

Genetic diversity and screening of rice genotypes for drought tolerance under rainfed upland ecosystem of Tamil Nadu

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(Received 27 May, 2024; Accepted 24 July, 2024)

ABSTRACT

The present investigation was undertaken to decipher the extent of diversity in 120 rice genotypes under natural stress condition during the years 2020-21 and 2021-22. Analysis of variance revealed that significant variability with respect to all the nine traits *viz.*, days to fifty per cent flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, grain length, grain breadth, thousand grain weights and grain yield per plant under study. Mahala Nobis D² values and non-hierarchical Euclidean cluster analysis categorized the genotypes under study in ten clusters. The maximum intra cluster distance was obtained in cluster VII (35.58) and farthest inter cluster distance was between clusters VI and VII (74.49). The cluster IV, VI, IX, and X exerted superior clusters mean performance. The characters *viz.*, number of grains per panicles, plant height, days to fifty per cent flowering, grain length, grain breadth along with grain yield per plant were the major contributors for genetic divergence. Based on genetic diversity and *per se* mean performance of the genotypes AURC 3, AURC 4, AURC 10, GSR8, Kandakasala, IR 64 and Banshpata are more drought stress tolerant that could be used as donor parent in future drought varietal breeding programme.

Key words: Drought tolerance, Rice, Genetic diversity, Mahalanobis D², Yield traits

Introduction

Rice (*Oryza sativa* L.) is the prominent staple cereal food grain and consumed by nearly one-third of the world's population and two-thirds of the Indian population, thus holds the key for food security and plays a pivotal role in national economy. At the global level, 158.4 million hectares around the world was devoted to rice cultivation with an annual production of 769 million tons and productivity of around 4717 kg/ha. The area, production and productivity of rice in India is 46.38 million hectares, 130.29 million tons and 2809 kg ha⁻¹, respectively. In

Tamil Nadu, the area under rice cultivation was 2.21 million hectares with productivity 8.07 million tons and productivity of 3658 kg per hectare (Agricultural Statistics at a glance, 2022-23). In terms of rice production and consumption, Asia is in first place. According to FAO Report (2021), average production of rice is estimated as 499.1 million tons and due to rise in population; the needed is expected to increase up to 2000 million metric tons by the year 2030.

Globally, the major rice production constraints included several stress factors namely biotic and abiotic stress that lead to a decline in rice production

in the rain fed area (Sabesan *et al.*, 2009). Amongst abiotic stresses, drought is the most detrimental causes and more than 50% of world arable land is expected to be affected by drought in 2050 (Singhal *et al.*, 2016). However, rice is considered one of the most drought sensitive plant due to its small root system, thin cuticular wax and swift stomatal closure. Rice requires an ample amount of irrigated fresh water during its cropping period as compared to other cereals (i.e., about 5000 liters of water/kg of seeds production). The crop suffers either early drought or late drought as a consequence of erratic and uneven distribution of rainfall during the cropping season. Reportedly, nearly 43 million hectares rain fed rice faces to occasional or frequent drought stress in Asia. The global reduction in rice production due to drought averages 18 million tons annually. In Asia alone, it is estimated that a total of 23 Mha of rice fields (10Mha upland and 13Mha lowland) are drought prone (Wang *et al.*, 2019). Lack of high yielding varieties and low rates of their adoption are major reasons for the low productivity in water limiting environmental conditions. Most of the high yielding green revolution varieties developed so far are not bred specifically for drought prone situations.

Drought is threatening food security in this region of Tamil Nadu. Therefore, raising production in these areas is crucial for alleviating poverty and ensuring food of the rural poor. At present, suitable drought response rice cultivar is essential for the expansion of rice production in drought prone areas of Tamil Nadu such as Ramanathapuram, Sivangangai, Thiruvavur and Dharmapuri. In these regions of traditional landraces are important reservoirs of many valuable traits (Hanumaratti *et al.*, 2008). Generally, landraces are highly adapted to fluctuation environment and also have paramount of resistance to biotic and abiotic stress. Green Super Rice (GSR) varieties have highly stable yield even when grown with less agricultural inputs or under unfavorable natural calamities. Selection for drought tolerance based on grain yield under natural stress was effective in identification of superior drought response genotypes. Hence, it is essential to screen crop varieties tolerance to drought stress under natural stress condition.

To further analyze the estimation of genetic diversity would help the plant breeder in choosing the potential parents for the success of drought breeding programme. It is imperative to understand of the

true genetic diversity pattern, individual trait contribution, cluster distance and genetic relationships of the close relatives of rice accessions will facilitate more effective conservation and utilization of germplasm for the improvement of the drought tolerant rice varieties. With this background, the present study was focused to identify suitable genotypes to augment better drought tolerance rice donors for improving tolerance as well as yield under natural stress condition.

Materials and Methods

Plant materials

The experimental material for this genetic divergence study comprised of 120 rice genotypes which were collected from different sources of the country. It consisted of 60 traditional varieties obtained from Northern India and Tamil Nadu origin, 20 advanced rice cultures were collected from Department of Genetics and Plant breeding, Annamalai University, five germplasm accessions were procured from genetic stock of International Rice Research Institute (IRRI), Philippines; 20 genotypes originated from Andhra Pradesh and Meghalaya along with 15 ruling varieties of Tamil Nadu collected from Tamil Nadu Rice Research Institute (TRRI) Aduthurai, Regional Research Station, Ambasamudiram, Regional Research Station, Paramakudi, Tamil Nadu, India were utilized in present study. The one hundred and twenty rice genotypes are presented in (Table 1). The germplasm were studied in detail for their physiological nature of drought tolerance.

Experimental site

The field experiment was conducted at the Plant breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar, Tamil Nadu, India during rice growing season (Navara season, 2020 and 2021 December to April). The pooled data was taken for D² analysis. The site geographic coordinates are 11° 24' N latitude, 79° 44' E longitude with an elevation of + 5.79 m above sea level. The meteorological parameters were recorded throughout the cropping period, which is represented in (Figure 1).

Experimental design and cultural practices

The experiment was laid out in randomized block design with three replications. The genotypes were

direct seeded in plot of 6 rows with each row of 5 meter length. The spacing was maintained at 20 x 15 cm (row to row and plant to plant). The recommended agronomic practices were followed up to active flowering stage. The crop before flowering stage was irrigated at weekly interval and after blooming stage irrigation was completely stopped to study the drought tolerance of selected rice genotypes under drought condition.

Data observations recorded and Analysis

Nine quantitative traits were measured and recorded on five randomly selected plants per replication at appropriate stages following, SES (IRRI, 2013). Multivariate analyses were performed on the following phenological (days to 50% flowering), morphological (plant height, number of productive tillers per plant, panicle length, number of grains per panicle), seed traits (length of grains, breadth of grains, thousand grain weight and grain yield per

Table 1. List of 120 genotypes for D² analysis

G.NO	Name of the Genotypes	G.NO	Name of the Genotypes	G.NO	Name of the Genotypes
G1	Anai komban	G41	Kerala Sundari	G81	GSR 8
G2	Chinnar	G42	Krishnakamod	G82	AU1 GSR
G3	Chitraikar	G43	Kudai Vazhai	G83	IR 20
G4	Karunkuruvai	G44	Kumbersale	G84	IR 64
G5	Kichadi samba	G45	Kuruvai Kalanjiyam	G85	IR 36
G6	Kuliadichan	G46	Lakhisar	G86	ADT 37
G7	Kullakar	G47	Lilabati	G87	ADT 36
G8	Kuzhiyadichan	G48	Madhumalati	G88	ADT 54
G9	Kuzhivedichan	G49	Mappillai samba	G89	ASD 16
G10	Norunkan	G50	Mehijawain	G90	ASD 19
G11	Seeraga samba	G51	Milagu Champa	G91	CO 43
G12	Sigappukavuni	G52	Moirang Phou	G92	C0 R 50
G13	Sornamashuri	G53	Mundan Kayama	G93	C0 51
G14	Thangam samba	G54	Navara Black Skin	G94	TPS R (4)
G15	Thengai poo samba	G55	Rakthasali	G95	TRY 3
G16	Thooyamalli	G56	Shapasad	G96	IW Ponni
G17	Varappu kudaichan	G57	Sivappu Kuruvikar	G97	MDU 5
G18	Aadam Cheeni	G58	Sukhadass	G98	PMK 2
G19	Ambhemohar	G59	Thulsi Bas [White]	G99	PMK 3
G20	Anadanoor Sanna	G60	Thulsi Manjari	G100	ANNA R 4
G21	Badsha Bhog	G61	AURC1	G101	SHABAGIDHAN
G22	Banshpata	G62	AURC2	G102	SIGAPPI
G23	Chak Hao Poretton	G63	AURC3	G103	BPT 5202
G24	Dadshial	G64	AURC4	G104	BPT 5204
G25	Dayala Modina	G65	AURC5	G105	Varadhan
G26	Dudheshwar	G66	AURC6	G106	Gold Saivam
G27	Ghansal	G67	AURC7	G107	Gold Amman
G28	Gobinda Bhog	G68	AURC8	G108	Saheo
G29	Illuppai poo samba	G69	AURC9	G109	Mohanand
G30	Irrawaddy Delta	G70	AURC10	G110	CAU R1
G31	Jeeraga Champa	G71	AURC11	G111	Chandrashini
G32	Kakcheng Phou	G72	AURC12	G112	Swarna
G33	Kalajeera	G73	AURC13	G113	CR DHAN 40
G34	Kalanamak	G74	AURC14	G114	Protazin
G35	Kamini Bhog	G75	AURC15	G115	Zincodhan
G36	Kandakasala	G76	AURC16	G116	Kalasanth
G37	Kari Basumathi	G77	AURC17	G117	Shasharang
G38	Karuppu Kavuni	G78	AURC18	G118	PB1121
G39	Karusiraka Champa	G79	AURC19	G119	Mala
G40	Katarni	G80	AURC20	G120	Gotra

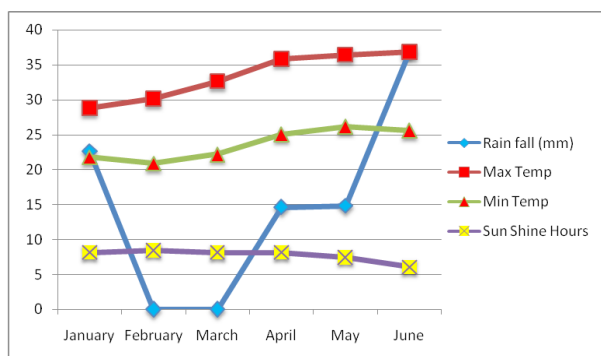


Fig. 1. Metrological parameters throughout the cropping period

plant) were estimated under natural stress condition. The distances between the genotypes were worked out using (Mahalanobis, 1936) and grouping of varieties were done following the Tocher's method as detailed by (Rao, 1952). The data were analyses with the technique of D^2 statistics. The software package INDOSTAT version 8.5 was used to analyse the statistical data.

Results and Discussion

The analysis of variance revealed that substantial significant differences for all the nine traits studied in 120 rice genotypes under natural drought stress condition. This is indicated that genotypes selected for this study were genetically divergent, which could be utilized in progressive drought breeding programme. Significant differences among the genotypes were earlier reported by Ahmad *et al.* (2014).

Clustering Pattern

Multivariate analysis giving the D^2 values between 120 genotypes revealed that these genotypes could be grouped into ten distinct clusters in natural drought stress condition. The pattern of clustering is depicted in (Table 2). Among these clusters, maximum numbers of 47 genotypes are possessed in cluster I. The next largest cluster II comprises of 39 genotypes while cluster III had 16 genotypes. Cluster VI and cluster VIII having 9 and 6 genotypes respectively. The rest of five clusters (IV, V, VII, IX and X) are mono-genotypic containing one genotype each. Cluster consisting of mono-genotypic provide information that the genetic constitution of the genotype belonging to the cluster is entirely different among the all genotypes. The tendency of genotypes (Exotic & Indigenous collections) occurring in clus-

ters cutting across geographical boundaries demonstrates that geographical isolation not only factor causing genetic diversity. The pattern distribution of genotypes showed that genotypes of different geographical origins were clubbed in the same cluster, whereas the genotypes from same geo-graphical origin fell in different clusters, indicates that there is no formal relationship between geo-graphical and genetic diversity. Possibly genetic drift and selection under different environments could have cause great divergence than geographical distance and desirable diverse genotypes may be selected from the locally adopted varieties. Keep in this view, selection of parents for hybridization should not be on geographic diversity alone. Genetic diversity must be given greater importance in the selection of parents. Similar findings of non-correspondence of geographic origin with genetic diversity were also reported by Shafina Haque *et al.* (2014) and Sheeba and Mohan (2021).

Cluster-distances among the rice germplasm

The mean intra and inter cluster distance among ten clusters were computed and presented in (Table 3). The intra and inter cluster mean values were arise due to different genetic architecture of various genotypes belonging to different clusters. In the present study, it is indicated that more prominent inter cluster distances when compared to intra-cluster distances and there is genetic diversity shown among the genotypes of the genetic distant groups. Similar results were also suggested by Korada *et al.* (2021).

The mean intra-cluster D^2 values were ranged from 0 (Cluster IV, V, VI, IX and X) to 35.58 (Cluster VIII). The highest intra-cluster distance was noticed in cluster VIII ($D^2=35.58$) possessing 4 genotypes, followed by VI ($D^2=34.25$) consisted 9 genotypes and lowest distance was recorded by cluster I ($D^2=28.40$) indicated that homogenous nature of the genotypes within clusters. Hence, selection will be ineffective. No intra cluster distance was observed in cluster IV, V, VII, IX and X.

The minimum inter cluster distance was observed between cluster V and VII (17.79) indicating close relatedness among the genotypes included. The maximum inter cluster distance was found between cluster VI and cluster VII ($D^2=74.49$) followed by the cluster VI and IX ($D^2=73.34$), which indicated that plethora variation in genotypes. Hence, selection of genotypes from these assorted clusters may be tailored based on the highest areas

for the desirable traits, which would be utilized made use of in improvement through inter-varietal hybridization. Similar findings were reported by Mukul *et al.* (2019) and Pathak *et al.* (2020).

Cluster means

The cluster mean values for nine quantitative traits were presented in (Table 4). Mean values of traits varied in different clusters. The cluster mean for days to 50% flowering was lowest in cluster IX (61.66) while it was the highest in cluster VII (117.68). Taller plants were present in cluster IV (147.53) while shorter plant types were observed in cluster X (85.74). For number of productive tillers per plant, cluster mean was highest in cluster IV (21.55) and lowest in cluster V (10.93). Longer panicle length was grouped in cluster IV (31.32) while cluster V (22.29) had short panicle. Number of

grains per panicle was highest in cluster VI (408.50) while cluster IX (72.68) had the least. Cluster mean for grain length was longer in cluster X (11.15) and shorter in cluster IV (6.61). Cluster III (3.00) had the longest grain width while cluster X (1.76) had the least. Cluster mean for thousand grain weight was highest in cluster III (27.41) and lowest in cluster IX (16.31). Grain yield per plant was highest in cluster VI (52.52) and lowest in cluster X (16.83).

The genotypes with maximum mean value are used as parental material in progressive breeding. Based on the genetic distance values, cluster constellation, the most divergent genotypes were from clusters IV, VI, VII and X which could be involved in a crop improvement programme. The accessions *viz.*, G63- AURC 3, G64- AURC 4, G70- AURC 10 and G81- GSR8 present in cluster VI has highest grain yield per plant and number of grains per

Table 2. Clustering pattern among 120 rice collections in 10 clusters

Cluster No.	Number of Genotypes	Genotypes included
I	47	G-4 Karunkuruvai, G-6 Kuliadichan, G-12 Sigappukavuni, G-13 Sornamashuri, G-20 Anadanoor Sanna, G-25 Dayala Modina, G-26 Dudheshwar, G-29 Illuppai poo samba, G-30 Irrawaddy Delta, G-34 Kalanamak, G-39 Karusiraka Champa, G-40 Katarni, G-41 Kerala Sundari, G-42 Krishnakamod, G-43 Kudai Vazhai, G-44 Kumbarsale, G-48 Madhumalati, G-52 Moirang Phou, G-56 Shapasad, G-61 AURC 1, G-62 AURC 2, G-65 AURC 5, G-66 AURC 6, G-67 AURC 7, G-69 AURC 9, G-71 AURC 11, G-72 AURC 12, G-73 AURC 13, G-78 AURC 18, G-80 AURC 20, G-85 IR 36, G-87 ADT 36, G-88 ADT 54, G-89 ASD 16, G-92 C0 R 50, G-93 C0 51, G-95 TRY 3, G-96 IW Ponni, G-97 MDU 5, G-99 PMK 3, G-100 ANNA R 4, G-101 SHABAGIDHAN, G-105 Varadhan, G-106 Gold Saivam, G-108 Saheo, G-109 Mohanand, G-119 Mala
II	39	G-2 Chinnar, G-5 Kichadi samba, G-7 Kullakar, G-8 Kuzhiyadichan, G-9 Kuzhivedichan, G-10 Norunkan, G-17 Varappu kudaichan, G-18 Aadam Cheeni, G-19 Ambhemohar, G-21 Badsha Bhog, G-23 Chak Hao Poretton, G-24 Dadshial, G-27 Ghansal, G-28 Gobinda Bhog, G-32 Kakcheng Phou, G-33 Kalajeera, G-35 Kamini Bhog, G-37 Kari Basumathi, G-38 Karuppu Kavuni, G-45 Kuruvai Kalanjiyam, G-46 Lakhisar, G-50 Mehijawain, G-55 Rakthasali, G-60 Thulsi Manjari, G-68 AURC 8, G-74 AURC 14, G-83 IR 20, G-86 ADT 37, G-91 CO 43, G-94 TPS R (4), G-102 SIGAPPI, G-103 BPT 5202, G-104 BPT 5204, G-111 Chandrashini, G-112 Swarna, G-113 CR DHAN 40 Z, G-114 Protazin, G-115 Zincodhan, G-120 Gotra
III	16	G-1 Anai komban, G-3 Chitraikar, G-11 Seeraga samba, G-14 Thangam samba, G-47 Lilabati, G-49 Mappillai samba, G-51 Milagu Champa, G-54 Navara Black Skin, G-58 Sukhadass, G-75 AURC 15, G-76 AURC 16, G-77 AURC 17, G-79 AURC 19, G-90 ASD 19, G-98 PMK 2, G-117 Shasharang
IV	1	G-36 Kandakasala
V	1	G-116 Kalasanth
VI	9	G-31 Jeeraga Champa, G-53 Mundan Kayama, G- 57 Sivappu Kuruvikar, 59 Thulsi Bas [White], G-63 AURC 3, G-64 AURC 4, G-70 AURC 10, G-81 GSR 8, G-107 Gold Amman
VII	1	G-118 PB1121
VIII	4	G-15 Thengai poo samba, G-16 Thooyamalli, G-82 AU1 GSR, G-110 CAU R1
IX	1	G84- IR 64
X	1	G22- Banshpata

Table 4. Cluster mean values for nine quantitative traits in rice genotypes

Cluster	X1	X2	X3	X4	X5	X6	X7	X8	X9
I	82.96	104.13	16.43	23.64	183.76	8.39	2.52	22.49	36.19
II	96.80	115.72	17.43	23.72	128.94	7.38	2.49	18.27	24.22
III	87.41	132.60	17.95	25.04	123.44	8.83	3.00	27.41	32.23
IV	91.23	147.53	21.55	31.32	283.29	6.61	2.60	21.05	33.17
V	110.85	77.04	10.93	22.29	178.69	9.76	2.46	23.10	32.35
VI	80.81	97.44	16.01	23.71	408.50	7.67	2.49	24.72	52.52
VII	117.68	119.74	16.49	26.96	139.42	10.25	2.41	21.53	30.71
VIII	100.49	87.77	13.33	22.72	248.69	6.92	2.69	26.60	38.11
IX	61.66	92.73	15.95	23.53	72.68	8.85	2.30	16.31	32.17
X	74.49	85.74	17.61	22.99	98.29	11.15	1.76	21.43	16.83
General mean	83.93	110.75	16.83	23.90	175.24	8.04	2.56	21.96	32.66

Table 3. Average intra and inter cluster D² values of 10 clusters of 120 genotypes of rice

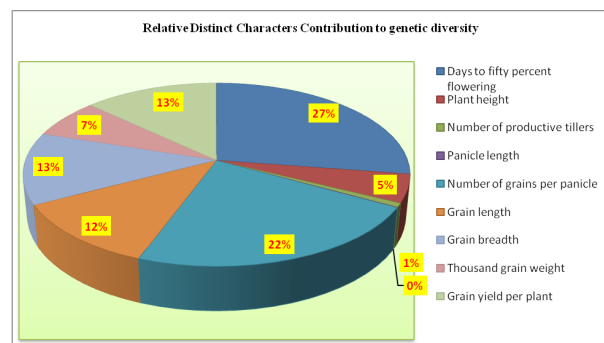
Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X
I	28.40	37.57	38.48	34.58	37.96	55.51	43.31	38.65	35.25	40.70
II		28.80	40.96	38.69	36.94	71.48	36.41	42.89	43.64	45.51
III			34.10	47.50	44.70	73.30	44.25	49.02	41.46	47.36
IV				0	44.81	46.42	47.82	34.88	51.44	53.13
V					0	64.65	17.79	36.13	53.06	43.59
VI						34.25	74.49	52.84	71.61	73.34
VII							0	45.14	55.78	44.55
VIII								35.58	56.65	57.92
IX									0	34.45
X										0

panicle. The genotype (G36- Kandakasala) was grouped in cluster IV has number of productive tillers per plant and panicle length. Early flowering (61.66) and dwarf plant (85.74) and slender genotypes (1.76) *viz.*, IR64 and Banshpata was clubbed in cluster IX and X respectively. Under natural drought stress, cultivars with earlier reproductive stage can be more tolerant at the end of season and they produce more yields because premature blooming is an important mechanism to escape from drought stress. Therefore, difference in flowering

time among the genotypes under this condition could be used in future breeding programmes for developing with earliness variety of rice. These findings were supported by the results of Abarshahr *et al.* (2011). The G63- AURC 3, G64- AURC 4, G70- AURC 10, G81- GSR8 G36- Kandakasala, G84- IR 64 and G22- Banshpata crosses involving genotypes of clusters IV, VI IX and X could produce recombinants that would be high yielding as well as early maturing progenies.

Character's contribution to diversity

The ranking technique was adopted to rank the characters in the order of the contribution to total genetic divergence. The contribution towards the total genetic divergence is presented in (Figure 2). The relative contribution of individual character towards the expression of genetic diversity estimated over character wise D² value revealed that days to fifty percent flowering (27.39 per cent) contribution and number of grains per panicle (22.54 per cent) and grain yield per plant (13.04 per cent) were the three major contributors under natural drought stress conditions. Similar findings were made

**Fig. 2.** Relative contribution of distinct characters to D² values

Perween *et al.* (2020) for number of fertile grains per panicle (15.07 per cent) under drought stress condition.

Conclusion

The experiment unraveled the hidden buffering capacity of the rice genotypes for the study. The 120 rice genotypes were grouped into ten clusters under natural drought stress condition. This indicates that several factors of clustering that played role under condition were rendered obsolete under natural drought stress. The intra cluster distance ranged from 28.04 to 34.25. The values indirectly revealed the untapped hidden diversity among the genotypes under study. The characters contribution to the genetic diversity observed revealed that days to fifty percent flowering, number of grains per panicle, grain yield per plant, grain length and grain breadth and as major source of divergence under natural drought stress condition. Based on divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes for drought tolerance. From the study can concluded that genotypes namely AURC 3, AURC 4, AURC 10, GSR8, Kandakasala, IR 64 and Banshpata from clusters VI, IX and X were the most diverse parents which would be used in drought tolerance varietal improvement programme.

Acknowledgement

The Authors are grateful to the Department of Genetics and Plant Breeding, Faculty of Agriculture, Annamalai University, Annamalai Nagar for providing research facility to conducting the field trails.

Conflict of Interest- None

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