COMPARATIVE ANALYSIS OF ROOT SYSTEM ARCHITECTURAL TRAITS IN GENOTYPES OF *VIGNA RADIATA* L. AND *VIGNA MUNGO* L.

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Abstract

`Investigation of root system architecture (RSA) has a huge potential to support the crop improvement under suboptimal nutrient and water conditions. The present study was carried out using eight genotypes of each mungbean and urdbean for comparative analysis of RSA traits among the genotypes. Presence of significant variations and medium to high heritability was observed for RSA traits. The genotypes KM 12-29 followed by PUSA 9072 among the mungbean genotypes and LBG 623 followed by PU 11-14 among the urdbean genotypes showed higher proportion of RSA traits. The higher percentage distribution of root traits was observed under diameter intervals in the order of 0-0.5 > 0.5-1.0 > 1.0-1.5 > 1.5-2.0 >> 2.0 mm in both mungbean and urdbean genotypes. Thus, the study shows the clear depiction and comparison of RSA traits among mungbean and urdbean genotypes, which can be exploited for cultivar development in future breeding programmes.

Introduction

Root is an indispensable plant organ for uptake of water and nutrients by expanding its surface area and enhancement of explored soil volume. The root system architecture (RSA) is mainly refers to the spatial configuration of roots and is made up of structural features like root length, number, diameter and spread (Khan *et al*. 2016). The RSA traits are critical for selection of crop genotypes efficient in water and nutrient absorption. Besides, each genotype varies in root morphology, the presence of fine roots will determine the percentage of root traits (Zobel and Waisel 2010). Based on root diameter, the classification of fine roots is a simple method and allows the assigning of each root into a specific order (Liu *et al*. 2018). The RSA traits predominantly total root length, root surface area and root number are significantly and positively associated with dry weight and grain yield (Xie *et al*. 2017). Thus the plant with vigorous root system not only supports the healthy establishment but also tolerance to abiotic stresses.

After cereals, grain legumes are economically and nutritionally important crops with rich in protein content. Among the pulse crops, mungbean and urdbean are important after chickpea and pigeon pea with area of 7.3 m ha and production of 5.3 m tonnes in the world (Nair *et al.* 2020). Both crops are short duration (60-90 days) legumes with good stress tolerance ability. Mungbean is an excellent source of digestible protein and its seeds are nutritive, palatable and non-flatulent than other pulse crops (Sadeghipour *et al*. 2010). Besides, mungbean sprouts are having six times higher antioxidant activity than normal seeds (Guo *et al.* 2012). Whereas, urdbean is consumed as

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dal and can be used as nutritive fooder for milch animals. In terms of balanced nutrition, the higher value of lysine content in urdbean makes it an excellent complement to rice. These crops are nature's gift to mankind and can be used as potential food supplement to alleviate malnutrition (Ganesan and Xu 2018).

The yield potential of these pulse crops is mainly limiting by abiotic stresses and climate change. The RSA of plants is one of the neglected area and is having potential for improving growth potential and environmental adaptability. Keeping in view of the importance of root traits in stress tolerance ability of crop plants, the present study was carried for comparative analysis of RSA traits in genotypes of mungbean and urdbean. The aim of the present study of carrying out RSA studies in crop plants is to understand areas of interest within the root system and incorporate this information in crop improvement programs

Materials and Methods

The experiment was carried out with eight genotypes of mung bean including Pusa 0672, Pusa 9072, M 1354, M 418, HUM 12, SML 1815, KM 12-29 and DMS 10 and eight genotypes of urd bean including KU 6, PU 11-14, TU 103, SPS 5, LBG 623, IPU 2000-9, IPU 02-43 and MASH 114 for comparative analysis of the RSA traits. The study was conducted in greenhouse with controlled environment facility at Division of Genetics, Indian Agricultural Research Institute, New Delhi. The weather parameters maintained in the greenhouse includes 90% relative humidity, $30^o/18^oC$ day/night temperature and 12 h photoperiod. Initially, the seeds of all the genotypes were washed with $HgCl_2$ (0.1% w/v) and kept for germination. After emergence of cotyledons, the uniform germinated seedlings were transferred to the hydroponic trays containing modified Hoagland's solution. The nutritional composition of the solution includes $MgSO_4$ (1mM), K_2SO_4 (0.92 mM), KH_2PO_4 (0.25 mM) $CaCl_2.2H_2O$ (0.75 mM), Fe-EDTA (0.04mM), Urea (5 mM), and micronutrients [H_3BO_3 (2.4 μM), $MnSO_4$ (0.9 μM), $ZnSO_4$ (0.6 μM), $CuSO_4$ (0.62 μM), and Na_2MoO_4 (0.6 μM)] (Sivasakthi *et al.* 2017).

The experiment was carried out in completely randomized design with three replications per genotype. After 21 days, the complete root system was isolated from each plant for recording of RSA traits in each plant. The isolated roots from individual plants were washed with tap water and used for measurement of root traits using root scanner (Epson professional scanner) with WinRhizo (Pro version 2016a; Regent Instrument Inc., Quebec, Canada) software. The WinRhizo software provided data on root parameters including total root length (TRL) (cm/plant), total root surface area (TSA) (cm^2/plant), root average diameter (RAD) (mm), total root volume (TRV) (cm^3/plant), total root tips (TRT), total root forks (TRF) and total root crossings (TRC). The root trait, primary root length (PRL) (cm/plant) was measured manually using the meter scale. Besides, the additional information provided by WinRhizo software allowed us to categorize the root traits viz., root length, root surface area, root volume and root tips into different classes as 0-0.5, 0.5-1.0, 1.0-1.5, 1.5-2.0 and >2.0 mm based on diameter intervals (Reddy *et al.* 2020a).The descriptive statistics and analysis of variance of the measured data on RSA traits were carried out by using STAR (Statistical tool for Agricultural Research) 2.1.0 software (Gulles *et al.* 2014)

Results and Discussion

The present investigation was carried out using hydroponic system to evaluate RSA traits in genotypes of mungbean and urdbean. The analysis of variance and descriptive statistics of eight RSA traits were explored to study the presence of significant variation among the evaluated mungbean and urdbean genotypes (Table 1). The variance analysis revealed the presence of highly significant differences among the evaluated genotypes for all studied RSA traits. The *in vitro*

screening methodology of hydroponics proves to be the best method for maintenance of root system accuracy and screening of genotypes with little environmental effects (Rajkumar and Ibrahim 2014). The coefficient of variation among the root architectural traits ranges from 5.12 (RAD) to 22.94 (TRC). This indicates that existence of sufficient variability among the root architectural traits. The broad sense heritability ranges from 0.64 (TRT) to 0.89 (TRL and TSA) among the root architectural traits. The presence of sufficient significant variability coupled with high heritability of traits is the requirement for improving genetic gain under selection (Reddy *et al.* 2020b).

Table 1. Analysis of variance and descriptive statistics for the root architectural traits among mungbean and urdbean genotypes.

Trait	Genotype mean sum of squares	CV (%)	Heritabil ity	Mean ± Standard error		t value
				Mungbean genotypes	Urdbean genotypes	
df	15					
PRL	99.03***	8.91	0.79	31.08 ± 2.50	32.43 ± 1.56	-0.46
TRL	266886.26***	12.49	0.89	1039.34 ± 73.19	578.13 ± 57.26	4.96***
TSA	3232.44***	13.75	0.89	109.63 ± 6.39	54.5 ± 5.54	6.52***
RAD	0.002***	5.12	0.68	0.33 ± 0.01	0.30 ± 0.0004	2.01
TRV	0.064***	14.70	0.78	0.58 ± 0.05	0.41 ± 0.04	2.86**
TRT	238335.58***	20.78	0.64	1053.79 ± 94.86	820.67 ± 91.64	1.77
TRF	1525764.17***	18.04	0.77	2548.25 ± 191.06	1548.33 ± 168.25	3.93***
TRC	136278.35***	22.94	0.68	514.25 ± 91.03	432.67 ± 58.36	0.75

The mean significant difference values of RSA traits between genotypes of mungbean and urdbean were studied using independent *t*-test using 0.05 level of significance. The root architectural traits TRL, TSA, TRV and TRF were found to be significantly higher in mungbean genotypes compared to urdbean genotypes. The root trait TRL represents the sum of primary, crown, seminal, lateral and basal roots. The variation in TRL representing entire RSA in contrasting genotypes of mungbean (PUSA 9072 and PUSA 0672) and urdbean (LBG 623 and KU 6) are presented in Fig. 1. Reddy *et al.* (2020a) found that root traits TRL, TSA and TRV are major contributing traits of root variability and plays an important role in phosphorus uptake in mungbean at seedling stage. At early stage of plant, roots with higher length and surface area allow the efficient absoption of water and nutrients (Wang *et al.* 2016). Kyu *et al.* (2021) studied the response of mungbean and urdbean genotypes to water logging and found that formation of adventitious roots at seedling stage is crucial under stress condition.

The detailed mean values of root architectural traits of studied mungbean and urdbean genotypes are presented in the Table 2. For PRL, the genotypes KM 12-29 (44 cm) followed by DMS 10 (38.67 cm) and IPU 02-43 (38 cm) followed by PU 11-14 (37.17 cm) recorded higher PRL among mungbean and urdbean genotypes, respectively. The higher TRL was recorded by PUSA 9072 (1378.29 cm) followed by KM 12-29 (1317.39 cm) among mungbean genotypes and LBG 623 (944.33 cm) followed by PU 11-14 (636.61 cm) among urdbean genotypes. The genotypes PUSA 9072 (145.73 cm^2) followed by KM 12-29 (123.94 cm^2) among mungbean genotypes and LBG 623 (88.48 cm^2) followed by PU 11-14 (59.06 cm^2) among urdbean genotypes showed higher TSA. For RAD, the genotypes PUSA 0672 (0.38 mm) followed by PUSA 9072(0.36 mm) and IPU 02-43 (0.33 mm) followed by IPU 2000-9 (0.32 mm) recorded higher

Table 2. Mean and standard error values for root architectural traits of mungbean and urdbean genotypes.

Traits	PRL	TRL	TSA	RAD	TRV	TRT	TRF	TRC
Mungbean genotypes								
PUSA 0672	25.00 ± 1.15	796.84 ± 41.35	102.71 ± 7.00	0.38 ± 0.01	0.64 ± 0.05	675.67 ± 35.20	2075.00 ± 105.67	414.67 ± 96.25
PUSA 9072	24.33 ± 1.45	1378.29 ± 54.55	145.73 ± 11.27	0.36 ± 0.01	0.50 ± 0.01	924.33 ± 18.98	2977.33 ± 331.17	391.00 ± 55.68
M 1354	31.67 ± 1.76	1001.93 ± 97.22	106.53 ± 7.70	0.31 ± 0.01	0.45 ± 0.04	917.33 ± 105.19	2157.33 ± 204.40	364.00 ± 45.40
M 418	30.83 ± 2.20	853.97 ± 75.03	84.22 ± 6.29	0.30 ± 0.01	0.38 ± 0.04	756.33 ± 93.25	2265.33 ± 249.92	405.00 ± 118.51
HUM 12	29.50 ± 1.44	957.20 ± 60.72	104.00 ± 5.68	0.35 ± 0.01	0.58 ± 0.04	1299.67 ± 37.88	1839.33 ± 250.96	174.33 ± 5.17
SML 1815	24.67 ± 0.89	1049.43 ± 54.84	104.48 ± 3.01	0.30 ± 0.00	0.70 ± 0.02	1197.67 ± 56.86	2998.00 ± 158.20	724.33 ± 82.98
KM 12-29	44.00 ± 0.58	1317.39 ± 26.81	123.94 ± 7.35	0.30 ± 0.00	0.77 ± 0.01	1373.00 ± 18.88	3369.33 ± 280.16	989.67 ± 91.05
DMS 10	38.67 ± 1.76	959.62 ± 94.34	105.44 ± 9.37	0.32 ± 0.01	0.65 ± 0.07	1286.33 ± 38.44	2704.33 ± 125.77	651.00 ± 83.61
Urdbean genotypes								
KU 6	24.33 ± 0.88	428.86 ± 43.05	41.53 ± 6.10	0.30 ± 0.01	0.28 ± 0.02	569.67 ± 64.43	1201.33 ± 154.24	309.67 ± 59.57
PU 11-14	37.17 ± 3.61	636.61 ± 65.99	59.06 ± 8.04	0.29 ± 0.01	0.43 ± 0.07	907.33 ± 114.65	1623.00 ± 253.38	456.67 ± 64.09
TU 103	32.33 ± 0.88	553.62 ± 59.30	52.40 ± 6.21	0.30 ± 0.01	0.46 ± 0.05	907.00 ± 234.16	1971.00 ± 233.13	679.67 ± 118.82
SPS 5	31.67 ± 1.86	556.40 ± 37.96	53.58 ± 3.62	0.30 ± 0.00	0.39 ± 0.04	814.00 ± 154.70	1289.67 ± 266.06	299.67 ± 45.03
LBG 623	33.67 ± 1.20	944.33 ± 51.56	88.48 ± 6.57	0.30 ± 0.01	0.60 ± 0.06	1367.33 ± 116.18	2503.67 ± 214.86	691.00 ± 89.32
IPU 2000-9	33.67 ± 1.20	492.84 ± 43.50	47.03 ± 1.66	0.32 ± 0.00	0.41 ± 0.04	745.67 ± 238.21	1267.00 ± 194.61	361.00 ± 85.98
IPU 02-43	38.00 ± 1.53	556.83 ± 30.24	56.95 ± 1.45	0.33 ± 0.01	0.46 ± 0.01	546.67 ± 70.05	1441.33 ± 112.58	377.33 ± 64.09
MASH 114	28.67 ± 1.33	455.57 ± 41.15	36.96 ± 4.46	0.28 ± 0.01	0.26 ± 0.03	707.67 ± 57.17	1089.67 ± 104.52	286.33 ± 78.54

higher RAD among mungbean and urdbean genotypes, respectively. The higher TRV was recorded by KM 12-29 (0.77 cm^3) followed by SML 1815 (0.70 cm^3) among mungbean genotypes and LBG 623 (0.60 cm^3) followed by IPU 02-43 and TU 103 (0.46 cm^3) among urdbean genotypes. The genotypes KM 12-29 (1373) followed by HUM 12 (1299.67) among mungbean genotypes and LBG 623 (1367.33) followed by PU 11-14 (907.33) among urdbean genotypes showed higher TRT. For TRF, the genotypes KM 12-29 (3369.33) followed by SML 1815 (2998) and LBG 623 (2503.67) followed by TU 103 (1971) recorded higher TRF among mungbean and urdbean genotypes, respectively. The higher TRC were recorded by KM 12-29 (989.67) followed by SML 1815 (724.33) among mungbean genotypes and LBG 623 (691) followed by TU 103 (679.67) among urdbean genotypes.
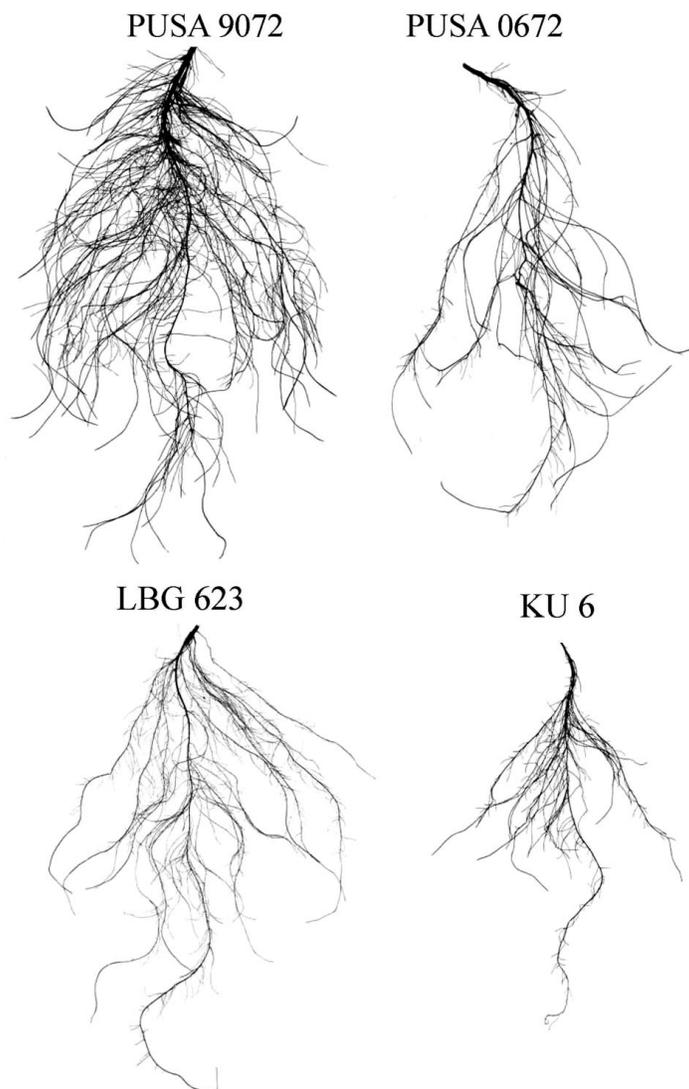

Fig. 1. Variation in root system architecture in contrasting genotypes of mungbean and urdbean.

Overall, the genotypes KM 12-29 (PRL, TRL, TSA, TRV, TRT, TRF and TRC) followed by PUSA 9072 (TRL, TSA and RAD) among the mungbean genotypes and LBG 623 (TRL, TSA, TRV, TRT, TRF and TRC) followed by PU 11-14 (PRL, TRL, TSA and TRT) among the urdbean genotypes showed higher proportion of root architectural traits. Pandey *et al.* (2014) observed the significant variation among the mungbean genotypes for root surface area, volume and biomass traits. Similarly, Jakkeral *et al.* (2009) observed the significant variation in root length, surface area, volume and lateral root number among the urdbean genotypes. The presence of significant variation in RSA traits can be exploited for improvement of water and nutrient use efficiency in crop plants (Malamy and Benfey 1997). Ao *et al.* (2010) reported that presence of highly variable RSA traits coupled with high heritability allows the efficiency of soybean genotypes under phosphorus limiting environment.

Interestingly, the root architectural traits TRL, TSA, TRV and TRT were categorized into five diameter intervals of 0–0.5 mm, 0.5-1.0 mm, 1.0-1.5 mm, 1.5-2.0 mm and >2.0 mm based on root diameter (Fig. 2). The relationship between root orders and root diameter mainly provides the accurate prediction of root characteristics of crop plants (Liu *et al.* 2010). The differences in the order of fine roots and their diameter classes are the key to more accurate determination of the lifespan of fine roots (Eissenstat and Yanni 2002). The mean trait values of TRL, TSA and TRV under all diameter intervals were significantly higher in mungbean genotypes compared to urdbean genotypes. Whereas the mean trait value of TRT was significantly higher in urdbean genotypes except under the diameter interval of 1.5-2.0 mm. In both categories of genotypes, the higher percentage distribution of root traits were observed under diameter intervals in the order of 0-0.5 mm > 0.5-1.0 mm > 1.0-1.5 mm > 1.5-2.0 mm >>2.0 mm. The formation of root cortical aerenchyma enables the greater root diameter results in higher porption of fine and very fine roots in crop palnts (Postma and Lynch 2011, McCormack and Guo 2014).
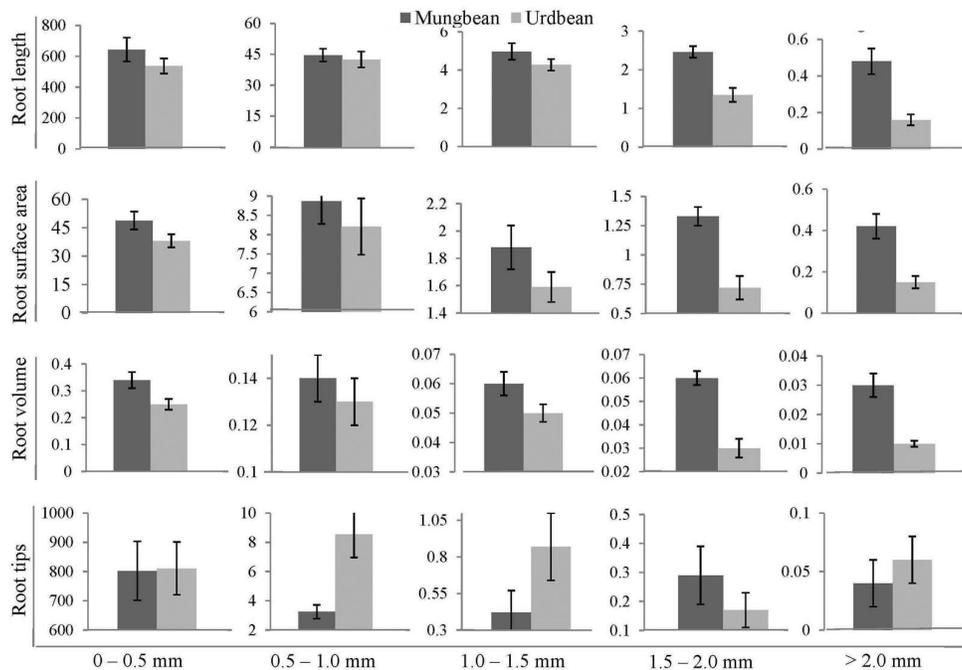

Fig. 2. Comparison of root architectural traits in diameter intervals in mungbean and urdbean.

Among the studied mungbean genotypes, KM 12-29 showed the higher proportion of root traits TRL, TSA, TRV and TRT under 0-0.5 mm diameter interval (Fig. 3). Whereas under 0.5-1.0 mm interval, the same genotype showed higher proportion of all root traits except TRT. The genotype DMS 10 showed higher TRL, TSA and TRV except TRT under root diameter intervals of 1.0-1.5 mm and 1.5-2.0 mm. Whereas the genotype HUM 12 recorded higher proportion of all root traits under the diameter interval of > 2.0 mm. Among the studied urdbean genotypes, LBG
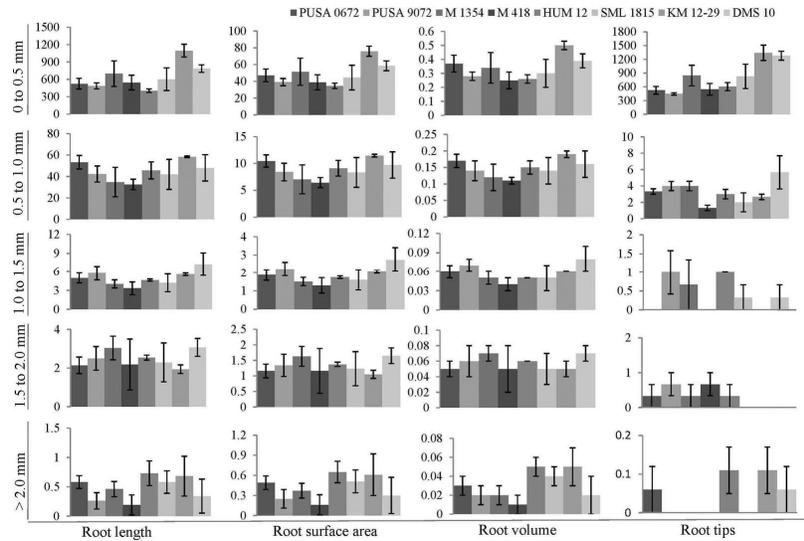

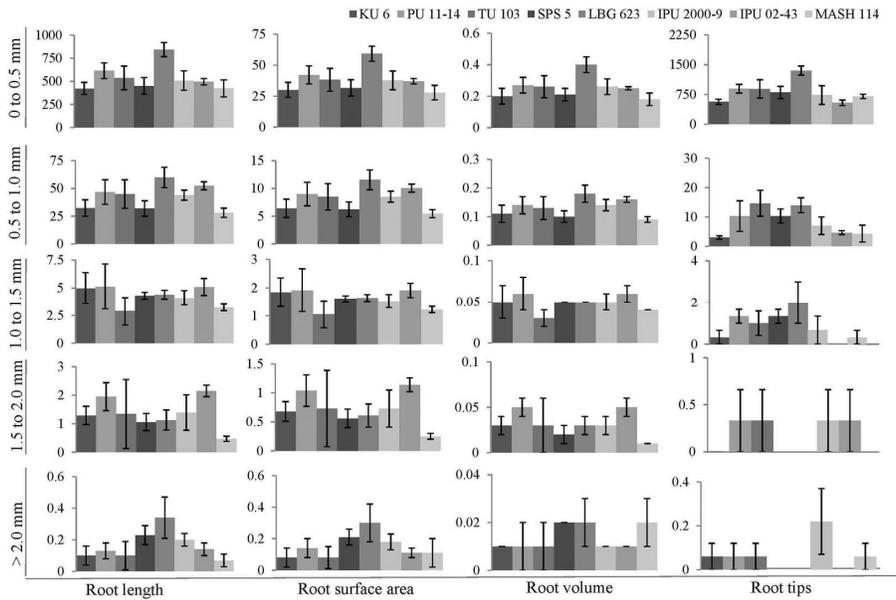Fig. 3. Comparison of root architectural traits in diameter intervals in eight mungbean genotypes.

Fig. 4. Comparison of root architectural traits in diameter intervals among eight urdbean genotypes.

623 showed the higher proportion of root traits TRL, TSA, TRV and TRT under 0-0.5 mm diameter interval (Fig. 4). Whereas under 0.5-1.0 mm interval, the same genotype showed higher proportion of all root traits except TRT. The genotypes PU 11-14 and IPU 02-43 recorded higher proportion of TRL, TSA and TRV under the diameter interval of 1.0-1.5 mm and TRV and TRT under 1.5-2.0 mm interval. The genotype IPU 02-43 only recorded higher proportion of TRL and TSA under 1.5-2.0 mm interval. Under the diameter interval of >2.0 mm, the genotype LBG 623 showed higher proportion of all root traits except TRT. Reddy *et al* (2020a) reported the significant variation in very fine and fine roots among mungbean genotypes while screening for P deficiency. Arif *et al.* (2019) reported that plants with higher fine root production allow the enhancement of root absorption area, which is an adaptive strategy under stress condition.

In conclusion, the veracity of RSA traits was maintained by growing the seedlings under hydroponic system with least environmental effects. The present study identified the differences in RSA traits among the genotypes of mungbean and urdbean. The genotypes KM 12-29 followed by PUSA 9072 among the mungbean genotypes and LBG 623 followed by PU 11-14 among the urdbean genotypes showed higher proportion of RSA traits. The presence of very fine (0-0.5 mm) and fine roots is important for water and nutrient uptake and determines the most percentage of root trait distribution. The genotypes KM 12-29 and LBG 623 among mungbean and urdbean genotypes respectively showed higher proportion of root traits under 0-0.5 mm diameter interval. Thus the importance of RSA in many plant functions has become a need of research in scientific communities.

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