Genetic Diversity of Sorghum Genotypes for Drought Tolerance based on Morpho-Physiological Traits

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In this study 100 sorghum accessions were evaluated at post flowering drought stress condition based on eight different morpho-physiological traits viz., days to 50 per cent flowering, leaf area index, SPAD chlorophyll, relative water content, plant height, proline, stay-green and grain yield. The analysis was subjected to mean performance and genetic diversity. Further, the diversity of 100 genotypes was studied based on D^2 statistics and grouped into 11 different clusters and each cluster revealed considerable amount of genetic diversity. Inter cluster distance and cluster mean have also been studied for these genotypes. The genotypes IS23399, DRT1030, MS7735, KO5SS53, KO5SS186 and B35 under cluster III were identified as superior genotypes with high mean performance for all the eight traits for post-flowering drought tolerance and could be used in genetic improvement programmes.

Key words: Sorghum, Genetic diversity, Drought tolerance and Genotypes

Sorghum is the most important food crop in the world particularly in the semi-arid tropics. It is also used as fodder and industrial value such as ethanol production mainly for fuel purpose. Drought response in sorghum has been characterized at vegetative (pre-flowering) and reproductive phases (post-flowering). The post-flowering stress significantly affects the grain yield (Rajarajan and Ganesamurthy, 2014). Drought tolerance in sorghum is a complex trait and involves various traits contributing towards its tolerance (Blum, 1979). Stay-green trait is significantly contributes as the ability of the plant to retain green leaves during grain maturity under water deficit conditions (Xu *et al.*, 2000) and hence associated with drought tolerance. Knowledge on genetic diversity among the genetic stocks plays importance of breeding programs for enhances the genetic potential of a genotype. However, the success in breeding under drought stress conditions highly depends on understanding the genetic basis of drought tolerance in crop plants based on various morpho-physiological traits (Mitra, 2001). This will help in choice of selection of genotypes to improve the trait under consideration without yield decline through hybridization.

The aim of the present study is to assess the sorghum genotypes for its divergence based on morpho-physiological traits under drought stress conditions. This could help in identification of superior genotypes under managed drought stress condition to improve sorghum drought tolerance breeding programmes.

Materials and Methods

Plant materials and location

The experiment was carried out at Tamil Nadu Agricultural University, Coimbatore during *kharif* 2016.

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The experiment was laid out under randomized block design (RBD) with two replications as under post flowering moisture stress imposed by withholding irrigation from flowering to maturity. In this study, one hundred sorghum genotypes were evaluated for its drought tolerance, which includes genotype B 35, and CO 26 (TNAU released grain sorghum) was used as the drought resistant and susceptible check respectively (Table 1). It was ensured that no rain was recorded during the moisture stress imposition i.e., from anthesis to crop maturity phase along with normal recommended cultural practices were adopted during the crop period. Data were recorded for days to 50 per cent flowering, leaf area index, SPAD chlorophyll, relative water content, plant height, proline, stay-green and grain yield.

Plant physiological traits and statistical analysis

Water stress indicator traits like relative water content (RWC) were calculated using the formula suggested by Barrs and Weatherly (1962) and total leaf chlorophyll contents were measured with a Minolta chlorophyll meter SPAD-502. The stay-green was estimated visually on a plot basis as follows; suggested by Wanous *et al.,* (1991) in sorghum.

Decimal score	Stay-green nature
1	Leaves have natural green colour
2	1/3rd of leaves yellowing
3	Intermediate
4	1/3rd of leaves green
5	All leaves yellow or dead

Proline estimation was done for stress condition based on Bates *et al.* (1973).

Diversity and construction of phenotypic dendrogram

The data on eight morpho-physiological traits for one hundred sorghum genotypes under drought

stress condition were subjected to multivariate hierarchial cluster analysis. Cluster analysis was performed using INDOSTAT services Ltd (version 8.5), Hyderabad, India, further the tree diagram based on elucidation distances was developed by TOCHER clustering method. The D^2 statistics was calculated according to Mahalnobis (1936) and Rao (1952).

Results and Discussion

In this present study all genotypes under consideration were showed significant variation under water deficit stress environment for its morpho-physiological traits based on the estimates of analysis of variance and mean performance of a genotypes, as it was evident from the range of values (Table 2).

Based on D^2 statistics and Tochers method, the 100 genotypes were grouped into 11 clusters and each cluster revealing considerable amount of genetic diversity in among the material (Table 3). It was observed that cluster I had maximum number of genotypes i.e. 40 followed by cluster II with 23 genotypes, cluster IV had 16 with susceptible check CO 26 variety, cluster VI had 9 and cluster 3 with 6 genotypes including resistant check B-35. The remaining 6 clusters were represented by single genotypes, which remain diverged from the others. The formation of solitary clusters may be due to the gene flow or intensive natural/human selection for diverse adaptive complexes (Sujatha and Pushapavalli, 2015). Genotypes, which had delayed

Table 1. List of sorghum genotypes and sources used in the study

S.No	Genotypes (Source: TNAU)	Origin	S.No	Genotypes (Source: TNAU)	Origin
1	ICSR93001	ICRISAT	51	WAC01	ICRISAT
2	ICSV91028	ICRISAT	52	MTRS2336	ICRISAT
3	ICSV95022	ICRISAT	53	PMR18	ICRISAT
4	ICSR91020	ICRISAT	54	RS14432	ICRISAT
5	ICSV584	ICRISAT	55	ICSV202	ICRISAT
6	ICSV1025	ICRISAT	56	PC63	ICRISAT
7	ICSV587	ICRISAT	57	SSV89	ICRISAT
8	DRT1026	ICRISAT	58	KO5SS262	IIMR
9	DRT1019	ICRISAT	59	KO5SS545	IIMR
10	DRT1011	ICRISAT	60	KO5SS303	IIMR
11	ICSR25001	ICRISAT	61	KO5SS202	IIMR
12	ICSR24001	ICRISAT	62	KO5SS150	IIMR
13	ICSR196	ICRISAT	63	KO5SS201	IIMR
14	ICSR89052	ICRISAT	64	KO5SS25	IIMR
15	ICSR95034	ICRISAT	65	KO5SS53	IIMR
16	ICSR162	ICRISAT	66	KO5SS306	IIMR
17	ICSR108	ICRISAT	67	KO5SS23	IIMR
18	ICSR16	ICRISAT	68	KO5SS405	IIMR
19	ICSR24005	ICRISAT	69	KO5SS51	IIMR
20	DRT1030	ICRISAT	70	KO5SS56	IIMR
21	IS5005	ICRISAT	71	KO5SS302	IIMR
22	IS5479	ICRISAT	72	KO5SS232	IIMR
23	IS3308	ICRISAT	73	KO5SS267	IIMR
24	IS1130	ICRISAT	74	KO5SS135	IIMR
25	IS5972	ICRISAT	75	KO5SS22	IIMR
26	IS3246	ICRISAT	76	KO5SS51	IIMR
27	IS3552	ICRISAT	77	KO5SS154	IIMR
28	IS1484	ICRISAT	78	KO5SS178	IIMR
29	IS23399	ICRISAT	79	KO5SS226	IIMR
30	IS21813	ICRISAT	80	KO5SS244	IIMR
31	IS358	ICRISAT	81	KO5SS932	IIMR
32	IS1594	ICRISAT	82	KO5SS450	IIMR
33	IS25030	ICRISAT	83	KO5SS258	IIMR
34	AS5160	Unknown	84	KO5SS303	IIMR
35	AS3680	Unknown	85	KO5SS214	IIMR
36	AS521	Unknown	86	KO5SS38	IIMR
37	MS7735	Unknown	87	KO5SS150	IIMR

38	MS8444	Unknown	88	KO5SS116	IIMR
39	MS8387	Unknown	89	KO5SS286	IIMR
40	MS1142	Unknown	90	KO5SS811	IIMR
41	MS73	Unknown	91	KO5SS186	IIMR
42	MS8079	Unknown	92	KO5SS42	IIMR
43	MS8444	Unknown	93	KO5SS287	IIMR
44	MS73	Unknown	94	KO3SS231	IIMR
45	MS91749	Unknown	95	KO3SS200	IIMR
46	MS91309	Unknown	96	KO3SS127	IIMR
47	VS1565	Unknown	97	KO3SS325	IIMR
48	ASS9407	Unknown	98	KO3SS281	IIMR
49	R6774	Unknown	99	B35	ICRISAT
50	Selection from national trail 13	IIMR	100	CO26	TNAU

onset of senescence or stay-green genotypes, were found clustered in separately along with resistant check (B 35) as well as the genotypes which had early senescence or non stay-green were found grouped in different clusters with susceptible check (CO 26) variety (Rajarajan and Ganesamurthy, 2014). Further the stay-green trait is likely to be controlled by different genes that in turn, are triggered by the

Table 2. Mean, range, standard error difference (S.Ed), and critical difference (CD) for agronomic and physiological traits in sorghum

Characters	Mean	Range	SEd	CD
Days to 50% flowering	64.31	59.5-73.0	1.39	3.91
Leaf area index	3.60	23.28-65.86	0.32	0.90
Plant height (PHT) (cm)	222.59	108-308.3	10.11	28.29
SPAD chlorophyll reading	43.05	23.8-62.8	1.45	4.08
Relative water content (%)	46.88	23.3-65.9	1.70	4.77
Proline (mg/g)	1.40	1.04-7.67	0.24	0.67
Stay green	3.72	1-5	0.44	1.25
Grain yield (g)	32.61	0.20-4.26	2.27	6.36

specific pattern of stress development (Dunwell 2000). Genotypes with the moderate level of senescence had clustered separately, which indicate that they are less useful as the source of trait for drought tolerance genotypes with delayed onset of senescence. The grouping of accessions into different clusters (Table 3) describes the breeder to identify and select the drought tolerant genotypes, which can be used as the donor parents in breeding programme for drought tolerance.

Table 3. Clustering composition of 100 sorghum genotypes

No. of clusters	Name of the genotypes
I	ICSR95034, IS5479, IS1484, IS1594, AS5160, MS8444, MS8387, MS8445, MS73, Selection from national trial 13,WAC01, PMR18, PC63, KO5SS545, KO5SS303, KO5SS51, KO5SS232, KO5SS1351, KO5SS150, KO5SS42, KO5SS287, KO3SS231, KO3SS200, KO3SS325, ICSR91020, IS5005, IS3308, IS1130, IS3246, IS358, MS1142, MS91309, VS1565, SSV89, KO5SS22, KO5SS178, KO5SS226, KO5SS244, KO5SS303 and KO5SS811
II	ICSR93001, DRT1026, ICSR24001, ICSR108, IS21813, MS75, RS14432, ICSV202, KO5SS262, KO5SS202, KO5SS25, KO5SS306, KO5SS23, KO5SS405, KO5SS56, KO5SS302, KO5SS267, KO5SS51, KO5SS932, KO5SS450, KO5SS214, KO5SS38 and KO3SS127
III	IS23399, DRT1030, MS7735, KO5SS53, KO5SS186 and B35
IV	ICSV91028, ICSV95022, ICSV587, DRT1019, ICSR16, ICSR24005, IS5972, IS3552, AS3680, AS521, MS8079, MS91749, ASS9407, R6774, KO5SS258 and CO26
V	KO5SS116
VI	ICSV584, ICSV1025, DRT1011, ICSR25001, ICSR196, ICSR89052, IS25030, MTRS2336 and KO3SS281
VII	KO5SS154
VIII	KO5SS201
IX	KO5SS150
X	KO5SS286
XI	ICSR162

Average inter cluster D^2 values among 100 genotypes (Table 4) revealed maximum inter cluster distance values between cluster XI and cluster III (22.30) followed by cluster III and IV (21.56), IV and IX (21.51), X and III (21.30), VI and III (20.17), VIII and III (19.79), IX and VI (19.17) while minimum genetic distance was observed between cluster I and cluster II (7.04). The data on cluster means (Table 5) revealed considerable differences among the clusters for all the 8 characters studied. The cluster VII (KO5SS154) recorded the least value for days to 50 per cent flowering. The cluster III genotypes recorded the

Table 4. Inter and intra cluster distance of sorghum genotypes.

	Group 1	Group 2	Group 3	Group 4	Group 5	Group 6	Group 7	Group 8	Group 9	Group 10	Group 11
Group 1	7.04	10.35	18.14	10.53	8.82	12.12	12.22	9.73	15.70	11.16	11.99
Group 2	10.35	7.67	14.44	15.36	9.15	12.49	9.28	14.60	11.78	16.20	15.16
Group 3	18.14	14.44	8.42	21.56	18.20	20.17	16.26	19.79	12.41	21.30	22.30
Group 4	10.53	15.36	21.56	8.83	15.08	14.85	18.78	12.95	21.51	12.27	14.92
Group 5	8.82	9.15	18.20	15.08	0.00	14.19	7.69	11.14	12.54	13.47	14.63
Group 6	12.12	12.49	20.17	14.85	14.19	10.87	13.91	17.00	19.17	19.04	13.45
Group 7	12.22	9.28	16.26	18.78	7.69	13.91	0.00	14.81	12.32	18.44	16.81
Group 8	9.73	14.60	19.79	12.95	11.14	17.00	14.81	0.00	16.21	6.38	12.32
Group 9	15.70	11.78	12.41	21.51	12.54	19.17	12.32	16.21	0.00	18.10	18.13
Group 10	11.16	16.20	21.30	12.27	13.47	19.04	18.44	6.38	18.10	0.00	14.22
Group 11	11.99	15.16	22.30	14.92	14.63	13.45	16.81	12.32	18.13	14.22	0.00

highest for leaf area index, SPAD chlorophyll, relative water content, proline, and grain yield with lower plant height, however the lower stay-green score is advantage and further the cluster VII had the stay-green genotypes. The data on inter cluster distances and *per se* performance of genotypes can be used to select genetically diverse and agronomically superior genotypes. The cluster range (Table 6) showed high

Table 5. Cluster mean performance of one hundred sorghum genotypes

	DFF	LAI	PHT	CHS	RWC	PRL	SGR	GYP
Group 1	64.21	3.36	233.48	41.25	42.45	1.43	4.32	30.08
Group 2	62.85	3.83	240.37	49.26	57.31	1.09	2.96	36.16
Group 3	66.25	6.62	181.92	59.46	62.00	2.76	1.08	46.85
Group 4	66.38	2.54	161.38	37.79	32.66	1.27	4.25	27.32
Group 5	64.00	2.89	306.50	49.25	48.64	1.36	4.50	29.64
Group 6	64.28	3.25	223.56	33.45	57.08	1.34	3.67	31.86
Group 7	59.50	3.48	309.00	48.15	64.16	2.62	4.50	37.54
Group 8	61.50	4.73	274.00	29.29	30.56	2.53	4.50	33.29
Group 9	63.00	7.26	298.50	57.40	56.44	1.07	1.50	38.04
Group 10	62.00	4.47	226.50	42.46	23.45	0.99	5.00	35.10
Group 11	69.00	5.82	292.00	24.09	41.35	0.50	3.50	37.24

variation among the genotypes for each character as it was evident from the range of values. Thus in the breeding programmes, the elite genotype KO5SS154 can be used as a donor for reducing the crop duration in developing early maturing varieties which surpass terminal drought stress more effectively. The advanced breeding lines IS23399, DRT1030, MS7735, KO5SS53, KO5SS186 and B35 can be used in improvement of grain yield under drought stress condition. Based on *per se* performance and genetic divergence analyses, crosses between cluster III genotypes and the cluster XI, IV, X and VI genotypes may be attempted to combine the corresponding desirable traits, since the inter cluster distance is high so good transgressive segregants can be possible. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages (Thoday, 1960). The cluster III

genotypes represents as drought tolerant so it can be combined to produce base populations in order to develop drought tolerant lines. Alternatively the donors identified can be utilized as elite genetic stocks/pre breeding lines for imparting the corresponding traits.

Table 6. Cluster range performance of one hundred sorghum genotypes

		DFF	LAI	PHT	CHS	RWC	PRL	SGR	GYP
Group 1	Min	60.0	1.7	175.2	35.3	30.0	0.3	1.0	22.4
	Max	71.0	7.6	298.5	57.4	57.4	3.2	5.0	40.5
Group 2	Min	59.5	1.8	165.0	44.0	38.6	0.2	1.0	26.2
	Max	69.0	7.0	296.5	58.5	63.2	2.4	5.0	40.0
Group 3	Min	59.5	1.7	165.0	35.26	30.02	0.2	1.0	22.4
	Max	71.0	7.6	298.5	58.50	63.17	3.2	5.0	40.5
Group 4	Min	59.5	1.7	143.0	23.9	23.5	0.4	1.5	23.8
	Max	73.0	6.5	308.8	58.2	65.9	3.9	5.0	37.5
Group 5	Mean	64.0	2.9	306.5	49.3	48.6	1.5	3.5	29.6
Group 6	Min	59.5	1.7	143.0	23.86	23.45	0.2	1.0	22.4
	Max	73.0	7.6	308.8	58.50	65.86	3.9	5.0	40.5
Group 7	Mean	59.5	6.5	308.8	58.2	64.2	3.9	1.5	37.5
Group 8	Mean	61.5	5.2	274.2	49.2	30.6	3.1	2.0	33.3
Group 9	Mean	67.0	3.3	255.7	51.7	46.9	1.8	4.0	36.4
Group 10	Mean	62.0	5.0	226.5	52.7	23.5	0.9	5.0	35.1
Group 11	Mean	69.0	5.8	292.2	23.9	41.3	0.4	3.5	37.2

The traits contributing towards genetic divergence reveals that, the stress tolerance indicators like, relative water content (32.30 %) and SPAD chlorophyll reading (22.14) contributed largely to the total genetic divergence under drought stress condition. Simultaneously the genotypes which is under cluster III possess high in these stress tolerance indicator values along with low stay-green score can further helps in effective selection and in choosing the parents for drought improvement programme. These results are in conformity with the findings of (Sujatha and Pushapavalli, 2015).

Conclusion

This investigation has revealed that high diverse among one hundred genotypes by forming eleven different clusters. Based on this study, the genotypes IS23399, DRT1030, MS7735, KO5SS53, KO5SS186 and B35 identified as highly drought tolerant as it evident from high mean values for the stress indicator parameters also have been clustered with resistant check. These identified genotypes can be used as parental source for drought tolerance improvement program.

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