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Characterization of Converted Race Stocks of Upland Cotton (*Gossypium hirsutum* L.) For Seedling Root Morphology

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Abstract: The genetic diversity and genetic relationship among breeding material has an invaluable importance for crop breeders. A number of methods based on morphological data, agronomic performance data, biochemical data and molecular data have been used to analyze genetic diversity in germplasm accessions, breeding line and populations. In this study, 68 CRS accessions and 10 cotton genotypes were investigated to characterize the genotypes based on root morphological data and to identify a core set of Converted Race Stocks (CRS) accessions by using multivariate methods, including principal component and cluster analyses. Principal component and hierarchical cluster analysis grouped CRS accessions into 13 clusters and produced two different groups for cotton genotypes, representing different cotton production area in the USA. The first two principal components explained 75.10 and 90.45% of the total variation among 68 CRS accessions and cotton genotypes, respectively, with Total Root Dry Weight (TRDW) and Lateral Root Dry Weight (LRDW) being the most important characters in the first principal component. The results of this study would be of practical value to cotton breeders to select robust rooted CRS accessions and cotton genotypes from different group without duplicate parents for further investigation in cotton breeding for drought tolerance.

Key words: Cotton, converted race stocks, cluster analysis, root morphology

Introduction

For long term crop improvement breeders rely on the degree and distribution of genetic diversity and relationship among breeding materials. The estimation of the levels and the patterns of genetic diversity in crops have diverse application including identifying diverse parental combinations to create segregating progenies with maximum genetic variability for further selection (Barrett and Kidwell, 1998) and introgression desirable genes from diverse germplasm into the available genetic base (Thompson *et al*., 1998). Large number of germplasm collections or accessions would be classified and subset of core accessions for specific breeding purposes would be identified by using genetic diversity analysis. To analyze genetic diversity in crop plants, researchers have used different data sets such as pedigree data (Messmer *et al*., 1993) morphological data (Granati *et al*., 2003 and Terzopoulos *et al*., 2003) and biochemical data (Hamrick and Godt, 1997).

In general, plant breeders primarily use current and obsolete cultivars along with public germplasm in developing new cultivars. Also, intensive selection for high fiber yield and fiber quality

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characters has apparently led to a narrowing of cotton gene pool. Therefore, to overcome this problem more efforts have been focus on the diverse cotton germplasm including Converted Race Stocks (CRS) and wild *Gossypium* species to expand genetic diversity. The exotic race stock accessions (*Gossypium hirsutum* L.) were collected in the arid regions of Mexico and Central America and Seventy-nine of about 600 of these race stock accessions had been converted (CRS) to the day neutral fruiting habit by 1998 (McCarty *et al.*, 1998). Converted Race Stocks (CRS) have been identified an important source of useful genetic variability including drought tolerance (Quiseberry *et al.*, 1981; Perceival, 1987; Basal *et al.*, 2003; McCarty *et al.*, 2004a, b; Basal *et al.*, 2005).

The use of multivariate methods is an important strategy for characterization, evaluation and classification of plant genetic resources when large numbers of accession are to be assessed for several characters (Peeters and Martinelli, 1989). The multivariate analysis, especially the principal component and cluster analyses, have been commonly employed for the evaluation of various trait and a large number of accession for different crop species (Brown, 1991; Ayana and Bekele, 1999; Veasey *et al.*, 2001; Terzopoulos *et al.*, 2003; Granati *et al.*, 2003). Total variation in the in the original data would be broken into components by Principal Component Analysis (PCA). Each PC expresses the proportion of variation as the eigenvalues. The PCS with eigenvalue >1.0 are considered as inherently more informative (Iezzoni and Pritts, 1991). Among the five clustering method, namely UPGMA (Unweighted Paired Group Method using Arithmetic averages), UPGMC (Unweighted Paired Group Method using Centroids), Single Linkage, Complete Linkage and Median, UPGMA provided results most consistent with known heterotic groups and pedigree information (Kantety *et al.*, 1995). Also UPGMA method provides consistency with regard to the allocation of cluster, when the different size of groups, or different types and number of characters were used (Rincon *et al.*, 1996; Franco *et al.*, 1997).

The objectives of this study were to determine the extent and patterns of root morphological variation related to drought tolerance in 68 Converted Race Stocks (CRS) and 10 upland cotton genotypes representing different cotton production regions in the USA and to identify groups of CRS accessions with similar root characters using multivariate statistical methods.

Materials and Methods

Sixty-eight CRS accessions were planted in pots (20 cm ht × 11 cm diam.) filled with fritted clay (Absorb-N-Dry, Balcones Co., Flatonia, TX) on 22 May 2002. Ten pots of each genotype were established. Four seeds were planted in each pot and thinned to one plant per pot 2 weeks post emergence. The pots were watered each day and fertilized with 20-20-20 NPK fertilizer (Peterson Professional All Purpose Plant Food, Spectrum Group, Division of United Industries Crop., St. Louis, MO) and micronutrients (Peterson Professional M-77 Soluble Trace Element Mic.) added three times to the irrigation water on the 8th, 12th and 16th day of the 20 day experiment. Ten upland cotton genotypes (TAM94L-25, Acala 1571, Acala Max, Fm 832, Lankart 142, Pyramid, PD 90, PD 94063, SG 125 and Stonville) representing different cotton production area in the USA were planted in tubes (70 cm ht × 11 cm diam.) filled with fritted clay on 19 June 2002, on 19 July and 13 August 2002. Ten tubes of each genotype were established. Four seeds were planted in each tube and thinned to one plant per tube. Plants in the tubes were grown under the same conditions as described above for pots. Twenty DAP, plants removed from the pots and the tubes. Roots were washed free of clay and then spread on paper for determination of root length and lateral root number. Plants were cut into two parts, root and shoot and fresh weight determined. Shoot, taproot and lateral roots were dried for 48 h at 90°C and dry weight recorded. RL was determined by direct measurement of fresh tap roots; LRN was determined by direct count of roots prior to drying; TRDW was determined by direct measurement after drying for 48 h at 90°C; W/L was determined by dividing the TRDW (mg) by the

tap root length (cm). TRDW/SDW and LRDW/TRDW were calculated by dividing the TRDW (mg) by the SDW (mg) and by dividing the LRDW (mg) by the TRDW (mg), respectively. Genotypes were evaluated for Root Length (RL), Lateral Root Number (LRN), Root Fresh Weight (RFW), Lateral Root Dry Weight (LRDW), Total Root Dry Weight (TRDW), root weight per unit length of the tap root (W/L), total root dry weight ratio to shoot dry weight (TRDW/SDW) and lateral root dry weight ratio to total root dry weight (LRDW/TRDW).

The experiments were conducted in a greenhouse at the Borlaug Biotechnology Center on the campus of Texas A and M University with 32/27°C and 57/67% relative humidity (day/night) conditions. The experiments were repeated using a completely randomized design and, data analyzed by using Generalized Linear Model (GLM) in SAS System (SAS Institute, Cary, NC). Means for all traits were calculated and used in multivariate analyses. Principal component analysis was performed on the correlation matrix of seedling root morphology characters to define the patterns of variation among CRS accessions. Hierarchical clustering was then carried out using UPGMA (Unweighted Paired Group Method using Arithmetic averages), which was recommended when the different size of groups and number of characters were used (Rincon *et al*., 1996; Franco *et al*., 1997). Principal component scores were used for the clustering procedure. Principal component and cluster analyses were obtained by using JMP (SAS Inst., 1996).

Results

Converted Race Stocks (CRS)

Means, standard errors, range of variation and coefficient of variation estimated for each trait in all accessions are given in Table 1. Among the investigated root characters, while LRDW/TRDW showed less variation, ranging from 0.715 to 0.880 mg, RFW was more variable, ranging from 761 to 3580 mg.

The results of principal component analysis showed that the first two principal components, with eigenvalues greater than 1.0, explained 75.10% of the total variation among 68 CRS accessions for the root morphology (Table 2 and Fig. 1). The variance accumulated by the first two components (75.10%) was a relatively high percentage of the total variation to explain satisfactorily the variability between individual (Mardia *et al*., 1979). The first and second principal components accounted for 59.59 and 15.50% of the total variation, respectively. Brown (1991), reported that a coefficient can be generally considered high if its value is higher than 0.3. Therefore, in the first Principal Component (PC1) Lateral Root Number (LRN), Root Fresh Weight (RFW), Lateral Root Dry Weight (LRDW), Total Root Dry Weight (TRDW), weight per unit length of the tap root (W/L) and LRDW/TRDW, lateral root dry weight ratio to total root dry weight; in the second Principal Component (PC2), Root

Table 1: Mean values, Standard Error (SE), ranges, coefficient of variation observed in 68 CRS accessions of upland cotton (*Gossypium hirsutum* L.)

Traits	Mean±SE	Min	Max	CV
RL[§] (cm)	30.1±0.25	22.7	34.7	6.9
LRN (No)	52.2±0.95	28.8	65.3	15.1
RFW (mg)	2358±68.8	761	3580	24.1
LRDW (mg)	163±4.33	43	228	21.9
TRDW (mg)	199±4.97	56	266	20.6
W/L (mg)	6.65±0.146	2.38	8.53	18.2
TRDW/SDW (mg)	0.414±0.006	0.248	0.500	10.9
LRDW/TRDW (mg)	0.819±0.004	0.715	0.880	3.8

[§] RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

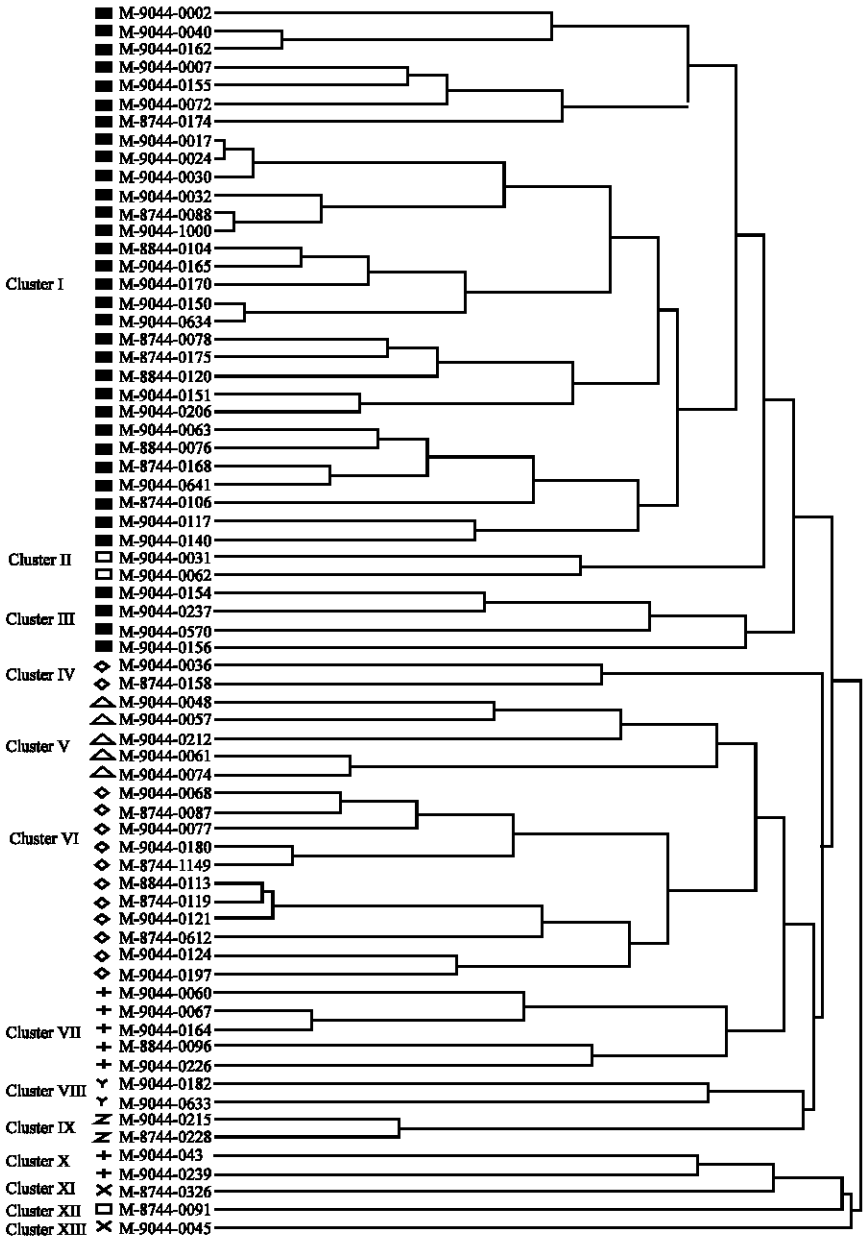

Fig. 1: Dendrogram showing hierarchical clustering of 68 CRS accessions

Length (RL) and Total Root Dry Weight ratio to Shoot Dry Weight (TRDW/SDW) had significant contribution (Table 2). Among the investigated root parameters, LRDW and TRDW and RL had highest values in PC1 and PC2, respectively.

Cluster analysis performed with the root characters classified the accessions into 13 groups. Clusters include different numbers of accessions, Cluster I include 30 CRS accessions with having considerable good parameters for all root characters. Cluster II formed only two CRS accessions, M-9044-0031 and M-9044-0062 and show the highest mean root values except for total root dry

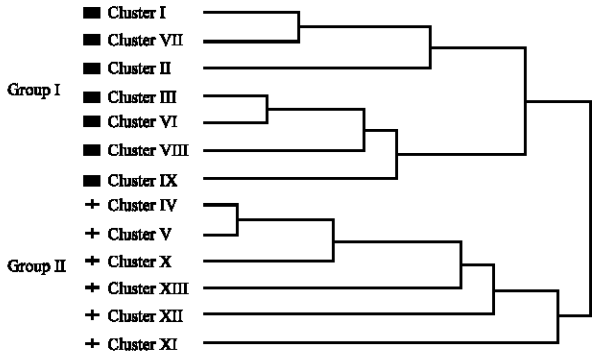

Fig. 2. Dendrogram from cluster analysis of 13 CRS cluster group

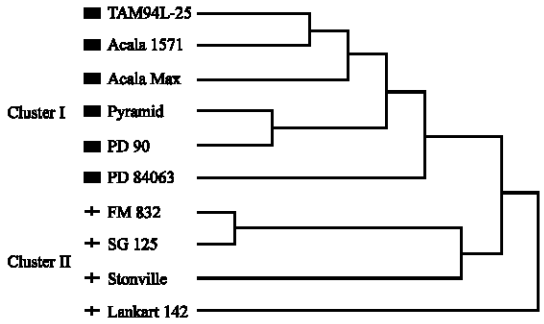

Fig. 3: Dendrogram showing hierarchical clustering of upland cotton genotypes

Table 2: Principal component analysis in 68 CRS accessions of upland cotton (*Gossypium hirsutum* L.): Eigenvalues, total variance and cumulative variance for the first two principal components for root morphological characters

Traits	PC1	PC2
Eigenvalues	4.77	1.24
% of total variance	59.59	15.50
% cumulative variance	59.59	75.10
RL§ (cm)	0.22	0.66
LRN (No.)	0.32	0.27
RFW (mg)	0.41	-0.09
LRDW (mg)	0.45	-0.11
TRDW (mg)	0.45	-0.08
W/L (mg)	0.41	-0.29
TRDW/SDW (mg)	0.14	0.58
LRDW/TRDW (mg)	0.30	-0.22

§ RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

weight ratio to shoot dry weight. Cluster III, four accessions and Cluster IV, two accessions, have root length over 30 cm while the Lateral Root Dry Weight (LRDW) and Total Root Dry Weight (TRDW) values are lower than that of Cluster I and II. Five CRS accessions formed in Cluster V has low Lateral Root Dry Weight (LRDW) despite of moderate Lateral Root Number (LRN). While over all root morphology values of Cluster VI, VII, VIII, IX close to each others in terms of root parameters, Cluster VI, VII, VIII, IX has the lowest value for Total Root Dry Weight ratio to Shoot Dry Weight (TRDW/SDW), Lateral Root Number (LRN), Lateral Root Dry Weight (LRDW) and weight per unit length of the tap root (W/L), respectively among this cluster group. Cluster X, including two CRS accessions and Cluster XI, XII and XIII, including only one CRS accession, has the lowest values for all investigated root parameters (Table 3).

Table 3: Cluster membership and mean of 68 CRS accessions

Genotype	RL[§] (cm)	LRN (number)	RFW (mg)	LRDW (mg)	TRDW (mg)	W/L (mg cm^{-1})	TRDW/SDW (mg)	LRDW/TRDW (mg)
a) Cluster I								
M-9044-0002	31.8	49.9	3024	182	221	7.09	0.449	0.880
M-9044-0040	31.2	45.6	2763	194	221	7.08	0.479	0.853
M-9044-0162	31.0	46.8	2360	186	218	7.06	0.464	0.813
M-9044-0007	30.5	60.1	2985	195	229	7.60	0.486	0.871
M-9044-0155	31.7	55.8	3082	196	229	7.25	0.460	0.814
M-9044-0072	32.1	55.1	3362	208	243	7.69	0.500	0.833
M-8744-0174	32.6	55.7	2921	199	242	7.61	0.498	0.807
M-9044-0017	30.1	55.3	3018	191	228	7.71	0.440	0.868
M-9044-0024	29.9	54.6	2920	191	229	7.69	0.439	0.863
M-9044-0030	30.1	56.9	2989	185	219	7.40	0.419	0.857
M-9044-0032	29.2	58.9	2594	174	208	7.19	0.416	0.856
M-8744-0088	29.2	53.9	2637	172	213	7.42	0.410	0.828
M-9044-1000	29.9	53.4	2545	177	220	7.56	0.412	0.715
M-8844-0104	31.3	56.2	2744	183	224	7.31	0.470	0.826
M-9044-0165	31.5	62.6	2622	180	222	7.13	0.468	0.811
M-9044-0170	32.5	54.8	2749	177	221	6.91	0.460	0.808
M-9044-0150	30.4	58.3	2343	174	213	7.23	0.448	0.816
M-9044-0634	30.5	61.0	2331	186	227	7.47	0.450	0.754
M-8744-0078	31.5	59.7	2870	177	219	6.98	0.378	0.830
M-8744-0175	31.6	61.3	2420	185	228	7.34	0.405	0.806
M-8844-0120	31.6	58.8	2386	180	215	6.81	0.375	0.822
M-9044-0151	31.9	53.9	2450	182	216	6.89	0.418	0.815
M-9044-0206	32.0	54.2	2608	196	230	7.20	0.382	0.804
M-9044-0063	29.7	60.0	2911	201	244	8.24	0.425	0.842
M-8844-0076	31.1	59.0	3127	214	262	8.53	0.432	0.831
M-8744-0168	31.3	58.8	2887	204	242	7.95	0.424	0.809
M-9044-0641	31.5	55.4	2595	208	251	8.05	0.432	0.752
M-8744-0106	32.1	65.3	2643	196	239	7.73	0.437	0.825
M-9044-0117	29.7	64.9	2412	192	240	8.27	0.376	0.824
M-9044-0140	31.5	61.7	2642	202	245	8.04	0.384	0.817
Mean	31.0	56.9	2731	189	229	7.48	0.435	0.822
b) Cluster II								
M-9044-0031	31.1	61.0	3539	216	257	8.40	0.442	0.856
M-9044-0062	31.2	54.3	3580	228	266	8.46	0.393	0.843
Mean	31.7	57.7	3560	222	261	8.43	0.418	0.850
c) Cluster III								
M-9044-0154	31.5	51.4	2229	154	180	5.81	0.468	0.815
M-9044-0237	29.4	50.7	2247	162	193	6.65	0.473	0.797
M-9044-0570	32.2	55.1	2361	145	178	5.62	0.460	0.788
M-9044-0156	34.7	59.0	2182	171	205	5.96	0.435	0.814
Mean	31.9	54.1	2255	158	189	6.0	0.459	0.803
d) Cluster IV								
M-9044-0036	31.7	39.3	1890	128	147	4.70	0.404	0.854
M-8744-0158	29.2	39.3	1715	132	150	5.05	0.448	0.813
Mean	30.5	39.3	1803	130	148	4.88	0.426	0.833
e) Cluster V								
M-9044-0048	28.6	48.8	1827	121	147	4.96	0.389	0.848
M-9044-0057	27.2	46.7	1860	114	139	5.67	0.383	0.846
M-9044-0212	29.6	40.3	1719	137	163	5.59	0.413	0.800
M-9044-0061	26.4	44.7	2071	130	161	6.12	0.350	0.845
M-9044-0074	26.4	44.2	2225	134	162	6.20	0.344	0.832
Mean	27.6	44.9	1940	127	154	5.71	0.376	0.834
f) Cluster VI								
M-9044-0068	29.5	46.3	2134	149	182	6.20	0.373	0.839
M-8744-0087	28.6	44.0	2134	155	186	6.57	0.384	0.829
M-9044-0077	28.3	47.9	2284	158	194	7.01	0.406	0.831
M-9044-0180	29.6	51.3	2060	160	195	6.59	0.387	0.806
M-8744-1149	30.0	52.6	2029	176	213	7.16	0.379	0.715
M-8844-0113	31.0	61.5	2066	160	199	6.50	0.368	0.824

Table 3: Continued

Genotype	RL§ (cm)	LRN (number)	RFW (mg)	LRDW (mg)	TRDW (mg)	W/L (mg cm^{-1})	TRDW/SDW (mg)	LRDW/TRDW (mg)
M-8744-0119	30.5	57.5	2232	165	203	6.73	0.376	0.822
M-9044-0121	31.5	57.3	2081	154	192	6.17	0.375	0.820
M-8744-0612	30.0	58.0	1832	147	180	5.98	0.419	0.773
M-9044-0124	28.9	58.2	1826	147	181	6.39	0.338	0.818
M-9044-0197	29.6	53.1	1749	139	166	5.68	0.364	0.805
Mean	29.8	53.4	2039	155	190	6.45	0.379	0.807
g) Cluster VII								
M-9044-0060	27.8	50.4	2598	179	209	7.33	0.403	0.845
M-9044-0067	28.9	43.7	2906	178	204	7.23	0.379	0.840
M-9044-0164	30.0	48.2	2891	183	213	7.27	0.400	0.813
M-8844-0096	27.3	43.6	2099	165	197	7.33	0.443	0.827
M-9044-0226	28.9	36.6	2242	168	196	6.92	0.420	0.798
Mean	28.6	44.5	2547	174	204	7.22	0.409	0.824
h) Cluster VIII								
M-9044-0182	32.5	49.0	1716	201	154	4.72	0.400	0.805
M-9044-0633	33.6	53.3	1601	141	177	5.40	0.397	0.769
Mean	33.0	51.2	1658	171	165	5.06	0.398	0.787
i) Cluster IX								
M-9044-0215	29.5	48.2	1368	121	152	5.17	0.474	0.798
M-8744-0228	29.2	52.0	1560	122	159	5.60	0.455	0.797
Mean	29.3	50.1	1464	122	155	5.39	0.465	0.798
j) Cluster X								
M-9044-043	29.5	43.0	1715	101	131	4.23	0.330	0.850
M-9044-0239	27.0	44.9	1334	89	113	4.10	0.385	0.796
Mean	28.2	43.9	1524	95	122	4.16	0.358	0.823
j) Cluster XI								
M-8744-0326	28.7	36.3	1214	81	106	2.38	0.248	0.849
k) Cluster XII								
M-8744-0091	22.8	32.5	1238	85	116	5.77	0.348	0.827
l) Cluster XIII								
M-9044-0045	22.7	28.8	761	43	56	4.04	0.430	0.794

§ RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

Thirteen cluster groups identified based on means for root traits, basically divided into two main groups (Fig. 2). First main group include Cluster I, II, III, VI, VII, VIII and IX. Second main group consist of Cluster IV, V, X, XI, XII and XIII. The mean root parameters values of first main group are higher than that of second main group, except for LRDW/TRDW. Therefore, first main group would be called as robust rooted and second main group non robust rooted accessions. In the Group I, Cluster III and IV and Cluster I and VII are the most similar ones. In the Group II, Cluster IV and V are the most similar ones. Cluster XI is the most distant and, consequently the least similar one.

Means, standard errors, range of variation and coefficient of variation estimated for each trait in 10 upland cotton (*Gossypium hirsutum* L.) varieties are given in Table 4. The results showed that differences among 10 upland cotton genotypes are significant for the investigated root characters. Root Fresh Weight (RFW), having the highest variation, ranges from 1391 to 4557 mg with a mean value of 3058 mg. On the contrary, LRDW/TRDW showed less variation, ranging from 0.661 mg to 0.771 mg. with a mean value of 0.710 mg.

The first two principal components with eigenvalues greater than 1.0 account for 90.45 % of the total variance of all traits (Table 5). Separate percentages of variation attributable to the first two components by decreasing order are 76.50 and 13.97%. Among investigated root parameters. TRDW in PC1 and LRDW/TRDW in PC2 had significant role in grouping the cotton genotypes.

Cluster analysis classified upland cotton genotypes into two cluster groups based on the root characters (Fig. 3 and Table 6). Cluster group I include six upland cotton genotypes, TAM94L-25,

Table 4: Mean values. Standard Error (SE), ranges, coefficient of variation observed in 10 upland cotton (*Gossypium hirsutum* L.) varieties

Traits	Mean±SE	Min	Max	CV
RL[§] (cm)	54.9±3.31	30.8	66.4	19.1
LRN (No)	65±4.42	33.9	80.7	21.4
RFW (mg)	3058±0.28	1391	4557	28.4
LRDW (mg)	135±11.91	54	182	28.0
TRDW (mg)	188±16.26	80	251	27.4
W/L (mg)	4.37±0.231	2.9	5.47	16.7
TRDW/SDW (mg)	0.319±0.011	0.309	0.367	10.6
LRDW/TRDW (mg)	0.710±0.009	0.661	0.771	4.3

[§] RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

Table 5: Principal component analysis in 10 upland cotton (*Gossypium hirsutum* L.) varieties: Eigenvalues, total variance and cumulative variance for the first two principal components for root morphological characters

Traits	PC1	PC2
Eigenvalues	6.12	1.11
% of total variance	76.50	13.94
% cumulative variance	76.50	90.45
RL[§] (cm)	0.37	-0.23
LRN (No.)	0.37	-0.01
RFW (mg)	0.39	0.01
LRDW (mg)	0.39	0.10
TRDW (mg)	0.40	0.01
W/L (mg)	0.37	0.17
TRDW/SDW (mg)	0.33	-0.32
LRDW/TRDW (mg)	0.10	0.89

§ RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

Table 6: Cluster membership and mean of cotton genotypes

Genotype	RL[§] (cm)	LRN (number)	RFW (mg)	LRDW (mg)	TRDW (mg)	W/L (mg cm^{-1})	TRDW/SDW (mg)	LRDW/TRDW (mg)
a) Cluster I								
TAM94L-25	59.1	80.2	3146	168	234	5.05	0.314	0.701
Acala 1571	65.4	70.8	2816	156	227	4.59	0.323	0.686
Acala Max	68.9	73.3	3222	183	253	4.48	0.358	0.724
Pyramid	57.9	58.4	2387	136	194	4.50	0.367	0.690
PD 90	47.9	71.4	2323	145	191	5.47	0.349	0.757
PD 94063	57.6	77.6	2839	167	227	5.47	0.330	0.726
Mean	59.5	70.3	2717	154	218	4.90	0.345	0.717
b) Cluster II								
Fm 832	56.6	71.5	2083	114	163	3.95	0.325	0.693
Lankart 142	31.6	33.3	1011	54	81	2.85	0.262	0.649
SG 125	48.7	60.0	1881	111	152	4.09	0.293	0.721
Stonville	36.4	51.4	1806	106	138	4.57	0.280	0.792
Mean	43.3	54.1	1695	96	134	3.87	0.290	0.714

[§]RL, Root Length; LRN, Lateral Root Number; RFW, Root Fresh Weight; LRDW, Lateral Root Dry Weight; TRDW, Total Root Dry Weight; W/L weight per unit length of the tap root; TRDW/SDW, total root dry weight ratio to shoot dry weight; LRDW/TRDW, lateral root dry weight ratio to total root dry weight

Acala 1571, Acala Max, Pyramid, PD 90, PD 94063 with having considerable robust root parameters for all investigated characters. Cluster group II formed four cotton genotypes, Fm 832, SG 125, Stonville and Lankart 142, had lower values for all investigated root parameters than that of Cluster group I. Although cotton genotypes, representing different cotton production area in the USA, were separated more than two statistical groups based on means of genotypes by using the Waller-Duncan LSD at k = 100 ratio (data not shown), cotton genotypes were classified only into two cluster groups based on the root characters. Thus, new gene resources would be used in breeding program to modify root morphology in cotton for drought tolerance.

Discussion

Genetic diversity limits vulnerability to pests and diseases and also provides allelic variation that can be used to create new favorable gene combinations. To overcome a narrowing of cotton gene pool problem due to intensive selection for high fiber yield and fiber quality characters more efforts have been focus on the diverse cotton germplasm including Converted Race Stocks (CRS) and wild *Gossypium* species to expand genetic diversity. Converted Race Stocks (CRS) have been identified an important source of useful genetic variability including drought tolerance (Quiseberry *et al.,* 1981; Perceival, 1987; Basal *et al*., 2003, 2005; McCarty *et al*., 2004a,b).

Categorizing germplasm accessions into morphologically similar and presumably genetically similar groups is necessary to create core collections which have been proposed to increase the efficiency of utilizations and management of germplasm collections. and to select parents for crossing (Souza and Sorrells, 1991; Liu *et al*., 1999). The cluster and principal component analysis with root morphological data of CRS accessions revealed the existence of variability. The available and potential phenotypic variability in CRS accessions for root parameters would be interesting for potential users of CRS accessions in relation to the prospect of improvement new cotton genotypes with modified root morphology for drought tolerance. In this study, CRS accessions and cotton genotypes, representing different cotton production area in the USA, were divided into 13 and two different cluster groups by using multivariate analysis, which would be of practical value to cotton breeders in order to avoid duplicate accessions or related accessions. Earlier study showed that robustness of seedling rooting parameters can be recovered easily and that seedling rooting robustness can be improved by crossing robust rooting parents (Basal *et al*., 2003). Thus, the results of this study would be of practical value to cotton breeders to select robust rooted CRS accessions and cotton genotypes from different group without duplicate parents.

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