

Root system architecture traits diversity and association with grain yield for drought adapted sorghum genotypes

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Abstract

Background and aims The roots system architecture of sorghum is a major morphological trait which strongly influences the capacity to access soil moisture and forage nutrients under drought condition. This study was conducted aiming to the extent of genetic diversity among sorghum genotypes adapted the dryland; to identify promising genotypes for key root and shoot traits for breeding purposes; and to determine the contribution of root related traits of sorghum on moisture stress area. **Methods** The experiment was conducted using 214 genotypes in greenhouse of Horticulture and Plant science Department, Jimma University using randomized complete block design. **Results** Cluster analysis indicated that the genotypes grouped into eight cluster. Number of genotypes per cluster varied from 100 (46.72%) in Cluster II and 2 (0.93%) genotypes both in Cluster III and VI. The maximum genetic distance ($D_2 = 151.36$) obtained between cluster III and VIII and minimum genetic distance ($D_2 = 9.38$) was found between cluster V and VII also the intra-cluster distance was highest in the cluster II ($D_2 = 43.93$) and the lowest cluster found VI ($D_2 = 0.93$). Root angle and root length exhibited strong negative ($r = -0.24$) and positive correlation ($r = 0.32$) with grain yield. Genotypes Acc#220249(58); Acc#220254(#59); Acc#234102(#102); Acc#235811(#118) Acc#20710(27) the most divergent on the principal axis of biplot and used direct sorghum improvement. **Conclusion** The information generated from this study could help to identified promising genotypes with suitable root traits for potential breeding under specific environmental conditions.

Introduction

In the dry land of Ethiopia, sorghum is an important food crop and staple local diet. It has grown for multipurpose human utilize as source food, fuel wood and construction material animal used as a source of animal feed, (Asfaw 2007). The major cereal crops in the dryland areas are sorghum, maize, tea and millet. These are the major food crops for human's diet and also provide feed for animals (Zidane, 2010). The most important factor influencing the productivity of crops in the region is the erratic rainfall pattern, uneven in its distribution and unpredictable in its inception (Gemechu et al. 2004).

Plant root system architecture play a major role in plant growth by exploiting soil resources via the uptake of water and nutrients (Ali et al. 2015). Root traits such as fine root diameter, specific root length, specific root area, root angle, and root length density are considered useful traits for improving plant productivity under drought conditions (Kumar et al. 2012).

The root system of sorghum is characterized by a single seminal root originating directly from the embryo and by multiple postembryonic nodal roots that emerge from the below-ground nodes of the stem (Singh et al., 2010). The seminal root plays an important part only in initial water and nutrient uptake and hence is of little importance in mature sorghum, for which the RSA is predominantly constituted by post embryonic nodal roots (Salih et al. 1999; Tsuji et al. 2005)

Significant progress has been made in understanding plant growth under drought stress. Water deficit is sensed by the roots which begin to synthesize ABA within 1 hour of the onset of the water stress. ABA is transported via xylem from roots to leaves within minutes to hours. Root length is an important trait against drought stress in plant varieties; in general, variety with longer root growth has resistant ability for drought (Kaydan and Yagmur 2008).

High throughput screening of agronomically relevant traits is often restricted by the availability of suitable phenotyping systems, rather than the availability of genetic information (Joshi et al. 2017).

Multivariate analysis is known by one of the most powerful statistical tool for quantity assessment and to estimate the extent of genetic diversity for selecting potential breeding lines for crossing blocks among the genotypes and gene introgression from distantly related germplasm in the breeding programme (Chozin et al. 2017; Dasgupta and Das 1984; Veronesi and Falcinelli 1988) Characterization of existing genotypes is a prerequisite for identifying potential genotypes for varietal improvement programme and to avoid duplication in the germplasm collection.

A better sympathetic of genetic diversity in sorghum genotypes will facilitate crop improvement. Keeping in view, the present study was carried out to determine the extent of genetic diversity among sorghum genotypes adapted the dry land; to identify promising genotypes for key root and shoot traits for breeding purposes; to determine the contribution of root related traits of sorghum on moisture stress area.

Material And Methods

Experimental platform

The experiment was conducted at greenhouse, Horticulture and Plant Science Department, College of Agriculture and Veterinary, Medicine Jimma University (JUAVM) in 2019/2020. JUAVM is situated in Oromia Regional state about 352 kilometers away from Addis Ababa in the of south west part of Ethiopia with a latitude and longitude of 7.667°N 36.833°E and its altitude is 1,780 meter above sea level. The greenhouse temperature varies 16 (night) to 40°C chamber method (Demelash et al. 2021). Each root chamber contained 1100 g of red, clay-textured soil. Stainless steel tubs (2 m) that had similar height and width was properly established in the greenhouse. The detail of the root platform described in Demelash et al., 2021.

Experimental materials

Two hundred fourteen sorghum genotypes were selected from 400 genotypes based grain yield variation and adaptation to the dryland's environment sown with the design of alpha lattice conducted in 2018/2019 main growing season at Sheraro (Appendix A). Sheraro is located in southern Tigray, northern Ethiopia. The site is situated at an altitude of 1006 m a.s.l., 14024'00" N, 37056'00" E with mean annual rainfall for the growing season about 676 mm (Weldegebriel et al. 2018). The genotypes were maintained by EIAR (Ethiopian Institute of Agricultural Research) under the national sorghum improvement research program of found MARC (Melkassa Agricultural Research Center).

The entire sets of experimental materials used under the greenhouse were composed of 110 (51.4%) genotypes from Ethiopian biodiversity institute collection (IBC), 91(42.52%) genotypes from International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) collection and 13 (6.07%) genotypes from released varieties. The detail of genotypes were presented in (Demelash et al. 2021).

Experimental procedure and design

Experimental procedure and design were done using the phenotyping platform consists of custom-built root chambers consisting of 300 pairs of perspex plates (40 cm high, 35 cm wide and 3 mm thick). Soil was filled in the void pair of plates. Fifty root chambers were placed vertically into slots (rows) in each of 10 large metal tubs (Demelash et al. 2021). The tops of the chambers were covered with polycarbonate covers to exclude light from the soil and roots with 5 cm long slits for the seedlings to emerge.

The chambers were watered to field capacity prior to planting and left until soil water saturation. Three seeds were planted in the center of each chamber on one side of the perspex with the embryo towards the base. The seedlings were thinned to one plant after emergence. The seeds were treated with ApronStar 42WS fungicide before sowing. Plants were watered one or two times per week, depending on the environmental conditions. Plant nutrients were applied in the form of diammonium phosphate (DAP, 1.5 kg) and urea (1kg) per experiment. DAP was applied during sowing in a granular form and urea when the plants reached 3rd leaf stage in liquid form equally in each chamber.

The experiment was conducted using randomized completely block design with column and row arrangement with three replications. Within each replication, there was three tubs (column) and 150-root chamber each tub held 50-root chamber (rows) with a total of 450-root chambers. There was two experimental runs for 214 genotypes, the first experimental run consisted 150 genotypes and the second experimental run consisted 64. The data collection was done when six leaves had fully expanded and the first flush of nodal roots visible. Shoot length, shoot diameter and leaf area was measured before root imaged. The Shoot fresh weight was also measured by cutting from the base of stem.

Leaf Area (cm²): The product of leaf length, width and coefficient (0.69) of larger leaf at six-leaf stage (Lafarge and Hammer 2002). At harvest, the shoot of each plant was removed by cutting at the base of the stem in order to measure shoot dry weight after drying at 60°C with in oven for 72 hours. Shoots were removed used to measure the root system that was visible through root imaged on both sides of each chamber using digital cameras (CANON SX610 HS) by connecting with two tables through Wi-Fi. The images were used to determine the root angle (RA), relative to the vertical plane, of the first flush of nodal roots at a distance of 2 cm from the base of the plant using Opengelpphoto software, which was designed by the University of Queensland (Singh et al. 2011).

The observed root angle for each plant was the mean of four observations (left and right of each plant for both sides of the chamber (Demelash et al. 2021) The roots were removed carefully from the chamber. The total number and root length of nodal root per plant was counted and measured respectively. The root was washed carefully with tap water and oven-dried at 60°C for 3 days. Root shoot ratio was calculated by dried root weight divided by dried shoot weight (Demelash et al. 2021).

Statistical analysis

The recorded data were subjected to analysis of variance (d Steel and Torrie 1986). Pearson correlations between root architectural traits and yield, and their associated were calculated (Maherali 2014). In order to study the genetic divergence, the generalized Mahalanobis distance matrix (D₂) was determined and used as similarity measure to analyze the clustering of genotypes by the method of Tocher and by the average linkage squared Euclidean Method Also, the relative contribution of the characters for the genetic divergence between coffee genotypes was determined according (Singh 1981). Statistical analyses were performed using the software SAS version 9.2 (2008)

The mean data of shoot root traits for sorghum genotypes were used for PCA in order to identify the major traits accounting for much of the gross observed variability among the genotypes. The function prcomp, included in the core package "facto extra" of R software environment (R core team, 2018), was used to generate PCA (Kassambara and Mundt 2017)

Results

Genetic diversity

The traits variance explained by Demelash et al., 2021. The result of cluster analysis indicated that from the composition of the entire sets of 214 genotypes were grouped into eight clusters. The number of genotypes per cluster varied from 100 (46.72%) in Cluster II to 2 (0.93%) genotypes in Cluster III and VI (Table 1).

Table1 grouping of 214-sorghum genotypes into eight different diversity classes.

Cluster I has consisted 28 (13.08%) genotypes, Cluster IV 29 (13.55%) 29 genotypes, Cluster V 41 (19.16%) genotypes, and Cluster VIII 9 (7.47%) genotypes (Table 1). From the group of cluster I 15(6.38%) genotypes were originated from set of ICRISAT collection, this cluster was explained by the highest root angle (21.62⁰) and lowest cluster mean value of shoot dry weight (1.44g). The genotype Acc#6094 with wider root angle (27.37⁰) originated from ICRISAT collection under cluster I. Cluster II was characterized by lower cluster mean value of root shoot ratio (0.39) and the cluster contained 100 genotypes from these the highest number of genotypes 57 (29.3%) were originated from the total set of IBC collection. Cluster III comprises 2 genotypes categorized by highest cluster mean value of root length (72.5cm) and the lowest root angle (15.93⁰) (Table.2).

The mean value of Custer IV described by the lowest leaf area (14.50m²) and 29 genotypes were grouped under this cluster 17(7.22%) were originated from ICRISAT (42.42%) collection (Table 2).The genotype Acc#19262 calculated (9.54m²) existed under cluster IV. Cluster V was comprised 41 genotypes with the composition of 22 genotypes from IBC, 16 genotypes from ICRISAT and 3 released Varieties. This cluster had lowest cluster mean of root dry weight (0.59g)

Cluster	Genotype Number	Code
CL I	28	13 (152,43,49,53,56,69,70,72,81,18,126,130,132,)
		15 (19,21,23,87,89,90,136,141,163,167,168,170,184,187,193)
CL II	100	57 (148,149,151,153,155,190,192,34,36,40,44,45,46,50,51,52,54,57,60,64,65,67,68,71,75,76,77,78,79,80,84,86,92,93,17,94,96,98,100,1)
		37 (202,4,91,6,134,135,22,24,28,29,30,31,143,83,85,88,145,146,172,140,174,156,157,159,164,165,180,175,177,178,169,181,198,199,2)
		6 (201,209,211,203,210,20)
CLIII	2	1 (12)
		1 (27)
CL IV	29	9 (147,150,41,47,74,103,104,106,197)
		17 (11,14,16,20,25,26,95,138,139,158,179,183,182,186,5,195,1)
		3 (212,204,214}
CL V	41	22 (144,154,191,35,37,39,42,48,55,58,59,61,62,63,66,82,99,125,113,118,119,121)
		16 (8,13,15,97,123,137,142,160,161,162,166,171,176,185,189 194)
		3 (213,206.207)
CL VI	2	1 (102)
		1 (7)
CL VII		3 (73)
		(32,173)
CLVI	9	6 (188,33,38,107,110,116)
		2 (9,10)
		1 205

and stem diameter (4.12mm).

Table 2
Mean of ten roots and shoot traits for the eight clusters of 214 sorghum genotypes tested under green house.

Cluster	CLI	CLII	CLIII	CLIV	CLV	CLVI	CLVII	CLVIII
Traits	Mean							
RA	21.62	19.37	15.93	19.82	20.53	19.50	18.66	20.93
RL	44.51	53.45	72.5	65.12	47.39	58.50	65.33	46.60
RN	11.05	10.05	10.66	10.78	9.14	10.83	11.33	8.81
RDW	0.61	0.62	0.61	0.64	0.59	0.86	0.62	0.61
RSR	0.40	0.39	0.34	0.43	0.41	0.52	0.34	0.45
SDW	1.44	1.62	1.78	1.53	1.49	1.88	1.82	1.45
SFW	9.29	9.11	9.50	8.24	9.71	7.50	10.18	10.77
SL	11.95	12.68	13.00	12.39	12.78	15.5	14.26	12.38
LA	14.81	15.92	15.86	14.50	23.12	32.45	24.77	30.49
SD	4.38	4.55	5.1	4.67	4.12	4.60	4.38	4.27

RA = Root angle, RL = Root length, RN = Root number, RDW = Root dry weight, RSR = Root shoot ratio SDW = Shoot dry weight = Root shoot ratio, SFW = Shoot fresh weight, SL = shoot length, LA = Leaf Area.

Cluster VI was assembled from two genotypes (Acc#234102) and (Acc#14963) which is determined by wider leaf area (32.45m²), maximum root dry weight (0.86g) and root shoot ratio (0.52) and lowest value of shoot fresh weight (7.5g). Cluster VII and Cluster VIII were illustrated by three and nine genotypes, respectively (Table 2). Cluster VII was determined by highest cluster mean of root number (11.33) and root number (12) In contrast Cluster VIII was explained by lowest root number (8.81) (Table.2).

Cluster distance

The result of the standardized Mahalanobis D² statistics had showed the existence of high genetic distance among the eight clusters. The χ^2 - test for the eight clusters computed out 28 pairs inter cluster squared distance 24 pairs were shown significant at P < 0.01 and a pair of cluster square distance was significant at p < 0.05 (Table.3). The rest three pairs of square distance were exhibited non-significant (Table 3). The maximum inter cluster distance was found between Custer III and Custer VIII with the value of (D² = 151.36) followed by Custer I and Cluster III with (D² = 111.53). The minimum inter cluster distance was found between Cluster I and Custer V with (D² = 10.91) (Table 3). The χ^2 - test for the eight clusters of the intra-cluster distance indicated highly significant at P < 0.01 in cluster II (43.93). The lowest intra-cluster calculated in cluster VI (0.93) (Table.3).

Table 3
Pair-wise generalized square distance (D²) between eight clusters constructed from 214 genotypes.

CL	I	II	III	IV	V	VI	VII	VIII
I	15.89**	11.01 ^{ns}	111.33**	62.64**	10.91 ^{ns}	69.85**	64.37**	36.81**
II		43.93**	53.04**	23.05**	15.54*	50.79**	27.58**	45.04**
III			1.40^{ns}	11.92 ^{ns}	109.86	98.58**	24.84**	151.36**
IV				13.08^{ns}	66.98**	74.21**	18.30**	107.10**
V					19.16**	37.52**	48.12**	9.38 ^{ns}
VI						0.93^{ns}	35.04**	34.92**
VII							4.21^{ns}	67.11**
VIII								3.74^{ns}

Significant ($\chi^2 = 15.50$) and highly significant ($\chi^2 = 20.09$), respectively

Principal component analysis

The principal component analysis the root and shoot traits were combined into a four-column matrix. The first four principal component which has eigenvectors values greater than one cumulatively explained about (67.38%) of the total variation among the studied traits describing the genotypes (Table 4). Out of the total four principal components PC1 had an eigenvalue of (2.24) and accounted for (22.38%) from the total variation. The five traits namely root length, root number; shoot fresh weight, root dry weight, and stem diameter were more contributed for variation in PC1.

Table 4
Components (PCA) analysis of root shoot traits in sorghum genotype showing eigenvectors.

Traits	Eigenvectors			
	PC1	PC2	PC3	PC4
Root angle	-0.07	0.08	0.56	-0.41
Root length	0.36	0.13	-0.49	0.21
Root number	0.40	0.07	0.12	-0.38
Root dry weight	0.47	-0.11	0.39	0.21
Root shoot ratio	0.29	-0.59	0.21	0.05
Shoot dry weight	0.06	0.62	0.15	0.1
shoot fresh weight	-0.36	0.23	0.24	0.01
Shoot length	0.14	0.23	0.19	0.57
Leaf area	-0.29	-0.2	0.31	0.51
stem diameter	0.40	0.29	0.16	-0.01
Eigenvalue	2.24	2.00	1.28	1.22
% variance	22.38	20.00	12.82	12.23
Cumulative	22.4	42.4	55.2	67.4

The PC2 had an eigenvalue of 2.00, contributing (20%) from the total of variation. In addition shoot dry weight and root shoot ratio were the traits with high value positive and negative of component loadings respectively which had contribute the variation and these two traits also demonstrated under PC2. Third Principal Component (PC3) had Eigen values of 1.28, indicating that root angle, leaf area, root length and root dry weight were contributing (12.82%) variation. Root angle had shown has highest positive loading score and highest contribution under PC3. PC4 had an eigenvalue of 1.22 with 12.23% of the variance estimated from the total variation. Shoot length, root angle and root number and leaf area were traits significantly important for contribution of a variation under PC4 (Table 4). The four principal components scores might be used to summarize the original root and shoot traits in any further analysis of the data. Root angle, root number, root dry weight, stem diameter and leaf area were contributed for variation more than one across the four principal components (Table 4).

The PCA biplot (Figure.2) demarcated the genotypes with trait of root and shoot characteristics explained by the first two dimensions. Most of the variation that responsible for genetic divergence under the biplot of PC1 and PC2 were root length, root dry weight and root shoot ratio, shoot fresh weight and stem diameter. The quadrant of biplot revealed that the outlier or distant/diverging from the major genotypes such as Acc#220249(58) had high number root; Acc#220254(#59) had high shoot dry weight (0.98g); Acc#234102(#102) had highest root shoot ratio; Acc#235791(#108) had lower root shoot ratio (0.29g); Acc#235811(#118) had lower root dry weight (0.29g) and Acc#20710(27) with narrow root angle (16.33°) and longest root length (72.33cm) (Figure.2).

Correlation RSA traits and grain yield

Root angle exhibited negative correlation ($r=-0.292$) with grain yield (Table 5) Root length showed strong Significant and positive association ($r = 0.329$) with grain yield. Root length showed significant and positive correlation with shoot fresh weight ($r=-0.261$), root number($r = 0.162$), root dry weight($r = 0.158$), stem diameter($r = 0.25$) and negative association with leaf area ($r = -0.231$).

Table 5
Pearson's correlation matrix for root and shoot traits trait that contain 214 genotypes

Traits	RA	RL	RN	RDW	RSR	SDW	SFW	SH	LA	SD	YLD
RA		-0.292**	0.064	-0.028	-0.041	0.066	0.055	0.024	-0.034	0.0521	-0.241**
RL			0.162*	0.158*	-0.008	0.104	-0.261**	0.12	-0.231*	0.252*	0.329**
RN				0.297**	0.142**	0.125	-0.164*	-0.056	0.272**	0.291**	0.027
RDW					0.571**	0.183**	-0.212*	0.139*	-0.016	0.313**	0.023
RSR						-0.665**	-0.330**	-0.102	0.112	0.004	-0.032
SDW							0.229*	0.237*	-0.12282	0.276**	0.015
SFW								-0.108	0.235*	-0.04943	0.03
SL									0.087	0.227*	0.081
LA										-0.282**	-0.077
SD											0.128
YLD											

Key: **and*significant at P = 0.01 and P = 0.05. RA = Root angle, RL = Root length, RN = Root number, RDW = Root dry weight, RSR = Root shoot ratio SDW = Shoot dry weight = Root shoot ratio, SFW = Shoot fresh weight, SL = shoot length, LA

Root number has showed strong significant positive correlation root dry weight ($r = 0.297$), root shoot ratio ($r = 0.142$) leaf area (0.272) and stem diameter ($r = 0.291$) and highly negatively associated with shoot fresh weight ($r = -0.164$). Root shoot ratio has showed high significant a positive and negative correlation with root dry weight ($r = -0.665$) and shoot fresh weight ($r = 0.330$) respectively. Shoot dry weight was significant and positively associated with shoot fresh weight ($r = 0.229$) and shoot length ($r = 0.237$) stem diameter ($r = 0.276$) (Table 5).

Discussion

Root system architecture traits revealed diversity among the drought adapted genotypes. This evidences the genetic heterogeneity of the evaluated population, what is quite relevant for the genetic divergence analysis and for breeding purposes, aiming at identify superior genotypes (Giles et al. 2019). The pattern of clustering of genotypes did not depend upon its seed source or origin, it means that genotypes from same origin do not group together i.e. genetic constituent of the genotypes is basically the main factor for predicting grouping genotype into distinct cluster (Bhanupriya et al. 2014). This indicates that the gene flow between Ethiopian sorghum (IBC) and ICRISAT genetic materials. Indeed, ICRISAT collected large number of materials from Ethiopia (Reddy et al. 2002).

Grouping the genotypes according to the characteristics might reveal that the lines have similarity in one or more traits (Seetharam and Ganesamurthy 2013) reported that promising genotypes can be identified from cluster means recorded for each trait. A better understanding genetically characteristics of different cluster is required by the breeder to increase the efficiency of selection of more diverse and adapted parents for crop improvement (Billot et al. 2013). Genotypes between the cluster were presumably shown the distinct nature which were genetically more divergent from each other which could be opportunity to exploit selection and crossing of sorghum genotype since, maximum recombination and segregation of the progenies is expected (Ayana and Mengistu 2006).

It is possible to develop some predictors of heterosis or specific combining ability between two lines using some surroundings of genetic distances in crop improvement (Qu et al. 2012). Heterosis effects discovered by crossing the populations reveal genetic divergences that are not expressed by populations themselves. In fact, similar phenotypes can be produced by different genotypes (Ayana and Mengistu 2006). Moreover, the amount of heterosis is a linear function of differences in allele frequencies for the loci having dominance or over dominance effects (Moll et al. 1965). Hence, providing higher heterotic groups of shoot and root traits for crop improvement is an advantageous opportunity developing variety for different constraints sorghum production in moisture stress area.

The genotype Acc#6094 with wider root angle (27.370) originated from ICRISAT collection under cluster-I which is vital for increase water extraction in wide or skip row dryland farming systems (Whish et al. 2005) which favors better crosswise access, which could Furthermore, genotypes with wider root angles and potentially denser but shallower root systems may be better able to exploit small events of in-crop rainfall (Liao et al. 2006; Sanguineti et al. 2007).

The result shown under Cluster III categorized by highest cluster mean value of root length (72.5cm) and the narrow root angle (15.930) the genotypes (Acc#15964) and (Acc#20710) were included under Cluster III. (Bibi et al. 2012; Singh et al. 2012) anticipated that the genetic potential of different sorghum accessions with the highest root length with narrow root angle at the seedling stage was the highest contributor towards drought tolerance. The genotypes allocating more roots at depth had on average 28 to 42% higher yield, probably due to a better capacity to capture deep soil moisture during grain filling (Lynch and Wojciechowski 2015).

The genotypes under this cluster significantly associated with drought. Root traits with highest root length and the proportion of fine to large roots are also important for drought tolerance (Ekanayake et al. 1985; Lopes and Reynolds 2010). The genotypes incorporated within this cluster (Acc#15964) and (Acc#20710) were more critical under moisture stress area (Pandey et al. 2015). Cluster V showed lowest mean root dry weight (0.59g) other study had predicted genotypes, which has low root dry weight genetic backgrounds had enabled to less adapted moister stress environment (Shinde et al. 2017).

The highest cluster mean of leaf area (32.45m²), root dry weight (0.86g), root shoot ratio (0.52) in cluster VI helped for breeding strategies aimed at enhancing biomass allocation to roots (Mathew et al. 2018). So the genotype must be pursued with due diligence to avoid compromising the above ground traits that are more favorably associated to grain yield. Plant size and root architecture thus represent two contrasting drought adaptation mechanisms, and the results for sorghum imply that these mechanisms could potentially operate independently, as it has been observed in rice (Price et al. 2002).

The maximum inter cluster distance (D₂ = 151.36) indicate that genotypes between the cluster were presumably shown the distinct nature which were genetically more divergent from each other which could be opportunity to exploit selection and crossing of sorghum genotype since, maximum recombination and segregation of the progenies is expected from these cluster (Zhu and Zhang 2013). (Amsalu et al. 1987) crossing genotypes belonging to distant clusters could maximize transgressive segregation however cluster mean for specific trait should be consider. The lowest intra-cluster was recorded in cluster VI (0.93) it can be observed that the intra-cluster distance was much less than the inter-cluster distance this indicating homogeneity within the clusters and heterogeneity between the clusters.

The principal component matrix decomposition was then used to create a set of loadings (eigenvectors of the correlation matrix) of length equal to the number of traits and a set of scores with length equal to the number of observations, thus enabling further investigation of the relationships between the trait observations and the trait correlations (loadings) Scores (Chatfield and Collins 1980). In consequence, can easily visualize the distances between the genotypes and decide on the best varieties to be selected, based on several traits, compressed in the two major principal components and analyzed simultaneously. The PCA analysis showed the most diverging genotype over the four quadrants based on the shoot and root traits, these pattern helps to brought up specific genotypes with particular traits for breeding pipe lines.

Group constellation was also independently derived by principal component analysis to verify grouping obtained through D₂ statistic in a two PC. Therefore, scores obtained for the first two principal components were plotted against two main axis and then superimposed with clustering (Figure. 2) this clustering pattern confirmed the results obtained by D₂ analysis. The appearance of traits more than one under the study is important that contribute more variation and brought the impact for further differentiation into eight clusters (Shegro et al. 2013).

Root length and angle reveled association with grain yield under drought condition. The negative association was observed between root angle and grain yield ($r = -0.292$) with similar the study of (Shinde et al. 2017). This result implied that narrow root angle genotypes tends to have relatively lengthy root and more vertical root growth this spectacles have implications for enhanced soil water extraction from depth in the soil profile as a result genotypes possessing deep penetrating root is more suitable for drought (Shinde et al. 2017).

Root length was positively correlated with grain yield. Additionally, positive correlation with traits like shoot fresh weight, root number, root dry weight, stem diameter and negative association with leaf area were observed. This result an agreement with wheat crop reported (Sanguineti et al. 2007). Root length could represent most of the root traits that contribute for searching and up taking plant nutrient and water under different environmental condition, not only for its easy measurement but also for its significant and positive relationship with several target root traits for breeding (Liang et al. 2014).

This experiment shown that root biomass was not contribute to sorghum grain in moister stressed area this finding concurred with reported by (Mathew et al. 2018). The association between variations in root architecture advances yield production of the crop, this is due predominantly the changes in water capture pattern root traits consequently root growth and architecture can thus have profound effects on shoot growth (Hammer et al. 2009).

Conclution

The Tocher's cluster analysis method clearly distinguished eight distinct clusters of 214-sorghum genotypes based on the values of different root and shoot traits. Four genotypes Acc#220249(58); Acc#220254(#59); Acc#234102(#102); Acc#235811(#118) Acc#20710(27) were found to be most potential towards direct utilization in sorghum improvement. Especially this finding was implicated narrow nodal root angle and largest root length genotypes such as Acc#15964 and Acc#20710 identified in the study can be involved in crossing programs to create maximum diversity for the benefit of new varieties' development as an indicator for specific adaptation in water-limited environments. May be further evaluated in multi-location trials. Molecular analysis of genetic diversity is recommended to optimize the use of the local sorghum genetic resources in varietal improvement. Pearson correlation coefficient analysis revealed significant association between grain yield versus root angle and root length traits this can be used in improvement of breeding activities in moisture stress area.

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Figures

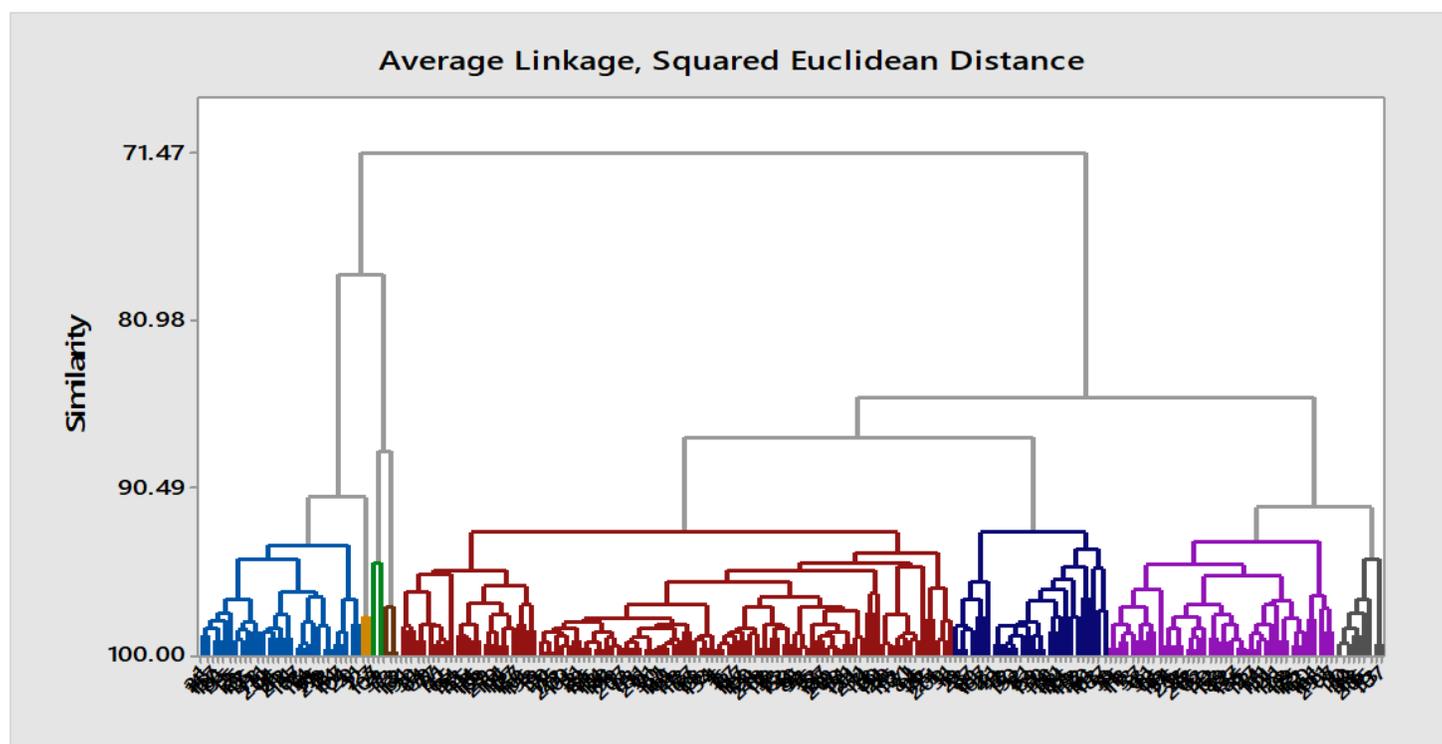


Figure 1

Dendrogram of 214 sorghum genotypes contracted using Ward's method based on 10 root traits under green House 2019/20

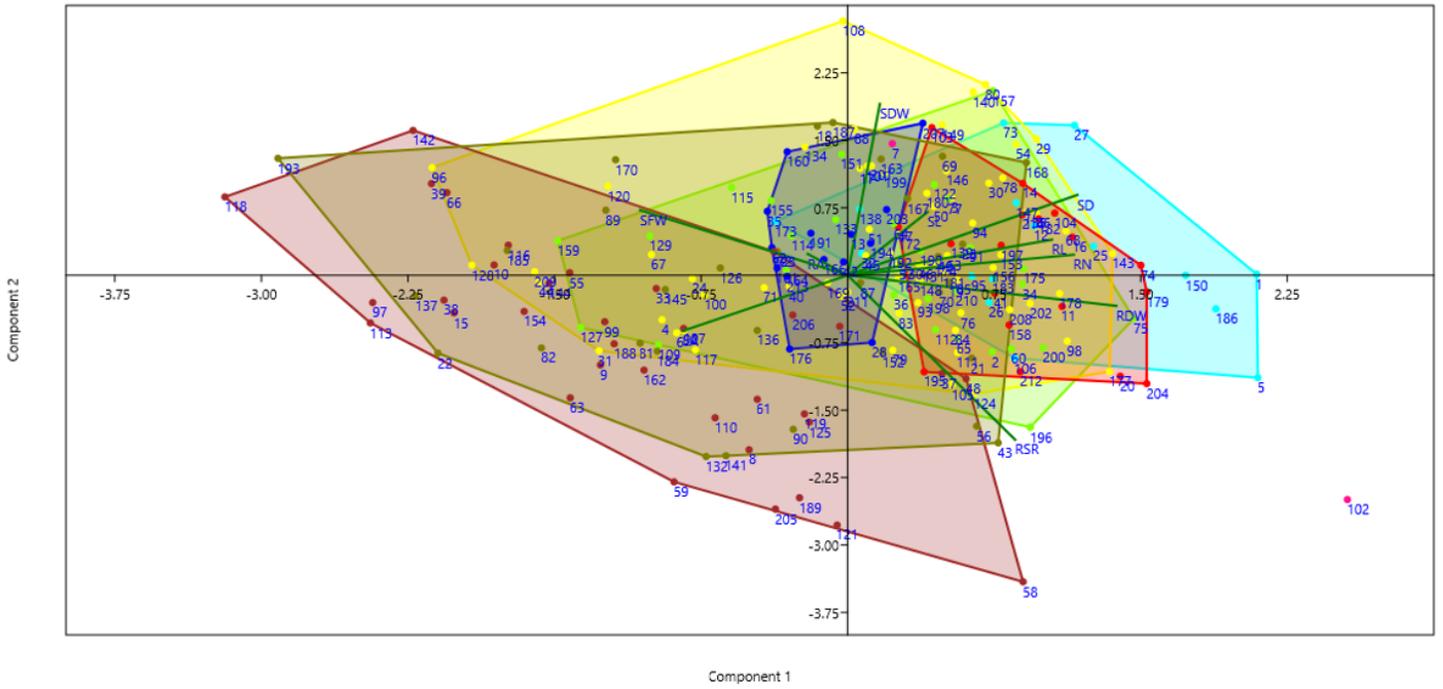


Figure 2

Biplot of PC1 and PC2 of 214 sorghum genotypes based on 10 root traits

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