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Salinity tolerance of *Panicum maximum* genotypes for germination and seedling growth

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Abstract
Twenty-eight diverse genotypes of Guinea grass (*Panicum maximum*) were screened against different salinity levels to select the tolerant genotypes. In general, a low or moderate level of salinity was found to have a stimulating effect on germination in most of the genotypes. More than 50% of genotypes showed higher germination per cent at EC 12 and 16 as compared to control. For seedling vigour measured in terms of radical and plumule length, the genotypes identified as tolerant included IG 01-169, IG 01-189, IG 97-48, IG 01-173 and IG 01-94 for radicle growth and IG 01-97, IG 01-196 and IG 01-119 for plumule growth. Analysis by susceptibility index revealed that most of the genotypes were tolerant to moderate level of salinity. Genotypes IG 97-48, IG 01-94, IG 01-173 and IG 01-97 were most tolerant. Eight genotypes viz. IG 01-125, IG 01-108, IG 01-188, IG 01-229, IG 01-104, IG 01-113, IG 01-165 and IG 01-216 possessing positive SSI values, were considered as most susceptible. Rest of genotypes possessed moderate tolerance to salinity condition. Field tolerance study revealed the genotypes such as IG 01-162, IG 01-189, IG 01-101, IG 01-183, IG 97-6 and IG 97-4 to possess tolerance to 9.5 pH. The study will help in identifying suitable genotypes for salinity prone areas in the country.

Keywords: Germination, *Panicum maximum*, Salinity, Seedling growth

Introduction

Panicum maximum Jacq. (Guinea grass) is an important multicut forage grass in tropical parts of the world. It is widely adopted because of its ease of propagation, fast growth and high-quality forage during the rainy season. The crop yield varies from 40-60 t/ha dry matter with crude protein content up to 14% and 41-72% dry matter digestibility (Bogdan, 1977; Sukhchain and Sidhu, 1992). It is highly suitable for rangelands receiving 900 to 1500 mm rainfall, although it can survive under less than 400 mm rainfall. Availability of annual as well as perennial types (Malaviya, 1996) makes the crop suitable for cultivated as well as rainfed conditions also. The vast diversity in the gene pool for various agronomic and morphological traits such as leaf length/width, leaf position (erect/ drooping/ semi-drooping), stem thickness, leaf hairiness, flowering behaviour (flowering after every harvest throughout year/once in year) (Malaviya, 1996, 1998; Jain *et al*., 2003a) offer ample opportunities for identification of genotypes suited to different agro-climatic zones and tolerant to various abiotic stresses. Guinea grass has been reported to out yield *Cenchrus ciliaris* and *Chrysopogon fulvus* in silvipasture system on non-arable land of semi-arid India (Kumar *et al*., 2017). The high level of genetic variability of the crop has been established at isozymic and cytological levels (Jain *et al*., 2003b, 2005) also.

Targeted breeding in *P. maximum* has its limitation because the transfer of genes into the line of interest through crossing is not possible in this apomictic grass. The only plausible breeding method appears to select the genotypes in the target environment. These apomictic grasses, although lack sexual mode of seed formation, possess substantial genetic variability in nature owing to residual sexuality, mutations and introgression of genes from another parent by way of apomeiosis followed with fertilization mode of seed formation (Kaushal *et al*., 2008).

Soil salinity is significant abiotic stress in plant agriculture which significantly affects crop productivity throughout the world (San Pietro, 1982). Around 7% of the world land

is salt-affected (Ruiz-Lozano *et al*., 2001, 2012) which amounts to approx 95 million hectares (Szabolcs, 1994). At a global level, salinity is further difficult problem in the arid and semi-arid regions. Hence, salt tolerance in crops is a critical trait. This becomes more important in the context of forage crops because the area under forage cultivation in India is not increasing and the country faces severe green forage deficit (Anonymous, 2012; Anonymous, 2016; Earagariyanna *et al*., 2017). Although some crops are moderately tolerant to saline conditions, many crops are adversely affected by even low levels of salinity (Greenway and Munns, 1980). The significant efforts to circumvent salinity in the past have been directed towards soil reclamation and water desalinization practices that are increasingly expensive. Identification of tolerant variety is the most economical and eco-friendly way towards improving biomass production and yield.

Salinity adversely affects seed germination and plant growth, resulting in a reduction in crop yield. Shannon (1984) demonstrated that tolerance observed at germination, early seedling, and the vegetative growth stage is of great importance in determining the ultimate tolerance of the species. Much of the work has been done on the development of grain/vegetable crops tolerant to salt stress. However, forages comprising of many wild and weedy germplasm offer a better choice for reclamation of saline land as they harbour genes for tolerance for biotic and abiotic stresses (Maas and Hoffman, 1977; Galluzzi *et al*., 2014; Malaviya *et al*., 2015; Roy *et al*., 2019). Medium tolerance to salinity in guinea has been reported (Grieve *et al*., 2012). Additionally, tolerance of guinea grass and its related species to saline-sodic conditions is also reported (Russell, 1976). Genotypic differences for salinity tolerance are also reported (Thakral *et al*., 2001).

The long-term goal of breeding for salinity tolerance is the development of germplasm with improved field level tolerance at all critical developmental stages under different levels of salinity. Germination is the major bottleneck in the establishment of any crop in saline condition. Hence, the study was planned to identify salt-tolerant genotypes of guinea grass (*Panicum maximum* Jacq). Additionally, some genotypes were also evaluated for field-level tolerance to salt stress for survival and establishment. This study, thus, presents results from screening for salinity tolerance of 28 genotypes for germination and seedling growth in controlled condition at different levels of salt stress as well as field tolerance of genotypes for survival under salt stress.

Materials and Methods

Experimental design: Twenty-eight genotypes of guinea grass selected from the global germplasm collection of IGFRI were evaluated for tolerance to four salinity levels of EC 4, 8, 12 and 16. One hundred seeds of each genotype were grown on sterilized filter paper in petri plates in two replications. In control sets, the filter papers were soaked with distilled water whereas in treatment sets, the soaking was done with saline water of electrical conductivity (EC) level of EC 4, EC 8, EC 12 and EC 16. The treatment solution was prepared by dissolving a different quantity of NaCl in water to get the desired EC level solution. The data on germination was recorded from day one to the 7th day, after which no increase in germination noticed, by recording the total number of seeds with radicle and plumule growth. Data presented here is germination per cent on 7th day. Observations on seedling growth i.e. radicle and plumule length were recorded on three seedlings in each replication on 15th day.

Data analysis: Salinity intensity index (SII) was calculated as SII=1-X_{ss}/X_{ns}, where X_{ss} and X_{ns} are the mean of all accessions under salinity stressed (SS) and non-stressed (NS) environments (Fisher and Maurer, 1978). Salt susceptibility index (SSI) was calculated as SSI= (1-Y_{ss}/Y_{ns})/SII (Y_{ss} and Y_{ns} are the mean values of a given accession in the stressed and non-stressed environment) following Bayuelo-Jimenez *et al*., (2002). Based on SSI values, the genotypes were grouped in susceptible, tolerant and highly tolerant genotypes. Lower SSIs values were treated as an indicator of high tolerance. Standard deviation, 't' test and two-factor analysis of variance with replication were performed using MS Excel programme. Per cent change under the stressed condition in germination, radicle length and plumule length over that in their respective value in control i.e. distilled water was calculated by the formula: Percent change = 100*(value in stressed condition-value in distilled water)/ value in distilled water.

Results and Discussion

Germination: In control set mean germination was 19.41%, whereas it was 26.79% in EC 4, 28.45% in EC 8, 26.64% in EC 12 and 22.34% in EC 16 (Fig 1; Table 1). Among twelve genotypes per cent germination was more than two times than their respective control *i.e*. germination in distilled water even at EC12 (Table 2); however, it drastically decreased at EC16. As per 't' test results, the germination per cent in distilled water was significantly lower than that at EC4, however differences between EC4-EC8 and EC8-EC12 was not significant.

Table 1. Mean, SII and SSI for germination in *Panicum maximum* genotypes

Genotype	Germination %					
	DW	EC4	EC8	EC12	EC16	SSI*
IG 01-104	35.5	43.5	18.0	15.0	15.5	1.4
IG 01-113	10.5	16.0	11.0	8.0	6.0	0.5
IG 01-170	12.5	37.0	37.0	25.0	26.0	-4.8
IG 01-120	8.5	19.5	17.0	14.5	21.5	-4.4
IG 97-34	16.0	22.5	23.0	32.0	18.5	-1.4
IG 01-163	6.5	8.0	14.5	15.5	10.5	-2.8
IG 01-166	11.0	27.5	16.0	19.0	20.5	-3.1
IG 01-169	28.5	23.0	27.0	18.0	17.0	1.1
IG 01-125	40.0	52.0	53.0	48.0	52.0	-1.0
IG 01-214	15.5	25.0	39.0	33.0	22.0	-2.7
IG 01-189	39.5	42.0	45.0	35.0	43.0	-0.2
IG 01-126	28.5	33.0	26.0	43.0	27.0	-0.3
IG 01-97	23.5	26.0	20.0	21.0	28.0	-0.2
JHGG1-1	20.5	14.0	19.0	18.0	20.0	0.4
IG 01-124	63.5	55.0	42.0	45.0	39.0	1.1
IG 01-196	19.5	25.0	29.0	38.0	16.0	-0.8
IG 01-119	6.5	17.0	23.0	13.0	9.0	-3.7
IG 01-229	15.0	17.0	13.0	6.0	11.0	0.8
IG 01-108	14.5	24.0	35.0	35.0	27.0	-3.6
IG 01-106	16.5	32.0	36.0	43.0	30.0	-3.7
IG 01-121	16.0	53.0	48.0	43.0	37.0	-5.9
IG 01-165	26.5	28.0	35.0	46.0	37.0	-1.4
IG 01-188	16.5	20.0	38.0	22.0	16.0	-1.0
IG 97-48	6.5	14.0	38.0	18.0	26.0	-9.5
IG 01-162	10.5	36.0	38.0	38.0	30.0	-7.8
IG 01-173	11.0	14.0	32.0	26.0	6.0	-1.4
IG 01-94	9.0	14.0	12.0	26.0	14.0	-2.7
IG 01-216	15.5	12.0	12.0	2.0	0.0	2.5
SII		-0.38	-0.47	-0.37	-0.15	
Mean	19.41	26.79	28.45	26.64	22.34	
Min	6.50	8.00	11.00	2.00	0	
Max	63.50	55.00	53.00	48.00	52	
SD	12.84	13.01	12.11	13.27	12.12	
t test p-value		0.000	0.198	0.146	0.006	

*Average of SSI at four EC levels. SII= Salinity intensity index; DW=Distilled water

Further, germination at EC12 was significantly different from EC16. Analysis of variance revealed a significant interaction effect between EC levels and the genotypes for germination (Table 4). In general, the salinity condition enhanced germination per cent. However, among four genotypes (IG 01-169, JHGG1-1, IG 01-124, IG 01-216), germination in stress condition was less in comparison to control in the lowest dose of salinity treatment. The per cent change varied from -13.4 to -31.7% in these four genotypes. At EC 8, eight genotypes recorded less germination as compared to control. At EC 12 and 16, the number of genotypes showing less germination increased to 9 and 11 respectively. Among some genotype ,lower germination a at a low level of salinity; however, at higher EC levels, the germination rate increased. In 16 genotypes, the per cent germination was always higher than the control level at all the four salinity levels, indicating thereby their high tolerance to the salinity. The per cent increase in germination ranged from 8.9 to 300.0 % at the highest level of salinity (EC 16) (Table 2). At a moderate level of salinity EC 8 and 12, the increase in germination was two to five-time over to the control. Thus, the study indicated genotypic variation for germination response to different salinity levels. Bayuelo-Jimenez *et al*. (2002) have also reported inter and intraspecies variation in *Phaseolus* for total seed germination as well

as time to 25, 50 and 75% germination at different EC levels. Percentage germination for different days from day 1 to 6 was 0.3, 4.4, 8.1, 19.7, 21.9 and 22.5% respectively. These figures indicated a linear increase in seed germination up to 4th or fifth day. The trend of germination rate was almost similar in distilled water and stressed condition.

In earlier reports, the germination rate under saline condition has been reported to increase with a decrease in germination per cent at lower saline concentrations (Panuccio *et al*. 2014; Kandil *et al*. 2017). However, in the present study, barring a few genotypes, germination per cent increased in the saline condition which is congruent with the study of Cordazzo (1999). The reason for such condition could be that specific seed-borne fungi/ bacteria inhibiting germination in normal condition could not grow in saline condition and that resulted in an overall increase in germination. Additionally, there could be some enzyme activation in saline condition which is involved in the germination process. It is reported that excess Na^+ and Cl^- have the potential to affect plant enzymes, resulting in reduced energy production and other physiological processes (Morais *et al.,* 2012*a, b*). NaCl has been reported to have more as well as lesser detrimental effect than seawater (SW) (Tirmizi *et al.,* 1993; Zia and Khan 2002;), however, Panuccio *et al.* (2014) found that the inhibition of different salt solutions on seed germination was in the order of SW > NaCl > KCl > $CaCl_2$ > $MgCl_2$ with no significant differences among the treatments in germination rapidity, except for the SW. The adverse effects of SW were attributed to ion toxicity on germination (Panuccio *et al*., 2014; Zehra *et al.,* 2013). Although NaCl is the predominant salt in SW, its effects on seed germination and seedling growth were less detrimental than SW itself. The adverse effects of SW on seedling growth may be ascribed to the induced accumulation of SO_4^{2-} in leaves and roots.

Table 2. Percent change in germination, radicle length and plumule length in *Panicum maximum* genotypes over their respective values in distilled water

Genotype	Germination				Radicle length				Plumule length			
	EC4	EC8	EC12	EC16	EC4	EC8	EC12	EC16	EC4	EC8	EC12	EC16
IG 01-104	22.5	-49.3	-57.7	-56.3	27.4	16.8	-11.3	6.1	-8.6	7.4	-2.6	-24.9
IG 01-113	52.4	4.8	-23.8	-42.9	-3.9	29.7	-23.7	-1.6	-6.3	5.6	-22.3	-35.7
IG 01-170	196.0	196.0	100.0	108.0	62.0	31.5	30.6	-10.1	20.5	-12.1	-13.2	-18.8
IG 01-120	129.4	100.0	70.6	152.9	39.8	-9.7	-8.2	26.2	44.6	15.7	-12.4	-2.6
IG 97-34	40.6	43.8	100.0	15.6	31.1	28.0	8.5	12.4	14.3	3.8	-12.8	-27.8
IG 01-163	23.1	123.1	138.5	61.5	21.3	20.5	25.6	33.7	28.5	20.2	-7.1	-42.2
IG 01-166	150.0	45.5	72.7	86.4	35.5	8.6	26.8	17.3	41.8	26.5	34.4	23.1
IG 01-169	-19.3	-5.3	-36.8	-40.4	45.7	9.8	44.2	30.4	50.6	56.4	30.0	-10.7
IG 01-125	30.0	32.5	20.0	30.0	9.8	-0.7	-5.6	-19.2	8.5	-5.9	-2.9	-7.6
IG 01-214	61.3	151.6	112.9	41.9	27.6	-1.9	0.7	-7.0	26.7	24.4	23.3	6.4
IG 01-189	6.3	13.9	-11.4	8.9	59.5	46.9	24.6	39.7	9.6	23.0	38.6	41.4
IG 01-126	15.8	-8.8	50.9	-5.3	35.0	29.1	23.8	32.4	-0.4	-12.4	15.8	16.9
IG 01-97	10.6	-14.9	-10.6	19.1	32.9	1.5	-5.4	19.5	204.7	117.0	129.2	138.7
JHGG1-1	-31.7	-7.3	-12.2	-2.4	-1.0	-9.5	-9.5	0.1	6.9	27.0	19.2	23.5
IG 01-124	-13.4	-33.9	-29.1	-38.6	4.7	-12.5	1.7	-7.7	6.7	40.7	33.1	32.6
IG 01-196	28.2	48.7	94.9	-17.9	12.1	-7.9	-20.5	-14.6	47.2	60.2	92.0	71.9
IG 01-119	161.5	253.8	100.0	38.5	-21.5	-26.2	-17.5	-17.1	24.9	51.7	88.3	37.1
IG 01-229	13.3	-13.3	-60.0	-26.7	3.8	-21.3	-1.7	-19.4	-6.7	24.8	8.4	-15.5
IG 01-108	65.5	141.4	141.4	86.2	-10.2	-10.9	-32.1	-26.6	-4.6	27.2	31.6	16.6
IG 01-106	93.9	118.2	160.6	81.8	30.1	-15.9	-12.4	-6.2	23.1	43.9	16.9	-5.7
IG 01-121	231.3	200.0	168.8	131.3	49.3	43.5	14.0	5.1	35.5	43.9	19.1	20.8
IG 01-165	5.7	32.1	73.6	39.6	-9.1	-4.8	-34.1	-37.8	-12.1	-15.5	-17.5	-9.8
IG 01-188	21.2	130.3	33.3	-3.0	-9.9	-18.8	5.3	-42.9	-34.0	-11.2	0.0	-26.5
IG 97-48	115.4	484.6	176.9	300.0	20.0	108.7	45.6	-5.6	-61.8	116.6	9.4	32.2
IG 01-162	242.9	261.9	261.9	185.7	26.1	77.4	33.5	-30.9	48.7	-6.8	-18.8	-50.4
IG 01-173	27.3	190.9	136.4	-45.5	199.5	124.3	105.8	-21.7	-10.9	-20.5	-21.8	-57.3
IG 01-94	55.6	33.3	188.9	55.6	225.1	213.6	64.2	44.5	4.2	5.0	-23.1	-49.6
IG 01-216	-22.6	-22.6	-87.1	-100.0	-68.4	-87.7	-93.6	-100.0	-72.9	-69.8	-71.1	-100.0

Table 3. Mean, SII and SSI for radical and plumule growth in *Panicum maximum* genotypes

Genotype	Radicle length (cm)						Plumule length (cm)						SSI**
	DW	EC4	EC8	EC12	EC16	SSI*	DW	EC4	EC8	EC12	EC16	SSI*	Overall
IG 01-104	2.2	2.8	2.6	2.0	2.3	1.0	4.5	4.1	4.8	4.4	3.4	1.8	1.4
IG 01-113	2.2	2.1	2.8	1.7	2.2	3.6	4.5	4.2	4.7	3.5	2.9	3.0	2.4
IG 01-170	2.0	3.2	2.6	2.6	1.8	-6.7	4.7	5.7	4.1	4.1	3.8	1.4	-3.4
IG 01-120	2.3	3.3	2.1	2.1	2.9	0.1	3.9	5.7	4.5	3.4	3.8	-0.5	-1.6
IG 97-34	2.1	2.8	2.7	2.3	2.4	-3.2	5.2	6.0	5.4	4.6	3.8	1.9	-0.9
IG 01-163	2.3	2.8	2.8	2.9	3.1	-6.9	4.0	5.2	4.9	3.8	2.3	2.3	-2.4
IG 01-166	1.9	2.6	2.1	2.4	2.3	-6.3	3.4	4.8	4.3	4.6	4.2	-3.5	-4.3
IG 01-169	2.2	3.2	2.4	3.2	2.9	-10.1	3.4	5.1	5.3	4.4	3.0	-1.6	-3.6
IG 01-125	2.7	3.0	2.7	2.6	2.2	1.7	3.9	4.3	3.7	3.8	3.7	0.5	0.4
IG 01-214	2.6	3.3	2.6	2.6	2.4	-0.1	2.9	3.6	3.6	3.5	3.1	-1.8	-1.5
IG 01-189	2.8	4.4	4.1	3.5	3.9	-8.2	3.6	4.0	4.5	5.0	5.1	-4.3	-4.2
IG 01-126	2.5	3.4	3.3	3.1	3.3	-6.9	4.3	4.3	3.8	5.0	5.1	-1.4	-2.9
IG 01-97	3.3	4.5	3.4	3.2	4.0	-0.3	1.9	5.9	4.2	4.4	4.6	-17.9	-6.2
JHGG1-1	3.1	3.1	2.9	2.9	3.2	2.0	3.8	4.1	4.9	4.6	4.7	-2.6	-0.1
IG 01-124	2.8	3.0	2.5	2.9	2.6	0.3	3.3	3.5	4.6	4.4	4.4	-3.7	-0.8
IG 01-196	4.0	4.5	3.7	3.2	3.4	4.4	2.6	3.8	4.1	4.9	4.4	-8.8	-1.7
IG 01-119	4.6	3.6	3.4	3.8	3.8	4.9	2.7	3.4	4.2	5.2	3.8	-5.8	-1.6
IG 01-229	3.5	3.6	2.7	3.4	2.8	1.6	4.0	3.7	5.0	4.3	3.4	0.7	1.0
IG 01-108	2.7	2.5	2.5	1.9	2.0	7.3	3.5	3.3	4.4	4.6	4.0	-2.2	0.5
IG 01-106	1.9	2.5	1.6	1.7	1.8	2.5	3.8	4.6	5.4	4.4	3.6	-1.0	-0.7
IG 01-121	2.6	3.9	3.7	3.0	2.7	-4.5	3.8	5.1	5.4	4.5	4.5	-3.1	-4.5
IG 01-165	3.1	2.9	3.0	2.1	2.0	8.0	4.9	4.3	4.2	4.1	4.5	1.5	2.7
IG 01-188	3.2	2.9	2.6	3.4	1.8	1.5	3.6	2.4	3.2	3.6	2.6	2.6	1.0
IG 97-48	1.5	1.8	3.1	2.2	1.4	-11.1	2.3	0.9	4.9	2.5	3.0	-2.9	-7.8
IG 01-162	1.8	2.3	3.2	2.4	1.2	-7.1	2.0	2.9	1.8	1.6	1.0	3.2	-3.9
IG 01-173	1.1	3.3	2.4	2.2	0.9	-24.0	4.0	3.6	3.2	3.1	1.7	5.0	-6.8
IG 01-94	1.0	3.3	3.2	1.7	1.5	-22.1	4.3	4.5	4.6	3.3	2.2	3.9	-7.0
IG 01-216	3.1	1.0	0.4	0.2	0.0	24.3	3.8	1.0	1.2	1.1	0.0	10.9	12.6
SII		-0.20	-0.08	0.01	0.07			-0.11	-0.16	-0.08	0.06		
Mean	2.50	3.04	2.74	2.52	2.38		3.66	4.06	4.24	3.94	3.44		
Min	0.97	0.77	0.38	0.20	0		1.92	1.03	1.15	1.10	0.00		
Max	4.59	4.47	4.07	3.78	4		5.22	5.97	5.42	5.15	5.12		
SD	0.80	0.77	0.71	0.75	0.93		0.83	1.25	0.99	0.97	1.20		
t test p-value		0.005	0.059	0.034	0.075			0.025	0.273	0.033	0.000		

*Average of SSI at four EC levels, **Average of SSI at each EC level for germination, radical length and plumule length. SII= Salinity intensity index; SSI= Salt susceptibility index; DW=Distilled water.

***Seedling growth*:** Seedling growth as indicated by radicle and plumule growth revealed a similar trend as that of germination. Average radicle growth in control set was 2.50 cm as against 3.04, 2.74, 2.52 and 2.38 cm at EC 4, EC 8, EC 12 and EC 16 respectively. This reflects that lower salinity levels (up to EC 8) have a positive effect on radicle growth and no significant adverse effect was seen even at EC 16. Average plumule length in control set was 3.66 cm as against 4.06, 4.24, 3.94 and 3.44 cm at EC 4, EC 8, EC 12 and EC 16 respectively (Fig 1; Table 3). Thus, on an average, at EC 16 only slight negative effect on radicle and plumule growth was observed whereas at lower doses, it has a positive effect on these two parameters. Genotypic variation was also marked among the genotypes to a different level of salinity treatment for radicle growth. Eight genotypes showed a negative effect at EC 4, whereas among 13 genotypes negative effect was observed at EC 8 and EC 12. Twelve genotypes showed a positive impact on radicle growth even at EC 16 which showed their tolerance to the salinity stress. Maximum per cent increase noticed at EC 4, EC 8, EC 12 and EC 16 was up to three times as compared to control.

Table 4. ANOVA for germination and seedling growth of *Panicum maximum* genotypes.

Attributes	Source of variation	SS	df	MS	F	F crit
Germination	Genotype	31553.13	27	1168.634	24.878**	1.566
	Salinity level	3119.593	4	779.898	16.602**	2.436
	Interaction	11832.61	108	109.561	2.332**	1.344
	Within	6576.5	140	46.975		
	Total	53081.83	279			
Radicle	Genotype	113.2375	27	4.194	18.809**	1.566
	Salinity level	13.17396	4	3.293	14.771**	2.436
	Interaction	69.39261	108	0.643	2.882**	1.344
	Within	31.21623	140	0.223		
	Total	227.0203	279			
Plumule	Genotype	182.5925	27	6.763	14.202**	1.566
	Salinity level	25.41956	4	6.355	13.346**	2.436
	Interaction	144.4858	108	1.338	2.810**	1.344
	Within	66.6639	140	0.476		
	Total	419.1617	279			

**P<0.01%

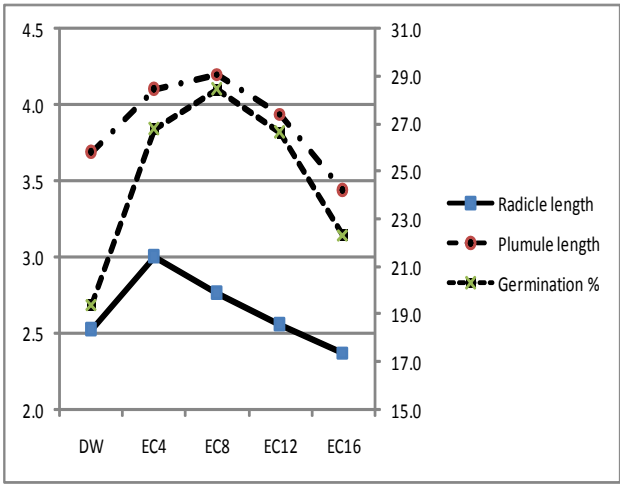

Fig 1. Average germination and seedling growth of *Panicum maximum* genotypes at four EC levels and control

Y1 axis (left) = radicle and plumule length (cm); Y2 axis (right) = germination percent; DW=Distilled water; EC4 to EC16= Electrical Conductivity of saline solution.

Plumule length decreased among 9, 8, 12 and 15 genotypes at EC 4, EC 8, EC 12 and EC 16 respectively as compared to non-stress condition. The analysis of variance revealed significant differences (P<0.01) between genotypes, treatments and interaction for germination and seedling growth (radicle and plumule length) (Table 4). It was also noticed that genotypes with good growth under low stressed condition also performed well at high EC levels.

Bayuelo-Jimenez *et al*. (2002) reported that NaCl stress significantly reduced seedling dry weight in addition to differential response of different accessions and species of *Phaseolus*. Salt stress has been reported to inhibit hypocotyl growth more than radicle growth and hypocotyl fresh weight reduced at all salinity levels whereas radicle fresh weight reduced only at higher levels of salinity in *Phaseolus* (Bayuelo-Jimenez *et al*., 2002). Similar observations have been reported in barley (*Hordeum vulgare* L.) (Huang and Reddman, 1995), tomato (*Lycopersicon*) (Foolad, 1996), pigeon pea (*Cajanus cajan*) (Subbarao *et al*., 1991).

The average performance and the stress susceptibility index (SSI), alternatively stress tolerance index (STI) (Fernandez, 1993) have been used for comparing genotypic performance across environments whereas SSI was used to identify genotypes that perform well under both stress and non-stress conditions. In the present study, genotypes were identified which showed tolerant behaviour at different EC levels using SSI. The overall SSI ranged from -7.8 to 12.6; however, the genotypes showing overall SSI < -5 were considered as highly tolerant because in this analysis, the least the value of SSI was indicative of high tolerance. Thus, genotypes IG 97-48, IG 01-94, IG 01-173 and IG 01-97 were most tolerant. Eight genotypes viz. IG 01-125, IG 01-108, IG 01-188, IG 01-229, IG 01-104, IG 01-113, IG 01-165 and IG 01-216 possessing positive SSI values were considered as most susceptible (Table 3). Rest of genotypes possessed moderate tolerance to salinity condition. Further to mention that germination of seeds

is an essential factor for maintaining the population in the natural condition under high salinity condition, hence, the genotypes IG 97-48, IG 01-162 and IG 01-121 with high salinity tolerance for germination are also important. Seven genotypes were susceptible to salinity with positive SSI values.

Identification of genotypes at different stages of growth has great significance because salinity tolerance is known to differ with ontogeny (Shannon, 1984). For biological reclamation of salinity affected soil, the germination of perennial species like *P. maximum* and its early vigour is very important for successful establishment. Kinsburry and Epstein (1984) also suggested screening at high salinities over a single generation as a useful tool in identifying salt-resistant genotypes. Thus, tolerance observed at different growth stages starting from germination to reproductive growth stage is of great importance as it will help in identifying the donor genotypes for hybridization and gene pyramiding programmes to develop a complete tolerant plant. Positive correlation for salt tolerance between the seedling stage and later development stages in mustard was reported by Jain *et al.* (1990, 1991).

In the present study, salinity tolerant genotypes were identified based on the response at germination and seedling vigour in a stressed condition. The study indicated genetic variation among the genotypes for tolerance to different salinity levels at different growth stages. Salt stress has been reported to affect germination through osmotic effects (Welbaum *et al*., 1990) or by ion toxicity (Huang and Reddman, 1995) or in turn the low water potential (Bradford, 1995). Growth stage-dependent salinity tolerance together with genotypic differences, was also observed by Sun *et al*. (2018).

The germination process that facilitates rapid germination under salt stress and no stress condition possibly are controlled by similar genetic and physiological mechanisms among some species (Foolad, 1996) whereas in some other species wherein germination in non-stress condition was good but severely reduced under high salt stress condition, physiological process required for germination were sensitive to salt and such plants might be deficient in genetic elements as are necessary for coping with salinity (Foolad and Lin, 1997). In the present study, the accessions represent wide genetic variability of single species which is reported to possess a high level of genetic variability (Kaushal *et al.,* 1999). Hence, the genotypes evaluated also exhibited large variability for tolerance to salinity. Genotypes showing tolerance for germination and that for seedling growth were different in some cases showing that salt tolerance in guinea grass at germination and at the seedling stage might be controlled by more than one gene as reported earlier by Foolad and Jones (1993).

Conclusion

Screening of twenty-eight diverse genotypes of Guinea grass against different salinity levels revealed that moderate level of salinity had stimulating effect on germination. Initial seedling growth was also not much affected at low to moderate salt stress among some genotypes In field condition also, a few genotypes possessed tolerance up to 9.5 pH. The germplasm lines possessed high genetic variation among the genotypes for tolerance to different salinity levels at different growth stages which indicates that different sets of genes are probably involved in conferring tolerance. The study will help in identifying the donor genotypes for hybridization and gene pyramiding programmes.

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