

## Delineation of selection indices for identification of asiatic cotton (*Gossypium arboreum* L.) genotypes for drought tolerance ability

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### ABSTRACT

Categorization of genotypes under low moisture conditions is essential for the identification and development of drought tolerant genotypes in cotton. In the present study, 48 diverse Asiatic cotton genotypes were categorized for drought tolerance ability using two different techniques. The significant interaction between genotypes and drought treatment indicates that the studied genotypes were significantly affected by imposed treatment for measured drought tolerance related traits. The categorization of genotypes based on the cumulative score assigned for each genotype revealed the linear relationship between biomass production and drought tolerance ability. The categorization of genotypes based on comprehensive drought tolerance measurement is the finest way to identify the contrast cotton genotypes for drought tolerance ability. The Asiatic cotton genotypes NDLA 2963, NDLA 2965, NDLA 3113, NDLA 3139-3 and NDLA 2708 are identified as drought tolerant, which can be exploited for the improvement of drought tolerance ability in Asiatic cotton breeding programs.

**Keywords:** Drought, Categorization, Comprehensive measurement, Desi cotton

### INTRODUCTION

Cotton (*Gossypium spp.*) is an important fiber crop that provides the raw material to the textile industry. It is the livelihood for millions of people in various sectors like agriculture, ginning factories, textile mills and the garment industry (Manan *et al.*, 2022). Globally, cotton is cultivated in an area of 33.18 m ha and production of 25.73 m tonnes with a productivity of 775 kg ha<sup>-1</sup> (International Cotton Advisory Committee Data Portal 2021-22) (ICAC <https://icac.org/>). Cotton is cultivated in more than 60 countries covering nearly 2.5% of the world's arable land and making it one of the major industrial crops of the world (FAO, 2021). Among the cotton growing countries, India (25%) ranks first in global cotton production followed by China (22%), USA (15%) and Brazil (10%) and it is expected to touch 28.4 m tonnes in that same order continue to dominate in production till 2030 (OECD/FAO, 2021).

Globally more than 50% of the cotton area is under a rainfed agricultural system and thereby productivity of cotton is mainly affected by many abiotic stresses. Among the abiotic stresses, drought is the major destructive cause, which limits the fiber yield and lint quality in cotton production (Chattha *et al.*, 2021). At the

seedling stage, drought stress can affect the seedling growth and establishment including early root growth, shoot length, leaf area and size of the plant (Li *et al.*, 2019). The success of the drought tolerance improvement program is mainly based on the selection of drought tolerant parameters and the identification of tolerant genotypes (Riaz *et al.*, 2013). More than 30 morphological and physiological traits have been used as selection criteria for screening drought tolerance genotypes in cotton (Loka *et al.*, 2011). An indicator based on a single trait can reflect the sensitivity of that trait to stress but not the comprehensive performance of genotypes during the particular stress (Yan *et al.*, 2020). The study of genotypes by synthesizing comprehensive indexes based on membership functions and other methods will make the assessment more reliable and practicable (Bo *et al.*, 2017). Besides, the categorization of genotypes with different methods in the same environment will provide the differences in the drought tolerance ability of genotypes (Ghodrat and Bahrani, 2022). Based on the clear understanding of measured parameters and drought tolerance estimated methods, the present study is aimed to identify the drought tolerant genotypes of Asiatic cotton by comparing two different categorization methods.

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## MATERIALS AND METHODS

The study was carried out using 48 *G.arboreum* cotton genotypes developed from Regional Agricultural Research Station (RARS), Nandyal, India. The pot culture experiment was conducted in a polyhouse at RARS, Nandyal, India to screen the diverse genotypes for drought tolerant related traits. The genotypes were grown under both treatment (stress) and control (non stress) conditions and were watered till the development of the first leaf. Thereafter, the genotypes grown under control condition were only watered regularly. Water stress condition was created by withholding water supply to the genotypes grown under treatment. The experiment was continued for 45 days from the date of emergence of the seedlings (Dahab *et al.*, 2016).

The root and shoot portions of control and treatment plants were separated and used for measurement of drought tolerant related traits including primary root length (PRL) (cm/plant), root dry weight (RDW) (g/plant), shoot dry weight (SDW) (g/plant), total dry weight (TDW) (g/plant), root to shoot ratio (RSR) and relative water content (RWC) (%). The PRL was measured manually using a meter scale. Later, the root and shoot portions were dried at 60°C until constant mass for measurement of RDW and SDW, respectively using a precision weighing balance. The dried root and shoot mass of each genotype were summed and divided to get the TDW and RSR, respectively. The RWC of genotypes was measured by using the formula (Ahmad *et al.*, 2020)

$$\text{RWC (\%)} = \frac{\text{Fresh weight} - \text{dry weight}}{\text{Turgid weight} - \text{dry weight}} \times 100$$

The fresh weight of the sample was measured immediately after the detachment of the leaf. For measurement of turgid weight, the detached leaf samples were kept in a plastic bag having distilled water and left for 24 hours under laboratory condition with the maintenance of light intensity 20  $\mu\text{mol m}^{-2}\text{s}^{-1}$ . The leaves were removed and weighed to get a turgid weight. Later, the leaf samples were dried at 70°C for 72 hours to obtain the dry weight of the sample (Ahmad *et al.*, 2020).

The genotypes in the present investigation were evaluated in a completely randomized design (CRD) with five replications per genotype. The data obtained in the study

were subjected to descriptive statistics, analysis of variance, correlation analysis and Principal component analysis (PCA) using Statistical Tool for Agricultural Research according to Reddy *et al.* (2020). Further, the 48 genotypes were categorized based on drought tolerant related traits for identification of drought tolerant genotypes. The two techniques used in the study are as follows.

Technique 1: As per the method given by Reddy *et al.* (2021), the diverse Asiatic cotton genotypes were classified into tolerant (T), medium (M) and sensitive (S) categories based on the absolute values assigned to each genotype using population mean ( $\mu$ ) and standard deviation (SD) for each trait under normal and drought conditions. The mean value of the tolerant genotype was  $>\mu+SD$ , for medium, it ranges between  $\mu+SD$  to  $\mu-SD$ , for sensitive, it was  $<\mu-SD$ . The scores assigned to each genotype are 3, 2 and 1 for tolerant, medium and sensitive types, respectively. Later the scores of each parameter were summed to get the cumulative scores of the respective genotypes.

Technique 2: The Comprehensive drought tolerance measurement (D) value was used to evaluate the drought tolerance ability of all Asiatic cotton genotypes. The D value of genotypes was estimated across the traits using the formula (Reddy *et al.*, 2020)

$$D = \sum_{j=1}^n [U_{ij} \times |DTC_{ij}|] / \sum_{j=1}^n |DTC_{ij}| \quad (j = 1, 2, 3, \dots, n)$$

Where  $U_{ij}$  is the subordinate function value of  $j^{\text{th}}$  trait for the  $i^{\text{th}}$  cultivar for drought tolerance. DTC is the drought tolerance coefficient of  $j^{\text{th}}$  trait for  $i^{\text{th}}$  cultivar.

The  $U_{ij}$  and DTC were measured using the formulas

$$U_{ij} = \frac{DTC_{ij} - DTC_{j\min}}{DTC_{j\max} - DTC_{j\min}} \quad (j = 1, 2, 3, \dots, n)$$

Where  $DTC_{j\max}$  is the maximum value of the DTC for the  $j^{\text{th}}$  trait and  $DTC_{j\min}$  is the minimum value of DTC for the  $j^{\text{th}}$  trait.

$$DTC = \frac{X_{ijt}}{X_{ijc}}$$

Where,  $X_{ijt}$  and  $X_{ijc}$  are the values of  $j^{\text{th}}$  trait for the  $i^{\text{th}}$  cultivar measured under treatment and control conditions, respectively.

Based on D value, the genotypes were classified into three groups namely tolerant, medium and sensitive.

## RESULTS AND DISCUSSION

Drought is an important stress that has a huge impact on cotton growth and development from seed germination to the boll open stage (Ul-Allah *et al.*, 2021). The analysis of variance revealed the presence of highly significant differences among the studied genotypes for six measured traits under both conditions (Table 1). Besides, the study revealed a significant

interaction between genotypes and drought treatment indicating the effect of drought treatment on genotypes for measured traits under control and treatment conditions. The coefficient of variation ranges from 2.25 (RWC) to 16.04 (PRL) among the measured traits. The highest and lowest broad sense heritability was observed for RDW (0.97) and PRL (0.23), respectively among the measured drought tolerant related traits. The presence of significant genetic variation combined with heritability is the key to breeding drought tolerance in cotton (Sen *et al.*, 2022).

Table 1: Analysis of variance for the measured traits under control and treatment conditions

Variables	Mean sum of squares			F value			P value significance			CV	h <sup>2</sup>
	G	D	× D	G	D	× D	G	D	D		
df	47	1	47	47	1	7	7	1	7		
PRL	29.47	30.58	2.60	9.2	977.46	7.06	***	***	***	6.04	0.23
RDW	0.07	0.35	0.00	.48	712.7	4.75	***	***	***	0.25	0.97
SDW	0.75	.33	0.08	28.15	24978.81	115.24	***	***	***	3.08	0.89
RSR	0.05	0.30	0.00	72.5	460.3	4.75	***	***	***	9.68	0.93
TDW	1.14	23.75	0.10	491.09	10265.52	41.96	***	***	***	4.39	0.91
RWC	28.31	22908.34	18.57	8.02	6489.03	5.26	***	***	***	2.25	0.34

df: degrees of freedom, G: genotype, D: drought, CV: coefficient of variation, h<sup>2</sup>: broad sense heritability, PRL: primary root length, RDW: root dry weight, SDW: shoot dry weight, RSR: root to shoot ratio, TDW: total dry weight, RWC: relative water content

The success of a plant breeding program mainly depends on the identification of efficient genotypes for specific traits of interest. In cotton, different methods and traits were used by previous researchers for the categorization and identification of drought tolerant genotypes (Mahmood *et al.*, 2022). Besides, tolerant genotypes under stress conditions may not give a similar type of performance under normal conditions (Hammond and White, 2008). The genotypes having superior performance under normal and stressful situations are well adaptable to varied stress conditions (Bilal *et al.*, 2018). Therefore, the categorization of genotypes under both normal and stress conditions is an essential requirement for the improvement of drought tolerance in crop plants. Based on the cumulative score derived considering both conditions, the genotypes NDLA 3113 (26 out of 30) followed by NDLA 2963 (25 out of 30), NDLA 2708 (24 out of 30), NDLA 2965 (24 out of 30), NDLA 3094 (24 out of 30) NDLA 3139-3 (24 out of 30) showed the

highest scores among the studied genotypes (Table 2). While the genotypes NDLA 3148-2 (14 out of 30) followed by NDLA 3155-2 (17 out of 30) and NDLA 3155-3 (17 out of 30) recorded the lowest score combined under both conditions. Further, the genotypes NDLA 2963, NDLA 2965 and NDLA 3109-4 recorded the highest score of 13 out of 15 under control condition. Whereas, the genotypes NDLA 3113 (14 out of 15) followed by NDLA 3139-3 (13 out of 15) recorded the highest score under treatment condition. The genotypes NDLA 3148-2 (6 out of 15) and NDLA 3155-3 (7 out of 15) recorded the lowest scores under control and treatment conditions, respectively among the studied genotypes. The poor performance is due to lower production of root and shoots biomass and inferior performance for other traits like PRL and RWC under control and treatment conditions. This technique clearly showed the justification for the linear relationship between biomass production and the drought tolerance ability of genotypes.

Table 2: Variation in tolerance level of ten contrasting genotypes based cumulative score recorded under control and treatment conditions

Genotypes	Control						Treatment						Total score/ out of 30
	PRL	RDW	SDW	RSR	RWC	Score/ out of 15	PRL	RDW	SDW	RSR	RWC	Score/ out of 15	
Top five genotypes													
NDLA 3113	M	T	M	T	M	12	T	T	T	T	M	14	26
NDLA 2963	M	T	T	M	T	13	M	T	T	M	M	12	25
NDLA 2708	M	M	T	M	T	12	M	T	M	M	T	12	24
NDLA 2965	T	T	T	M	M	13	M	T	T	S	M	11	24
NDLA 3139-3	M	M	T	M	M	11	T	T	T	M	M	13	24
Bottom five genotypes													
NDLA 2946	S	S	M	M	M	8	T	M	M	S	M	10	18
NDLA 3146-2	M	M	M	M	M	10	M	M	M	S	S	8	18
NDLA 3155-2	T	S	M	S	M	9	M	M	M	S	S	8	17
NDLA 3155-3	T	S	M	S	T	10	S	S	M	S	M	7	17
NDLA 3148-2	S	S	M	S	S	6	M	M	M	S	S	8	14

PRL: primary root length, RDW: root dry weight, SDW: shoot dry weight, RSR: root to shoot ratio, TDW: total dry weight, RWC: relative water content, T: tolerant, M: medium, S: sensitive

The other technique is based on the estimation of comprehensive drought tolerance measurement (D) value of 48 Asiatic cotton genotypes. Based on the D value, the genotypes were classified into tolerant, medium and

sensitive groups based on the mean and standard deviation of the D value. Among the 48 genotypes, the tolerant, medium and sensitive groups include 9, 34 and 5 genotypes, respectively (Table 3).

Table 3: Categorization of 48 Asiatic cotton genotypes into tolerant, medium and susceptible types based on Comprehensive drought tolerance measurement (D value)

D value	Condition	No	Name of genotypes
$>\mu+SD$ ( $>0.53$ )	Tolerant	9	NDLA 2708, NDLA 2463, NDLA 2933, NDLA 2985, NDLA 2974, NDLA 2946, NDLA 2963, NDLA 3113, NDLA 3139-3
$\mu+SD$ to $\mu-SD$ (0.53 to 0.27)	Medium	34	NDLA 3116-4, NDLA 2953, NDLA 3005, NDLA 3066, NDLA 3014, NDLA 3038, NDLA 3043, NDLA 3037, NDLA 2930, NDLA 2965, NDLA 3028, NDLA 2958, NDLA 2976, NDLA 3020, NDLA 3094, NDLA 3104-4, NDLA 3116-3, NDLA 3109-4, NDLA 3111-5, NDLA 3109, NDLA 3128-2, NDLA 3105-5, NDLA 3129-1, NDLA 3140, NDLA 3143-1, NDLA 3147-1, NDLA 3151-1, NDLA 3152-1, NDLA 3154-3, NDLA 3148-2, NDLA 3155-2, NDLA 3155-3, NDLA 3149-2, NDLA 3142-1
$<\mu-SD$ ( $<0.27$ )	Susceptible	5	NDLA 3115-2, NDLA 3091, NDLA 3147-2, NDLA 3146-2, NDLA 3146-1

$\mu$ : mean, SD: standard deviation

The nine genotypes under the tolerant group include NDLA 2708, NDLA 2463, NDLA 2933, NDLA 2985, NDLA 2974, NDLA 2946, NDLA 2963, NDLA 3113 and NDLA 3139-3. Whereas, the genotypes under the sensitive group include NDLA 3115-2, NDLA 3091, NDLA 3147-2, NDLA 3146-2 and NDLA 3146-1. Based on D values, the variation in drought tolerance related traits of tolerant and sensitive genotypes are presented in Table 4. The genotype NDLA 2946 with the highest D value (0.72) showed a high PRL value under

treatment condition. Interestingly, the genotype NDLA 2963 under the tolerant group showed high values for RDW, SDW and TDW compared to other genotypes under treatment condition. The genotype NDLA 3147-2 with the lowest D value (0.08) showed a low value of PRL compared to other sensitive genotypes under treatment condition. Further, the same genotype showed inferior performance for RDW, SDW and TDW under treatment condition compared to control condition. Further, the contrast genotypes (NDLA 2946,

Table 4: Variation in drought tolerant related traits between tolerant and susceptible genotypes selected based on D value under controlled and treatment condition

Genotypes	D value	Drought tolerant related traits											
		PRL		RDW		SDW		RSR		TDW		RWC	
		C	T	C	T	C	T	C	T	C	T	C	T
Tolerant genotypes													
NDLA 2708	0.70	9.57	12.39	0.33	0.32	1.86	0.83	0.18	0.38	2.19	1.16	93.92	85.52
NDLA 2463	0.53	6.01	11.49	0.17	0.15	1.11	0.62	0.15	0.24	1.28	0.77	90.89	80.55
NDLA 2933	0.53	7.35	17.49	0.17	0.14	1.21	0.61	0.14	0.23	1.38	0.75	91.24	79.83
NDLA 2985	0.55	7.39	15.81	0.16	0.1	1.12	0.33	0.14	0.29	1.28	0.42	91.25	77.21
NDLA 2974	0.57	5.94	12.81	0.14	0.08	1.03	0.29	0.13	0.28	1.17	0.37	92	78.22
NDLA 2946	0.72	5.77	25.77	0.13	0.09	0.91	0.5	0.14	0.18	1.04	0.59	91.97	74.01
NDLA 2963	0.58	6.93	16.43	0.48	0.46	1.57	1.39	0.31	0.33	2.05	1.85	93.76	76.33
NDLA 3113	0.59	7.3	21.3	0.46	0.41	1.22	0.99	0.37	0.42	1.68	1.4	93.59	76.93
NDLA 3139-3	0.54	7.87	21.6	0.32	0.29	1.69	1.26	0.19	0.24	2.01	1.55	91.38	72.31
Susceptible genotypes													
NDLA 3115-2	0.23	8.2	12.9	0.22	0.12	0.7	0.32	0.32	0.36	0.92	0.43	93.18	75.16
NDLA 3091	0.27	9.67	15.13	0.38	0.22	0.99	0.45	0.39	0.49	1.37	0.67	91.41	73.98
NDLA 3147-2	0.08	9.87	12.4	0.3	0.12	1.48	0.52	0.2	0.23	1.78	0.64	93.27	67.87
NDLA 3146-2	0.17	7.63	12.6	0.2	0.1	1.27	0.63	0.16	0.17	1.46	0.73	91.38	67.28
NDLA 3146-1	0.17	9.97	14.3	0.24	0.12	0.72	0.33	0.34	0.37	0.96	0.45	91.84	70.67

C: control, T: treatment, PRL: primary root length, RDW: root dry weight, SDW: shoot dry weight, RSR: root to shoot ratio, TDW: total dry weight, RWC: relative water content

NDLA 2963 and NDLA 3147-2) identified based on the D value for drought tolerance measurement traits can be exploited in recombination breeding for the development of drought tolerant cultivars (Xiao *et al.*, 2021). The mean values of DTC for six drought tolerance related traits in three groups with different tolerance abilities are shown in Fig.1. The mean values of DTC are highest in the tolerant group, moderate in the medium group and lowest in the sensitive group indicating the genotypes with high D values also have high DTC values. The

categorization of genotypes based on a comprehensive index derived from all the studied traits was used in cotton (Sun *et al.*, 2021). Overall two techniques revealed that the genotypes NDLA 2963 followed by NDLA 3113, NDLA 3139-3 and NDLA 2708 are found to be drought tolerant genotypes among the 48 studied genotypes. The proposed methods showed high accuracy in identifying the tolerant genotypes and therefore they may be used for the selection of drought tolerant genotypes in large scale screening.

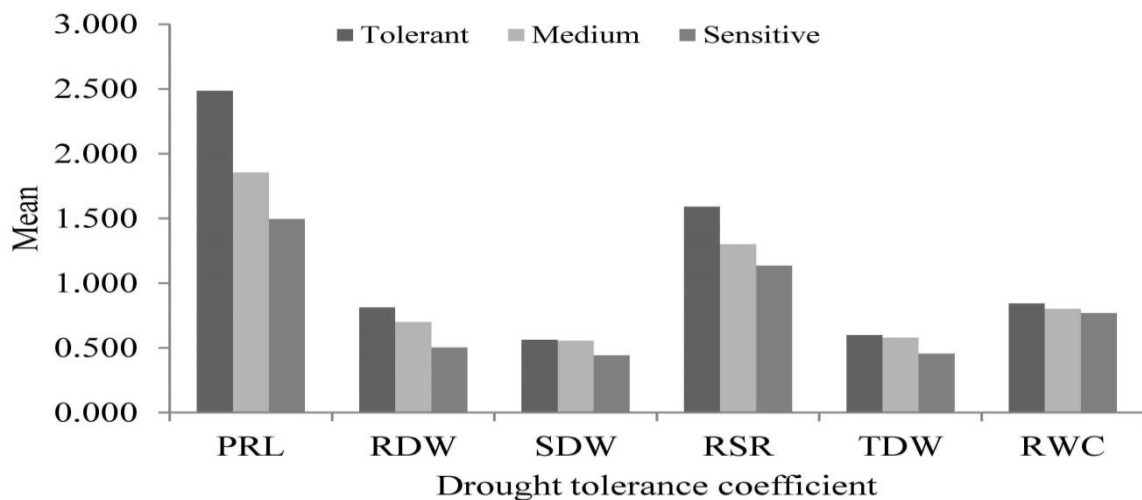


Fig. 1: The mean values of drought tolerance coefficient for six traits in three groups (tolerant, medium and sensitive) for drought tolerance ability. PRL: primary root length, RDW: root dry weight, SDW: shoot dry weight, RSR: root to shoot ratio, TDW: total dry weight, RWC: relative water content

In conclusion, the categorization and identification of tolerant genotypes is the critical step for breeding tolerance ability in cotton. The study revealed the presence of significant variation among the genotypes for the traits PRL, RDW, SDW, RSR, TDW and RWC. Besides, the significant interaction between genotypes and the treatment imposed can be exploited for the development of drought tolerant genotypes. The drought tolerant tolerance ability of genotypes varies with the traits and methods of categorization used under normal and stressful conditions. The two techniques used for

the categorization of genotypes are the best strategies for studying the minor discrepancy in the drought tolerance ability of genotypes. Besides, categorization based on comprehensive drought tolerance measurement is the efficient method to anticipate the contrast genotypes considering all the traits under stress condition. However, the performance of genotypes should be confirmed with adult stage traits in field conditions. The outcome of the study could be used for the enhancement of drought tolerance ability in Asiatic cotton genotypes.

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