

Materials and Methods

A field experiment with 14 genotypes was conducted in randomized block design with three replications on medium black soils during the post-rainy season 2000/01 at the Sorghum Research Station, Marathwada Agricultural University, Parbhani, Maharashtra. The crop was sown on 10 October 2000 and harvested on 27 February 2001. The crop was grown on residual soil moisture and was not irrigated. The spacing adopted was 45 cm between rows and 15 cm between plants. The gross plot size was 2.7 m x 5.0 m and net plot size was 1.8 m x 4.4 m. Recommended fertilizer doses were given. Five plants were selected from each plot for recording observations on different physiological characters.

Results and Discussion

The genotype RSP 1 and Sel 3 matured earlier than rest of the genotypes (Table 1). The plant height differences were not significant; however, M 35-1 recorded maximum plant height. Leaf area index (4.21) at flowering and total biomass production (696 g m⁻²) at physiological maturity was significantly high in RS 29. Panicle partitioning was maximum in PBS 2 (62.8%) followed by CR 6 (62.2 %) and CR 9 (62.0 %).

Among the 14 genotypes evaluated, CSV 14R recorded significantly higher grain yield (1.58 t ha⁻¹) followed by M 35-1 and CR 4 (1.49 t ha⁻¹). The genotype RS 29 possessed significantly higher fodder yield (4 t ha⁻¹) than rest of the genotypes except CSV 14R (3.8 t ha⁻¹). Relative water content (%) at panicle initiation was significantly high in Sel 3 while at 50% flowering, it was high in M 35-1 followed by CSV 14R and RSLG 383. The genotype RSLG 241 had lowest chlorophyll stability index.

The difference in leaf stay greenness was not significant; however, maximum non-senescence score (%) at physiological maturity was recorded in PBS 2. The increase in grain yield in PBS 2, CR 4, CR 6 and CR 9 was due to increase in total biomass (520 g m⁻², 541 g m⁻², 505 g m⁻² and 543 g m⁻², respectively), panicle partitioning (62.8%, 59.0%, 62.2% and 62.0%, respectively), harvest index (54.9%, 50.1 %, 53.1 % and 53.1 %, respectively) and test weight (47.6 g, 41.8 g, 39.1 g and 38.4 g, respectively).

The same genotypes performed better for drought tolerance parameters like relative water content at flowering (74.8%, 77.9%, 77.8% and 70.9%, respectively), chlorophyll stability index at 50% flowering (0.338, 0.299, 0.367 and 0.522, respectively) and leaf stay greenness at physiological maturity (44.7%-, 39.4%., 31.1% and 34.8%, respectively) in comparison with checks M 35-1, Sel 3 and CSV 14R. On the basis of the

above yield and drought tolerance parameters studied, the genotypes PBS 2, CR 4, CR 6 and CR 9 were found to be high yielding with tolerance to drought.

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Screening Sorghum Germplasm for Tolerance to Soil Salinity

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Introduction

Sorghum (*Sorghum bicolor*) is known to be relatively more tolerant to salinity than other crops, such as maize (*Zea mays*) or legumes and thus has the potential to replace maize in saline soils (Igartua et al. 1994). The existence of large interspecific (Yang et al. 1990) and intra-specific (Maas 1985, Azhar and McNeill 1988, De La Rosa-Ibarra and Maiti 1995) variation for salinity tolerance offers a scope for integrating these tolerant crop genotypes with appropriate management practices to better exploit the saline soils.

Most crops are sensitive to salt stress at all stages of plant development, including seed germination, vegetative stage and reproductive stage. In sorghum, seed germination and seedling establishment seem to be more sensitive to soil salinity than subsequent development stages. However, screening methods aimed at crop productivity as a goal, need to concentrate on the quantity and quality of the yield of either fodder (shoot biomass) and/or grain. Variation in the whole-plant reaction to salinity has been considered as the best means to identify salinity tolerant genotypes (Shannon 1984). Salt-tolerant plants at vegetative stage are also less sensitive to stress at later stages of growth. Therefore, the objective of this study

was to screen a diverse set of improved hybrid parents and germplasm lines of sorghum for their ability to produce higher biomass under saline soil conditions during pre-anthesis stage.

Materials and Methods

One hundred entries comprising popular varieties, hybrids and improved lines of sorghum were screened in a greenhouse at 20-28°C in a randomized complete block design (RCBD) with three replications at ICRISAT, Patancheru, India. There were two salinity treatments: (1) Control: irrigated with deionized water; and (2) Saline: irrigated with 250 mM NaCl solution (EC 23.4 dS cm⁻¹) once at the time of sowing and later irrigated with deionized water. Sixteen seeds of each entry were sown in one 12.5-cm diameter plastic pot on 29 March 2003 and irrigated with deionized water or saline solution to field capacity previously estimated for the soil (Krishnamurthy et al. 2003). To avoid waterlogging during subsequent irrigations, the water needed was determined by regular weighing of representative pots. A maximum of four plants pot⁻¹ were retained after thinning at 10 days after sowing (DAS) in the control. One plant per pot was sampled at 18, 25, 32 and 39 DAS. Sampling was done as described by Krishnamurthy et al. (2003).

The total plant biomass for each sample was subjected to ANOVA as a two factor RCBD and the genotypic means were obtained. All the four individual sample genotypic means of total biomass produced under saline condition and the four calculated ratios of total biomass under saline condition as that of the control were used for clustering the entries into different classes using Numerical Taxonomy and Multivariate Analysis System (NTSYS-PC), version 2.1 from Exeter Software, New York, USA. Similarity/dissimilarity matrix was obtained based on Euclidean distances and thus the entries were grouped on the basis of UPGMA (unweighted pair-group method of arithmetic average).

Results and Discussion

Germination and seedling emergence were delayed under salinity stress. Seedlings emerged in 8 to 10 DAS under salinity compared to 4 DAS in the control. The total plant biomass of entries under salinity showed significant variation at all stages of sampling. However the salinity x genotype interaction was significant in the first three samples only (Table 1). The cluster analysis of the entries on the basis of total biomass production under salinity in all stages and the relative production inclusive of all growth stage samples has indicated at least 4 major

Table 1. Analysis of variance and its significance for salinity treatments, sorghum genotypes and their interactions for total dry matter plant⁻¹ of samples at different days of sowing (DAS).

Source of variation	Mean sum of squares and significance level ¹			
	14 DAS	25 DAS	32 DAS	39 DAS
Salinity levels (S)	12.500***	73.790***	189.250***	15275***
Sorghum genotypes (G)	0.014***	0.120***	0.280**	1.080**
S x G	0.011*	0.100***	0.290**	063 INS
Residual	0.009	0.06	0.190	0.706

1. * = Significant at $P = <0.05$; ** = Significant at $P = <0.01$; *** = Significant at $P = <0.001$; NS = Not significant.

Table 2. Cluster group means of total biomass (g plant⁻¹), the ratio of total biomass under 250 mM saline condition to that of control at 18, 25, 32 and 39 days after sowing (DAS) and the comparative reaction of the tested sorghum entries¹.

Sorghum entries	18 DAS		25 DAS		32 DAS		39 DAS		Reaction
	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	Biomass	Ratio	
13	0.067	0.222	0.193	0.248	0.241	0.169	0.626	0.315	Sensitive
55	0.074	0.205	0.271	0.294	0.448	0.303	1.251	0.575	Tolerant
13	0.105	0.261	0.276	0.259	0.340	0.197	1.908	0.666	Tolerant (needs confirmation)
19	0.113	0.306	0.380	0.382	0.700	0.479	2.056	0.856	Highly tolerant

1. Pair-wise analysis of means by multivariate analysis showed that the clusters listed were different at 0.001 probability level.

Table 3. Sorghum entries grouped on the basis of pre-anthesis total biomass production under 250 mM saline water irrigated condition and the ratio of biomass under salinity to that of control.

Group	Entries
Sensitive	ICSV 96020, SP 20614B, ICSR 91012, ICSB 677, ICSB 678, ICSB 406, ICSB 89002, SP 20666B, SPDM 94014 (ICSB 517), ICSB 415, ICSR 93033, ICSB 88010, SPDM 94024 (ICSB 218)
Highly tolerant	CSV 15, ICSB 766, ICSV 95030, NTJ 2, ICSV 145, S 35, ICSB 676, ICSV 112, ICSB 300, ICSR 196, SP 40669, SPA2 94029 (ICSB 725), SP 40672, SPV 1022, SPDM 94006 (ICSB 203), ICSR 91005, ICSR 89010, SP 40646, ICSR 93034

groups at a similarity coefficient of 60%, excluding one entry. The consideration of the relative biomass production is expected to account for the variation of the entries in growth vigor. The genotypes that performed consistently across all the sampling stages can be grouped into sensitive, tolerant and highly tolerant entries based on the group means of the total biomass and its ratio relative to control plants, for all the sampling dates (Table 2). Almost all entries that have only partially emerged under salinity in all three replications were grouped under the sensitive category (Table 3). As in pearl millet (*Pennisetum glaucum*) (Krixnamurthy et al. 2003), some of the elite germplasm lines of sorghum that are particularly known for their specific desirable characters also exhibited better tolerance to salinity. These putative salinity tolerant entries have other desirable characteristics: (1) stable across environments (CSV 15 and ICSV 112); (2) stay-green after maturity (ICSB 676, SP 40646 and SP 40672); (3) resistance to grain mold (ICSV 95030); (4) resistance to leaf blight (ICSB 300); (5) resistance to downy mildew (SPDM 94006); (6) resistance to *Striga* (ICSV 145); and (7) high grain and fodder yield and quality (CSV 15 and ICSR 93034).

A selected set of sorghum lines based on their contrasting performance are being tested again for confirmation. Also, determination of various ionic compositions of the plant tissues is being carried out to delineate the mechanisms of salt tolerance. The same material is being tested at the International Center for Biosaline Agriculture (ICBA), Dubai, UAE as part of a collaborative project on salinity tolerance.

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