

Selection of End-of-Season Drought Stress Tolerant Greengram (*Vigna radiata* (L). Wilczek) Genotypes of Different Maturity Groups

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ABSTRACT

Direct selection of genotypes for high grain yield under moisture stress free (MSF) environment with minimal reduction in grain yield under terminal drought stress (TDS) environment is considered as the most effective and sustainable strategy to breed crops (including green gram) for drought tolerance. Identification of indices that discriminate genotypes for TDS tolerance and that have high correlation with grain yield under MSF and TDS environment is critical for success of this strategy. The present study was aimed at identifying desirable indices from among those reported for quantification of genetic variability and selection of TDS tolerant genotypes. A total of 52 Short duration and 77 long duration genotypes including three checks were evaluated in augmented design for grain yield in two locations (Bidar and Gulbarga) during summer season across two years (2018 and 2019) under managed TDS and MSF environments. Four reported indices namely Stress Tolerance Index (STI), Arithmetic Mean Productivity (AMP), Harmonic Mean Productivity (HMP) and Geometric Mean Productivity (GMP) were calculated based on grain yield of genotypes under MSF relative to TDS environment. The correlation coefficients of these indices with grain yield under TDS and MSF were estimated. Desirable indices were identified as those with high correlation coefficients (>0.91) with grain yield under TDS and MSF environments. Genotypes of both the maturity groups differed significantly for responses to TDS as in both the tested years and locations. Three of the four indices viz., STI, AMP and GMP were found desirable. On an average, short and long duration genotypes were comparable for TDS tolerance. Two and three genotypes from short and long duration groups, respectively were found highly tolerant to TDS based on the combination of the three desirable indices. These genotypes are suggested for use in breeding in green gram for TDS tolerance.

Keywords : Green gram, Moisture stress free, Indices, Terminal drought stress

GREEN gram is one of the important grain legume crop grown extensively in India. It is believed to be originated from India (De Candolle, 1988). It is a short duration crop predominantly grown in rice fallows in peninsular India. Depending on the time of sowing and hence harvesting of rice, green gram planted in rice fallows most often is grown during the

period which overlaps between late post rainy season and early summer season. India produces about 1.5 to 2.0 million tons of green gram annually from about 3 to 4 million hectares of area, with an average on-farm productivity of 0.5 t ha^{-1} which is far below the attainable productivity (2 t ha^{-1}) in research stations (Ministry of Agriculture, Government of India). This

large gap in productivity is attributed to several biotic and abiotic stresses. Among these, abiotic stresses especially terminal drought stress (TDS) is reported as the one of the major causes for low productivity in farmer's field. Almost all the traits are affected due to TDS (Hussain *et al.*, 2004 and Ghanbari & Javan, 2015).

Development and deployment of cultivars tolerant to TDS is the most effective and sustainable approach to reduce the effect of TDS on grain yield (Carrow *et al.*, 1990 and Siddique *et al.*, 2000). From farmer's point of view, the ideal crop cultivars are those that are better yielders under moisture stress free (MSF) environments and suffer least reduction in grain yield under TDS environment (Ramesh & Byregowda, 2016; Susmitha & Ramesh 2020 and Kalpana *et al.*, 2023). This is because, occurrence of TDS is random and that during some years, crop experience MSF environment and in a few other years, crop experiences TDS environments.

Direct empirical selection for grain yield has been reported to be successful for breeding crops to improve yield under drought stress (Richards, 1996). Two selection strategies have been used to breed crops for tolerance to TDS environment (Mitra, 2001). In the first strategy, direct selection for grain yield under MSF environment is practiced. The basic hypothesis of this strategy is that genotypes that perform better under MSF environment do so under TDS environment as well (Blum, 2011). Most often, this strategy may not necessarily be true. In the second strategy, direct selection for high grain yield under TDS environment is practiced. Due to significant genotype \times TDS interaction coupled with low heritability, direct selection for grain yield potential under TDS environment has been less effective resulting in low grain yield. Hence, progress of breeding crops for tolerance to TDS is rather slow (Mitra, 2001). Considering the demerits of the two selection strategies, an alternative one which is the combination of the two is suggested. In the alternative selection strategy, direct selection for high grain yield under MSF environment with minimal reduction in grain yield under TDS environment is practiced

(Bennani *et al.*, 2017). This alternative selection strategy is attempted in the present study.

Detection, quantification and exploitation of genetic variability within working germplasm for responses to TDS environment is not only a prerequisite, but also a short-term strategy for identification of TDS tolerant green gram genotypes for use as cultivars to cater to immediate needs of the farmers. An objective criterion is necessary for quantification of TDS tolerance of test genotypes and identification of tolerant ones for use as cultivars. Several indices such as stress tolerance index (STI) (Fisher and Maurer, 1978), arithmetic mean productivity (AMP) (Rosielle and Hamblin, 1981), geometric mean productivity (GMP) and harmonic mean productivity (HMP) (Fernandez, 1992), yield index (YI) (Gavuzzi *et al.*, 1997), drought susceptibility index (DSI) (Lan, 1998), modified STI (K_1 STI and K_2 STI) (Farshadfar and Sutka, 2002), abiotic tolerance index (ATI) and stress non-stress production index (SNPI) (Moosavi *et al.*, 2008) have been developed and frequently used for quantification and selection of genotypes for tolerance to TDS environments. All these proposed indices are based on the extent of reduction in grain yield under TDS environment relative to that under MSF environment. Of these 10 indices, STI, AMP, GMP and HMP have been suggested as most effective ones for quantification and selection of TDS tolerant genotypes in legume crops (Susmitha & Ramesh, 2020 and Kalpana *et al.*, 2023). Identification of indices that enable effective discrimination of test genotypes for responses to TDS environments and selection of those with high grain yield under MSF environments and acceptable stability of grain yield under TDS environments is the key (among others) for enhancing the progress in breeding for tolerance to TDS environment in any crop (Bennani *et al.*, 2017) with no exception of green gram.

Considering that germplasm accessions have evolved under natural and/or human selection environment which constitute a population of MSF and TDS environments, we hypothesize that, there exist substantial genetic variability for responses to TDS environment and that it is possible to identify and

select genotypes tolerant to TDS environment with optimum yield under MSF environment. To test this hypothesis, the present study was envisaged with three objectives. These are (1) identify indices that most discriminate the test genotypes for responses to managed TDS environment (2) indices that are significantly correlated with grain yield under both MSF and TDS environments and (3) identify TDS tolerant genotypes using the combination of indices that most discriminate and correlated with grain yield under TDS and MSF environments.

MATERIAL AND METHODS

Experimental Material

The material for the present study consisted of 126 germplasm accessions. Of these, 49 accessions were of short duration (45-50 days to 50% flowering) and remaining 74 accessions were of long duration

(55-60 days to 50% flowering) along with three checks (Table 1). The accessions were deliberately classified into two maturity groups such that the accessions within the group are comparable for days to flowering. This classification was to ensure that the accessions, especially those which belong to short duration group will not escape from imposed terminal drought stress. The major objective of the present study is not to exploit drought stress escape mechanism associated with the short duration accessions/genotypes. Instead the major objectives is to identify both short and long duration accessions with terminal drought stress tolerance and acceptable grain yield. The accessions (here after referred to as genotypes) used in the present study were procured from the Scientist in/charge of Department of Genetics and Plant Breeding, College of Agriculture, University of Agricultural Sciences (UAS), Gandhi Krishi Vignana Kendra (GKVK), Bengaluru and Agricultural Research Station (ARS), Bidar, UAS, Raichur.

TABLE 1
List of short and long duration group genotypes

Short duration group					Long duration group					Checks		
Sl. No.	Genotypes	Sl. No.	Genotypes		Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
1	T 74	26	T 33		1	T 41	26	T 124	51	T 57	1	Selection 4
2	T 113	27	KMS 13 57		2	T 79	27	T 36	52	T 199	2	BGS 9
3	KM13 42	28	T 108		3	T 96	28	T 109	53	T 123	3	China Mung
4	T 159	29	KM 13 45		4	T 25	29	T 62	54	T 194		
5	T 45	30	GG 13 9		5	T 206	30	T 49	55	T 90		
6	KM13 02	31	T 157		6	T 122	31	T 80	56	T 52		
7	T 168	32	T 186		7	T 10	32	T 175	57	T 46		
8	T 103	33	KM 13 22		8	T 195	33	T 205	58	T 100		
9	T 153	34	KM 13 73		9	T 24	34	T 171	59	T 203		
10	KM13 26	35	T 75		10	T 162	35	T 163	60	T 208		
11	T 66	36	KM 14 51		11	T 8	36	T 152	61	T 16		
12	T 1	37	Gangavati		12	T 14	37	T 190	62	T 160		
13	Bangalore	38	T 156		13	T 26	38	T 198	63	XXX		
14	T 38	39	T 104		14	T 91	39	T 134	64	T 201		
15	T 72	40	KM 13 09		15	T 23	40	T 89	65	T 88		
16	T 32	41	KM 13 20		16	T 82	41	T 197	66	T 20		

Continued....

TABLE 1 Continued....

Short duration group				Long duration group				Checks			
Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes	Sl. No.	Genotypes
17	KM 13 45	42	KM 13 30	17	T 120	42	T 204	67	T 193		
18	Pusa Baisaki	43	T 116	18	T 51	43	T 56	68	T 137		
19	KM 14 61	44	KS 13 26	19	T 202	44	T 169	69	T 47		
20	KM 14 34	45	KM 14 41	20	T 174	45	T 39	70	T 54		
21	T 129	46	KM 14 47	21	T 21	46	T 18	71	T 178		
22	KMS 13 29	47	KM 13 32	22	T163/164	47	T 87	72	T 151		
23	T 9	48	T 112	23	T 200	48	T 58	73	T 27		
24	KM 14 54	49	KM 14 18	24	T 29	49	T 12	74	T 125		
25	KM 13 23			25	T 106	50	T 102				

Field Evaluation of Genotypes under Managed TDS and MSF Environments

The seeds of 126 genotypes of two maturity groups along with three checks (Selection 4, China Moong and BGS 9) were planted at Zonal Agricultural Research Station (ZARS), Gulbarga and ARS, Bidar in Augmented design (Federer, 1956) at two locations (Bidar and Gulbarga) during summer season across two years (2018 and 2019) under two managed moisture regimes (MR) namely TDS and MSF environments in two separate trials.

The seeds of each genotype were dibbled in a single row of 4m length. Following germination, after 15 days of dibbling of seeds, the seedlings were thinned-out by maintaining a spacing of 0.2 m between plants within a row. In each maturity group, one trial was maintained by regular irrigation through-out the crop life cycle. In the second trial, TDS was imposed by with-holding irrigation from pod-filling stage until pod harvesting stage. All the other recommended crop production and protection practices were followed to maintain the crop free from other abiotic stresses and biotic stresses in both the maturity groups and trials. Following mortality of a few plants, 15 plants in each accession survived to maturity.

Sampling of Plants and Collection of Data

Dry pods were harvested from five randomly selected plants from each genotype of the two trials in each

experiment. The pods were hand-threshed, the resulting grains were sundried, weighed. The data was recorded on grain yield plant⁻¹.

Statistical Analysis

Adjusted means of grain yield plant⁻¹ were used for statistical analysis. Experiment wise and trial-wise ANOVA of genotypes belonging to two maturity groups for grain yield were performed to detect variability among the genotypes, MR and genotypes x MR interaction. The analysis was implemented in R version 4.2.1 (R core team, 2021). Pooled ANOVA was performed to detect interaction of accessions with two MR for grain yield plant⁻¹. Homogeneity of error mean squares as indicated from Bartlett test ($P < 0.05$) (Bartlett, 1937) provided statistical validity to pool the data from the two locations in each year. The analysis was implemented using Microsoft (MS) excel software's statistical analysis option. The mean grain yield plant⁻¹ of genotypes in both MR was used to estimate a statistic namely yield relative to environment maximum (YREM). YREM of genotypes was estimated as, $Y_{ij} = X_{ij} / \text{Max } X_{ij}$ (Yan, 1999), where Y_{ij} and X_{ij} are the YREM and trait value, respectively of 'ith' genotype in moisture stress 'j'. Max_{ij} is the maximum grain yield (of any genotype) observed in environment 'j'. YREM was estimated using MS Excel software.

TABLE 2
The reported indices and their formulae used to quantify the responses of green gram genotypes to terminal drought stress (TDS) environment

Indices	Code	Formula	Reference
Arithmetic Mean productivity	AMP	$(Y_p + Y_s)/2$	Rosielle and Hamblin (1981)
Geometric mean productivity	GMP	$\sqrt{Y_s \times Y_p}$	Fernandez (1992)
Harmonic mean productivity	HMP	$2*(Y_p + Y_s)/(Y_p + Y_s)$	Fernandez (1992)
Stress tolerance index	STI	$(Y_s \times Y_p)/(\bar{Y}_p^2)$	Fischer and Maurer (1978)

Y_p = Mean grain yield plant⁻¹ under MSF environment; Y_s = Mean grain yield plant⁻¹ under TDS environment;
 \bar{Y}_p = Mean grain yield plant⁻¹ under MSF environment

Quantification of Responses of Genotypes to TDS

Based on the recorded grain yield plant⁻¹ of genotypes under TDS and MSF environments, reported four indices (Table 2) were calculated to quantify the responses of genotypes to TDS environment for grain yield plant⁻¹.

All the indices were calculated based on the extent of reduction in grain yield plant⁻¹ of the genotypes evaluated under TDS environment relative to those evaluated under MSF environment. Correlation coefficients of four indices with grain yield plant⁻¹ of genotypes evaluated under MSF and TDS environments were calculated. All these statistical analyses were implemented using Microsoft (MS) excel software's statistical analysis option. Higher the magnitude of these indices higher is the tolerance of that genotype to TDS environment.

Selection of Desirable Indices

Two criteria were used for selection of desirable indices for use in identification of TDS tolerant genotypes. These are (1) indices with better ability to discriminate the genotypes for responses to TDS environment and (2) indices with high correlation ($r > 0.91$) (Kalpana *et al.*, 2023) with grain yield under TDS and MSF environments. Statistics such as standardized range (SR) and phenotypic coefficient of variation (PCV) for grain yield plant⁻¹ were estimated as $SR = \text{highest grain yield} - \text{lowest grain yield} / \text{mean grain yield}$ and $PCV = (\text{phenotypic}$

standard deviation/mean grain yield) $\times 100$. The indices which exhibited highest magnitudes of SR and PCV were considered as those with good discriminating ability.

The correlation coefficients of indices with mean grain yield plant⁻¹ of genotypes evaluated under both MSF and TDS environments and among the indices were estimated. The indices which significantly correlated (>0.91) with grain yield under both TDS and MSF environments were considered as desirable for selection of TDS tolerant genotypes.

Criteria to Identify TDS Tolerant Genotypes

TDS tolerant genotypes were identified as those with (i) higher magnitudes of STI, AMP, GMP, HMP and/or their combination along with better ability to discriminate the genotypes and (ii) high correlation ($r = >0.91$) of such indices with grain yield of genotypes evaluated under MSF and TDS environments.

Description of Rank Sum (RS) Method

As TDS tolerant genotypes varied with the indices, rank sum (RS) method (Farshadfar *et al.*, 2012) which combines all the indices into one integrated index was used to select TDS tolerant genotype. By virtue of the formulae used to estimate the indices, higher the magnitude of the indices, higher is the TDS tolerance of the genotypes. Considering this relationship between magnitude of the indices and TDS tolerance of the genotypes, the genotypes with

TABLE 3
Schematic description of rank sum (RS) method to identify TDS tolerant genotypes based on hypothetical magnitudes of three indices

Genotype Code	Stress tolerance index (STI)	Rank	Mean productivity (MP)	Rank	Yield index (YI)	Rank	Rank mean (RM)	Standard deviation of ranks (SDR)	Rank sum (RS) (RM+SDR)
G1	0.9	1	14	1	0.8	1	1.0	0.0	1.0
G2	0.8	2	08	4	0.6	3	3.0	1.3	4.3
G3	0.5	4	12	2	0.5	4	3.3	1.3	4.3
G4	0.6	3	10	3	0.7	2	2.7	0.3	3.0

highest and lowest magnitudes of indices estimated based on grain yield plant⁻¹ were assigned rank '1' and highest rank, respectively. The ranks of each genotype were summed across all the indices. The rank mean (RM) and standard deviation of ranks (SDR) were estimated. The RS was calculated as $RS = RM + SDR$ (Table 3). The genotypes with lowest and highest magnitudes of RS were considered as most TDS tolerant and least TDS tolerant, respectively.

Selection of TDS Tolerant Genotypes Based on the Combination of the Estimates of Mean Grain Yield under MSF and TDS Environments and Best Index Identified based on RS Method

Using the indices identified as desirable to select TDS tolerant genotypes and the estimates of mean grain yield plant⁻¹ under MSF and TDS environments,

the genotypes of two maturity groups were grouped into four classes (A, B, C and D) of responses to TDS environment (Fernandez, 1992). Three dimensional graphs were drawn by plotting mean grain plant⁻¹ of the genotypes under MSF and TDS environments on X-axis and Y-axis, respectively and the best index (AMP) on Z-axis (Fig. 1) to group the genotypes into classes A, B, C and D responses. These graphs were plotted using 'NCSS' software (NCSS software, 2023).

RESULTS AND DISCUSSION

Analysis of Variance

Genotypes differed significantly for grain yield plant⁻¹ in both short and long duration groups as revealed from significant mean squares attributable to genotypes (Table 4). These results justified the selection of the genotypes for the study.

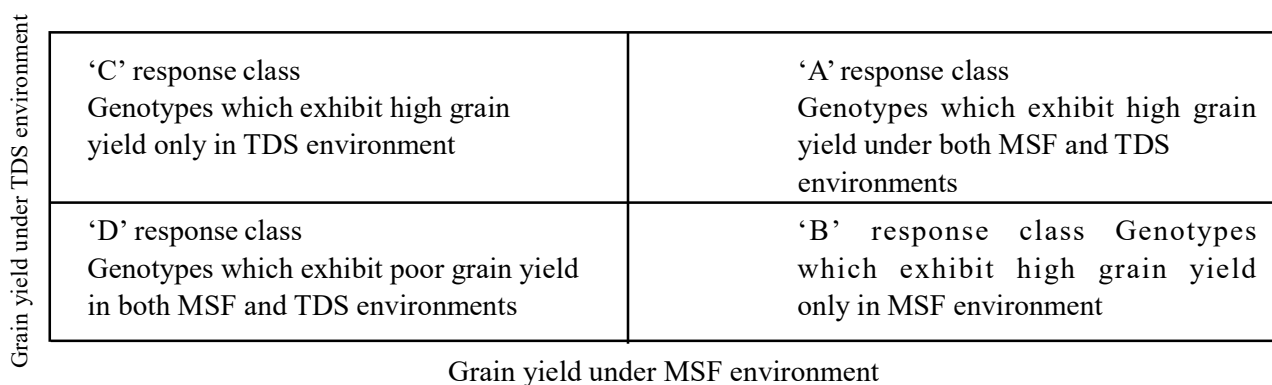


Fig. 1 : Schematic illustration to demonstrate the protocol to classify the genotypes into 'A', 'B', 'C' and 'D' response classes

TABLE 4
Pooled analysis of variance of genotypes evaluated for grain yield plant⁻¹
under stress and non-stress environments

Source	Degrees of freedom		Mean sum of squares		F Statistics		Probability	
	Short duration group	Long duration group	Short duration group	Long duration group	Short duration group	Long duration group	Short duration group	Long duration group
Moisture Regime (MR)	01	01	38.95 **	24.58 **	156.20	100.54	<.0001	<.0001
Location	01	01	0.03	3.27 **	0.14	13.36	0.7114	0.0005
Year	01	01	215.65 **	255.99 **	865.15	1046.94	<.0001	<.0001
Block	03	02	0.71 *	0.40	2.83	1.64	0.0433	0.2018
Check	02	02	0.68	0.62	2.71	2.53	0.0721	0.0883
Genotypes	79	77	1.55 **	0.80 **	6.17	3.28	<.0001	<.0001
MR × Genotypes	80	78	0.28	0.05	1.11	0.20	0.3170	1.0000
MR × Location	01	01	1.81 **	0.17	7.28	0.69	0.0085	0.4085
MR × Year	01	01	0.15	0.45	0.62	1.85	0.4349	0.1793
Location × Genotypes	80	78	1.15 **	0.47 **	4.60	1.91	<.0001	0.0048
Year × Genotypes	80	78	1.57 **	0.42 *	6.30	1.73	<.0001	0.0141
Location × Year	01	01	0.90	25.43 **	3.61	104.00	0.0608	<.0001
MR × Location × Year	01	01	0.75	0.15	3.01	0.60	0.0863	0.4399
MR × Location × Year × Genotype	320	312	0.35 *	0.17	1.39	0.70	0.0360	0.9721
Residual	83	60	0.25	0.25				
Model R-Square %			97	97				

Non-receipt of rains during intended crop growth stage, *i.e.*, during pod filling and grain maturity stages in both locations suggested successful imposition of TDS, which is amply reflected by significant mean squares attributable to moisture regime (MR) in pooled ANOVA (Table 4) and substantial reduction in mean grain yield plant⁻¹ of genotypes in the two MR (Table 5). However, non-significant mean squares attributable to genotypes x MR interaction suggested comparable responses of genotypes in both MSF and TDS environments. Further, the F-test used is less sensitive to detect genotype x MR interaction because of large degrees of freedom obtained in the conventional ANOVA. Significant mean squares attributable to location x genotypes indicated differential response of genotypes in different locations *viz.*, Bidar and Gulbarga in both the maturity

groups. However, non-significant mean squares attributable to location in short duration group suggest that genotypes could not receive sufficient time to expose to TDS environment in both the locations. On the other hand, significant mean squares due to location in long duration group indicates differential effect of location environment on genotype performance. The high magnitude of r^2 (97%) suggested linear model used for partitioning total variation into components attributable to different sources indicate reliability of these interpretations made based on the results of ANOVA.

Effect of TDS on Grain Yield of Genotypes

TDS environment considerably affected grain yield plant⁻¹ of the genotypes of both the maturity group (Table 5). The genotypes varied widely for grain yield

TABLE 5
Descriptive statistics of % reduction in grain yield plant⁻¹ of green gram genotypes of short and long duration group evaluated under MSF and TDS environments

Maturity Group	Mean			Absolute Range			Minimum			Maximum			Standardized Range						
	Bidar	Gulbarga		Bidar	Gulbarga		Bidar	Gulbarga		Bidar	Gulbarga		Bidar	Gulbarga					
	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18	2017-18				
Short duration	15.56	28.63	18.48	52.91	46.06	89.77	63.49	0.20	0.63	6.26	0.27	53.11	46.70	96.02	63.76	3.40	2.60	3.14	3.44
	13.09	17.59	12.25	49.18	32.75	66.21	41.33	0.21	2.41	0.66	0.43	49.40	35.16	66.86	41.76	3.76	2.38	3.76	3.37
Long duration																			

plant⁻¹ under TDS environment relative to that under MSF environments. The range of mean per cent reduction in grain yield plant⁻¹ of genotypes of both maturity groups was narrower in Bidar compared to that in Gulbarga (Table 5). Further, the range in per cent reduction in grain yield of genotypes of long duration group was narrower compared to those of short duration group (Table 5). The wider range of reduction in grain yield plant⁻¹ suggest that the imposed level of TDS was sufficient enough to discriminate the genotypes of the two maturity groups for their responses and hence their degree of tolerance to TDS environment. Further, the comparable lower range of mean per cent reduction in grain yield plant⁻¹ in long duration group and high mean per cent reduction in grain yield plant⁻¹ in short duration group suggest that the genotypes of short duration did not have adequate time to recover from the stress shock compared to those of long duration group. These results based on the estimates of absolute range suggest that breeding for long duration genotypes is advantageous as such genotypes recover from the stress shock. However, the estimates of standardized range (SR) (which correct for the mean values) suggest comparable responses of genotypes of both maturity groups across years and locations. Thus, results based on the estimates of SR suggest that, it is possible to breed green gram for improved tolerance to TDS environment even in short maturity groups, of course, with a little compromise in grain yield *per se*.

Relationship between Grain Yield of Genotypes under MSF and TDS Environments

Higher phenotypic correlation co-efficient between grain yield under MSF and TDS environments of both the duration groups could be attributed to similar performance ranks and as reflected even from non-significant genotype x MR interaction (Table 4). These results also suggest that the genotypes' performance for the grain yield under MSF is a good indication of their performance under TDS environments and *vice-versa*. Theoretical results reported by Rosielle and Hamblin (1981) implicitly indicate that at each of the several loci controlling

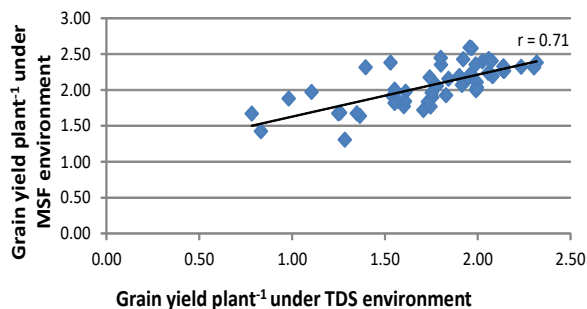
the target trait (grain yield in the present study), alleles controlling grain yield under MSF environment are different from those controlling grain yield under TDS environment. It is therefore argued that grain yield measured under MSF and TDS environments must be treated as two different traits and are likely to be influenced to certain extent by different genes, though partly also by same genes (Falconer, 1990). The two traits are genetically correlated and the magnitude of correlation reflects the extent to which the same genes are involved. High correlation of grain yield between TDS and MSF environments in both short duration genotypes (Fig. 2) and long duration genotypes (Fig. 3) in the present study suggest that at least a few same set of genes are likely to control grain yield under MSF and TDS environments in both maturity groups. These results further suggest that good prospectus of maximizing grain yield of both short and long duration genotypes under both MSF and TDS environments.

Selection of Indices for Identification of TDS Tolerant Genotypes

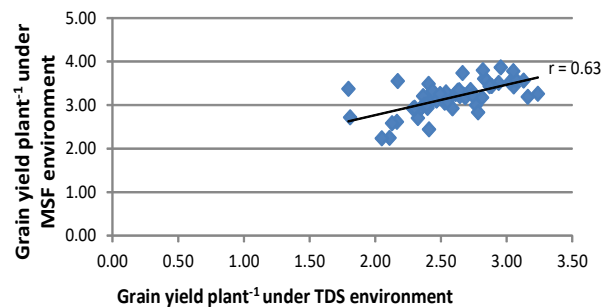
Indices with Good Discriminating Ability

Good discriminating ability of indices helps effective identification of most desirable indices for selection of TDS tolerant genotypes. The results of the present study suggest that STI as the most effective index to discriminate the genotypes for their responses to TDS environment as reflected from high magnitude of estimates of both SR and PCV (Table 6). This means that, STI can discriminate the genotypes which produce high grain yield in both MSF and TDS environments from those which produce relatively low grain yield under MSF and TDS environments. It is therefore desirable to preferentially use STI for screening the genotypes for responses to TDS environment in green gram. Safavi *et al.* (2015) in sunflower, Uday *et al.* (2016) in chickpea, Bennani *et al.* (2016) and Bennani *et al.* (2017) in bread wheat

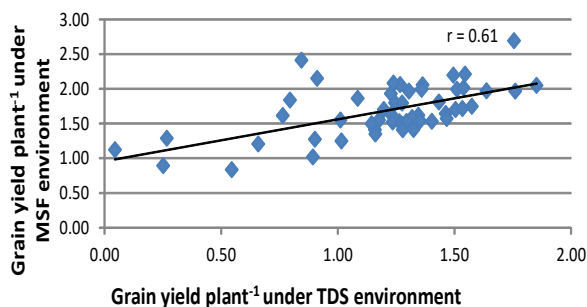
A. Bidar 2017-18



B. Bidar 2018-19



C. Gulbarga 2017-18



D. Gulbarga 2018-19

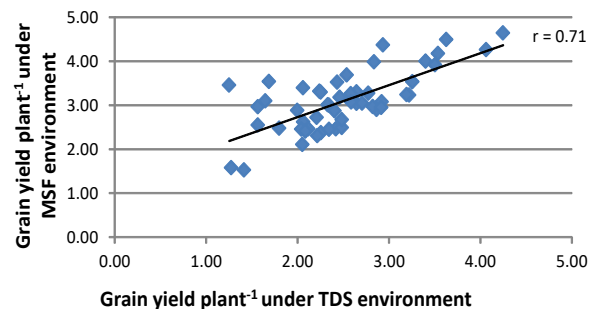


Fig. 2 : Relationship of short duration green gram genotypes for grain yield plant⁻¹ between MSF and TDS environments

& Susmitha & Ramesh (2020) and Kalpana *et al.* (2023) in dolichos bean, have also suggested the use of STI for discriminating the test genotypes for their responses to TDS environment.

Indices of High Correlation with Grain Yield under TDS and MSF Environments

Based on correlation criterion, two of the four indices namely AMP (Fig. 4 and Fig. 5) and GMP (Fig. 6 and Fig. 7) with significant positive and high magnitude of correlation ($r > 0.91$) with grain yield plant^{-1} under both MSF and TDS environments were considered as desirable ones. Further, these two indices are highly correlated among themselves ($r > 0.98$) in both maturity groups.

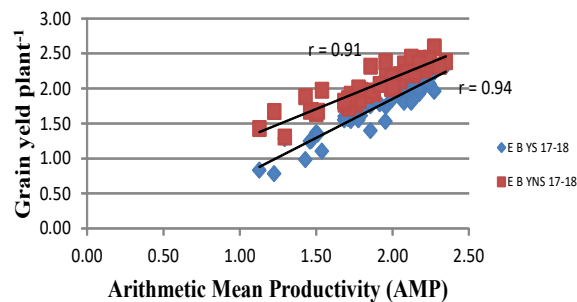
These results suggest any one or the combination of these two indices could be used to select TDS tolerant genotypes based on correlation criterion. Several researches have used this criterion and identified AMP and GMP as most desirable indices for selection of drought tolerant genotypes in different crops. To

illustrate a few, Moosavi *et al.* (2008) and Seyyed *et al.* (2014) in soybean, Bennani *et al.* (2016) and Bennani *et al.* (2017) in wheat have reported the utility of AMP and GMP for selection of drought tolerant genotypes based on the correlation criterion.

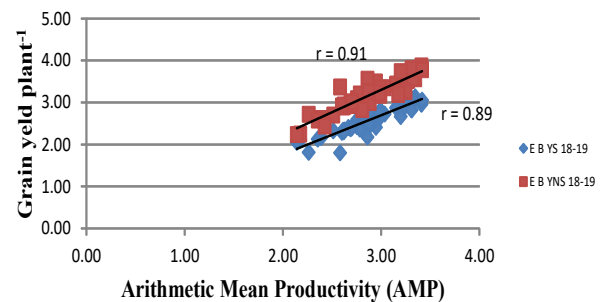
Identification of TDS Tolerant Genotypes Based on Combination of Indices

Mere drought tolerance alone doesn't guarantee acceptance and adoption of varieties of crop including green gram by farmers. This is because, the farmers prefer the genotypes which produce optimum grain yield under MSF environments and suffer least grain yield under TDS environments (Serrai *et al.*, 2011; Dixit *et al.*, 2014; Susmitha and Ramesh, 2020 and Kalpana *et al.*, 2023). Such genotypes are regarded as TDS tolerant one's and could be identified based on the indices which exhibit high discriminating ability (STI) and those with high magnitude of correlation (AMP & HMP) with grain yield under TDS (YTDS) and grain yield under MSF (YMSF)

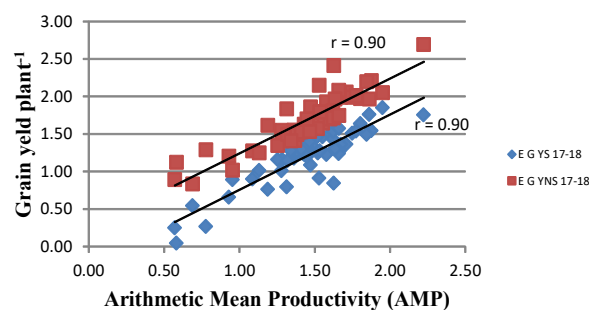
A. Bidar 2017-18



B. Bidar 2018-19



C. Gulbarga 2017-18



D. Gulbarga 2018-19

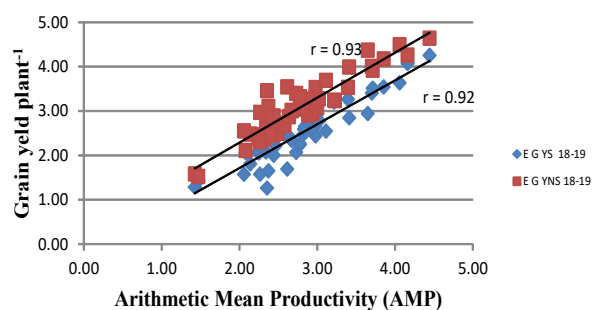
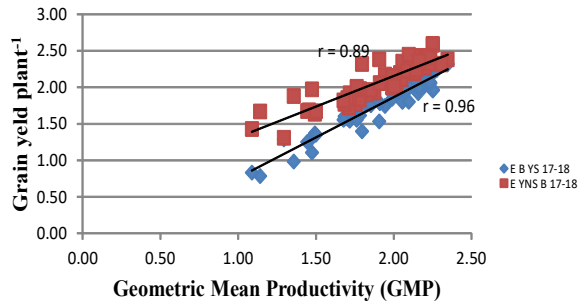
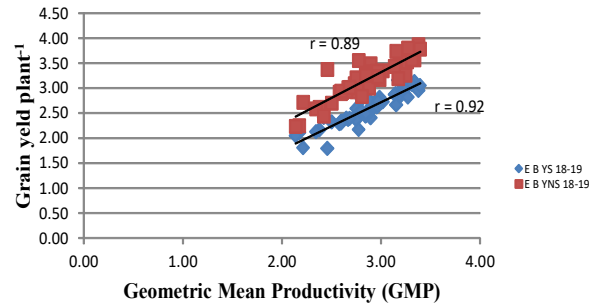


Fig. 4 : Estimates of correlation coefficients between AMP and grain yield of green gram genotypes of short duration group during 2017-18 and 2018-19 in Bidar and Gulbarga

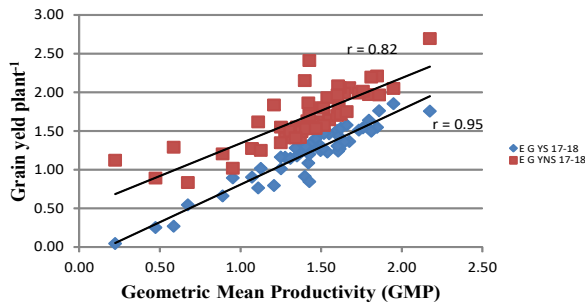
A. Bidar 2017-18



B. Bidar 2018-19



C. Gulbarga 2017-18



D. Gulbarga 2018-19

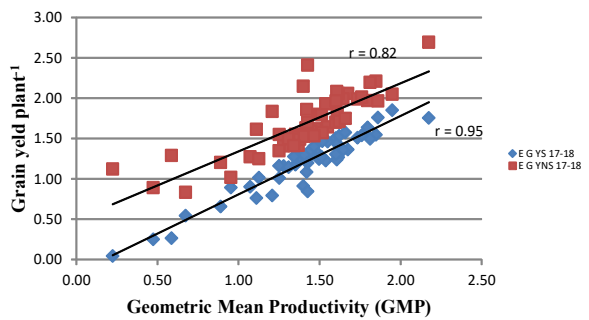
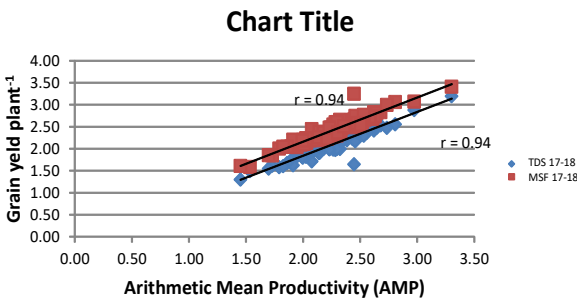
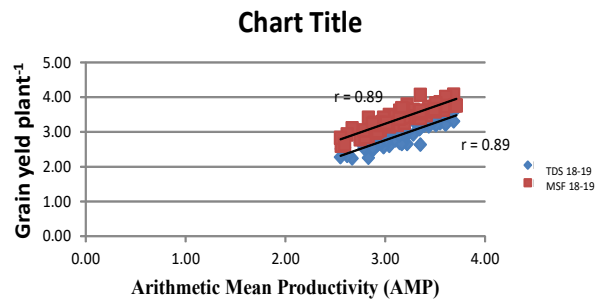


Fig. 5 : Estimates of correlation coefficients between GMP and grain yield of green gram genotypes of short duration during 2017-18 and 2018-19 in Bidar and Gulbarga

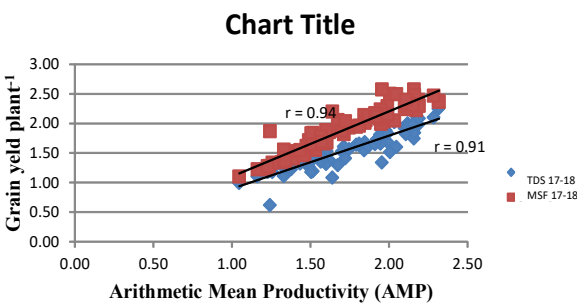
A. Bidar 2017-18



B. Bidar 2018-19



C. Gulbarga 2017-18



D. Gulbarga 2018-19

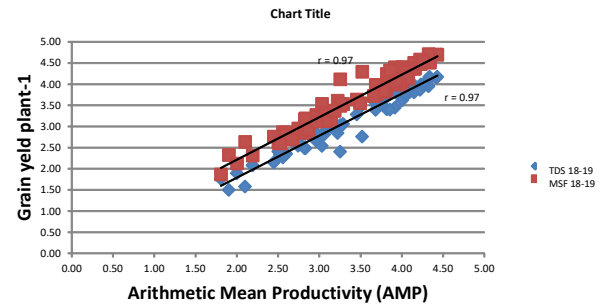
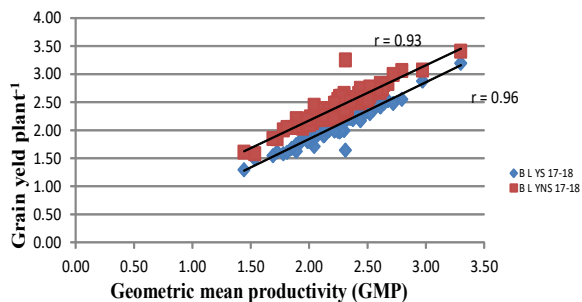
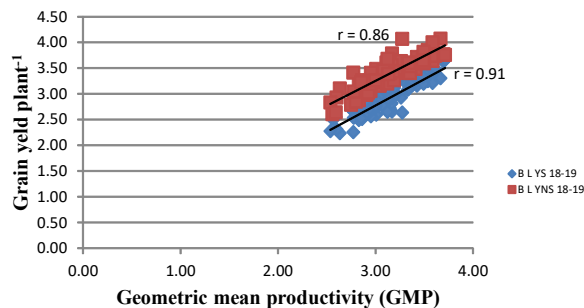


Fig. 6 : Estimates of correlation coefficients between AMP and grain yield of green gram genotypes of long duration during 2017-18 and 2018-19 in Bidar and Gulbarga

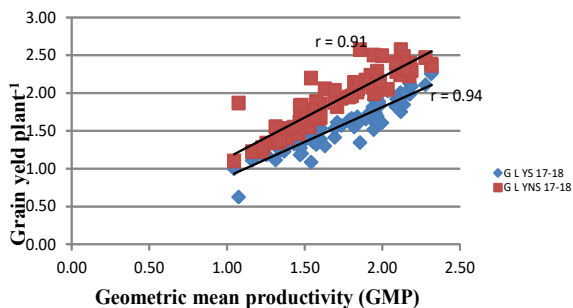
A. Bidar 2017-18



B. Bidar 2018-19



C. Gulbarga 2017-18



D. Gulbarga 2018-19

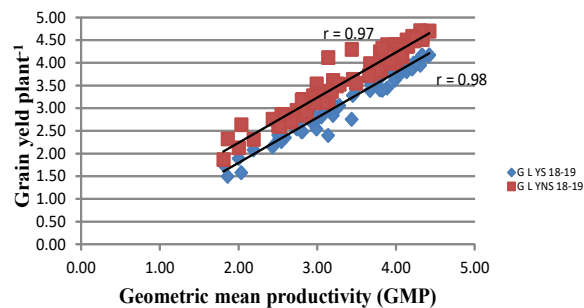


Fig. 7 : Estimates of correlation coefficients between GMP and grain yield of green gram genotypes of long duration during 2017-18 and 2018-19 in Bidar and Gulbarga

environments. Based on this argument, we used combination of three of the four indices using rank sum method (as described in the material and methods section) to identify TDS tolerant genotypes. Based on the rank-sum method, genotypes such as T 45, T 108, T 103, KM 13 45 and T 159 in short duration group and T 190, T 26, T 80, T 205, T 198, T 52 and T 106 in long duration group were found TDS tolerant (Table 7). Genotypes selected based on RS method are characterized by TDS tolerance with high yield under both MSF and TDS environments (Thiry *et al.*, 2016).

Identification of TDS Tolerant Genotypes based on Combination of Indices (AMP) and YTDS and YMSF Environments

Considering the cues from other studies, we identified TDS tolerant genotypes in both short and long duration groups based on the combination of the two indices which showed high correlation with YTDS and YMSF as well as YTDS and YMSF *per se*. Based on this criterion, in short duration group, three genotypes (with class ‘A’ response) namely, T 108, T 159 and KM 13 45-2 were identified as TDS tolerant (Fig. 8).

TABLE 7

Mean Ranks and rank-sum of green gram genotypes of short and long duration based on the combination of four indices for grain yield plant⁻¹ of genotypes evaluated under MSF and TDS environments

Short duration group			Long duration group		
Genotype	Mean RS	Rank	Genotype	Mean RS	Rank
T 45	12.55	1	T 190	10.27	1
T 108	12.94	2	T 26	14.47	2
T 103	14.02	3	T 80	15.10	3
KM 13 45	14.31	4	T 205	20.56	4
T 159	14.85	5	T 198	21.16	5

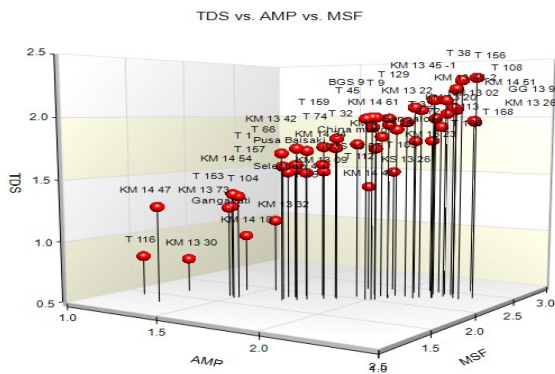
Continued....

TABLE 7 Continued....

Short duration group			Long duration group		
Genotype	Mean RS	Rank	Genotype	Mean RS	Rank
KM 13 02	15.43	6	T 52	21.64	6
T 72	17.09	7	T 106	22.30	7
BGS 9	19.01	8	T 91	23.14	8
T 186	19.4	9	T 58	24.08	9
T 112	21.07	10	T 29	24.42	10
T 156	21.26	11	T 10	24.67	11
KM 13 23	21.27	12	T 36	25.77	12
KM 14 51	21.35	13	T 208	26.52	13
T 168	21.94	14	T 169	27.16	14
GG 13 9	21.96	15	T 87	27.35	15

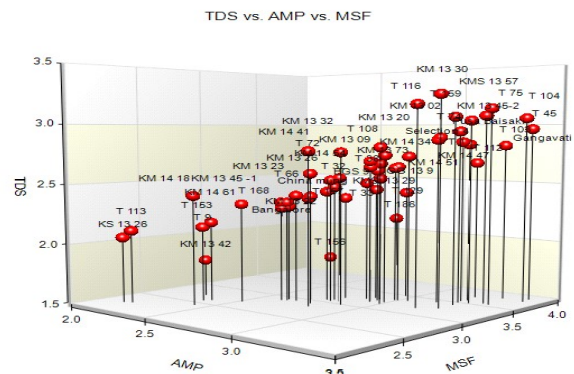
A-Short Duration Bidar 2017-18

Class 'A' response genotypes



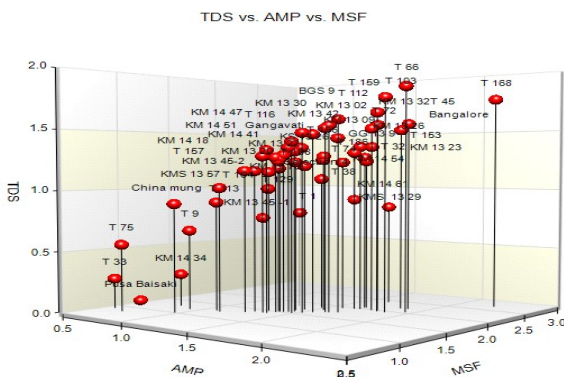
B - Short Duration Bidar 2018-19

Class 'A' response genotypes



C- Short Duration Gulbarga 2017-18

Class 'A' response genotypes



D- Short Duration Gulbarga 2018-19

Class 'A' response genotypes

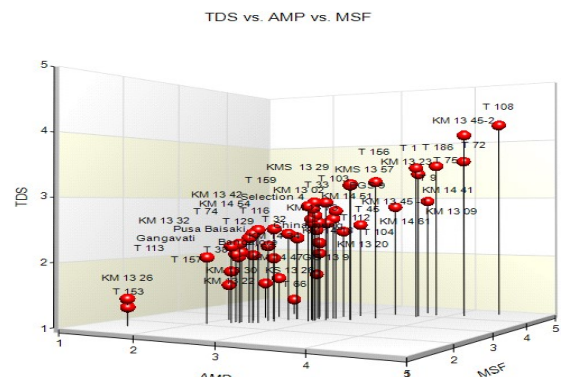


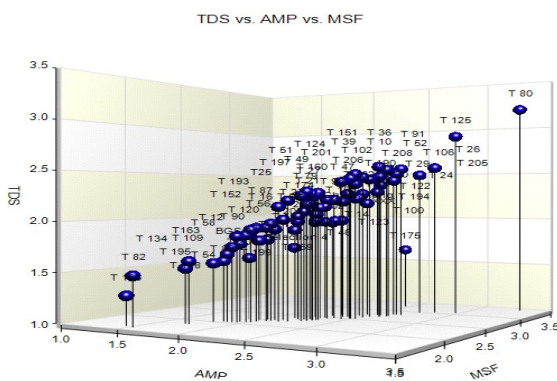
Fig. 8 : 3D graphs for grouping of the genotypes into A, B, C & D classes of responses of short duration group genotypes for tolerance to TDS environments for grain yield based on AMP and YTDS and YMSF over two locations and two years

In long duration group, the genotypes T 80, T 190, T 26 and T 205 were identified as best with class ‘A’ response (Fig. 9). Previous researchers such as Farshadfar and Javadinia (2011) in chickpea and Farshadfar and Elyasi (2012) and Farshadfar *et al.* (2012) in bread wheat have also identified class ‘A’ response genotypes. It is likely that a complex interplay of antioxidant enzymes such as peroxidase, catalase, superoxide dismutase, glutathione reductase and polyphenol oxidase and non-enzymatic components such as ascorbate, glutathione, phenols, etc. (D’souza & Devaraj, 2011) could be playing a significant role in imparting TDS tolerance in the aforementioned genotypes. Taking clues from report by Yao

et al. (2013) on the key genes associated with the drought tolerance using suppression subtraction hybridization in dolichos bean (a comparable legume) it is hypothesized that the genes encoding enzymes involved in the phenylalanine metabolism and flavonoid biosynthesis pathways are likely to have over-expressed in the green gram genotypes identified as TDS tolerant. It is also possible that β -amylase, a metabolic enzyme which plays a major role in cell survival (Kokila *et al.*, 2014) could be involved in imparting TDS tolerance to green gram genotypes identified in the present study. It is evident from the results that some of the TDS tolerant genotypes (of both the maturity groups) identified based on the

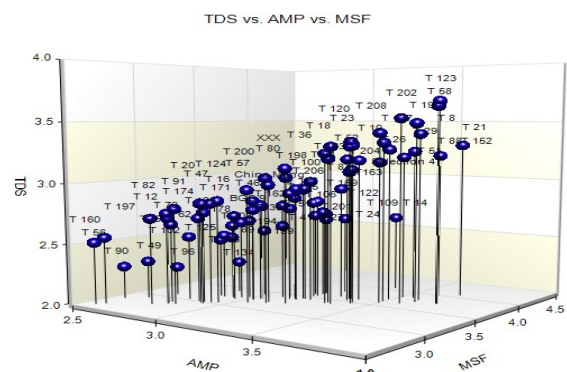
A- Long Duration Bidar 2017-18

Class 'A' response genotypes



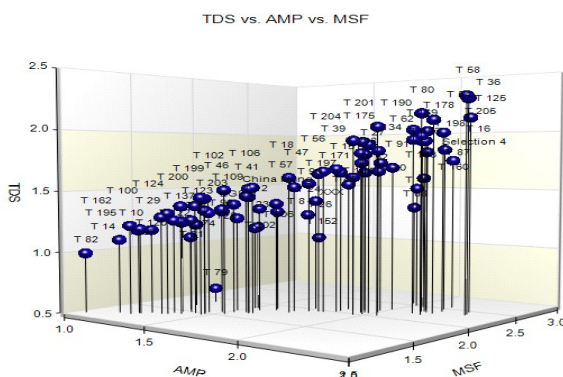
B. Long Duration Bidar 2018-19

Class 'A' response genotypes



C. Long Duration Gulbarga 2017-18

Class 'A' response genotypes



D. Long Duration Gulbarga 2018-19

Class 'A' response genotypes

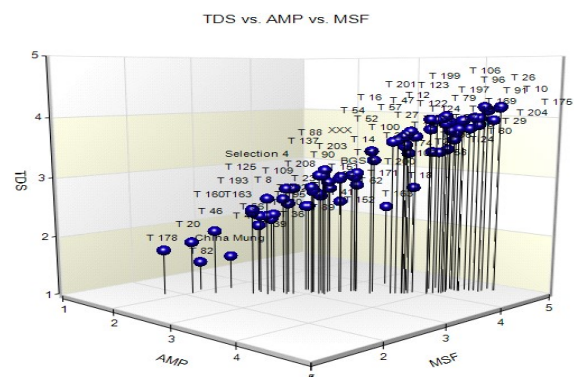


Fig. 9 : 3D graphs for grouping of the genotypes into A, B, C & D classes of responses of long duration group genotypes for tolerance to TDS environments for grain yield based on AMP and YTDS and YMSF over two locations and two years

TABLE 8
Estimates of YREM of best green gram genotypes evaluated under MSF and TDS environments for grain yield plant⁻¹

Short duration group					Long duration group				
Genotypes	TDS	Genotypes	MSF		Genotypes	TDS	Genotypes	MSF	
T 108	0.87	T 186	0.86		T 80	0.91	T 26	0.9	
KM 13 45	0.86	T 108	0.83		T 190	0.88	T 80	0.9	
T 159	0.84	T 168	0.83		T 58	0.85	T 175	0.88	
T 72	0.83	T 72	0.82		T 91	0.83	T 190	0.87	
T 103	0.82	T 45	0.82		T 201	0.82	T 205	0.87	
KM 13 02	0.81	GG 13 9	0.82		T 205	0.82	T 169	0.86	
T 45	0.8	KM 13 45	0.81		T 204	0.82	T 198	0.86	
C2	0.78	KMS 13 29	0.81		T 52	0.81	T 87	0.86	
KM 14 51	0.76	T 103	0.79		T 26	0.81	T 91	0.85	
T 156	0.76	KM 13 23	0.78		T 198	0.81	T 24	0.85	
T 168	0.75	T 156	0.78		T 106	0.8	T 58	0.84	
T 186	0.74	KM 14 41	0.77		T 36	0.8	T 204	0.84	
KMS 13 57	0.74	KM 13 20	0.77		T 10	0.8	T 52	0.84	
KM 13 23	0.74	KM 13 02	0.77		T 125	0.8	T 106	0.83	
T 74	0.73	T 112	0.77		T 208	0.79	T 27	0.82	

indices as well as YREM are common and that YREM, being simple first-degree statistics, could be preferentially used to identify and select TDS tolerant genotypes much quicker time.

YREM, a Statistic to Predict Loss in Grain Yield of Genotypes under TDS Environment

YREM is an intuitive, genotypes' attendance independent dynamic statistics (Yan, 1999). The best genotype's performance is its potential grain yield attainable in a particular given environment. Therefore, expected YREM of genotypes tested across diverse environments such as MSF and TDS environments should be unity. Any deviation of a particular genotype's YREM from unity is attributable to reduction in grain yield due to cross-over genotype by environment interaction. The extent of reduction in attainable grain yield of a genotype depends on the extent of departure of its YREM from unity (Yan, 1999). In the present study, the estimates of

YREM suggested that two genotypes namely T 108 and T 72 from short duration group and three genotypes T 80, T 190 and T 205 of long duration group (Table 8) are expected to suffer a much lower loss in attainable grain yield plant⁻¹ than other genotypes in both duration groups.

This inference is based on the innate property of YREM. Higher the value of YREM of a genotype, lower is the extent of reduction in grain yield potential of that genotype even in presence of crossover MR x genotypes interaction. However, though the genotypes did not interact with MR in the present study, afore mentioned the genotypes with near to unity YREM values indicate that their interaction with the four test environments is of non-crossover type.

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