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ORIGINAL RESEARCH

Variability of root traits, seed size and tolerance to low soil phosphorus in common bean (*Phaseolus vulgaris* L.)

Nathan Aliel Kachiguma[1,2] · Beatrice E. Ifie[2] · John S. Y. Eleblu[2] · Moses F. A. Maliro[3] · Kwadwo Ofori[2] · Pangirayi B. Tongoona[2]

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Abstract
Common bean is an important food and cash crop, but its seed yield productivity is constrained by the soil phosphorus (soil-P) deficiency among other factors. This study was implemented to determine variability of root traits and seed size of 14 bean genotypes, and identify genotypes with tolerance to low soil-P. A pot experiment was laid out in split-plot design with two replicates. Highly significant ($P < 0.01$) mean square differences were observed among the genotypes and the genotype × soil-P interactions for all the root traits and seed size. Genotypes BFS-29, USRM-20 and SEF-15 all of Meso-American origin had the lowest values for seed size reduction rate and low fertility susceptibility index and were, therefore, considered tolerant to low soil-P. Cumulatively PC-1 and PC-2 accounted for about 99% of the total variability and were both highly correlated with Hypocotyl Root Length (HRL). PC-2 was also highly correlated with basal root whorl number, basal root growth angle, basal root length and tap root diameter. Quadrant-3 comprised of genotypes USRM-20, SEF-15, BFS-29 and SAB-560 that were tolerant to low soil-P and were characterized with longer basal roots, large tap root diameter, and high seed size. The tolerant genotypes need to be tested on a large scale, conserved and could be utilized in bean improvement programs for low soil-P tolerance.

Keywords Common bean · Genotypes · Root traits · Tolerance · Variability

Introduction

Common bean (*Phaseolus vulgaris* L.) is an annual crop and a diploid ($2n = 2 \times 11 = 22$) species that belongs to the *Fabaceae* family (Beebe et al. 2013). This leguminous nutritious crop is estimated to provide recommended dietary protein in the excess of 50% to the resource poor households in most developing countries in Africa (Wortman et al. 2004). The crop contributes to food and nutrition requirements of the resource poor farming communities. However, in Southern and Central African countries, about 70% of the area under the production of common beans is deficient in soil phosphorus (soil-P) needed for optimum crop growth, development and production (Aggarwal et al. 1997). It is also reported that in Eastern and Southern Africa, limited soil-P is common in 65%–80% of the area under common bean cultivation (Namayanja et al. 2014). According to Henry et al. (2010) soils for bean cultivation are considered deficient if they contain less than 15 mg/kg of available soil-P. Limited soil-P is common in Malawi where soil-P as low as 8 µg/g of soil was reported for some areas (Chilimba and Nkosi 2014).

Potential common bean seed yields are rarely realized because very small quantities of orthophosphate (Pi) are usually available for plant roots to acquire due to the chemical and biological reactions in the soil that quickly transform Pi into unavailable forms (Lynch and Brown 2008). Phosphorus is a very important composition of the Adenosine Diphosphate and Adenosine Triphosphate energy compounds that control biochemical processes including respiration, photosynthesis, nucleic acid, protein and plant cell production

✉ Nathan Aliel Kachiguma
nkachiguma@yahoo.co.uk

[1] Ministry of Agriculture, Department of Agricultural Research Services, Lunyangwa Agricultural Research Station, P.O. Box 59, Mzuzu, Malawi

[2] West Africa Centre for Crop Improvement (WACCI), College of Basic and Applied Sciences, University of Ghana, PMB LG 30, Legon, Accra, Ghana

[3] Lilongwe University of Agriculture and Natural Resources, Bunda College Campus, P.O. Box 219, Lilongwe, Malawi

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(Nesme et al. 2014). Phosphorus is very critical for early maturity, grain and root development in legume crops such as common bean and soils deficient in phosphorus result in poor plant development (Mitran et al. 2018). As such soil fertility need to be supplemented with organic and inorganic fertilizers. Most smallholder farmers are resource poor and cannot afford to pay for escalating prices of inorganic fertilizers. Therefore, it is very important to evaluate, identify and select genotypes that can yield relatively high under limited soil-P conditions.

Common bean plant roots grown in soils with limited phosphorus exhibit genetic variability that needs to be exploited to develop improved genotypes with root traits for efficient soil-P exploration and acquisition (Burridge et al. 2016; Lynch and Brown 2008). Namayanja et al. (2014) reported genotypic variability in root mass, total root length, basal and lateral root production. Mourice and Tryphone (2012) reported genotypic variability in root biomass and 100 seed weights after exposing the genotypes to different soil-P levels. Singh et al. (2011) also reported genotypic variation in 100 seed weight of cowpea genotypes due to varying phosphorus levels. Genotypes with tolerance to low soil-P have been reported, for example, *Carioca,* a widely cultivated cultivar in Brazil, and a Mexican genotype G2333 widely grown in Rwanda are well adapted to low soil-P conditions and respond well to added fertilizer (Lynch and Beebe 1995).

Not much has been done to evaluate specific root traits in common bean for responses to limited soil-P to identify and select tolerant genotypes. Lynch and Brown (2008) indicated that much of research on common bean plant responses to edaphic stress focus on the above ground plant traits and less on the roots, yet the roots directly react to the effect of stress due to limited soil-P. Information on common bean genotypic variability of specific root traits grown in low soil-P conditions is scarce. The specific objectives of this study were, therefore, to determine variability of root traits and seed size of common bean genotypes under low soil-P, and identify genotypes with tolerance to low soil-P.

Materials and methods

Experimental site

The experiment was conducted at Bolero agricultural trial site, located 10 km west of Rumphi district assembly headquarters in Malawi (11° 01′ and 33° 52′ E). Bolero trial site is under Lunyangwa Agricultural Research Station (LARS) which is the center for agricultural research in the northern region of Malawi. The site experiences a humid subtropical climate characterized by hot and humid summers, and cool to mild winters. The rainy season is usually from November to April, and the dry season is from May to October. The average temperatures ranged from 18.2 °C to 29.1 °C and 18.1 °C to 28 °C in February and March 2018, respectively. Rainfall for the months of February and March 2018 averaged 10 mm and 7 mm per day with a relative humidity of 70% (February 2018) and 66% (March 2018).

The soil is classified as Oxic Haplustalf. Soil analysis carried out prior to planting indicated that the soils are slightly acidic and low in phosphorus (Table 1). In bean cultivation, soils with less than 15 mg/kg of phosphorus are considered low in phosphorus (Henry et al. 2010). Phosphorus was determined using Bray-1 method.

Experimental materials

Fourteen common bean genotypes with contrasting root traits were used for this study. Eleven of the genotypes were of Meso-American origin and three were of Andean gene pool (Table 2). The genotypes were obtained from Chitedze Agricultural Research Station and the 'Improving Bean Production in Drought-Prone, Low Fertility Soils of Africa and Latin America-An integrated Approach' project coordinated by Pennsylvania State University.

Table 1 Soil characteristics at Bolero trial site in Rumphi district

Soil depth (cm)	pH	OM (%)	N (%)	P (ug/g)	CEC (me /100 g)	K (mg/Kg)	Zn (mg/Kg)	Mg (mg/Kg)
0–20	6.94	0.56	0.03	17.41	24	22	14	466
20–40	6.15	0.28	0.01	0.18	7	23.2	15.4	517
0–20	5.08	0.40	0.02	19.10	20	36.8	20.2	372
20–40	4.53	0.47	0.02	3.73	10	25	14	275
Mean	5.68	0.43	0.02	10.11	15.3	26.75	15.9	407.5
Critical levels	< 5.5	< 1.5	< 0.08	< 15	–	–	–	–

pH Power of Hydrogen; *OM* Organic Matter; *N* Nitrogen; *P* Phosphorous; *CEC* Cation Exchange Capacity; *K* Potassium; *Zn* Zinc; *Mg* Magnesium

Table 2 Characteristics of bean genotypes that were screened under low and optimum soil phosphorous conditions at Bolero trial site

Genotype	Flower color	Source of collection	Source of origin
BFS-81	Purple	Pennsylvania State University	Meso-American
Tepary-32	White	Pennsylvania State University	Andean
IJR	White	Pennsylvania State University	Andean
SAB-560	White	Pennsylvania State University	Meso-American
BFS-142	White	Pennsylvania State University	Meso-American
BSF-95	White	Pennsylvania State University	Meso-American
SAB-659	White	Pennsylvania State University	Andean
Quimbaya	Purple	Pennsylvania State University	Meso-American
BFS-29	White	Pennsylvania State University	Meso-American
SEF-15	White	Pennsylvania State University	Meso-American
USRM-20	Yellow	Pennsylvania State University	Meso-American
Kabalabala-UBR(92)25-LF	Purple	Department of Agric. Research	Meso-American
Kambidzi-A286	White	Department of Agric. Research	Meso-American
Kalima-PVA-692[a]	Purple	Pennsylvania State University	Meso-American

[a]Check

Experimental design

The experiment was implemented from February to March 2018. The experiment was laid out in a split-plot design with two replicates. The main plots comprised of two soil phosphorus levels: (A) Normal Phosphorus (NP) and (B) Low Phosphorus (LP). NP was achieved by applying NPK fertilizer (23:21:0 + 4 s) at 200 kg/ha to supply 46 kg N, 42 kg P_20_5 and 8 kg S, while LP was achieved by applying Urea (23:10:5: + 6S + 1.0Zn) at 200 kg/ha to supply 46 kg N, 20 kg P_2O_5, 10 kg K_2O, 12 kg S and 2 kg Zn. Multifeed P 5:2:4 (43) foliar inorganic fertilizer was applied in all the main plots twice at seven and 14 days after crop emergence at the rate of 2 kg/25 L water/hectare to supply for any possible deficiencies in the other nutrients. The sub-plot entries (genotypes) were randomly applied to the main plots. Genotype Kalima-PVA-692 was included as a check. Genotype Kalima-PVA-692 was reported to superior performance for seed yield under low soil-P in Malawi (Aggarwal et al. 1997).

Ten plants were grown per experimental unit per replicate. The experimental unit comprised of ten pots. Fifty kilogram polypropylene woven bag (60 cm in diameter and 102 cm in length) used as planting pots were filled with soil to 50 cm high. Two seeds were planted per pot at 2 cm depth and thinned to one plant per pot 7 days after emergence. The polypropylene woven bag was ideal because according to Halterlein (1983) half of common bean roots are distributed within the top 30 cm and less than 10% of the roots are distributed to a soil depth of more than 30 cm. The field soil (pretested for soil nutrients) was used as the substrate for plant growth. The top-soil (20 cm deep) was removed, and the sub-soil from the deeper soil profile (> 20 cm deep) was used to fill the pots because the soil had much lower soil-P content. The pots were laid out in an open field. All agronomic practises such as irrigation, hand weeding and pesticide spraying were done when necessary.

Data collection and analysis

Root phenotypic data were collected at flowering stage. Root development is expected to decrease at flowering stage because photosynthates are allocated more towards flower and grain development (Araujo et al. 2005). Data were taken on five randomly selected plants per experimental unit. The soil surrounding the root zone was carefully removed with as much minimal damage to the roots as possible by use of running water from a hose pipe. The excavated roots were then dipped into water containing soap solution. A protractor on the phenotyping board was used to measure the basal root growth angle from the horizontal axis perpendicular to the direction of gravitational force. Hypocotyl root length (cm), basal root length (cm) and primary root length (cm) were measured by aligning a piece of string along the root and then the string was measured using the ruler. Tap root diameter (mm) was measured using a digital calliper. Seed size (g) was measured from the remaining three plants. Basal roots number, basal root whorl number and hypocotyl roots number were also counted.

The following derived variables were calculated from data on seed size using the adopted formulae: Low Fertility Intensity Index (LFII) (Fischer and Maurer 1978), Reduction Rate (RR) (Rosielle and Hamblin 1981), and Low Fertility Susceptibility Index (LFSI) (Fischer and Maurer 1978).

Results and discussion

Variability for root and seed size traits of 14 common bean genotypes

The mean squares for seed size and all the root traits except for basal root whorl number, basal root growth angle and basal root length were significant ($P < 0.05$) under the soil-P levels (Table 3). The mean squares for the genotypes were much higher than the genotype × soil-P level interactions for all the variables except for basal root whorl number, basal root number and basal root length. The study revealed highly significant ($P < 0.01$) differences among the genotypes and the genotype × soil-P level interactions for all the root traits and seed size. Considerable high variation for root and seed size was observed among the bean genotypes under varying soil-P conditions probably due to varying genetic effects. Similarly, Trindade and Araujo (2014) reported genotypic variability of root traits in response to varying soil-P levels.

Hypocotyl Root Number (HRN) ranged from 6 for genotype BFS-29 to 22.5 for genotype Kabalabala-UBR(92)25-LF under low soil-P conditions (Table 4). Low soil-P increased HRN by 28.1%. Genotype BFS-81 had the shortest hypocotyl root (3.9 cm) while BFS-142 had the longest hypocotyl root (25.1 cm) after exposure to low soil-P treatment. Hypocotyl Root Length (HRL) for Kalima-PVA-692, the check genotype, was slightly reduced due to low soil-P compared to BFS-142 of Meso-American origin which had the longest hypocotyl roots. Miller et al. (2003) and Ochoa et al. (2006) reported a decrease in hypocotyl root length due to phosphorus deficiency. Under low soil-P conditions, Quimbaya had the highest number of basal roots (26) while genotype SAB-659 had the lowest number of basal roots (7.5). Low soil-P effect increased number of basal roots by 12%. The results revealed that hypocotyl root length decreased while basal root number and basal root length increased due to low soil-P (Table 4). The findings are consistent with earlier studies that reduction in hypocotyl root length is inversely proportional to the increase in basal root number and length (Walk et al. 2006). The study revealed highly significant ($P < 0.01$) differences among the genotypes and the genotype × soil-P level interactions for hypocotyl root number, hypocotyl root length and basal root number (Table 3). Low soil-P increased Basal Root Whorl Number (BRWN) by 3.5%. Genotypes BFS-81, BFS-95 and USRM-20 had two basal root whorls while Quimbaya had four basal root whorls. The soil-P treatment had no significant effect on BRWN, however, genotypic effect and the genotype × soil-P interaction were significant at $P \leq 0.01$ and $P \leq 0.05$, respectively (Table 3). The high number of basal root whorls probably contributed to increased basal root number observed in this study, and consequently, increased hypocotyl root number, basal root number and basal root length contributed to high root surface area which is beneficial for soil-P exploration and acquisition under limited soil-P conditions.

Under low soil-P, genotype Quimbaya had the lowest basal root growth angle (10°) while Kalima-PVA-692 (the check) had the highest basal root growth angle (55°). Quimbaya had the shortest basal roots (16 cm) while SAB-560 had the longest basal roots (46.6 cm). Exposure to low soil-P increased the basal roots growth angle and basal root length when compared to normal soil-P level. The treatment effects were not significant suggesting that the effects of soil-P levels on basal root growth angle and basal root length were similar. However, the genotypic effect and the genotype × soil-P treatment interactions were highly significant at $P \leq 0.01$ (Table 3). Genotypes with shallow basal root growth angle after exposure to soil-P deficiency

Table 3 Mean squares for root traits and seed size of 14 genotypes evaluated under low and optimum soil phosphorus

Source of variation	DF	BRWN	BRGA (^{0})	BRN	BRL (cm)	PRL (cm)	HRN	HRL (cm)	TRD (mm)	SdWt (g)
Block/Replication	1	0.07	0.45	0.286	0.15	1.479	2.161	0.411	3.018	0.982
Soil-P Level (SL)	1	0.07 ns	279.02 ns	20.643*	207.90 ns	15.122*	95.161*	211.383*	11.161*	4008.455*
Main Plot Error	1	0	54.02	0.071	11.07	0.03	0.446	0.231	0.018	1.083
Genotypes (G)	13	1.22**	454.29**	26.286**	118.68**	39.072**	32.853**	77.373**	0.826**	140.773**
SL × G	13	2.41*	223.25**	34.643**	245.65**	18.072**	18.315**	52.401**	0.738**	35.853**
Sub Plot Error	26		31.08	0.948	34.90	0.982	1.150	0.432	0.172	0.373

DF degrees of freedom; *BRWN* basal root whorl number; *BRGA* basal root growth angle (°); *BRN* basal root number; *BRL* basal root length (cm); *PRL* primary root length (cm); *HRN* hypocotyl root number; *HRL* hypocotyl root length (cm); *TRD* tap root diameter (mm); SdWt weight of 100 Seeds (g)

^{ns}Non-significant

*Significance at $P \leq 0.05$

**Significance at $P \leq 0.01$

Table 4 Effect of optimum and low soil phosphorus on hypocotyl root number, hypocotyl root length, basal root whorl number, basal root number, basal root growth angle, basal root length, primary root length and tap root diameter of 14 genotypes

GENOTYPE	HRN		HRL (cm)		BRWN		BRN		BRGA (^{0})		BRL (cm)		PRL (cm)		TRD (mm)	
	NP	LP	NP	LP	NP	LP	NP	LP	NP	LP	NP	LP	NP	LP	NP	LP
BFS-81	8	10	22.2	3.9	3	2	7.5	11.5	20	20	25.4	30.9	15	16.2	4	3.5
Tepary-32	7	11.5	4.8	8.2	3.5	3	11	17	35	20	21.1	19	22.2	20	3.5	2
IJR	9	14	22.3	12.4	4	3.5	11	12	20	40	18.9	26.2	13.5	6.7	2.5	2.5
SAB-560	7.5	6.5	13.5	10.1	3	2.5	10	12.5	40	45	31.2	46.6	16.6	14.9	2	2
BFS-142	9.5	12.5	18	25.1	2.5	3	10.5	10	25	45	18.7	42.4	11	14.9	3	1
BSF-95	12	16.5	22.1	22.2	2.5	2	9.5	9.5	30	48	44	23.4	16.4	15.7	3.5	2
SAB-659	10	15.5	13.2	11	2	2.5	13	7.5	30	15	19.3	30.7	14.4	15	3.5	2
Quimbaya	11	12	24.9	12.1	4	4	8.5	26	20	10	36.8	16	15.8	16	3.5	2
BFS-29	11.5	6	11.1	11.8	2	3	11	8.5	30	15	23.5	26.1	12.1	15.9	3.5	2.5
SEF-15	10.5	8	19.9	9.3	3	2.5	9.5	9.5	25	25	22.5	25.6	11.7	8.8	2.5	2.5
USRM-20	5.5	8.5	13.7	6.3	3	2	8.5	11	50	45	40	37	16.1	11.6	3	3
Kabalabala-UBR(92)25-LF	9.5	22.5	15.7	10.1	2	3	10.5	12	30	55	24.4	32.1	23	15.9	4.5	2
Kambidzi-A286	9.5	11.5	14.2	14.3	2.5	3	11	9	35	50	25.9	31.8	21.7	16	2.5	2.5
Kalima-PVA-692[a]	14.5	16.5	15.2	19.6	3.5	3.5	20	12.5	35	55	44.7	25.5	11.2	18.5	3	2.5
Mean	9.6	12.3	16.5	12.6	2.9	2.8	10.82	12.0	30.4	34.8	25.7	29.5	15.7	14.7	3.2	2.3
SE±	0.74	0.78	0.46	0.47	0.31	0.31	0.72	0.66	4.76	2.90	5.33	2.55	0.89	0.44	0.26	0.33
Reduction (%)	–	− 28.1	–	23.6	–	3.5	–	− 0.12	–	− 14.5	–	− 14.8	–	6.4	–	28.1
Heritability (H^2)	0.97	0.88	0.99	0.99	0.74	0.80	0.94	0.98	0.92	0.88	0.60	0.94	0.94	0.98	0.80	0.76
GA as %age of the mean	53.07	19.86	41.13	49.03	20.66	30.78	30.53	43.82	58.86	25.99	28.77	39.79	24.80	31.09	18.53	29.01
GCV (%)	22.26	4.68	32.76	47.12	21.08	18.72	42.52	24.08	26.03	44.98	39.95	21.92	25.47	23.17	18.24	22.56
PCV (%)	23.69	32.89	32.89	47.26	23.60	21.71	42.95	24.82	27.72	47.02	41.17	28.41	25.63	23.94	20.88	25.17

HRN hypocotyl root number; *HRL* hypocotyl root length (cm); *BRWN* basal root whorl number; *BRN* basal root number; *BRGA* basal root growth angle (°); *BRL* basal root length (cm); *PRL* primary root length (cm); *TRD* tap root diameter (mm); *NP* normal phosphorus; *LP* low phosphorus; *SE* standard error H^2 broad sense heritability; *GA* genetic advance; *GCV* genetic coefficient of variation; *PCV* phenotypic coefficient of variation

[a]Check genotype

conditions can be selected from this study. A shallow basal root growth angle under low soil-P condition is desirable for soil-P exploration and acquisition in the top-soil profile which is expected to contain more soil-P compared to the lower soil profile.

The length of primary roots decreased under low soil-P. The genotype IJR had the shortest primary root (6.7 cm), while Tepary-32 had the longest primary root (20 cm). The genotypic effect and the genotype × soil-P interactions were highly significant at $P \leq 0.01$ for primary root length (Table 3). Low soil-P conditions increased the number and length of basal roots and decreased primary root length, and these characteristics contribute to tolerance of bean genotypes grown under soil-P deficiency conditions. Therefore, genotypes with such traits for tolerance to soil-P deficiency can be selected and included in bean crop improvement programs. According to Burridge et al. (2016) deep primary roots in legume crops are more useful for extracting soil moisture from the deep soil profiles while the short primary roots, increased number and length of basal roots are useful attributes for extracting available soil-P in the top-soil profile. The findings of this study are also consistent with Lopez-Bucio et al. (2002) and Al-Ghazi et al. (2003) who reported that an increase in basal roots reduced primary root length in *Arabidopsis thaliana* after exposure to low soil-P growth conditions.

Genotype BFS-142 had the smallest tap root diameter (1 mm), while BFS-81 had the largest tap root diameter (3.5 mm) under low soil-P conditions. Generally, soil-P deficiency decreased tap root diameter (Table 4). The genotypic effect and the genotype × soil-P treatment interactions were highly significant at $P \leq 0.01$ for tap root diameter (Table 3). Tap root diameter provides an indication of the strength of the tap root. A large tap root diameter may be useful against lodging and also contribute to total root surface area which is ideal for acquiring available soil-P. Zhu and Lynch (2004) reported that tap root diameter decreased with low soil nutrient content. Similarly, Lynch and Brown (2008) indicated that specific root diameters are more likely to decrease in response to soil nutrient deficiency.

The broad sense heritability with their corresponding genetic advance values were highest for hypocotyl root length, basal root number, basal root length and primary root length under low soil-P conditions (Table 4). This is an indication that these traits can reliably be used in the screening and selection of genotypes with genetic tolerance to low soil-P conditions. According to Panes and Sukhatme (1995) variables that exhibit high heritability and genetic advance can be used in the selection process because such variables are expected to be controlled by additive genes and are less influenced by the environment. Contrary to this study, Araujo et al. (2005) reported lower broad sense heritability values for bean root traits under low soil-P conditions. High coefficients of variation were observed for root traits in this study suggesting that common bean adaptive strategy to low soil-P include characteristics such as roots plasticity which enables the roots to grow until they reach localized soil portions with optimum available soil-P. Similar observations have been reported in maize by Zhu and Lynch (2004). Root morphological variables that were used in this study can be effectively used in conventional breeding programs to identify genotypes that are tolerant to low soil-P. The findings are consistent with Burridge et al. (2016) and Lynch and Brown (2008) who reported that efficient top-soil profile foraging and phosphorus acquisition is a combination of several root traits with different adaptive functions.

Variability of seed size and indices for selecting genotypes tolerant to low soil phosphorus

Seed size ranged from 20 to 49 g under normal soil-P and from 11 to 29 g under low soil-P (Table 5). Seed size decreased due to the effect of low soil-P conditions. Seed size reduction rate and low fertility susceptibility index were

Table 5 Effect of optimum and low soil phosphorus on 100 seed weight, reduction (%) in seed weight and low fertility susceptibility index of 14 bean genotypes

Genotype	100 Seed Weight (SdWt) in grams/plant/genotype		Reduction rate (%)	LFSI
	NP	LP		
BFS-81	24	11	54.2	1.2
Tepary-32	37	14	62.2	1.3
IJR	37	19	48.6	1.1
SAB-560	49	26	46.9	1.0
BFS-142	36	19	47.2	1.0
BSF-95	27	12	55.6	1.2
SAB-659	46	22	52.2	1.1
Quimbaya	34	18	47.1	1.0
BFS-29	27	23	14.8	0.3
SEF-15	35	21	40.0	0.9
USRM-20	33	29	12.1	0.3
Kabalabala-UBR(92)25-LF	20	18	54.2	1.2
Kambidzi-A286	32	26	62.2	1.3
Kalima-PVA-692[a]	48	23	52.1	1.1
Mean	23.6	20.1	14.7	–
SE ±	2.42	1.86	–	–
GCV	26.30	20.94	–	–
PCV	27.45	24.17	–	–

SE standard error; *LFSI* low soil-P fertility susceptibility index; *NP* normal phosphorus; *LP* low phosphorus; *GCV* genotypic coefficient of variation; *PCV* phenotypic coefficient of variation

[a]Check genotype

used as principal criteria in discriminating between susceptible and tolerant genotypes under low soil-P. Five genotypes, SAB-560 of Andean evolutionary origin, BFS-142, BFS-29, SEF-15 and USRM-20 of Meso-American gene pool, had lower values for seed size reduction rate and low fertility susceptibility index compared to the check genotype Kalima-PVA-692. These genotypes were considered less susceptible to low soil-P. Genotypes BFS-29, USRM-20 and SEF-15 all of Meso-American evolutionary origin were considered tolerant to low soil-P for the lowest values both in seed size reduction rate and low fertility susceptibility index (values ˂ 1). However, while similar seed size was observed for BFS-29 and the check genotype Kalima-PVA-692, SEF-15 had smaller seed size. Genotype USRM-20 which had the highest seed size, lowest value for seed size reduction rate and lowest fertility susceptibility index was identified as the most tolerant to low soil-P conditions. The tolerance in the three genotypes could be attributed to longer basal roots for USRM-20 and BFS-142; a larger tap root diameter for BFS-142; and the highest number of basal roots and whorls for BFS-29 compared to the check genotype Kalima-PVA-692. Lynch and Brown (2008) explained that the most tolerant bean genotypes under low soil-P conditions are able to explore and acquire the soil nutrients at very minimal metabolic costs and allocate more photosynthates towards grain development.

Relative contribution of root variables to observed variability

Principal Component Analysis (PCA) is one of the tools that is used to understand the extent of genetic variation and relationships of the genotypes. PCA enhances the selection of ideal genotypes and identification of traits that best depict the genotypic variation. The first Principal Component (PC-1) and second Principal Component (PC-2) accounted for 99% of total variability observed in this study (Fig. 1). Variability was based on eight root variables and the genotypes were spread across the four quadrants of the principal components. Kambidzi-A286 was solely categorized in Quadrant-1, and BFS-142, BFS-95 and Kalima-PVA-692 (the check) in Quadrant-2 (all of Meso-American gene pool), BFS-142 had long hypocotyl roots while Kalima-PVA-692 had the highest number of hypocotyl roots and the deepest basal root growth angle. Genotypes SEF-15, USRM-20 and BFS-29 considered as tolerant to low soil-P were categorized in Quadrant-3 together with SAB-560 that had high seed weight size and long basal roots. Generally, the genotypes in Quadrant-3 had the least number of hypocotyl roots, longest basal root length, shortest basal root length, least number of basal root whorls and largest tap root diameter. Quimbaya was in between Quadrant-3 and Quadrant-4 and was characterized with the highest number of basal roots and root whorls. Quadrant-4 comprised of genotypes with the lowest number of basal roots and the highest number of hypocotyl roots. Quadrants 3 and 4 comprised of genotypes of both Meso-American and Andean origins.

Variables with high factor loadings were identified by examining the latent vectors (Eigen vectors) for the first two principal components (Table 6). Score on the PC-1 was highly and positively correlated to hypocotyl root length. The PC-2 was highly and positively correlated with hypocotyl root length and basal root length. PC-2 was also highly and negatively correlated with basal root whorl number,

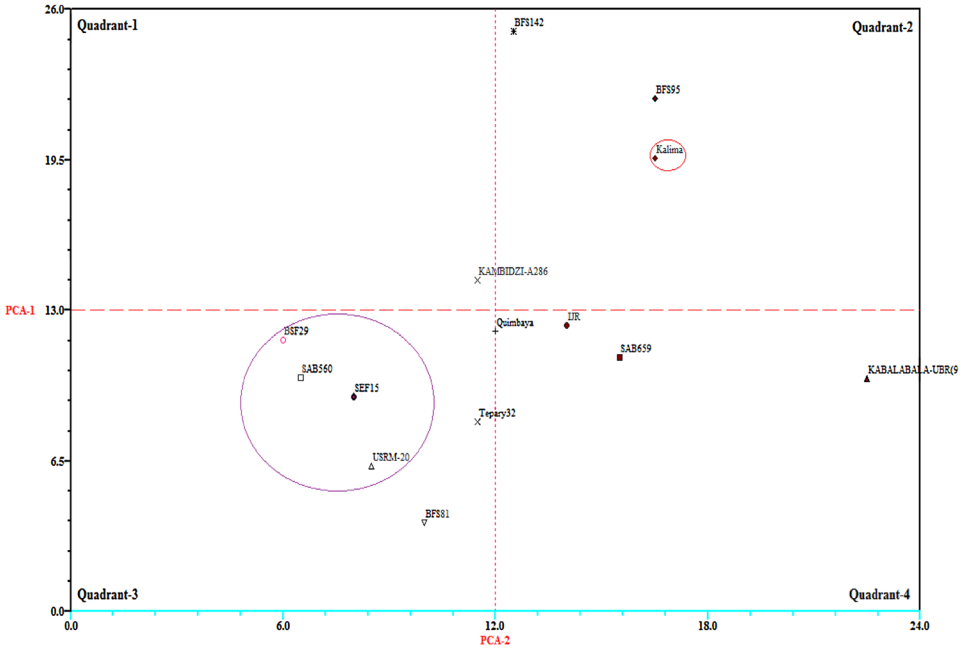

Fig. 1 Distribution across the principal component axes of 14 common bean genotypes screened under low soil-P

Table 6 First two principal components for root traits under low soil moisture conditions

Variable	Principal Component (PC) factor loadings	
	PC-1	PC-2
HRN	1.05	3.55
HRL	6.95	5.47
BRWN	1.05	− 5.76
BRN	2.35	− 3.75
BRGA	− 2.12	− 5.02
BRL	− 1.55	5.38
PRL	− 1.19	1.44
TRD	1.10	− 5.99
Eigen value	1082.99	57.63
Variance	31.43	20.32
Proportion of variance (%)	94.30	5.02
Cumulative (%)	94.30	99.31

HRN hypocotyl root number; *HRL* hypocotyl root length; *BRWN* basal root whorl number; *BRN* basal root number; *BRGA* basal root growth angle; *BRL* basal root length; *PRL* primary root length; *TRD* tap root diameter; *LFSI* low fertility susceptibility index

basal root growth angle and tap root diameter. The findings suggest that hypocotyl root length, basal root length, basal root whorl number, basal root growth angle and tap root diameter can effectively and efficiently be used to phenotype bean roots at flowering stage under low soil-P conditions.

Relatedness of common bean genotypes based on selected root traits

The average linkage grouping method produced three major clusters at the mid-point (9.0) distant between cluster centroids (Fig. 2). Cluster analysis based on hypocotyl root length, basal root length, basal root whorl number, basal root growth angle and tap root diameter rearranged the association of genotypes as compared to the distribution of the genotypes on the principal component axes. Cluster-A comprised of genotypes that were characterized with the longest hypocotyl and basal roots. Genotypes that were identified as tolerant to low soil-P, BFS-29, SEF-15 and USRM-20 including the check genotype Kalima-PVA-692 were all in Cluster-B suggesting close genetic relatedness of these genotypes. Cluster-B comprised of genotypes that were characterized with the shortest basal roots, shallow basal root growth angle, longest hypocotyl roots and high number of basal root whorls. The shallow basal root growth angle, high number and long hypocotyl root characteristics of some genotypes in Cluster-B contribute to large root area enhancing soil-P exploration and acquisition from the top-soil substrate (Burridge et al. 2016; Lynch and Brown 2008; Miller et al. 2003). The principal components and cluster analyses revealed the existence of genotypic variation among the fourteen bean genotypes.

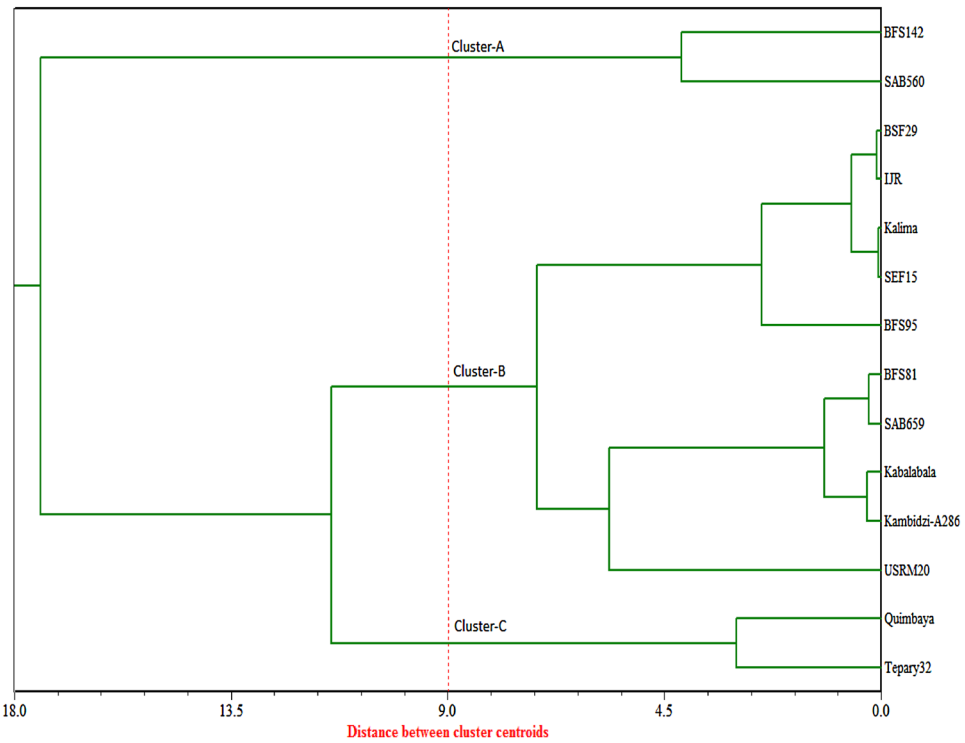

Fig. 2 Hierarchical clustering of 14 bean genotypes under low soil-P

Conclusion

Genotypic variability existed for root traits and seed size among the common bean genotypes evaluated under low soil-P conditions. Genotypes BFS-29, USRM-20 and SEF-15 were identified as tolerant to limited soil-P. The three genotypes exhibited lowest seed size reduction rate and low fertility susceptibility index. USRM-20 was considered the most tolerant based on its high seed size, lowest seed size reduction rate and low fertility susceptibility index. Genotypes BFS-29, USRM-20 and SEF-15 could be utilized in bean crop improvement programs for low soil-P tolerance.

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Declarations

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