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Genetic analysis for extra earliness in Rice (*Oryza sativa* L.) among different age groups

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Abstract
Flowering time is one of the critical factors in the rice cultivars. The basic objective of the present study is the development of very early/ extra early rice cultivars by utilizing various duration of rice genotypes collected from different regions of India. Totally thirty seven rice genotypes were evaluated which includes very early, short, medium, long and very long duration age groups.The genotypes were grouped into 11 diverse clusters. Cluster one with five genotypes *i.*e., DHALA HEERA, JALDHI DHAN-6, ANJALI, CB 12593 and ASD 20 had the traits required for earliness with superior mean value *viz*., Days to panicle initiation (66.429), Days to fifty per cent flowering (72.700) and plant height (91.392). Cluster I also exhibited highest inter cluster distance (64.378**)** with cluster XI with two genotypes CR 1009 Sub. 1 and GEB 24 had other extreme traits for extra earliness. Hence, hybridization between these seven genotypes will also through transgressive segregants which offer scope for further selection.

Keywords: Rice, genetic divergence, extra early, very early, very short duration

Introduction
The world with highly diversified climatic conditions shows that the different peoples with various cultures and varietal food habits. The nature Posses its vast amount of genetic diversity to feeds the lives, from the beginning of civilization, man collected and selected for their requirements were finally domesticated and cultivated several crop plants mean while they become human, then the sources of genetic diversity has been utilized and some were preserved for the future use.To meet the future food requirements effective utilization of different plant genetic resources is necessary to produce new plant types in crop improvement which is suitable for the modern world. Global demand for food is rising because of population growth, increasing affluence and changing dietary habits. The UN/FAO forecasts that the global food production needs to increase 40% by 2030 and 70% by 2050 **(**FAO, 2009). Yet globally, water is anticipated to become scarce and there is increasing competition for land, putting added pressure on agricultural production. In addition, climate change will reduces the reliability of food production through weather pattern changes and increased pressure from biotic factors of pests and diseases. Rice is very most important food crop of the developing world and the staple food for more than 60% of Indian populace, so it forms the bedrock of food security. Expectation in the future, India needs to produce 120 million tons by 2030 to feed its one and half a billion plus population. But unavailability of water and pressure on cultivating area constrains the rice production. To meet the prevailing global demand extra earliness is one of the emerging areas to produce extremely early duration rice varieties. The present evaluation aims to know the duration, yield and special features for earliness then only the best lines and tester will be elected based on their performance for the new cultivar development through crossing programme. In future these developing cultivars will be suitable for the upland conditions and also for the water scary regions of the Tamil Nadu and other states of India.

Materials and Methods
The experiment material consisted of thirty seven genotypes (Table 1) collected from various places of India which includes I. Central Rice Research Institute (CRRI), Cuttack, Orissa. II. Tamil Nadu Agricultural University (TNAU) Coimbatore, III. Agricultural College and Research Institute, Madurai. IV. Rice Research Station, Ambasamudram. V. Agricultural Research Station, Thirupathisaram. VI. Rice Research Station, Tirur, Thiruvallur. VII.

Agricultural Research Station, Paramakudi and among all the varieties one variety were released from International Rice Research Institutre, Las Banos, Manilla, Phillipines, also used for the divergence studyconducted at Agricultural College and Research Institute, Madurai during *Rabi* 2015 in randomized block design with two replications. Twenty days old seedlings were transplanted in well ploughed main field applied with recommended dose of fertilizer.

Table 1: The rice genotypes employed in the present study along with their age, parentage and special features

S No.	Variety	Parentage	Duration (Days)
1	DHALA HEERA	CR 404-48/ CR 289-1208	80-85
2	JALDHI DHAN -6	DULAR MUTANT/ NAGINA 22 MUTANT	65-75
3	ANJALI	RR-19-2 X RR 149-1129	90-95
4	PRASANNA	IRAT 8/ N22	75
5	SNEHA	ANNADA / CR 143-2-2	70-75
6	SATTARI	NSJ 200 X PADMA) GAMMA IRRADIATED	70-80
7	KALYANI- II	SATTARI X RASI X KALINGA-III	60-62
8	KALLINGA III	AC- 540/ RATNA	80-85
9	KATTA NEL	TRADITIONAL LANDRACE	90-95
10	ARUBATHAM KURUVAI	TRADITIONAL LANDRACE	70-80
11	POONGAR	TRADITIONAL LANDRACE	80-82
12	SAVULU SAMBA	TRADITIONAL LANDRACE	95-98
13	IR 36	IR 1561-228/1 IR 244/O.NIVARA/CR 94-13	120- 125
14	MDU 5	O.GLABERRIMA X POKKALI	95-100
15	MDU 6	MDU 5/ ACM96136	110-115
16	CO 41	CUL.2410 X IR 22	100 -105
17	CO 47	IR 50/ CO 43	110-115
18	CO 51	ADT 43 / RR 272 – 1745	105 -110
19	CB 12593	CB 04110-ADT (R) 43	100-105
20	CB 12599	CB 04110-JJL 1798	95-100
21	ADT 3	PURELINE	95
22	ADT 4	PURELINE	100
23	ADT (R) 30	IR 262 / ADT 27	90
24	ADT (R) 36	TRIVENI X IR 20	110
25	ADT (R) 37	BG 280-12/ PTB 33	105
26	ADT (R) 43	IR 50/WHITE PONNI	105-110
27	ADT (R) 45	IR 50/ADT 37	110
28	ADT (R) 47	ADT 43/JEERAGASAMBA	118
29	ADT (R) 48	IET 11412/ IR 64	94-99
30	ANNA (R) 4	PANTDHAN 10 X IET 9911	100-105
31	ASD 16	ADT 31/CO 39	110-115
32	ASD 17	ADT 31/RATNA/ASD 8/IR 8	95-101
33	ASD 20	IR 18348/IR25863/IR 58	105-115
34	TKM 6	GEB 24 / CO 18	115-120
35	TPS(R) 4	TS 29/ASD 16	95
36	CR 1009 Sub. 1	PANKAG X JAGANNATH (Sub. 1 LOCUS INTROGRESSED FROM FR 13A)	155-165
37	GEB 24	SPONTANEOUS MUTANT	150

Each entries transplanted in two rows of three metre length and based on the age group the spacing has been followed (Table 2). Single plant observations were observed in ten plants selected randomly at every genotypes in both the replication and their means were used for statistical analysis. The different components taken for the study are Days to panicle initiation, Days to 50 per cent flowering, Plant height(cm), Total number of tillers per plant, Number of productive tillers per plant, Panicle length (cm), Flag leaf length(cm), Flag leaf width(cm), Number ofgrains per panicle, 100 grain weight(cm) and Single plant yield(g). The genetic diversity between the genotypes computed by the means of Mahalanobis (1928) D^2 statistics and the genotypes were grouped in to clusters by following the Tocher's method.

Table 2: Duration and spacing according to Indian Rice Research Institute, Rajendranagar, Hyderabad.

Sl No.	Category	Days	Spacing
1	Very early	About 100 days	20x10
2	Short	100-120 days	20x10
3	Medium	121-140 days	20x15
4	Long	141-160 days	20x20
5	Very long	Above 160 days	20x20

Results and Discussion

Genetic Diversity

Rice cultivars show a wide range of natural variation in heading date and day-length response. Although knowledge of the genetic diversity is being accumulated, the wide range of natural variation not fully understood yet. The exact place and time of domestication for rice is not to be known but in general it may considered as in (Asia) China, India and Indonesia. Rice has acquired highest diversity and wide adaptability to survive in the wetland, deep water, hilly slopes, swamps, rainfed and semi dry conditions that quality which may induce to develop as three major varietal groups of

Asia (*japonica, javanica and indica*). In the varietal development programme, genetic diversity is the most important and potential tool. Hence measuring the variation present in the materials may select and useful in hybridization to promote new varieties.

For discussion, one must define what early variety, early maturing is and early season rice mean. For cultivation, a rice variety maturing before the 7th month is called early, early-season or early-producing, a term for regions with twice-yearly rice cultivation. Early maturing rice is the variety that matures earlier than those planted concurrently, therefore this variety exists in early, mid- or late-season rice. As climate may cause different maturation timing in different places for the same variety, they may have strong regional traits. (Peng and Shijiang)

In the present study all the 37 genotypes were grouped in to 11 clusters (Table 3.) for the eleven traits were studied. In this investigation, the cluster X with six genotypes *viz*., ADT 4, ADT (R) 36, ADT (R) 37, ADT (R) 43, ASD 16 and TKM 6 found to be having maximum intra cluster distance 26.679 (Table 4). The next best cluster with high intra cluster distance 25.374 was IX, which had seven genotypes *viz*,. KALYANI, KATTA NEL, SAVULU SAMBA, CO 41, CB 12599, ASD 17, TPS 4. The mean values of genotypes were found to be inferior for the traits *viz*., Days to panicle initiation, Days to 50 per cent flowering, Panicle length, Flag leaf width Number of grains per panicle and Single plant yield when compared to those of cluster X. Hence, the genotypes in cluster X could be better to utilize either directly for hybridization programme.

Table 3: Distribution of 37 rice genotypes into different clusters

Cluster number	Number of genotypes	Genotypes
I	5	DHALAHEERA, JALDHIDHAN 6, ANJALI, CB 12593, ASD 20
II	2	ADT 3, ADT (R) 30
III	5	PRASANNA, SNEHA, SATTARI, ARUBATHAM KURUVAI, POONGAR
IV	2	CO 47, ADT (R) 47
V	2	MDU 6, ANNA 4
VI	2	MDU 5, ADT (R) 48
VII	2	CO 51, ADT (R) 45
VIII	2	KALLINGA III, IR 36
IX	7	KALYANI, KATTA NEL, SAVULU SAMBA, CO 41, CB 12599, ASD 17, TPS 4
X	6	ADT 4, ADT (R) 36, ADT (R) 37, ADT (R) 43, ASD 16, TKM 6
XI	2	CR 1009 Sub. 1, GEB 24

The magnitude of intra cluster distance measures the extent of genetic diversity between the genotypes of same cluster which the inter cluster distance measures the extent of genetic diversity between two clusters.A comparison of inter cluster distances (Table 4) between the 11 clusters revealed that the maximum values of 64.378 was between clusters I consisted five genotypes *viz*., DHALAHEERA, JALDHI DHAN-6, ANJALI, CB 12593 and ASD 20and cluster XI consist of two genotypes *viz*., CR 1009 Sub. 1 and GEB 24. The two genotypes of cluster XI had high mean values for days to panicle initiation (106.250) and days to fifty per cent flowering (114.000) and ranked second in single plant yield (30.265 g). Onthe other extreme, the genotypes of cluster I was poor in performance for the traits *viz*., days to fifty per cent flowering (72.700) and plant height (91.392). The genotypes are different from each other in duration and yield.

Table 4: Inter and intra cluster average distances in 37 rice genotypes

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	22.575	29.400	24.583	31.237	28.553	17.582	25.596	30.921	28.403	31.157	64.378
II		7.671	21.766	23.455	25.407	25.775	22.382	29.577	25.666	23.601	50.061
III			21.613	29.402	27.396	19.418	22.740	26.006	22.784	25.855	58.397
IV				9.673	27.122	24.634	14.837	29.430	34.047	25.406	46.810
V					10.121	24.980	28.040	21.717	31.865	26.008	44.389
VI						10.852	16.405	22.764	23.450	25.145	59.959
VII							11.726	24.895	26.513	22.908	54.188
VIII								11.751	27.207	24.113	49.787
IX									25.374	28.224	62.427
X										26.679	52.091
XI											23.245

Bold diagonal values shows intra cluster distance

The second high inter cluster distance of 62.427 was observed between the clusters IX and XI. The cluster IX consist of seven genotypes *viz*., KALYANI, KATTANEL, SAVULU SAMBA, CO 41, CB 12599, ASD 17 and TPS 4 and the cluster XI consisted of long and very long duration genotypes. The third position of inter cluster distance (59.959) occurred between cluster VI and cluster XI. The clusters VI consist of two genotypes *viz*., MDU 5, ADT (R) 48. These inter cluster genotypes will be very effective for the new varietal development programme.

The relative contribution of characters (Table 5), (Fig.1) towards genetic divergence was assessed. The highest contribution towards genetic divergence was recorded by total number of tillers per plant followed by single plant yield, number of productive tillers per plant, hundred grain weight, flag leaf length, panicle length, days to 50 per cent flowering, plant height, days to panicle initiation, flag leaf width and number of grain per panicle

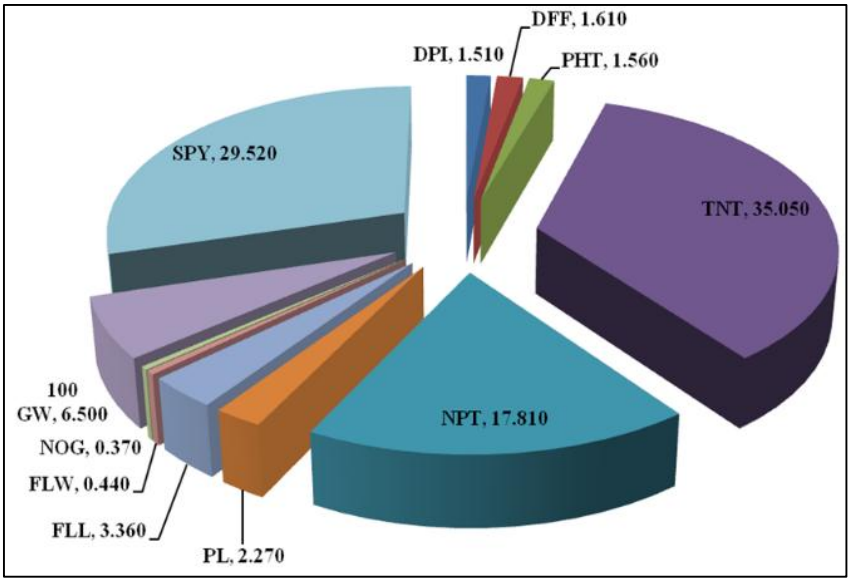

Fig 1: Contribution of characters towards diversity in rice genotypes

Table 5: Contribution of characters towards diversity in rice genotypes

Source	Times Ranked1st	Contribution (%)
Days to panicle initiation	62	1.51
Days to 50 per cent flowering	66	1.61
Plant height	64	1.56
Total number of tillers per plant	1439	35.05
Number of productive tillers per plant	731	17.81
Panicle length	93	2.27
Flag leaf length	138	3.36
Flag leaf width	18	0.44
Number ofgrains per panicle	15	0.37
100 grain weight	267	6.50
Single plant yield	1212	29.52
Total	4105	100

Considering the mean performance of clusters (Table 6) for different traits, cluster one with five genotypes (DHALAHEERA, JALDHI DHAN-6, ANJALI, CB 12593 AND ASD 20) and the traits required for earliness is present in this cluster i.e., Days to panicle initiation (66.429), Days to fifty per cent flowering (72.700) and plant height (91.392) and also it exhibited highest inter cluster distance with cluster XI which was the other extreme for these traits. Hence, hybridization between these seven genotypes will also throw transgressive segregants which offer scope for further selection. These results were in accordance with Kandamoorthy and Govindarasu, 2005[3]; Muthuramu and Sakthivel, 2017[5] and Ranjith *et al.*, 2018[6].

Table 6: Cluster mean for different quantitative traits among 37 rice genotypes

Clusters	DPI	DFF	PHT	TNT	NPT	PL	FLL	FLW	NOG	SPY	100 GW
I	**66.429**	**72.700**	**91.392**	16.966	15.172	25.151	31.974	1.325	148.300	24.614	2.453
II	76.500	83.000	**158.842**	**12.632**	**10.510**	**28.610**	35.372	1.367	**145.000**	**19.670**	2.140
III	68.900	75.700	125.463	19.840	18.232	26.865	36.447	1.164	156.600	24.207	2.239
IV	82.250	87.250	100.705	17.978	16.230	23.627	28.443	1.543	**218.250**	24.028	**1.615**
V	82.500	87.500	106.550	16.650	15.000	26.180	31.780	**1.625**	200.250	29.858	**2.588**
VI	69.250	74.750	92.057	20.757	19.208	24.013	27.960	1.335	166.750	28.170	2.233
VII	74.250	80.750	102.935	21.540	**19.698**	**21.935**	**27.123**	1.457	209.250	26.057	1.750
VIII	74.000	80.750	98.637	**21.830**	19.435	25.100	33.910	1.388	163.250	**40.525**	2.135
IX	69.100	73.286	128.005	18.509	16.204	25.291	**37.302**	1.262	148.143	28.131	2.234
X	75.417	81.667	121.104	17.715	16.134	25.990	34.803	1.454	200.750	29.207	2.005
XI	**106.250**	**114.000**	133.335	18.102	15.628	25.785	31.280	**1.143**	188.750	30.265	1.775

Bold numbers show the maximum and minimum values for their respective characters

Conclusion

Mahalanobis D^2 analysis revealed considerable amount of diversity in the material handled. In future, from the cluster I, the first three genotypes will be selected and used as very early donors for the hybridization with selected germplasms from the highest inter cluster distance andalso with various range of inter cluster distances to produce valuable Transgressive Segregants.

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