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Evaluation of Indigenous Rice Genotypes for Drought Tolerance under Induced Moisture Condition

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ABSTRACT

The present study was undertaken to evaluate 28 traditional rice genotypes for various physio-morphological characters towards drought tolerance. Two experiments were conducted to assess the responsiveness of genotypes for induced moisture stress. Field level screening for drought stress was carried at three different environments and the pooled data were subjected to D^2 Mahalonobis analysis of genetic divergence. In second experiment, laboratory screening at growth stages was subjected to four levels (0, 20, 30 and 35%) of polyethylene glycol (PEG-6000). Data on seed germination percentage, shoot length, root length and dry weight were recorded. Most of the genotypes showed significant differential responses for growth parameters towards the increasing concentration of PEG. Among the 28 genotypes, Kuzhiadichan, Karupu Kavuni, Mysore Malli, Sornamasuri and Raja pokame recorded better growth parameters under drought stress conditions indicating their capability to combat with severe moisture situation. Using D^2 analysis, the 28 rice genotypes were grouped into 10 clusters. The maximum intra-cluster distance was observed between Cluster I and Cluster VII. The maximum inter-cluster distance was noticed between clusters III and X. It showed that intra-cluster distances were significantly lower than the inter-cluster distances indicating the existence of wider genetic diversity among the genotypes. Genotypic correlation studies revealed that grain yield had positive significant correlation with productive tillers, grains per panicle and 100-seed weight. Grain yield exhibited positive significant association with number of productive tillers per plant, number of grains per panicle and 100-seed weight, while it was negatively correlated with days to 50% flowering. The genotypes Karudan samba, Kichadi samba, Kattuyanam, Karupukavuni, Mapillai samba, Kuzhiadichan and Thanga samba showed superior values in terms of grain yield under drought stress. It was/is advantageous to select genotypes as donor parents from clusters showing high inter-cluster distance (Clusters III and X) for crop breeding program.

Key words : Rice, polyethylene glycol, drought tolerance, cluster

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple cereal food grain and consumed by more than half of the world population (Han *et al.*, 2018). It also provides stable income and employment for more than 100 million population in Asia (Singh *et al.*, 2015). Rice is the rich source of dietary energy (27%) and dietary protein (25%) which play an important role in Indian diet and consumed by all races in the world. Globally, rice is cultivated on an area of 154 million hectares of area with an annual production of 700 million tonnes. Worldwide, the major production constraints included several stress factors such as biotic and abiotic, which led to significant yield loss in rice production. However, its productivity was significantly reduced due to abiotic stresses such as drought and salinity (Omisun *et al.*, 2018). It has been reported that drought severely affects rice productivity (66%) in rainfed and also upland ecosystems (McCabe and Wolock, 2015). Drought is among the most destructive of abiotic causes, and more than 50% of the world's arable land is expected to be affected by drought in 2050 (Singhal *et al.*, 2016).

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Increasing rice production by reducing constraints is very critical for fulfilling UN global sustainability goals and thus ensuring food security for the ever-increasing global population. The improvement of high yielding rice genotype with a high level of protection against biotic and abiotic stresses is a pre-requisite by 2050 (Chukwu *et al.*, 2019; Oladosu *et al.*, 2019).

Plant tolerance for both biotic and abiotic stress may be enhanced by selecting particular agents, such as NaCl for salt tolerance and polyethylene glycol (PEG) for drought tolerance. The PEG is a polymer compound with several functions. It has a large molecular weight, does not infiltrate plant tissues and is a perfect osmotic for application in a hydroponics root mean. The PEG has been extensively applied to induce water stress. Moreover, drought-tolerant cultivars have been achieved in several crops by expanding approaches derived from PEG application. Genetic variations in the rice genes responsible for drought tolerance have been revealed via the screening and characterization of rice germplasm at different molecular, genetic and morphological levels while under drought stress. Thus, it becomes necessary to understand the variability and genetic diversity that existed among the selected genotypes at seedling stage. In the present study, 28 land races of rice were simulated at three different concentrations, namely, 20, 30 and 35% of water potential created by dissolving 200, 300 and 350 g of PEG 6000, respectively. Also, studying genetic diversity of the genotypes helps in selection of genotypes for utilization as donors in crop improvements. With this background, the present study was undertaken to screen 28 upland traditional rice genotypes for drought tolerance, and to characterize various physio-morphological characters responsible for drought tolerance in the selected genotypes.

MATERIALS AND METHODS

To examine the impact of drought stress on traditional rice genotypes, 28 rice genotypes collected from various Tamil Nadu Agro-climate Zones. The drought tolerant varieties such as PMK-3 and MDU-5 were used as drought tolerant check and TN-1 was utilized as susceptible check. The collected rice samples were kept at 4°C for 3 to 4 months in a laboratory refrigerator for regular uses. The list of 28 rice genotypes collected from various sources is presented in Table 1.

Table 1. List of traditional rice genotypes used for drought screening

S. No.	Genotypes	Sources of collection	Region
1.	Basmathi	Thirutraipundi	Tamil Nadu, India
2.	Thooyamalli	Thirutraipundi	Tamil Nadu, India
3.	Karudan samba	Thirutraipundi	Tamil Nadu, India
4.	Milagu samba	Thirutraipundi	Tamil Nadu, India
5.	Kichadi samba	Thirutraipundi	Tamil Nadu, India
6.	Boommi	Thirutraipundi	Tamil Nadu, India
7.	IIlapai poo samba	Radhapuram	Tamil Nadu, India
8.	Vasanai seeraga samba	Radhapuram	Tamil Nadu, India
9.	Mysore malli	Radhapuram	Tamil Nadu, India
10.	Navara	Radhapuram	Tamil Nadu, India
11.	Kattuyanam	Radhapuram	Tamil Nadu, India
12.	Kalan namak	Radhapuram	Tamil Nadu, India
13.	Poonkar	Pattukottai	Tamil Nadu, India
14.	Selam sanna	Pattukottai	Tamil Nadu, India
15.	Seeraga samba	Pattukottai	Tamil Nadu, India
16.	Karupu kavuni	Pattukottai	Tamil Nadu, India
17.	Mapillai samba	Pattukottai	Tamil Nadu, India
18.	Kuzhiadichan	Pattukottai	Tamil Nadu, India
19.	Sorna masuri	Vedaranyam	Tamil Nadu, India
20.	Attur kichali samba	Vedaranyam	Tamil Nadu, India
21.	Vakai samba	Vedaranyam	Tamil Nadu, India
22.	Thanga samba	Vedaranyam	Tamil Nadu, India
23.	Arcode kichali samba	Vedaranyam	Tamil Nadu, India
24.	Tulasi vasanai samba	Vedaranyam	Tamil Nadu, India
25.	Raja pokame	Vedaranyam	Tamil Nadu, India
26.	TN-1	DRRI, Hyderabad	Andhra Pradesh, India
27.	PMK-3	Agricultural Research Station Paramakudi	Tamil Nadu, India
28.	MDU-5	AC&RI, Madurai	Tamil Nadu, India

Field screening of selected rice genotypes for their drought tolerance was carried out in a separate field of the Plant Breeding Farm with respective check varieties as control.

The field experiments were conducted up to reproductive stage under two different drought environmental conditions. The experiment was carried out with three replications of randomized block layout in each region. Field was thoroughly prepared and levelled before transplantation in such a way water should not be stagnant during rainfall in drought stress field. Since July-October, seeds of 28 genotypes were planted in a raised bed. After 25 days in a plot size four rows, and a spacing of 20 cm between rows and 15 cm between plants, one seedling per hill was transplanted in each genotype. Standard agronomic practices and measures were followed. All tests of vegetative drought stress were carried out in upper fields that did not hold standing water. Initially, watering was done at intervals of 3-4 days and the soil was kept saturated in pressure areas up to 25 days after sowing or 4 weeks after transplantation. Then, by stopping irrigation, the stress treatment began. As the soil was dried up, the amount of gravimetric soil water was measured by soil sampling at a depth of 15-30 cm at three different places in each replication. In order to calculate moisture 2-3 days after sampling, fresh ground sample was weighed and then oven-dried [(fresh sample wt. - dry sample wt.) /(dry sample wt.) x 100]. The dry stress treatment was maintained every season, until symptoms of stress such as severe rolling of leaves and tip drying began to appear in the plants. The stress treatments were re-watered by flushing the field with water when gravimetric soil moisture was about 12% and the soil water potential was about -15 kpa at a depth of 30 cm.

All the 28 genotypes were raised separately under normal and drought conditions at seedling stage using a paper towel in the PG Laboratory of Department of Genetics & Plant Breeding, Faculty of Agriculture during August 2018. *In vitro* drought tolerance screening was conducted using Polyethylene Glycol (PEG 6000). A horizontal line was drawn at 5 cm from the top of the germination paper and labelled at 1 cm interval with 10 lines. On the moistened paper towel, 10 seeds of each genotype were placed at the indicated point to ensure that the seeds did not touch each other and a moistened second paper towel was carefully placed over the seeds. The paper towels were then loosely rolled along with a polythene sheet to form a tube and held together with a rubber band. The rolls were packaged in various PEG concentration containers.

The desired strengths of PEG were artificially induced during water deficit screening (Swapna and Shylaraj, 2017). The study was planned in a completely randomized design model (CRD) with three levels of drought pressure and three replications. Drought stress was simulated at three different concentrations, namely, 20, 30 and 35% of the water potential generated by the dissolving of 200, 300 and 350 g of PEG 6000. The distilled water was used as a control unit. This experiment was carried out in growth chamber at 2.5±0.5°C and 80% of relative humidity. The number of germinated seeds was recorded at an interval of 24 h. The height of seedling and the dry weights of seedling were determined on the 14th day. Seeds were considered to germinate when plumule and radicle spread out from the seeds to more than 2 mm. The Standard Evaluation System (SES) for rice was used for the screening of dry-tolerant rice genotypes. Physical ratings on scale 1 to 9 for stress symptoms, where lower scores indicated sensitivity, and higher scores denoted vulnerability.

The genotypes (landraces + checks) and PEG treatments (control and drought stress) were the key influences in the study of analysis of variance (ANOVA) on all parameters. Analysis of variation (ANOVA) was also calculated to find the significant variation among the genotypes. The genetic variability parameters, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were determined. Genetic divergence and clustering pattern were undertaken as the correlated variables were transformed into uncorrelated variables by pivot condensation method and grouping the genotypes into different clusters.

RESULTS AND DISCUSSION

The phenotypic data of 28 genotypes were subjected to Mahalonobis D^2 analysis. The analysis of variance for dispersion was significant, for almost all the characters which satisfied the requirement of diversity analysis.

Pooled analysis over two environments (E_1 and E_2) was used for genetic diversity studies as it reduced the environmental effect and genotype x environment effect of the genotypes studied. The mean performance for grain yield per plant ranged from 12.12 to 49.42 g in Illapai poo samba and Kuzhiadichan in pooled analysis, respectively. In pooled analysis, nine genotypes recorded significantly higher value than general mean value (Table 2).

The 28 genotypes were categorized into 10 clusters. Cluster II was the largest with the maximum number of seven genotypes. This was followed by cluster VII with five genotypes and the cluster V which had four genotypes. However, the least number i. e. only a single genotype was found in clusters I, VI and X (Table 3). The classification of genotypes revealed that genetic diversity and geographical diversity were not directly linked as genotypes of a different geographical origin were included in one cluster. The genotypes of same genetic origin may not have the same geographical origin or the genotypes arising from same geographical region may be genetically dissimilar, hence, they fall in different clusters. It appeared that geographic and genetic diversity did not necessarily correlate.

Among the clusters, high intra-cluster distance was recorded by cluster VII (73.258) followed by cluster IX (53.434) and cluster VIII (50.197). This suggested wider divergent genotypes within these clusters. With regard to inter-cluster distances, clusters III and X (93.263) were found to be highly divergent followed by clusters VI and VII (92.652), clusters III and VIII (89.276) and VI and IX (89.276) in that order (Table 4). It is well known that high inter cluster distance between two clusters indicated high genetic divergence. Hence, it would be logical to select genotypes from these clusters as parents for further crop improvement, as selection of parents from

Table 2. Mean performance of rice genotypes for seed yield per plant

S. No.	Genotypes	Mean			S. No	Genotypes	Mean		
		E1	E2	Pooled			E1	E2	Pooled
1.	G1	28.06**	19.94	24.00	17.	G17	40.41**	35.23**	37.82**
2.	G2	21.29	14.89	18.09	18.	G18	49.66**	49.19**	49.42**
3.	G3	35.52**	32.22**	33.87**	19.	G19	17.95	12.94	15.45
4.	G4	18.40	13.20	15.80	20.	G20	21.86	19.05	20.45
5.	G5	31.33**	25.80**	28.56**	21.	G21	19.96	17.63	18.79
6.	G6	22.07	16.82	19.45	22.	G22	40.85**	34.99**	37.92**
7.	G7	15.95	8.29	12.12	23.	G23	18.06	14.93	16.50
8.	G8	28.11**	21.24	24.67*	24.	G24	7.32	5.33	6.33
9.	G9	10.92	8.37	9.65	25.	G25	29.60**	24.18**	26.89**
10.	G10	18.56	10.10	14.33	26.	G26	24.44	13.70	19.07
11.	G11	32.19**	29.89**	31.04**	27.	G27	26.21	24.21**	25.21*
12.	G12	19.36	16.05	17.70	28.	G28	40.69**	37.14**	38.91**
13.	G13	24.96	21.88	23.42	General mean		25.79	21.14	23.47
14.	G14	24.79	21.69	23.24	Range		7.32-49.66	5.33-49.19	12.12-49.42
15.	G15	15.01	9.29	12.15	C. D. (P=0.05)		1.17	1.15	0.940
16.	G16	38.76**	33.70**	36.23**	C. D. (P=0.01)		1.56	1.53	1.249

Table 3. Cluster composition of 28 rice genotypes under three different environments

Clusters	No. of genotypes	Name of the genotypes
I	1	Thooyamalli
II	7	Basmati, Boommi, Illapai poo samba, Vasanai seeraga samba, Mysore malli, Navara, Aercad kichilli samba
III	2	Thanga samba, Swarna masuri
IV	3	Seeraga samba, Athur kichadi samba, Poonkar
V	4	Raja bogam, TN1, Milagu samba, Kichadi samba
VI	1	Karudan samba
VII	5	Kuzhi Adichan, Karupu kavuni, Thulasi vaasam samba, Salem samba, Mappillai samba
VIII	2	Kaattu yaanam,Vadan samba
IX	2	PMK 3, MDU 5
X	1	Kalanamak

Table 4. Intra and inter-cluster distance (D^2) for 28 traditional rice genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X
I	110.497 (10.512)	1307.75 (36.163)	5580.63 (74.704)	467.576 (21.624)	1975.930 (44.451)	4419.367 (66.478)	1145.637 (33.847)	4365.953 (66.075)	3400.520 (58.314)	3805.559 (61.689)
II		1335.72 (36.548)	3118.226 (55.841)	1137.097 (33.721)	1067.303 (60.517)	3809.409 (61.720)	2285.752 (47.810)	3197.122 (56.543)	2464.545 (51.415)	4454.736 (66.744)
III			192.635 (13.879)	4595.665 (67.791)	1528.429 (39.095)	2384.450 (48.831)	5999.176 (77.454)	7970.131 (89.276)	3545.662 (59.545)	8698.040 (93.263)
IV				360.318 (18.879)	1665.943 (40.816)	5669.264 (75.295)	1350.502 (36.749)	2874.780 (53.617)	2663.599 (51.610)	2739.252 (52.338)
V					476.879 (21.838)	3752.563 (61.258)	3162.476 (56.236)	2784.439 (52.768)	1980.344 (44.501)	5473.11 (73.983)
VI						572.560 (23.928)	8584.384 (92.652)	3360.305 (57.968)	5169.966 (89.276)	7455.480 (86.345)
VII							5366.678 (73.258)	581.395 (24.112)	5905.631 (76.848)	2591.108 (50.903)
VIII								2519.714 (50.197)	3685.850 (60.711)	3704.311 (60.863)
IX									2855.231 (53.437)	7703.250 (87.768)
X										0.000 (0.000)

divergent genetic origin would yield potential recombination. This was in accordance with the study of Kumar *et al.* (2017). Based on these criteria, the genotypes of clusters III & X, IV & VII, III and VIII and VI and IX can be considered for further exploitation.

Days to 50% flowering had positive correlation with the number of tillers and productive tillers. Plant height had positive correlation with number of tillers, panicle length, grains per yield, 100-seed weight and the negative correlation with productive tillers. Number of tillers had positive correlation with productive tillers and the number of tillers had negative correlation with 100-seed weight. Productive tillers had a positive correlation with seeds/ grain yield and a negative correlation with crop production. Panicle length had a significant correlation with grains per crop. Grain yield and 100-grain weight had a positive correlation with seeds/grain yield (Table 5).

Cluster V (85.514) reported the minimum cluster mean value for the number of grains per panicle and the maximum cluster mean value was 174.703 in cluster VI (Table 6). The grain yield per plant ranged from 9.24 to 43.91 g, respectively. Cluster VII (43.91 g) observed the highest cluster mean value for this individual. Whereas the minimum cluster mean value for pooled analysis was exhibited by the cluster VII (9.24 g). Three clusters (VI, VIII and IX) showed grain yield higher than the general mean of 24.04 g for this trait.

The relative contribution of each character to the total divergence is another important criterion in the choice of parents (Kumari *et al.*, 2015). In the present study, the maximum contribution to the total genetic divergence was by grain yield per pant followed by days to 50% flowering. The characters plant height and 100-seed weight also contributed significantly to the total divergence. Hence, these two

Table 5. Genotypic correlation among 28 traditional rice genotypes

Characters	DFF	PH	NT	PT	PL	GPP	100-SW	SPGY
DFF	1.000	0.091	-0.276	-0.27	0.645**	0.279	-0.023	0.095
PH		1.000	-0.457**	-0.267	0.344*	0.363*	0.401*	0.256
NT			1.000	0.702**	-0.318*	0.006	-0.06	0.291
PT				1.000	-0.045	0.204	0.238	0.707**
PL					1.000	0.567**	0.027	0.159
GPP						1.000	0.249	0.645**
100-SW							1.000	0.695**
SPGY								1.000

DFF – Days to 50% flowering, PH – Plant height, NT – Number of tillers, PT – Productive tillers, PL – Panicle length, GPP – Grains/panicle, 100-SW – 100-Seed weight and SPGY – Seeds/grain yield.
*,**Significant at P=0.05 and P=0.01 level, respectively.

Table 6. Cluster mean analysis of 28 rice genotypes for various characters

Clusters	Days to 50% flowering	Plant height	No. of tillers/ plant	No. of productive tillers/plant	Panicle length	No. of grains/ panicle	100-seed weight	Grain yield/ plant
I	107.057	82.959	20.815	12.927	23.894	119.372	1.379	16.95
II	96.714	98.341	18.427	12.232	23.523	112.751	1.758	19.862
III	65.882	128.406	19.863	13.205	22.352	107.624	2.064	24.318
IV	110.798	97.015	18.748	12.452	30.012	146.985	1.606	21.85
V	87.516	100.818	18.747	15.022	24.861	85.514	1.981	22.983
VI	94.391	145.741	17.797	14.206	26.105	174.703	2.414	43.626
VII	108.412	115.264	13.178	9.442	29.226	125.92	1.041	43.91
VIII	118.488	121.379	15.489	11.177	27.643	139.946	2.56	28.689
IX	91.958	84.075	19.618	15.86	31.418	144.342	2.043	38.421
X	146.16	143.42	12.25	9.162	25.358	152.712	1.743	17.708
General mean	102.737	111.741	17.493	12.568	26.439	130.986	1.858	24.364

characters could be given due importance while selecting genotypes for breeding program.

From the foregoing discussion, it could be concluded that the genotypes from the clusters VI, IX, VIII and III with superior mean performance for yield and yield component characters could be chosen for further hybridization base on morphological diversity.

Drought is regarded as a way to determine the extent of crop drought (Fen *et al.*, 2015). Visual scoring is a reliable tolerance measure of plant oxidative damage estimation that reflects plant tissue dehydration. When water pressure is increasing, the plants have developed a natural protective mechanism to minimize the energy charge on the leaves and to roll and dry their leaves, thereby reducing the net amount of radiation on the leaf.

PEG 6000 is an osmotic agent, which plays a significant part in regulating minerals, hormones, protein metabolism and signal transduction effects. PEG mainly acts to slow down the seed humidity level. All the 28 genotypes were subjected to PEG treatment and scored visually. Fourteen genotypes were found highly tolerant at 20% PEG concentrations. At 35% concentration, only five genotypes survived. Therefore, drought stress affected seed germination greatly in the present investigation, but the strength of response and adverse effect of stress depended on the genotypes.

In general, germination was severely affected by 35% PEG and all the selected genotypes had germination of less than 80%. However, differential tolerance of rice genotypes was observed. In the present study, PMK-3, Kuzhiadichan, Selamsanna, Karudan samba and MDU-5 showed 76.5, 76.15, 76.5, 71.25 and 71.5% germination, respectively, during 35% of PEG treatment. Regarding seedling height, the maximum value was observed in the controlled condition and the minimum was in the highest drought stress level of 35% PEG. Maximum seedling height was found in Thulasivasam samba, Sornamasuri, Kuzhiadichan and Raja pokame. In all the genotypes, the seedling dry weight decreased due to increased PEG concentration. At 35% PEG treatment, the highest seedling dry weight was found to be maximum in PMK-3, MDU-5, Raja pokame and Kuzhiadichan. The genotype Kuzhiadichan recorded less reduction in vigour index I followed by MDU-5 in vigour Index II with an average of 1453.48 and 2.433, respectively, under high drought stress of 35% PEG (Table 7).

CONCLUSION

It was concluded that the genotypes were divided into 10 clusters in the study of morphological diversity. The genotypes, Kuzhidichan and Salem samba were highly tolerant and were grouped into one cluster as well as Kuzhiadichan and Mapillai samba, which were high yielders and highly tolerant to drought PEG treatment but having moderate quality may be crossed with other high quality (slender type) rice. This would throw superior hybrids or may yield potential recombinants during hybridization and selection program. The genotype Karuppukavuni possesses rich medicinal value and is also a high yielder, and highly tolerant to drought with black coloured grains. This may be used as a donor for incorporating medicinal value to other superior

Table 7. Mean data for normal and drought condition

S. No.	Genotypes	SL		RL		TSL		RSR		G%	
		N	D	N	D	N	D	N	D	N	D
1.	G1	9.25	7.45	13.58	8.395	22.83	15.845	1.47	1.125	85.0	38.00
2.	G2	8.15	6.20	12.29	8.05	20.44	14.25	1.97**	1.295	100.0**	41.50
3.	G3	8.68	7.41	9.01	7.205	17.695	14.62	1.545	0.97	75.00	71.25**
4.	G4	8.6	7.35	7.885	5.15	16.485	12.50	1.10	0.705	75.00	42.50
5.	G5	8.865	6.84	12.24	8.205	21.105	15.045	1.82**	1.195	65.00	41.50
6.	G6	13.75	12.45**	16.125	12.55	29.875	25.00	1.63	1.01	65.00	39.50
7.	G7	11.70	9.20	9.525	7.30	21.225	16.50	0.74	0.79	100.00**	51.50
8.	G8	9.55	7.86	15.14	12.93	24.695	20.79	1.76*	1.64**	65.00	53.75
9.	G9	14.15	12.43**	13.95	11.445	28.10	23.88	0.855	0.92	75.00	44.75
10.	G10	10.00	7.25	12.375	9.175	22.37	16.425	1.22	1.265	100.00**	28.00
11.	G11	11.25	9.67	19.83**	16.98**	31.11	26.56**	1.215	1.76**	95.00**	36.50
12.	G12	10.17	8.37	11.50	9.00	21.675	17.375	1.15	1.075	95.00**	63.75**
13.	G13	12.40	10.52	20.75**	19.12**	33.15**	29.64**	1.305	1.82**	75.00	66.25**
14.	G14	11.15	10.06	21.5**	19.5**	32.65**	29.56**	1.93**	1.93**	100.00**	76.50**
15.	G15	10.31	9.06	15.25	13.70	25.565	22.765	1.67*	1.51**	85.00	66.50**
16.	G16	16.40	15.23**	24.25**	21.5**	40.65**	36.73**	1.56	1.41**	100.00**	68.75**
17.	G17	10.67	9.84	21.08**	20.04**	31.76*	29.88**	0.775	2.04**	100.00**	65.00**
18.	G18	14.25	17.59**	21.57**	20.16**	35.82**	33.41**	0.91	1.52*	100.00**	76.50**
19.	G19	18.37**	13.25**	16.75	15.90	35.12**	33.49**	1.00	0.90	100.00**	63.75**
20.	G20	12.75	11.91**	12.275	10.85	25.025	22.76	0.96	0.91	100.00**	66.25**
21.	G21	14.73	13.10**	14.015	12.55	28.75	25.65*	1.225	0.95	100.00**	61.50*
22.	G22	17.75*	16.47**	6.50	5.80	24.25	22.275	0.305	0.35*	95.00**	64.00**
23.	G23	13.81	12.80**	16.95	14.22*	30.765	27.03	1.82**	1.11	100.00**	65.00**
24.	G24	17.34**	16.10**	25.5**	23.26**	42.84**	39.36**	1.535	1.44**	100.00**	61.50*
25.	G25	17.89**	15.5**	20.15**	17.88**	38.04**	33.38**	1.175	1.155	100.00**	59.00
26.	G26	28.77**	6.78	14.64	8.90	43.41**	15.68	0.505	1.32	98.60**	56.00
27.	G27	27.04**	14.45**	24.30**	17.37**	44.41**	31.82**	0.89	1.20	100.00**	76.50**
28.	G28	27.085**	10.80	19.12**	15.46**	44.05**	26.26**	0.70	1.42**	100.00**	71.50**
	GM	14.10	10.92	16.00	13.30	29.78	24.23	1.23	1.24	91.02	57.75
	Range	8.6-28.77	6.20-17.59	6.50-25.50	5.15-23.26	17.69-44.41	12.50-39.36	0.30-1.97	0.35-1.76	65.00-100.00	28.00-76.50
	C. D. (P=0.05)	0.66	0.61	1.41	0.92	1.71	1.09	0.44	0.10	0.12	3.29
	C. D. (P=0.01)	0.88	0.82	1.88	1.22	2.28	1.45	0.59	0.146	0.16	4.39

S. No.	Genotypes	FSW		DSW		SV I		SV II		LRR	
		N	D	N	D	N	D	N	D	N	D
1.	G1	0.12	0.11	0.045	0.03	1940.37	602.19	3.825	1.135	5	7
2.	G2	0.29	0.185	0.14**	0.045	2044.00	591.32	14.00	1.85	5	7
3.	G3	0.15	0.115	0.04	0.02	1327.12	1041.41	3.375	1.41	1	3
4.	G4	0.135	0.125	0.05	0.035	1236.37	531.13	4.125	1.48	5	7
5.	G5	0.11	0.105	0.03	0.03	1371.82	624.40	2.275	1.235	3	5
6.	G6	0.18	0.14	0.05	0.04	1941.87	987.30	3.575	1.60	5	7
7.	G7	0.15	0.135	0.04	0.045	2122.50	849.75	4.50	2.31	3	5
8.	G8	0.19	0.135	0.05	0.045	1605.175	1117.32	3.575	2.41	3	5
9.	G9	0.50	0.24**	0.06	0.025	2107.50	1068.485	4.875	1.12	5	7
10.	G10	0.31	0.16	0.05	0.01	2237.50	460.06	5.00	0.835	7	9
11.	G11	0.21	0.175	0.06	0.05	2955.45**	969.51	6.175	1.835	3	5
12.	G12	0.21	0.115	0.06	0.035	2059.12	1107.77	5.70	2.25	1	1
13.	G13	0.36**	0.23**	0.09	0.05	2486.62**	1963.89**	7.12	3.325	1	1
14.	G14	0.28	0.22**	0.07	0.035	3265.00	2262.39**	7.50	2.68	1	1
15.	G15	0.24	0.06	0.06	0.025	2173.025	1513.75	5.525	1.645	1	1
16.	G16	0.365**	0.20	0.04	0.03	4065**	2524.47**	4.00	2.06	1	1
17.	G17	0.20	0.13	0.05	0.045	3176**	1942.44**	5.00	2.91	1	1
18.	G18	0.29	0.21	0.05	0.09	3582.5**	2555.45**	5.00	3.41	1	1

Contd.

Table 7 contd.

19.	G19	0.31	0.20**	0.05	0.03	3512.50**	2135.74**	5.00	1.91	1	3
20.	G20	0.18	0.15	0.05	0.04	2502.50	1507.80	5.50	2.65	3	3
21.	G21	0.28	0.14	0.06	0.05	2875.00**	1578.21*	6.50	3.05	3	5
22.	G22	0.13	0.13	0.04	0.03	2303.75	1425.47	4.275	1.91	3	3
23.	G23	0.325	0.25**	0.05	0.025	3076.50**	1757.65**	5.00	1.61	1	3
24.	G24	0.30*	0.12	0.12	0.05	4284.00**	2419.94**	12.00**	3.06	3	5
25.	G25	0.26	0.20	0.09	0.07**	3804.00**	1968.55**	9.50	4.12	3	5
26.	G26	0.31	0.10	0.10	0.03	3922.00**	879.02	9.40*	1.69	5	5
27.	G27	0.23	0.25**	0.11*	0.095**	3866.00**	2434.13**	8.00	7.26	1	1
28.	G28	0.26	0.20*	0.11*	0.075*	3512.00**	1878.04**	7.80	5.35**	1	1
	GM	0.24	0.16	0.06	0.041	2287.68	1453.48	5.10	2.43	2.71	4
	Range	0.12-0.36	0.06-0.25	0.14-0.03	0.09-0.01	1236.37-4284.00	460-2555.45	2.27-12.00	0.83-5.35	1-7	1-9
	C. D. (P=0.05)	0.08	0.05	0.04	0.02	139.78	102.00	4.51	1.54	0.00	0
	C. D. (P=0.01)	0.10	0.77	0.063	0.036	186.78	136.00	6.023	2.05	0.00	0

N – Normal, D – Drought, SL – Shoot length, RL – Root length, TSL – Total seedling length, RSR – Root-shoot ratio, G% – Germination percentage, FSW – Fresh seedling weight, DSW – Dry seedling weight, SV I – Seedling vigour index I, SV II – Seedling vigour index II and LRR – Leaf rolling ratio.

genotypes which are better in quality viz., Basmathi, Karudan samba and Kichadi samba which are also genetically divergent to Karuppukavuni. Thus, it was concluded that the genotypes Kuzhiadichan and Mapillai samba could be selected as superior genotypes for further exploitation in breeding program.

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