Metzger, 1995), by 2050 (Vance *et al.*, 2003). Therefore, identifying genotypes that respond to high P applications need to be emphasized, as it helps maximize productivity of the crop for resource rich farmers on low P, and acidic soils. For the resource poor farmers, genotypes tolerant to low soil P levels will be beneficial on acid soils.

Developing crop varieties that are tolerant to and efficiently utilize both the soil and applied P on low soil fertility and low P conditions is considered as a sustainable and environmentally safe practice (Yan *et al.*, 2006; Li *et al.*, 2010; Wang *et al.*, 2010). Individual genes that respond to low P were reported, and grouped into two *i.e.*, 'early' and 'late' genes (Vance *et al.*, 2003). The 'early' genes have immediate and specific response to P; while the 'late' genes change the morphology, physiology or metabolism of plants upon extended P deficiency (Vance *et al.*, 2003).

The literature indicates that soybean genotypes have variable responses to P levels which form the basis for identifying

stress tolerant genotypes. Li et al. (2010) classified 156 cultivars into 29 tolerant, 59 moderate and 68 sensitive cultivars. The authors also identified eight highly tolerant genotypes. Xiangwen et al. (2008), classified 96 soybean genotypes into three categories: high, moderate, and low P efficiency using principal component analysis. Furlani et al. (2002) also classified 29 soybean genotypes into efficient-responsive (ER); efficient non-responsive (ENR); inefficient responsive (IR); inefficient non-responsive (INR).

Analytical tools, such as Genotype x Environment interactions and Additive Main Effect and Multiplicative Interaction (AMMI) model have been employed to interpret large genotype x environment x replicate tables without missing values (Cossa et al., 1991; Romagosa and Fox, 1993). In this particular study, the P levels were considered as environments. Additive Main Effect and Multiplicative Interaction uses PCA to explain pattern in the GXE, or residual matrix through extracting genotype and environment main effects (Romagosa and Fox, 1993). It is a combination of ANOVA and PCA analysis (Yan and Hunt, 1998), and the most effective model to explore the G×E interaction with a minimum number of degrees of freedom (Ramagosa and Fox, 1993). Over 90% of the total sum of squares is explained by an AMMI biplot with main effects plotted against the IPCA1. IPCA1 value of close to zero indicates that the genotypes have general adaptation to the tested environments (Ramagosa and Fox, 1993), and are the most stable genotypes (Yan and Hunt, 1998). IPCA1 scores of larger value depict specific adaptation to environments having similar IPCA1 score sign. Environments were reported to have little interaction with the genotypes when the IPCA1 scores are small and vice versa (Yan and hunt, 1998).

These authors also reported that the biplot of IPCA1 versus IPCA 2 explains only a small portion of the total variation, and genotypes that are far from the origin are reported to be responsive. In this

biplot the two axis partition the plot into four sectors, and genotypes that occur in the same sector interact positively; while those occurring in the opposite sector interact negatively (Yan and Hunt, 1998). The 36 soybean genotypes used in this study had not been previously evaluated for their response to varying P regimes, on acidic soils. Therefore, the objectives of this study were to understand the G×P×L interactions of soybean genotypes, and especially to identify genotypes that are low P tolerant and responsive to high P applications.

## MATERIALS AND METHODS

### Experimental sites, designs, and management

The study was conducted in three locations of Western Ethiopia, namely: Jimma, Mettu, and Assosa in the year 2010 main cropping season (Table 1). The three sites are characterized by strong to moderate acidic soil and low P availability (Table 2).

A total of 36 soybean genotypes were used in the study. A split plot design, where levels of P were the main plots and genotypes were subplots, were used in the experiment. Three levels of P i.e., 0, 100, and 200 kg ha<sup>-1</sup> P were used, representing low, medium, and high levels, respectively. Triple super phosphate (TSP) was used as the source of P. The 36 genotypes within each of the main plots were laid-out in a 6×6 lattice design with two replications. The seeds of all the genotypes were uniformly dressed with Rhizobium bacteria, and no commercial N-fertilizer was applied.

In the statistical analysis of split-plot designs, it is important to consider the presence of two different sizes of experimental units used to test the effect of whole plot treatment and split-plot treatment. Factor A effects are estimated using the whole plots and factor B and the A\*B interaction effects are estimated using the split plots. Since, the size of whole plot and split plots are different, and have different precisions.

Therefore, 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 and  $(\alpha\beta)_{ij} + (\alpha\tau)_{ik} + (\beta\tau)_{jk} + (\tau\alpha\beta)_{ijk}$  represents main plot  $\times$  subplot, main plot  $\times$  location, subplot  $\times$  location, and main plot  $\times$  subplot  $\times$  location interactions, respectively.

**Table 1:** Agro-ecological characteristics of Jimma, Assossa and Mettu 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°03' 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,

AEZ= agro-ecological zone according to EIAR classification; NA=Not available

### Soil sampling and analyses

Soil samples from the experimental plots were collected from the plough layer (0-20 cm) before the experiments. Three samples were collected from each location and analyzed for nutrient content according to various procedures described in Sahlemedin and Taye (2000), such as 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 in Sahlemedin and Taye (2000) were used to analyze pH and exchangeable acidity, Al and H<sup>+</sup>. Data on yield and related traits were collected at maturity.

**Table 2:** Soil analysis results for soil samples collected from the plots before the experiment at Jimma, Assossa and Mettu sites in the 2010 main cropping season

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 <sup>+</sup> (meq/100g soil)
1	Jimma	5	0.14	1.73	2.98	2.96	5.35	0.24	nd*	0.24
2	Jimma	55	0.13	1.99	3.43	4.77	5.34	0.24	nd	0.24
3	Jimma	10	0.14	1.79	3.08	6.96	5.68	0.08	nd	0.08
4	Assossa	10	0.13	2.19	3.77	4.90	4.92	0.24	nd	0.24
5	Assossa	5	0.12	2.33	4.02	5.28	5.5	0.24	nd	0.24
6	Assossa	5	0.12	2.02	3.48	3.35	4.5	1.68	0.08	1.6
7	Mettu	20	0.28	2.30	3.97	1.80	5.11	1.52	0.8	0.72
8	Mettu	15	0.28	2.62	4.52	2.84	4.86	0.72	0.32	0.4
9	Mettu	20	0.26	2.82	4.87	1.16	4.5	2.48	1.28	1.2

\*nd=not detected

### Statistical analysis

Data collected in the experiment were analyzed using SAS Statistical Software package (SAS Institute, 2008). Test of homogeneity of error variances for the locations was made before combined analysis. The combined analysis of G×L, G×P, and G×L×P was analyzed using SAS, split plot analysis program. Square root transformation was performed for count data, such as number of seeds per pod and pod number, as suggested by Gomez and Gomez (1984). AMMI analysis was performed to examine the responses of genotypes to the varying levels of P. Mean separation was done using LSD at 5% level of probability.

## RESULTS

### Response of genotypes to different levels of P in each location

Genotypes showed highly significant differences for all the studied traits, except for pod number at Jimma (Table 3). The P main effects and G × P interactions were non-significant for all the traits at Jimma. At Assossa, the genotypes showed highly significant differences for all the traits, except days to flowering. The P main effects also showed significant differences ( $P < 0.05$ ) for 100 seed weight and days to flowering. The G×P interaction effects were significant ( $P < 0.05$ ) for grain yield, 100 seed weight, days to flowering, days to maturity, and pod length at Assossa. At Mettu, the genotypes showed highly significant difference for all the traits, except for pod length and pod number. It was only days to maturity that showed highly significant G×P interactions at Mettu. The presence of highly significant differences for most of the studied traits indicates that there is sufficient variability among the soybean genotypes for further genetic improvement, and Chiezey and Odunze (2009) reported similar finding.

### Response of genotypes to different P levels over locations

The homogeneity test revealed that there was no significant difference among the

error variances for all the traits. Therefore, results from the combined analysis of variance are reported (Table 4). The genotypes showed highly significant differences for grain yield, days to flowering, days to maturity, fresh biomass and plant height; and significant difference for pod length and pod number, which is similar to the findings of Chiezey and Odunze (2009). The genotype × P-levels (G×P) interaction was significant only for 100-seed weight; while all the traits showed highly significant genotype × location (G×L) interactions, except for fresh biomass weight, and pod number. The presence of significant genotype × P interactions indicates the presence of differential response of the soybean genotypes to the different P levels.

### Performance of genotypes in each location

Genotypes: such as Essex-1, IAC-11, AGS-3-1, HS 82-2136 and Tunia were high yielding at 200 kg ha<sup>-1</sup> P at Assossa (Table 5). Several genotypes, like IAC-11, Hawassa-04, Alamo, Hardee-1, HS 82-2136, Essex-1, Clark-63-K, PR-142 (26), SR-4-1, AA-42-52, AA-7138, and PR-143 (14) at 100 kg ha<sup>-1</sup> P level, were statistically at par with the top yielding genotypes at the rate of 200 kg ha<sup>-1</sup>. Genotypes, such as IAC 11, AA-7138, G 9945, and Hawassa-04 produced the highest grain yield without P application, and were among the top performing genotypes across the different P levels. The performance of genotypes AA-7138, G-9945, and H16 was relatively higher without P application compared to their performance at 100 and 200 kg ha<sup>-1</sup> of P, which might indicate that these genotypes are tolerant to low soil phosphorus. Essex-1, and IAC-11 showed increasing performance with increasing P level. Three genotypes i.e., IAC 6, Ocepara-4, and Protana-2 produced nearly stable performance across the three levels of P.

**Table 3:** Mean squares of genotypes, levels of phosphorus (P), and genotype × phosphorus (G×P) interaction for each of the three locations i.e., Jimma, Assosa and Mettu in the 2010 main cropping season

Traits	Jimma		Assosa		Mettu	
	G	G × P	G	G×P	G	G × P
Grain yield (kg ha <sup>-1</sup> )	750846**	75615ns	235445**	86523*	295002**	132696ns
100-seed weight (g)	24.14**	2.102ns	36.919**	1.564*	19.54**	3.51ns
Days to flowering	106.55**	5.21ns	13.89ns	23.59*	59.49**	15.12ns
Days to maturity	174.27**	4.7ns	19.20**	5.32*	92.85**	18.2**
Fresh biomass (gplant <sup>-1</sup> )	39190**	7771ns	11200**	3220ns	28238**	11754ns
Plant height (cm)	841.22**	36.47ns	232.42**	12.73ns	451.97**	67.55ns
Pod length (cm)	0.685**	0.0743ns	0.8895**	0.1015*	0.276ns	0.211ns
¥Pod number	1.794ns	0.798ns	0.965**	0.342ns	1.299ns	0.741ns

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

**Table 4:** Mean squares for P levels, genotypes, and locations and their interactions for the combined analysis across three locations i.e., Jimma, Mettu and Assosa in the 2010 main cropping season

Traits	Genotypes	P-Levels X	Location X	Location X	P-
		Genotypes	Genotypes	levels X	
Grain yield (kg ha <sup>-1</sup> )	513333**	91490ns	391218**	95974ns	
100-seeds weight (gm)	68.66**	3.02*	5.97**	2.08ns	
Days to 50% flowering	37.5**	12.97ns	56.26**	12.24ns	
Days to maturity	75.29**	11.20ns	66.86**	13.1ns	
Fresh biomass (gm/plant)	21993**	9257ns	16505ns	9748ns	
Plant height (cm)	467.4**	64.22ns	292.9**	88.53ns	
Pod length (cm)	0.3179*	0.1321ns	0.381**	0.173ns	
¥Pod number	1.18*	0.646ns	0.788ns	0.758ns	

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

The performance of most genotypes at 200 kg ha<sup>-1</sup> showed decline compared to their performance at 100 kg ha<sup>-1</sup> P, even though the decline was significant only for two genotypes i.e., Hawassa-04 and SCS-1, which might indicate the application P fertilizer in excess of the optimum level might not give the desired response.

The 100-seed weight of Alamo, HS 82-2136, Ocepara-4 and SCS-1 was significantly higher at both 100 and 200 kg ha<sup>-1</sup> P levels than the control treatment; while PR-143 (14), AGS 217, AGS 3-1 and Hawassa-04 produced significantly higher weight of 100 seeds only at 100 kg ha<sup>-1</sup> P, as compared to the control (no P application) (Table 6). Similarly, number of days to 50%

flowering of SCS-1 and G-9945 was significantly higher at 100 kg ha<sup>-1</sup> than the control. The increase in the P level from zero to both 100 and 200 kg ha<sup>-1</sup> has resulted in significant increase in number of days required to maturity of two genotypes IAC 11 and AA-42-52. Increasing the level of P from zero to 100 kg ha<sup>-1</sup> significantly increased the number of days required to the maturity of genotypes PR 142 (26), and H3; while significantly reducing the maturity of AGS-234.

The difference for P response in each location can be justified by the relatively high P and pH at Jimma, and vice versa at Assosa and Mettu (Table 2). The absence of significant genotype × P level interaction for all the traits at

Jimma, and most of the traits at Mettu and Assossa indicates that there is very limited change in the relative performance of the genotypes with changing P level.

The genotype  $\times$  P interaction was significant for grain yield, 100 seed weight, days to flowering, days to maturity and pod length at Assossa, and days to maturity at Mettu. This validates the need to conduct, such variety evaluation trials in different P regimes, and the need to identify tolerant and responsive varieties. Thus, the relative performance of genotypes in each of the three levels of P for grain yield was determined based on the analysis of Assossa data.

The bi-plot of IPCA1 versus the P-levels main effects that accounted for 31% of the total treatment sum of squares (Table 7) showed that zero and 200 kg ha<sup>-1</sup> P showed relatively higher IPCA1 scores of opposite signs (figure 1), indicating that these two levels of P are highly discriminating the genotypes in contrasting directions. The bi-plot of IPCA1 scores versus the genotype and P levels main effects accounted for more than 80.1% of the total treatment sum of squares. The IPCA1 score of 100 kg ha<sup>-1</sup> P level was small and close to zero, indicating this P level is not strong in discriminating the genotypes. The main effect of 100 kg ha<sup>-1</sup> P level was the highest; while the main effect of 200 kg ha<sup>-1</sup> was close to average. Zero P-level showed the lowest main effect (Figure 2). The released variety, Clark 63 K, Bossire-2 and Protana-2 showed nearly average main effect, and very small IPCA scores, indicating that these genotypes relatively have stable performance. Genotypes: IAC 6 and AA 42-52 produced IPCA1 score of close to zero and above average main effect, which might indicate that these genotypes are relatively stable across the different P levels with above average performance. The highest main effects with relatively small IPCA

scores were produced by genotypes AA-7138, PR-142 (26) and H3, which might show the relative stable and high performance of these genotypes.

There was no genotype with, exceptionally, high IPCA1 score closer to the IPCA 1 score of 200 kg ha<sup>-1</sup> of P. However, AGS-3-1, Hardee-1, Tunia and SR-4-1 are the genotypes with relatively high negative IPCA1 scores and high main effects

**Table 5:** Mean grain yield values of 36 soybean genotypes evaluated at each of the three levels of P i.e., 0, 100 and 200 kg ha<sup>-1</sup> at Assossa in the 2010 main cropping season

Genotypes	Grain yield kg ha <sup>-1</sup>		
	0	100	200
1. Davis	704	1080	1026
2. Tunia	1087	1108	1466
3. PR-142 (26)	1418	1538	1382
4. IAC 11	1604	1783	1881
5. Alamo	1058	1715	1384
6. FB1-7636	1014	1262	1297
7. PR-143 (14)	1386	1484	1039
8. AGS 217	977	1200	1243
9. HS 82-2136	1335	1660	1498
10. AA-7138	1600	1517	1308
11. IAC 73-5115	958	1056	809
12. AA-42-52	1145	1533	1325
13. AGS 234	885	1412	970
14. Coker 240	1192	1006	600
15. AGS-3-1	1136	1313	1549
16. Essex-1	1249	1613	1920
17. Hardee-1	803	1674	1282
18. Bossire-2	1337	1030	1312
19. HAWASA-04	1514	1747	925
20. TGX-297-6E-1	1144	1043	1081
21. AGS-62	989	1151	676
22. Protana 2	1265	1115	1314
23. H 16	1348	1222	1058
24. H 3	1258	1790	1269
25. H 6	1005	1062	1322
26. Ocepara 4	1065	1153	1130
27. SCS-1	879	1414	705
28. Clark 63-K	1121	1559	1109
29. G 9945	1563	1227	1369
30. JSL 1	667	1315	1123
31. SR-4-3	1047	1365	976
32. IAC 6	1363	1321	1394
33. H 7	923	1157	974
34. PR-162-11	899	1168	1060
35. OC-78503	870	1377	978
36. SR-4-1	797	1535	1264
Mean	1128	1353	1195
Level of significance	*		
LSD 5%	486.6		
CV %	19.7		

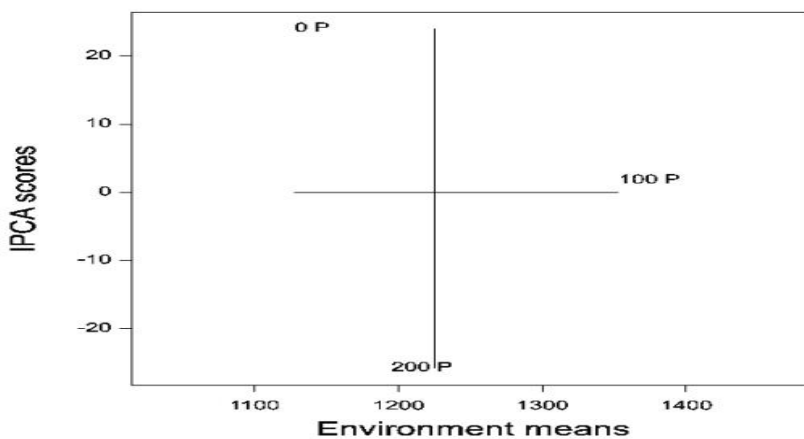


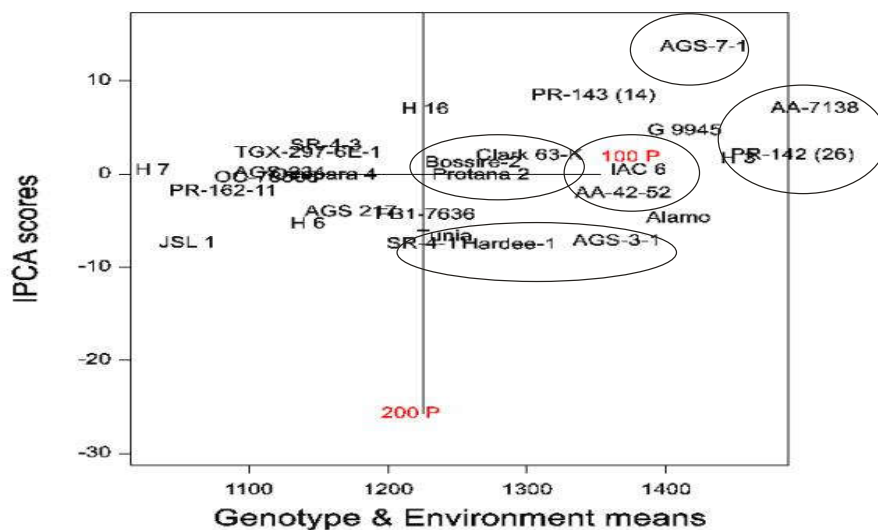
**Table 6:** Mean values of 36 soybean genotypes for some yield related traits evaluated at each of the three levels of P i.e., 0, 100 and 200 kg ha<sup>-1</sup> at Assossa in the 2010 main cropping season

Genotypes	100 seed weight (gm)			Days to flowering			Days to maturity			Pod length (cm)		
	0	100	200	0	100	200	0	100	200	0	100	200
1. Davis	16.5	15.5	14.0	46	44	45	114	115	116	3.5	3.6	3.6
2. Tunia	14.0	15.5	15.0	47	44	53	115	115	115	3.5	3.7	3.8
3. PR-142 (26)	19.5	20.5	19.5	52	48	47	118	123	121	4.5	4.4	4.4
4. IAC 11	16.0	16.5	18.0	48	55	44	116	121	122	4.1	4.0	4.1
5. Alamo	14.5	20.5	19.0	45	44	51	115	115	116	3.8	3.6	4.0
6. FB1-7636	13.0	14.0	14.0	44	51	44	115	115	116	4.0	3.9	4.1
7. PR-143 (14)	14.0	17.0	15.5	46	47	45	118	115	116	3.7	4.0	4.0
8. AGS 217	13.5	17.0	15.0	43	47	46	117	115	115	4.1	3.3	3.7
9. HS 82-2136	13.0	15.5	14.0	50	49	48	118	115	116	3.1	3.3	3.3
10. AA-7138	14.5	16.5	15.5	50	52	43	117	115	116	4.4	4.2	4.4
11. IAC 73-5115	12.5	13.0	12.5	47	48	43	114	115	116	3.5	4.1	4.1
12. AA-42-52	16.0	16.5	15.5	46	45	49	117	125	125	4.4	4.1	4.5
13. AGS 234	13.0	14.0	15.0	46	51	45	120	115	116	3.3	3.1	2.8
14. Coker 240	13.0	14.0	14.5	44	45	44	114	115	116	3.7	3.6	3.2
15. AGS-3-1	15.0	17.5	16.0	44	54	45	115	115	116	3.4	3.7	3.7
16. Essex-1	18.0	20.0	18.5	45	53	44	121	122	116	3.8	4.1	3.7
17. Hardee-1	14.0	16.0	16.0	46	51	44	114	115	115	3.4	4.0	4.0
18. Bossire-2	16.0	17.5	16.5	47	55	44	118	115	116	4.4	4.2	4.1
19. Hawassa-04	17.0	19.5	19.0	48	44	45	115	115	116	4.0	4.1	4.5
20. TGX-297-6E-1	12.5	13.0	14.5	48	51	50	114	115	116	3.9	4.2	3.9
21. AGS-62	13.5	14.0	12.5	48	48	42	115	115	116	3.9	3.6	3.7
22. Protana 2	18.5	20.0	21.0	46	49	50	114	115	116	3.7	4.4	3.9
23. H 16	17.0	19.0	17.5	54	47	47	115	115	116	4.1	3.8	3.9
24. H 3	13.5	14.0	13.5	44	48	49	117	122	116	3.8	3.6	3.9
25. H 6	20.0	21.5	21.0	44	52	44	114	115	116	5.2	4.6	4.8
26. Ocepara 4	15.5	19.5	18.5	46	51	49	117	115	116	4.0	3.7	4.1
27. SCS-1	16.5	19.5	20.0	44	53	50	119	115	116	3.5	3.9	3.7
28. Clark 63-K	14.0	16.0	16.0	47	50	43	114	115	116	4.0	4.1	4.3
29. G 9945	19.5	21.5	20.5	44	53	43	115	115	116	4.4	4.4	4.2
30. JSL 1	17.5	19.0	18.5	45	46	50	114	115	116	3.3	3.7	3.9
31. SR-4-3	14.5	18.0	19.0	45	49	50	114	115	116	4.0	4.2	3.7
32. IAC 6	21.0	21.5	21.0	47	47	53	117	115	116	5.1	4.5	4.7
33. H 7	15.5	17.5	18.0	50	44	47	119	115	116	4.0	4.0	4.4
34. PR-162-11	12.0	13.0	11.5	42	50	44	115	115	116	3.7	4.1	3.8
35. OC-78503	12.5	15.5	13.5	53	48	51	118	115	116	3.2	3.2	3.2
36. SR-4-1	18.0	19.0	20.0	54	46	45	115	115	116	3.3	4.0	3.9
Mean	15.4	17.2	16.7	47	49	46	116	116	116	3.86	3.9	3.92
Level of significance	*			*			*			*		
LSD 5%	2.04			8			4			0.523		
CV %	6.1			8.3			1.6			6.7		

**Table 7:** Analysis of variance for the G×P interaction using the AMMI model for Assossa site

Source	Df	SS	MS	F	F Probability	% variation
Total	215	24479010	113856	*	*	
Treatments	107	16218039	151570	2.59	0.000	
Genotypes	35	8240589	235445	4.03	0.000	50.8
P levels	2	1920824	960412	1.36	0.262	11.8
Block	3	2126033	708678	12.13	0.000	13.1
Interactions	70	6056626	86523	1.48	0.034	37.3
IPCA 1	36	3098705	86075	1.47	0.067	19.1
IPCA 2	34	2957921	86998	1.49	0.065	18.2
Error	105	6134938	58428			

**Figure 1:** The IPCA1 scores of P levels versus the P levels main effect for Assossa site



**Figure 2.** The bi-plot of IPCA1 scores of genotypes and P levels versus the main effects of genotypes and P levels main effect for Assossa site Performance of genotypes over locations

The analysis of variance across locations revealed that the released variety Hawassa-04, and genotypes G-9945 and SCS-1 were the highest yielding, across locations and P levels (Table 8). Hardee 1, Davis, H-7, AGS-3-1, Alamo, Essex-1, Cocker 240, H 3, Tunia, Protana-2, H 16, AGS 62, and FB1-7636, were also among the highest yielding genotypes. Genotypes: G-9945, Protana-2, and the released variety were among the highest yielding genotypes that also produced the highest weight of 100-seeds. Essex-1 and Tunia were late maturing genotypes; while Cocker 240, AGS 62, and Protana 2 were early maturing.

Table 8: Mean performance of soybean genotypes over three locations i.e., Jimma, Assossa and Mettu, and three levels of P in the 2010 main cropping season  $\sqrt{\text{€}}$  values are based on square root transformation

Genotypes	100-seed weight (g)	Days to flowerin g	Days to maturity	Fresh biomass Weight (gm)	Pod number	√Pod number	Pod length (cm)	Number of seeds per pod	Plant Height (cm)	GYLD kg ha-1
1. Davis	16.66	62	127	213.92	37.97	(6.01)	4.22	2.60	48.61	1684.46
2. Tunia	15.81	63	129	285.68	40.64	(6.08)	4.14	2.56	65.04	1617.63
3. PR-142 (26)	18.26	66	131	294.89	32.76	(5.61)	4.36	2.48	63.26	1146.57
4. IAC 11	16.34	66	130	320.19	42.83	(6.33)	4.24	2.63	61.77	1478.13
5. Alamo	17.74	63	126	217.39	36.84	(5.86)	4.10	2.57	57.48	1641.69
6. FBI-7636	13.94	63	125	225.8	39.79	(6.09)	4.27	2.59	47.67	1585.37
7. PR-143 (14)	15.53	64	129	231.21	39.91	(6.09)	4.29	2.67	52.85	1554.20
8. AGS-217	14.96	65	128	286.31	39.99	(6.14)	4.19	2.60	54.07	1411.38
9. HS 82-2136	13.59	64	126	230.82	38.69	(6.02)	3.82	2.54	58.26	1533.38
10. AA-7138	14.71	66	129	238.22	37.16	(5.94)	4.19	2.58	55.29	1411.3
11. IAC 73-5115	13.02	63	124	200.66	33.73	(5.62)	4.07	2.56	43.89	1340.37
12. AA-42-52	14.65	65	131	270.56	36.64	(5.82)	4.14	2.53	56.04	990.32
13. AGS 234	14.50	61	124	240.89	42.88	(6.34)	4.16	2.60	58.71	1572.38
14. Coker 240	15.21	63	123	209.91	41.58	(6.17)	4.11	2.66	46.89	1628.41
15. AGS-3-1	16.90	64	126	256.03	43.63	(6.36)	4.26	2.53	54.29	1671.29
16. Essex-1	17.53	65	130	291.26	39.99	(6.07)	4.20	2.58	54.22	1630.87
17. Hardee-1	15.87	62	126	251.88	40.29	(6.11)	4.19	2.64	59.21	1699.25
18. Bossire-2	15.40	65	126	260.95	42.11	(6.27)	4.29	2.69	47.47	1455.24
19. HAWASA-04	18.56	62	126	248.08	39.6	(6.07)	4.22	2.58	58.55	1911.86
20. TGX-297-6E-1	13.63	63	124	201.19	38.67	(6.03)	4.19	2.64	47.92	1539.69
21. AGS-62	14.66	62	123	170.45	32.99	(5.56)	4.05	2.49	45.13	1596.76
22. Protana 2	19.59	62	124	221.69	36.81	(5.87)	4.41	2.52	55.51	1601.99
23. H 16	17.19	63	126	266.68	39.72	(6.09)	4.48	2.70	48.83	1598.44
24. H 3	14.17	65	128	309.46	47.93	(6.62)	4.22	2.66	58.51	1627.66
25. H 6	19.18	65	127	272.21	37.59	(5.94)	4.39	2.46	52.93	1468.48

Table 8 (continued)

26. Ocepara 4	17.26	62	127	280.37	40.79	(6.11)	4.27	2.64	50.12	1550.95
27. SCS-1	17.08	66	127	280.92	42.20	(6.31)	4.02	2.61	55.08	1721.89
28. Clark 63-K	15.27	64	129	261.23	38.94	(6.04)	4.29	2.64	53.74	1566.67
29. G 9945	20.01	62	127	206.37	33.95	(5.68)	4.31	2.52	50.15	1792.06
30. JSL 1	16.52	64	127	236.76	35.51	(5.77)	4.08	2.52	50.59	1480.83
31. SR-4-3	16.82	64	126	234.93	39.24	(6.06)	4.15	2.56	54.57	1443.39
32. IAC 6	19.87	62	127	267.08	35.71	(5.78)	4.52	2.57	55.55	1490.63
33. H 7	17.27	65	126	306.74	45.76	(6.35)	4.23	2.50	56.43	1679.26
34. PR-162-11	13.18	64	127	275.06	43.38	(6.32)	4.33	2.70	49.83	1351.24
35. OC-78503	13.96	65	127	281.69	46.49	(6.5)	4.14	2.62	56.37	1384.43
36. SR-4-1	18.31	65	125	250.23	45.08	(6.43)	4.16	2.52	59.31	1532.82
Mean	16.20	63.73	126.69	252.71	39.66	(6.07)	4.21	2.58	54.00	1538.65
Level of significance	**	**	**	**	*	*	*	ns	**	**
LSD 5%	1.799	5.011	4.63	122.47	15.99	(1.15)	0.561	---	10.54	337.14

## CONCLUSIONS

The P-levels did not show significant difference for all the traits at Jimma, which is similar with the report of Payne *et al.* (1986); while the P levels were significantly different for 100 seed weight and days to flowering at Assossa, and significantly different for grain yield, days to flowering, fresh biomass weight, plant height, and pod number at Mettu.

Although, it was only at one location that the genotype  $\times$  P interaction for grain yield was significant, it signifies the existence of differential response of genotypes to varying P levels. This also indicates the possibility of identifying low P tolerant and high P responsive genotypes. The significant genotypic difference for most of the studied traits also indicates the existence of sufficient variation among the genotypes for improvement. Genotypes Essex-1, IAC 11 and AGS-3-1 showed best overall performance; while IAC 11, AA-7138, G 9945 and Hawassa-04 were tolerant to low-P, indicating that these genotypes are good for resource poor farmers who cannot afford to apply inorganic fertilizer and amend their soil with lime. Genotypes: Essex-1, IAC-11, HS 82-2136 and Tunia were high yielding at both 200 kg ha<sup>-1</sup> and 100 kg ha<sup>-1</sup> P at Assosa, indicating that these genotypes are relatively responsive to higher P application. Such genotypes might be recommended for resource rich farmers, who have the capacity to buy and apply inorganic fertilizer for good productivity. Genotypes: AA-7138, PR-142 (26) and H3 were stable across the different P levels. In general, the varieties identified for different desirable responses to P, will have much significance in breeding programs to improve soybean.

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