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Characterization of Common Bean (*Phaseolus vulgaris* L.) Genotypes for Drought Tolerance

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ABSTRACT

Background: Drought is a major constraint affecting the seed yield of common bean in smallholder farmers' fields in Malawi. Therefore, there is a need to develop genotypes that can perform well under drought conditions. The study was conducted to assess the variability of common bean genotypes under stressed and optimum soil moisture conditions.

Methods: Forty-three common bean genotypes were evaluated under low and optimum soil moisture in a split-plot pot experiment in 2017. Data were collected at flowering stage on five root traits and seed weight.

Result: Highly significant ($P<0.01$) differences were observed among the genotypes and the genotype × water treatment interactions for the root traits and seed weight. Water stress increased hypocotyl root number, basal root number and basal root growth angle by 127.1, 11.3 and 46.1% respectively, while hypocotyl root length, basal root whorl number and seed weight were reduced by 7.1, 1.9 and 9.4% respectively. Broad sense heritability and genetic advance (%) was highest for hypocotyl root length. Genotypes CER-78, SAB-560 and SER-125 were considered tolerant to soil moisture stress and should therefore be tested in various drought conditions for release and used for genetic enhancement focusing on root traits and seed yield.

Key words: Common bean, Genotypes, Drought tolerance, Root traits, Variability.

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INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) belongs to the legume family *Fabaceae* and is a diploid (2n=2x11=22) crop species (Beebe *et al.*, 2013). Common bean is an annual food crop and also a source of income to most farming households in Malawi and other developing countries. The crop originated from a wide geographic origin in the tropics and sub-tropics of Latin America and the major centres of domestication are the Andean and Middle American gene pools (Cortes, 2013).

Common bean seed yield productivity is greatly affected by intermittent drought (Sajitha *et al.*, 2022; Jincya *et al.*, 2021; Asfaw and Blair, 2014). However, common bean genotypes that give relatively high seed yield in drought prone areas have been reported (Darkwa *et al.*, 2016; Hu *et al.*, 2022). These genotypes tend to maintain seed weight higher than those less tolerant to drought conditions. Therefore, the objectives of this study were to determine variability of root traits and seed weight among common bean genotypes under low soil moisture; and to identify genotypes with characteristics for tolerance to low soil moisture. The findings of this study will guide genetic enhancement of genotypes that can perform well under drought conditions.

MATERIALS AND METHODS

Forty-three common bean genotypes of Andean and Meso-American origin were used in this study (Table 1). The experiment was conducted at Lunyangwa Agricultural Research Station (LARS), Malawi located on the Viphya Plateau, at 1,342 meters above sea level. LARS is on latitude 11°11′ South and longitude 34°03′ East. The soil had Sand (60.2%), Silt (3.01%) and Clay (36.8%).

The study was conducted during the dry season in the months of October and November 2017 with the treatments laid out in a Split-plot design with two replicates. The main plots comprised of two soil moisture levels; Non-Stressed (NST) (optimum soil moisture level was maintained by supplying water to field capacity until the crop had reached flowering stage) and Stressed (ST) (the soil was irrigated and soil moisture was maintained at field capacity from planting up to 10 days after emergence and thereafter irrigation was done whenever the soil moisture was depleted to less than 30% field capacity until the crop had reached flowering stage). The soil moisture levels were measured and monitored using the 3-in-1 Soil moisture, light and pH meters (Model YKS628). The sub-plot entries (genotypes) were randomly applied to the main-plots. Ten plants each per pot were planted per experimental unit per replicate. The pots were polypropylene woven bags and were filled with soil to 50 cm high. The field soil (pretested for soil nutrients) was used as the substrate for plant growth. Inorganic NPK fertilizer was applied at 20 kg/ha of N and P_2O_5. Multifeed P 5:2:4 (43) foliar inorganic fertilizer was also applied twice at seven and fourteen days after emergence at the rate of 2 kg/25 litre water/hectare. The experiment was laid out and left in the open air.

Root phenotypic data were collected at flowering stage. Five plants per experimental unit were randomly selected, root crowns were excavated and evaluated. A protractor on the phenotyping board was used to measure the basal root growth angle (BRGA) from the horizontal axis perpendicular to the direction of gravitational force. To measure hypocotyl root length (HRL), a piece of string was aligned along the hypocotyl root and then the string was measured using the ruler in centimetres. Seed weight was measured for seeds that were harvested from the remaining three plants. Data were also collected on basal root number (BRN), basal root whorl number (BRWN) and hypocotyl root number (HRN). Reduction (R%) and seeds weight stability index (SSI) were calculated from data on 100 seeds weight as per Rosielle and Hamblin (1981) and Bouslama and Schapaugh (1984). Analysis of variance was performed in GenStat 18th Edition.

RESULTS AND DISCUSSION

Variation in root traits

No significant mean square differences were observed between the soil water treatment regimes for all the root variables except for HRL ($P<0.05$) (Table 2). However, there were highly significant ($P<0.01$) mean square differences among the genotypes and the genotype × water treatment regime interactions for all the root traits measured and seed weight. The effect of soil moisture stress on expression of root traits and seed weight varied and that was probably due to genetic effects which is an indication that selection can be done for genotypes with tolerance to drought conditions utilising root traits. The genotype × water treatment regime interactions observed suggest that the phenotypic root and seed weight characters of the genotypes across the two main water treatment regimes were adaptable to specific environment. The findings of this study agree with those of Asfaw and Blair (2014) and Rezene *et al.* (2011) who reported variations in common bean roots response to low and optimum soil moisture conditions.

Table 1: Flower colour and origin of 43 common bean genotypes evaluated.

Genotype	Flower color	Origin
BFS-81	Purple	Meso-American
Tepary-32	White	Andean
BC-265	Purple	Meso-American
SER-78	Purple	Meso-American
IJR	White	Andean
CAL-143	White	Andean
SAB-560	Purple	Meso-American
BFS-142	White	Meso-American
Bonus	White	Andean
Tepary-22	Purple	Meso-American
Amadeus	White	Meso-American
BSF-95	White	Meso-American
Kalima-PVA-692	White	Meso-American
Colorado-3	White	Meso-American
Tio Canela	White	Meso-American
SAB-659	White	Andean
Quimbaya	Purple	Meso-American
EAL-14	Purple	Andean
SER-125	White	Meso-American
BFS-29	White	Meso-American
ER-118	Purple	Meso-American
SEF-15	White	Meso-American
DOR-364	Purple	Meso-American
CL-43	White	Andean
USRM-20	Yellow	Meso-American
SEN-56	White	Meso-American
SAP-1	White	Andean
SAB-686	Purple	Andean
DOR-390	White	Meso-American
CIM-RM06(BSM52-14)	Purple	Andean
CIM-SUG02-15-1	White	Andean
INTER-LAB31	White	Andean
MN13509-8-6	White	Meso-American
MR13508-2	White	Meso-American
CIM-RM-03-03-46	Yellow	Andean
CIM-RM07-ALS-62-1	White	Andean
CIM-KHAKHI-07-ALS-1	White	Andean
CIM-RM-04-04-04	White	Andean
SER-124	White	Meso-American
SER-83	White	Meso-American
Kabalabala-UBR(92)25-LF[a]	Purple	Meso-American
Kambidzi-A286[a]	White	Meso-American

[a]Check genotype.

The HRN ranged from 3.5 to 27 in the optimum water treatment and from 7.5 to 48.5 under water stress treatment (Table 3). The effect of water stress increased HRN by 127%. Genotypes BFS-29 and DOR-364 had the lowest HRN, while SER-124 had the highest HRN after exposure to low soil moisture. While the effect of low soil moisture increased HRN by 127%, the mean HRL was slightly reduced by only 7%. The HRL ranged from 2.1 to 27.3 cm with mean of 8.2 cm under optimum water treatment and from 1.7 to 25 cm with mean of 7.6 cm under water stress treatment. The increase in HRL and HRN observed under low soil moisture contributed to increased root surface area. This is crucial in enabling

Table 2: Mean squares for root traits and seed weight of 43 common bean genotypes evaluated.

Source of variation	DF	BRWN	BRGA	BRN	HRN	HRL (cm)	SdWt
Block/Replication	1	1.884	42.01	10.750	0.093	1.172	4.176
Water regime (WR)	1	0.093^{ns}	7358.28^{ns}	30.983^{ns}	5181.023^{ns}	13.846*	537.302^{ns}
Main plot error	1	0.093	348.98	2.099	41.023	0.075	7.266
Genotypes (G)	42	1.034**	415**	11.653**	107.457**	86.477**	391.665**
WR × G	42	0.938**	370.78**	13.804**	84.630**	79.282**	5.414**
Sub plot error	84	0.334	63.35	2.389	4.999	0.978	2.079

ns- Non-significant; **Significant at $P \leq 0.01$; DF- Degrees of freedom; BRWN,- Basal root whorl number; BRGA- Basal root growth angle; BRN- Basal root number; HRN- Hypocotyl root number; HRL- Hypocotyl root length; SdWt- 100 seeds mean weight.

tolerant genotypes explore and access soil moisture resource under limited conditions. For example, genotype SER-124 had the highest HRN and longest HRL after exposure to low soil moisture and this genotype is known to be drought tolerant. Contrary to the findings of this study, Amane *et al*. (2016) reported more hypocotyl roots of the bean genotypes after exposure to unlimited soil moisture conditions.

Low soil moisture effect reduced BRWN by 1.9% (Table 3). Under low soil moisture, genotypes CAL-143 and BC-265 had one basal root whorl, while genotypes that had the highest number of basal root whorls include Tepary-22, CL-43, the checks Kambidzi-A286 and Kabalabala-UBR (92) 25-LF. Exposure to low soil moisture increased the BRN and BRGA (Table 3). Genotypes SER-124 had the lowest number of basal roots (3.5), while Kabalabala-UBR (92) 25-LF (check) had four times more basal roots than genotype SER-124 under low soil moisture conditions. Genotypes Qwimbaya followed by Inter-lab-31 and SER-118 were among the genotypes with the deepest basal root growth angle (> 45°) after exposure to low soil moisture conditions. The study revealed genotypes with deeper basal root angles from the horizontal axis, longer roots and high number of root whorls under low soil moisture. Genotypes with such root systems are expected to explore and access soil moisture from the deep soil profile, relatively grow well and yield high under limited soil moisture conditions (Lynch, 2014). Similarly, Amane *et al*. (2016) reported an increase in basal root growth angles after exposure of the genotypes to low soil moisture conditions. The findings agree with Miguel *et al*. (2013) that drought tolerant landraces or adapted cultivars tend to have basal root whorl number reaching four and sometimes more. Similarly, Comas *et al*. (2013) screened and identified common bean genotypes tolerant to drought which had 16 basal roots from four distinct root whorls. Comas *et al*. (2013) further reported that drought tolerant genotypes preferentially increase elongation of roots and suppress basal roots branching in response to drought conditions.

Broad sense heritability ranged from 0.02 for BRN to 0.99 for HRL under low soil moisture (Table 3). The genetic advance (%) ranged from 10.37 for BRN to 106.84 for HRL under limited soil moisture conditions. The variables that exhibited high broad sense heritability and genetic advance can be used in the selection of genotypes with tolerance to drought conditions. Variables with high broad sense heritability and genetic advance are expected to be controlled by additive genes and are less influenced by the environment (Panes and Sukhatme, 1995).

Variability in seeds weight and indices for tolerance to low soil moisture

100 seeds mean weight (SdWt) ranged from 15.8 to 55 grams under low soil moisture (Table 4). The effect of low soil moisture reduced SdWt by 9.4%. Under low soil moisture, the genotype Bonus had the lowest SdWt, while Tio-Canela had the highest SdWt. Genotypes of Andean gene pool, including SBA-686 and EAL-14, performed well in terms of SdWt contrary to what was reported by Hayes and Singh (2007) that Andean gene pool is not a good source of drought tolerance compared to the Meso-American gene pool.

Under low soil moisture, twenty-five genotypes outperformed the checks having lower values for percent reduction (%) in SdWt and seeds weight stability index (SSI) values equal or greater than 0.90 (Table 4). Genotypes CER-78, SAB-560 and SER-125 of Meso-American origin had the lowest SdWt reduction and SSI values equal or greater than 1.0. The three genotypes, CER-78, SAB-560 and SER-125, are considered tolerant to low soil moisture conditions. These genotypes (CER-78, SAB-560 and SER-125) had high SdWt and the tolerance could also be attributed to the highest number of hypocotyl roots for CER-78 and SAB-560, the longest hypocotyl roots for CER-78 and SER-125 and a deeper Basal Root Growth Angle for CER-78. Genotypes CER-78 and SER-125, outperformed all other genotypes with regard to percent reduction in SdWt and SSI (Table 4) and therefore, considered as the most drought tolerant genotypes. Similarly, Golabadi *et al*. (2006) identified genotypes with tolerance to soil moisture stress in wheat based on tolerance indices.

CONCLUSION

There was variability in root traits and seed weight among the common bean genotypes. Genotypes CER-78, SAB-560 and SER-125 of Meso-American origin had the longest

Table 3: Effect of low and optimum soil moisture on root traits of 43 common bean genotypes.

Genotype	HRN		HRL (cm)		BRWN		BRN		BRGA	
	ST	NST	ST	NST	ST	NST	ST	NST	ST	NST
BS-81	16.5	9.5	5.8	4.8	2	1.5	9	7.5	30	45
Tepary-32	12.5	4.5	9.6	2.1	3	3.5	7.5	9.5	50	20
BC-265	21	7	3.4	3.4	1	3.5	8	8	55	15
CER-78	25.5	5.5	24.5	10.5	2.5	2	10	5.5	55	25
IJR	37.5	8	11.4	2.7	2.5	3.5	9	11.5	35	15
CAL-143	16.5	9	4.6	5.7	1	3.5	6.5	9.5	40	15
SAB-560	11.5	3.5	1.9	2.9	2.5	2.5	11.5	8.5	45	25
BFS-142	27.5	12.5	4.6	10.4	3	2.5	8	8	25	25
Bonus	10.5	8.5	6.8	3.3	3	2.5	12	9.5	55	20
Tepary-22	8.5	4.5	2.2	5.7	3.5	2	11.5	3	50	45
Amadeus	12	5.5	3.9	5.0	2	3.5	9.5	13.5	45	10
BSF-95	13.5	13.5	9.9	4.7	2	3	6.5	8	27.5	35
Colorado-3	27	13	12.9	12.2	2	1.5	6.5	2.5	55	45
Tio Canela	25.5	8.5	4.5	5.6	2	2	8.5	5	55	15
SAB-659	20	27	7.4	3.9	2.5	1	5.5	6.5	20	45
Quimbaya	15	7	17.7	6.2	3	3.5	9.5	12.5	72.5	35
EAL-14	32.5	10	5.5	3.2	2.5	3	13.5	7.5	35	15
SER-125	29	7	11.6	21.1	2	1.5	7	4	30	25
BFS-29	7.5	6	12.8	3.6	2	3	8	7	30	15
SER-118	29	6	4.2	7.0	1.5	2.5	5	8.5	65	15
SEF-15	14.5	9.5	3.6	2.6	2.5	2	10.5	7	20	25
DOR-364	7.5	12.5	3.3	3.6	3	2	9	7.5	42.5	30
CL-43	31	11.5	7.1	7.0	3.5	2.5	8.5	11	15	35
USRM-20	13.5	6	21.1	4.8	2	2	9	8.5	60	25
SEN-56	14	7	6.5	16.7	3	2.5	11	7	35	25
SAP-1	27.5	5	9.2	6.9	3	4	10	13	55	50
SAB-686	14.5	12	6.5	27.3	2.5	2	8	7.5	45	40
DOR-390	17.5	7.5	2.2	25.2	2.5	2	8.5	8	15	25
CIM-(BSM52-14)	16.5	5.5	3.9	3.3	3.5	3.5	12.5	12	25	35
CIM-SUG02-15-1	17	11.5	6.4	8.0	3	2	8.5	6.5	45	35
INTER-LAB31	15.5	3.5	8.3	12.0	2.5	2.5	7.5	9.5	67.5	30
MN13509-8-6	27.5	9.5	1.9	9.3	2.5	2.5	8.5	7	57.5	45
MR13508-2	21.5	7	16.2	22.9	2	2	5.5	7	25	25
CIM-RM-03-46	11	5.5	3.6	2.4	2.5	2	11	8	55	45
CIM-RM07-ALS-62-1	8.5	9	8.3	3.3	2.5	2	8	4.5	15	15
CIM-KHAKHI-07-ALS-1	11	7.5	3.8	2.5	3	4	8	7.5	30	10
CIM-RM-04-04-04	27	7.5	6.6	6.2	2.5	2	9	5	25	15
CIM-KHAKHI-O4-01-22	25	14.5	2.3	6.3	2	2.5	6.5	10	65	30
SER-124	48.5	9	25	6.7	2	4	3.5	13.5	40	40
SER-83	23	9.5	4.3	17.6	2	1.5	9.5	4.5	55	25
Kabalabala-UBR(92)25-LF	24	6	3.8	2.4	3.5	2	15.5	4	55	25
Kambidzi-A2864	10.5	4.5	1.7	25.7	3.5	3	8.5	9	35	25
Mean	19.6	8.6	7.6	8.2	2.5	2.6	9.5	7.9	41.5	28.4
SE±	1.94	1.12	0.53	0.83	0.46	0.48	4.96	1.19	5.45	5.80
Significance level	**	**	**	**	**	**	ns	**	**	**
Reduction (%)	-127.1	-	7.0	-	1.9	-	-11.3	-	-46.1	-
H^2	0.95	0.93	0.99	0.99	0.72	0.62	0.02	0.81	0.88	0.77
GA	12.16	5.23	8.12	9.73	0.73	0.86	0.99	3.43	20.74	14.69
GA as % of the mean	62.04	64.31	106.84	118.61	29.35	33.09	10.37	43.37	49.98	51.72

**Significant at $P \leq 0.01$; ns- Not significant; ST- Stressed; NST- Non-stressed; HRN- Hypocotyl root number; HRL- Hypocotyl root length; BRWN- Basal root whorl number; BRN- basal root number; BRGA- Basal root growth angle; SE- Standard error; H^2- Broad sense heritability; GA- Genetic advance.

Table 4: Effect of low and optimum soil moisture on seed weight and drought tolerance indices for 43 common bean genotypes.

Genotype	100 seeds weight (grams)		Tolerance indices	
	(NST)	(ST)	R (%)	SSI
BFS-81	46.3	43.5	6.2	0.94
Tepary-32	39.4	36.0	8.5	0.91
BC-265	26.7	23.1	13.7	0.86
IJR	34.4	29.0	15.6	0.84
CAL-143	34.5	30.8	10.9	0.89
BFS-142	51.4	49.3	4.1	0.96
Bonus	24.1	15.8	34.6	0.65
Tepary-22	29.5	23.7	19.8	0.80
Amadeus	43.5	40.1	7.8	0.92
BSF-95	46.5	45.1	3.0	0.97
Kalima-PVA-692	43.5	38.1	12.5	0.87
Colorado-3	51.7	48.3	6.7	0.93
Tio-Canela	29.8	22.6	24.2	0.76
SAB-659	28.3	22.1	21.8	0.78
Quimbaya	26.5	22.2	16.3	0.84
EAL-14	56.2	54.5	3.1	0.97
BFS-29	38.1	33.9	11.0	0.89
SER-118	33.2	31.3	5.9	0.94
SEF-15	29.8	27.5	7.7	0.92
DOR-364	39.2	37.9	3.4	0.97
CL-43	21.8	19.2	11.9	0.88
USRM-20	36.5	34.9	4.4	0.96
SEN-56	50.1	49.4	1.5	0.99
SAP-1	29.8	28.4	4.7	0.95
SAB-686	56.5	55.0	2.7	0.97
DOR-390	32.8	26.5	19.4	0.81
CIM-RM06(BSM52-14)	47.1	43.8	7.1	0.93
CIM-SUG02-15-1	34.1	31.0	9.1	0.91
INTER-LAB31	43.8	41.4	5.5	0.95
MN13509-8-6	35.7	33.8	5.5	0.95
MR13508-2	36	32.2	10.4	0.90
CIM-RM-03-03-46	51	49.6	2.7	0.97
CIM-RM07-ALS-62-1	26.9	24.3	9.7	0.90
CIM-KHAKHI-07-ALS-1	48.8	42.6	12.7	0.87
CIM-RM-04-04-04	34.4	29.3	14.7	0.85
CIM-KHAKHI-O4-01-22	28.3	25.9	8.5	0.92
SER-124	33.8	26.2	22.5	0.78
SER-83	26.1	20.6	20.9	0.79
[b]CER-78	49.2	49.5	-0.5	1.01
[b]SAB-560	32	32.0	0.2	1.00
[b]SER-125	39	39.9	-2.2	1.02
[a]Kabalabala-UBR(92)25-LF	37.8	29.3	22.5	0.77
[a]Kambidzi-A2864	24.7	17.7	28.2	0.72
Mean	37.4	33.9	-	-
SE±	0.47	1.36	-	-
Reduction (%)	-	9.4	-	-

[a]Check; [b]Tolerant; NST- Non-stressed; ST- Stressed; SdWt- 100 Seeds mean weight; R(%)- reduction (%); SSI- Seeds weight stability index; SE- Standard error.

hypocotyl roots, high seed weight and high number of basal roots respectively. These characteristics are typical of genotypes adaptable to drought conditions. The three genotypes CER-78, SAB-560 and SER-125 were considered the most tolerant genotypes to soil moisture stress conditions based on tolerance indices. Therefore, these three genotypes should be tested rigorously in drought prone environments for commercial release or may be conserved and used for genetic enhancement of common bean utilising root traits and seed yield.

Conflict of Interest: None.

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