

Genetic Diversity of Rice Genotypes Screened under Normal and Flash Flooded Condition

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ABSTRACT

The present investigation was undertaken to explore the extent of diversity in 30 rice genotypes under normal (E1) and flash flooded conditions (E2) during samba, 2020. Analysis of variance divulged significant variability with respect to all the nine traits viz., days to 50% flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth and grain yield per plant under study. Mahalanobis D^2 values and non-hierarchical Euclidean cluster analysis categorized into seven clusters in E1 and three clusters in E2. The maximum intra cluster D^2 was obtained in cluster V (80.618) in E1 and III (1626.542) in E2 and farthest inter cluster

distance between III and cluster VI (129.797) in E1, cluster II and III (2743.060) in E2. The clusters VI and II exerted superior mean performance in E1 and cluster III and II had in E2. The characters viz., number of grains per panicles, panicle length, number of productive tillers per plant, grain breadth along with grain yield per plant were the major contributors for genetic divergence in E1. In the flash flood tolerance environment E2, the traits of plant height, grain breadth, and grain yield per plant contributed more toward the genetic divergence. Based on genetic diversity and performance of the genotypes Poongar, seeraga samba, CR 1009 sub1 and Swarna sub 1 are the superior parents for flash flood tolerance. Hence, these genotypes could be lucidly utilized for the flash flood genetic improvement program.

Keywords Flash flood tolerance, Genetic diversity, Mahalanobis D^2 , Rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is the staple food crop globally consumed by more than half of the world population. Asia alone produces 705.39 million tonnes of rice, accounting for more than 90 % of global rice output of 782 million tonnes. In India, rice is being grown over a total area of 43.77 million hectares with a production of 169.14 million tonnes and a productivity of 3.86 tonnes per hectare (Directorate of Economics and Statistics 2020). Tamil Nadu is one of the major rice producing states in India with an area of 19.00

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lakh hectares and production and productivity of 68.66 lakh metric tonnes and 3.61 tonnes /hectare, respectively. Coastal rice ecosystems, covering more than 16% of rice areas worldwide 20 million hectares are adversely affected by annual flooding (Sathyaraj *et al.* 2023).

The extensive rice growing areas in South and South-East Asia especially India, Bangladesh, Thailand, Vietnam, Myanmar and Indonesia are exposed to flash flooding during monsoon season. Nearly 22 million hectares of rainfed lowland areas of South and South-East Asia get affected due to flooding, out of which about 6.2 million hectares of rice lands are in India (Azarin *et al.* 2017). Out of 22 million hectares, 15 million hectares of rainfed lowland are affected only due to short term flash flooding (Singh *et al.* 2017). Flash floods are highly unpredictable which may occur more than one time in a season and can affect at any growth stage of crops. Ten to 100% yield losses had been reported due to flash floods, which depend on water depth, duration of submergence, temperature, turbidity of water, soil fertility, light intensity and age of the crop (Wazifa *et al.* 2018).

The Indian rice cultivar FR13A stood out as extremely submergence tolerant; 100% of 10-day-old seedlings survived 7 days of complete submergence (Ismail *et al.* 2013). FR13A also has additional QTLs that contribute to its tolerance. Sub1 was subsequently fine-mapped and cloned, and three genes encoding putative ethylene responsive factors (ERF), Sub1A, Sub1B, and Sub1C, were identified, with Sub1A recognized as the primary determinant of submergence tolerance (Aslam *et al.* 2023). Cloning of Sub1A provided opportunities to gain more insight into the molecular mechanisms involved and to unravel the pathways underlying the submergence tolerance conferred by this gene (Mackill *et al.* 2010). Rice production is now at risk due to unprecedented effect of climate change. The threat is increasing day by day due to unpredictable rainfall. Rice cultivation is now riskier due to the prevalence of both excess and deficit rainfall in the same growing season. There is an urgent need to identify high yielding genotypes suitable for flashflood condition.

Mahalanobis's D^2 statistics is a powerful tool to

quantify the degree of genetic divergence between the genotypes and to relate clustering pattern with the geographic origin. Genetic diversity analysis is helpful in estimating and establishing of genetic relationship of genotypes in germplasm collection, identifying the diverse genotypes having wider variability for various characters and for efficient selection of parents for hybridization program. Changing climatic parameters has wanted frequent and unexpected occurrence of flash flood in Cuddalore district. Hence, the present study was conducted to know the untapped genetic potential of the traditional and released varieties under flash flood.

MATERIALS AND METHODS

The experiments were carried out at the Plant Breeding Farm, Department of Genetics and Plant Breeding, Faculty of Agriculture, Chidambaram during the samba season 2020, situated at 10.25 m MSL, with 11° 38' N latitude, 79 ° 72' E longitude. A set of 30 rice genotypes including fifteen well-characterized released varieties, two rice culture and 11 traditional varieties along with two submergence tolerant check Swarna Sub 1 and CR 1009 Sub1 were used in this study (Table 1). The experiment was laid out in a Randomized Block Design with three replications. The sowing date for our study was so planned that the flash flooding might coincide at active tillering stage and at the time of flowering. The crop was maintained under two conditions that is normal (E1) and flash flood (E2). Nursery was raised and twenty-one days old seedlings were transplanted in the field for evaluation under normal (E1) and low lying field evaluation under flash flood (E2). Weekly meteorological data from sowing including till harvest, rainfall, relative humidity, temperature and rainy days were presented in Table 2. Flash flood happened during the first week of December, 2020. The stage of the crop under flash flooded environment (E2) was presented in Table 3. Recommended agronomic and cultural practices were adopted to obtain good phenotypic expression of the traits. Data were recorded on five random plants in each replication of each genotype for nine quantitative traits viz., days to 50% flowering, plant height, number of productive tillers per plant, panicle length, number of grains per panicle, 1000 grain weight, grain length, grain breadth and grain yield per plant.

Table 1. List of genotypes selected for D² analysis.

Genotypes code	Varieties/ culture	Source
G1	CR-1009 Sub-1	Plant Breeding Farm, Annamalai University, Tamil Nadu.
G2	SWARNA Sub-1	Plant Breeding Farm, Annamalai University, Tamil Nadu.
G3	ADT-49	Tamil Nadu Rice Research Institute, Aduthurai
G4	ADT-43	Tamil Nadu Rice Research Institute, Aduthurai
G5	ADT-36	Tamil Nadu Rice Research Institute, Aduthurai
G6	TKM-13	TNAU, Coimbatore, Tamil Nadu
G7	TKM-9	TNAU, Coimbatore, Tamil Nadu
G8	ASD-18	TNAU, Coimbatore, Tamil Nadu
G9	BPT-5204	Bapatla Agriculture College, Andhra Pradesh
G10	CO-43	TNAU, Coimbatore, Tamil Nadu
G11	IR-64	TNAU, Coimbatore, Tamil Nadu
G12	IR-36	TNAU, Coimbatore, Tamil Nadu
G13	AURC-4	Plant Breeding Farm, Annamalai University, Tamil Nadu.
G14	AU-1 GSR	Plant Breeding Farm, Annamalai University, Tamil Nadu.
G15	ANPRC-9	Rice Culture, Arunachal Pradesh
G16	NDLR-7	Nandyal Rice Research Station, Andhra Pradesh.
G17	NDLR-8	Nandyal Rice Research Station, Andhra Pradesh.
G18	MTU-7029	Rice research station, Marteru , Andhra Pradesh
G19	JGL-384	Jagityala Rice Research Station, Andhra Pradesh
G20	White ponni	TNAU, Coimbatore, Tamil Nadu
G21	Mappillai samba	Thiruvannamalai, Tamil Nadu
G22	Kullakar	Sethurayan, Kudikadu Thanjavur, Tamil Nadu
G23	Aruvathm kuruvai	Mandalakottai, Thanjavur Tamil Nadu
G24	Kallimadayan	Thanjavur ,Tamil Nadu
G25	Kattu yanam	Vaduvur, Thanjavur Tamil Nadu
G26	Poongkar	Avaniyapuram, Thanjavur
G27	Seeraga samba	Thuramadi , Thanjavur
G28	Salem sannaam	Salem, Tamil Nadu
G29	Mutrina sannaam	Ulunthurpet, Tamil Nadu
G30	Adukunel	Vaduvur, Thanjavur Tamil Nadu

Multivariate D² analysis was done as per (Mahalanobis 1936) and quantitative diversity of genotypes were grouped into various clusters following Tocher's method (Rao 1952). The D² statistics were computed using the INDOSTAT software.

RESULTS AND DISCUSSION

The analysis of variance revealed that mean squares were highly significant differences for all the nine traits under both normal and flash flooded conditions, which reflected the presence of high magnitude of variability among the rice germplasm utilized for this study.

The genetic diversity is important for rice productivity improvement through selection for direct commercial use and for breeding to mitigate abi-

otic and biotic stress that affect the crop. Effective breeding for target traits requires careful selection of parents with a wide genetic base to enhance genetic gain. The complementary of normal and flash flood approaches in crop diversity help us to understand not only the variability of the germplasm but also value of the variability is observed. Multivariate analysis is very important tool to study morphologically complex individuals and for measuring the degree of divergence between different populations. Employing Mahalanobis generalized distance the divergence in 30 genotypes of rice was assessed for nine yield contributing characters.

Clustering pattern

In the present study, D² analysis of the 30 genotypes confirmed the presence of high diversity among the

Table 2. Weekly meteorological mean data from 2020 January to 2021 January.

Week no.	Period	Temperature (°C)		Relative humidity (%)	Rainfall (mm)	Rainy days
		Max	Min			
1	Sep 3 – 9	32.9	24.4	86	008.0	2
2	Sep 10 – 16	32.4	24.2	84	008.6	1
3	Sep 17 – 23	33.6	24.6	83	006.2	1
4	Sep 24 – 30	34.4	23.9	88	196.2	3
5	Oct 1 – 7	33.9	24.6	86	041.0	2
6	Oct 8 – 14	33.1	23.7	86	013.8	1
7	Oct 15 – 21	32.5	23.7	85	007.0	1
8	Oct 22 – 28	37.4	24.3	86	003.8	1
9	Oct 29- Nov 4	32.2	23.6	87	-	-
10	Nov 5 – 11	31.1	23.1	88	078.6	3
11	Nov 12 – 18	31.1	23.5	96	168.4	5
12	Nov 19 – 25	29.1	23.2	91	013.8	1
13	Nov 26 - Dec 2	29.4	22.8	92	171.8	4
14	Dec 3 – 9	26.2	22.7	99	661.3	7
15	Dec 10 – 16	28.9	21.7	91	037.0	1
16	Dec 17 – 23	27.9	21.9	92	086.4	3
17	Dec 24 – 31	28.4	21.4	91	049.6	2
18	Jan 1-7	28.2	22.3	95	121.4	5
19	Jan 8- 14	27.7	21.9	96	247.2	7
20	Jan 15 – 21	28.8	21.6	91	012.8	1
21	Jan 22 – 28	30.3	21.2	91	-	-
22	Jan 29 -Feb 4	29.7	21.4	89	-	-

Table 3. Crop stage under flashflood (E2).

Genotypes	Date of sowing	Crop stage at flash flood (December 3-9)
G1		Panicle initiation to booting
G2		Panicle initiation to booting
G3		Flowering
G4		Ripening Phase
G5		Ripening Phase
G6		Flowering
G7		Flowering
G8		Flowering
G9		Panicle initiation to booting
G10		Heading to flowering
G11		Ripening Phase
G12		Ripening Phase
G13		Flowering
G14		Flowering
G15	1/9/2020	Heading to flowering
G16		Flowering
G17		Flowering
G18		Flowering
G19		Flowering
G20		Flowering
G21		Panicle initiation to booting
G22		Ripening Phase
G23		Ripening Phase
G24		Ripening Phase
G25		Tillering to panicle initiation
G26		Ripening Phase

Table 3. Continued.

Genotypes	Date of sowing	Crop stage at flash flood (December 3-9)
G27		Panicle initiation to booting
G28		Heading to flowering
G29		Heading to flowering
G30		Flowering

genotypes by their resolution into seven clusters in E1 and three clusters in E2 (Table 4). Among the clusters, in E1 the cluster IV and V consist of 9 genotypes had maximum number of genotypes followed by III having 4 genotypes, cluster VI having 3 genotypes, cluster I and II having 2 genotypes and cluster VII are monotypic which indicates that these clusters contain the most diverse genotypes.

In E2, cluster I had twenty four genotypes and cluster II and III consisted of three genotypes in each cluster. The group of clustering constellation in the present study culled out that eco- geographical diversity was not related to the genetic diversity. The existence of genetic divergence in the rice germplasm

Table 4. Composition of D² clusters for 30 rice genotypes in E1 and E2.

Normal –E1 (7 Clusters)			Flash Flood –E2 (3 Clusters)		
Clusters	No. of genotypes	Name of genotypes	Clusters	No. of genotypes	Name of genotypes
I	2	G7 (TKM- 9), G9 (BPT-5204)	I	24	G1 (CR-1009 Sub-1), G2 (Swarna Sub-1), G3 (ADT49), G4 (ADT-43), G5 (ADT-36), G6 (TKM-13), G7 (TKM- 9), G8 (ASD-18), G9 (BPT-5204), G10 (CO-43), G11(IR64), G12 (IR36), G13 (AURC-4), G14 (AU-1 GSR), G15 (ANPRC-9), G16 (NDLR-8), G17 (NDLR-8), G18 (MTU-7029), G19 (JGL 384), (Whiteponni), G21 (Mappillaisamba), G22 (Whiteponni), G21 (Mappillaisamba), G22 (Kuliakar), G23 (Aruvathihaamkuruvai), G24 (Kallimadayan, G25 (Kattu yanam), G28 (Salem Sannam) 30 (Adukunel)
G20			II	3	G26 (Poonkgar), G27 (Seeragasamba), G29 (Mutrinassannam)
II	2	G4 (ADT-43), G5 (ADT-36)	III	3	
III	4	G1(CR-1009SUB-1), G2 (Swarna sub -1), G17 (NDLR-8), G19 (JGL 384).			
IV	9	G3 (ADT49), G6 (TKM-13), G8 (ASD 18 (CO43), G11 (IR64), G12 (IR36), G13 (AURC4), G22 (Kullakar), G29 (Mutrinassannam))	-	-	-
V	9	G14(AU1GSR), G15(ANPRC9), G16 (NDLR8), G18(MTU7029), G20 (Whiteponni),G21(Mappillasisa) G 23 (Aruvathaa-mkuvai),G24 (Kalimadayan), G25 (Kattu yanam)	-	-	-
VI	3	G26 (Poonkgar), G28 (Sallmaannam), G30 (Adukunel)	-	-	-
V	1	G27 (Seeraga Samba)	-	-	-

was earlier reported by (Sabesan 2018) and (Gnaneswari *et al.* 2023).

Cluster-distance

The intra and inter cluster distance among seven clusters in E1 while three clusters in E2 were computed and presented in (Table 5). The intra cluster distance for E1 and E2 analysis ranged from 15.059 (cluster I) to 80.618 (cluster V) and 1502.891 (cluster I) to 1626.542 (cluster III) respectively.

The highest value of intra cluster distance V ($D^2 = 80.618$) possessing 9 genotypes revealed that in E1 followed by VI ($D^2 = 77.155$) consisted 3 genotypes and minimum distance was observed by cluster I ($D^2 = 15.059$), while cluster III ($D^2 = 1626.542$) showed maximum intra cluster distance and minimum distance was recorded by cluster I ($D^2 = 1502.891$) in E2. Data further revealed that there is good scope for

selection for many traits of economic and agricultural importance within a cluster as indicated by the high magnitude of intra cluster distance among clusters. Hence, selection of divergent genotypes from the clusters namely V, VI, I and III which indicated these cluster consisted genotypes are highly diverse for flash flood tolerance. The maximum inter cluster distance in E1 was found between cluster III and cluster VI ($D^2 = 129.797$) followed by the cluster II and VII ($D^2 = 126.836$) while the minimum distance of 74.999 was observed between cluster IV and VI. In E2, the highest inter cluster distance observed between clusters II and III ($D^2 = 2743.060$). The lowest distance between clusters I and III ($D^2 = 1536.528$). To exploit genetic diversity through hybridization program inter-cluster distance must be taken into consideration. Therefore, genotypes of these divergence clusters when crossed to obtain may produce high heterotic hybrids. Similar findings were reported by (Rukmini Devi *et al.* 2020).

Table 5. Average inter and intra clusters D² and D value for 30 rice genotypes in normal and flash flood condition.

Cluster number	Environment	I	II	III	IV	V	VI	VII
I	Normal	15.059 (226.787)	82.409 (6791.296)	111.138 (12351.569)	58.070 (3372.138)	95.336 (9088.929)	77.582 (6018.924)	78.197 (6114.800)
	Flash flood	1502.891 (2258680.00)	2254.532 (5082915.500)	1536.528 (2360918.250)	—	—	—	—
II	Normal		15.905 (252.970)	114.873 (13195.721)	76.743 (5889.477)	77.440 (5996.956)	84.180 (7086.202)	126.836 (16087.408)
	Flash flood		1553.548 (2413511.750)	2743.060 (7524378.000)	—	—	—	—
III	Normal			55.643 (3096.157)	115.273 (13287.848)	93.233 (8692.381)	129.797 (16847.217)	78.867 (6220.049)
	Flash flood			1626.542 (2645638.250)	—	—	—	—
IV	Normal				69.419 (4819.050)	88.848 (7893.988)	74.999 (5624.889)	98.816 (9764.609)
V	Normal					80.618 (6499.264)	93.683 (8776.598)	107.630 (11584.316)
VI	Normal						77.155 (5952.887)	122.780 (15074.837)
VII	Normal							0.000

Cluster mean

The cluster means of the nine traits are presented in Table 6. In E1, cluster II exhibited the highest mean value for grain yield per plant, 100 grain weight while earliest in days to days to fifty percent flowering.

The low mean value for plant height was observed in cluster I and grain breadth in cluster III. Highest mean values for number of productive tillers per plant, panicle length, number of grains per panicle and grain length observed in clusters III and VI.

Table 6. Cluster means among two environments seven and three clusters for nine traits of 30 genotypes in rice.

Characters	Environments	Clusters							Grand mean
		I	II	III	IV	V	VI	VII	
DT 50% F	Normal	85.50	81.00	102.25	89.33	94.22	84.00	87.00	89.04
	Flash flood	96.45	113.13	87.33	-	-	-	-	98.97
PH (cm)	Normal	67.77	86.27	101.34	87.11	107.41	98.82	81.65	90.05
	Flash flood	100.19	129.25	89	-	-	-	-	106.16
NPTP	Normal	15.50	12.75	26.25	15.33	17.83	14.17	20.50	17.48
	Flash flood	14.85	13.00	14.00	-	-	-	-	13.95
PL (cm)	Normal	16.25	24.05	22.83	17.81	22.27	17.37	15.70	19.47
	Flash flood	19.61	20.07	14.93	-	-	-	-	18.21
NGPP	Normal	82.50	72.75	146.25	81.69	107.72	70.50	140.00	114.51
	Flash flood	35.01	28.00	38.00	-	-	-	-	33.67
1000 GW (g)	Normal	2.25	2.28	1.96	1.95	2.15	2.85	1.16	2.09
	Flash flood	2.02	2.76	1.92	-	-	-	-	2.24
GL (cm)	Normal	6.35	6.91	7.04	6.86	7.26	8.02	5.80	6.89
	Flash flood	6.92	7.82	7.06	-	-	-	-	7.27
GB (mm)	Normal	2.22	2.02	1.88	2.25	2.34	2.68	1.52	2.13
	Flash flood	2.16	2.65	2.12	-	-	-	-	2.31
GYPP (g)	Normal	22.65	24.65	23.94	18.51	21.48	11.50	24.20	20.99
	Flash flood	7.28	4.40	5.10	-	-	-	-	5.60

DT 50% F= Days to 50% flowering, PH= Plant height, NPTP= Number of productive tillers per plant, PL= Panicle length, NGPP= Number of grains per panicle, 100 GW= 100 Grain weight, GL= Grain length, GB= Grain breadth, GYPP= Grain yield per plant.

Table 7. Superior flash flood tolerance genotypes of rice based on mean performance and genetic divergence.

SL. No.	Cluster number	Genotype	Desirable traits
1	III	G26 (Poonkgar)	Days to fifty percent flowering, plant height,
2	III	G27 (Seeraga samba)	Number of grains per panicle
3	I	Swarna Sub 1	Productive tillers per plant
4	I	CR 1009 Sub1	Grain yield per plant

In E2, the flash flood environment, earliness in flowering was recorded in cluster III. Cluster I rank first and recorded highest grain yield per plant and number of productive tillers per plant while also recorded minimum grain breadth. Cluster II had short statured plants whereas maximum 1000 grain weight and grain length was exhibited in cluster II. Delayed flowering due to submergence caused by flash flooding was also reported by earlier workers (Kodihalli and Kumar 2014) and Mishra *et al.* 2019) in rice. The genotypes suggested for use as parents for hybridization based on their mean value and genetic divergence for traits are listed in Table 7. Genotype CR 1009 Sub1 present in cluster I has highest grain yield per plant and should be used in future breeding program for developing variety with high grain yield content. Genotype G26 Poonkgar (cluster III) may be used for breeding early variety rice.

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 (Fig. 1). The relative contribution of individual character towards

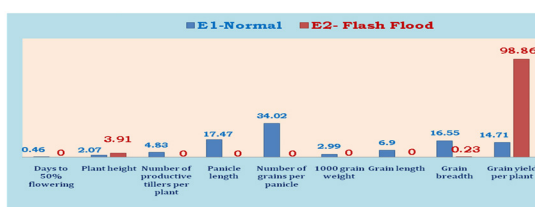


Fig. 1. Characters contribution to diversity E1- Normal, E2- Flash flood.

the expression of genetic diversity estimated over character wise D^2 value revealed that number of grains per panicle (34.02%) contribution and panicle length (17.47%) were the two major contributors in E1. Similar findings were made by Mutturaj *et al.* (2019) for the number of grains per panicle and grain yield per plant. Grain yield per plant with 98.85% contribution was the major force of discrimination among the genotypes tested in the flash flood environment E2.

CONCLUSION

The experiment unraveled the hidden buffering capacity of the rice genotypes for the study. The 30 rice genotypes which include 11 traditional, 15 popular rice varieties along with the two check varieties were grouped into seven clusters under normal (E1) and three clusters under flash flooded environment (E2). This indicates that several factors of clustering that played role under condition were rendered obsolete under flash flood environment.

Clustering distance showed significant variation under E1 and E2 as revealed by the intra and inter cluster distances. The intra cluster distance ranged from 15.059 to 80.618 under E1. While, it varied from 1502.891 to 1626.542 under E2. Also, the inter cluster distance but the clusters located apart was 129.797 in E1 and 2743.060 in E2. The values indirectly revealed the untapped hidden diversity among the genotypes under study.

The characters contribution to the genetic diversity observed revealed that number of grains per panicle, panicle length, grain breadth and grain yield per plant as major source of divergence under normal environment (E1). Whereas, grain yield per plant followed by plant height were forces of divergence under flash flooded environment (E2).

Based on divergence and cluster mean it may be suggested that maximum heterosis and good recombinants could be obtained in crosses between genotypes for flash flood tolerance. The genotypes namely Poonkgar, CR 1009 Sub1, Seeraga samba, Swarna sub 1 from clusters I and II were the most

diverse parents which would be used in flash flood varietal improvement program.

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