

## Research Note

### Studies on genetic diversity in rice TGMS lines

R. Rahul Roy<sup>1</sup> and D. Kumaresan<sup>2</sup>

1. Centre for Plant Breeding and Genetics, TNAU, Coimbatore, Tamil Nadu, 2. Hybrid Rice Evaluation Centre, Gudalur, Tamil Nadu

E-Mail: rahulagri15@gmail.com

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#### Abstract

One hundred and nineteen rice temperature sensitive genetic male sterile lines (TGMS) were used to study the magnitude of genetic diversity for ten yield traits using Mahalanobis  $D^2$  analysis. Based on Torcher's cluster analysis, the 119 genotypes were grouped into nine clusters. Cluster I was maximum with 85 genotypes followed by cluster II with 15 genotypes and cluster III with 11 genotypes. The clusters namely IV, VI, VII, VIII, and IX were solitary clusters with one genotype each. The maximum inter cluster distance was observed with clusters V and IX followed by cluster V and VIII which indicates the genotypes present in these cluster having more divergence. The highest intra cluster distance was observed in cluster III (22.08). Among the traits, number of grains per panicle (49.76 %) followed by number of productive tillers (23.43%), spikelet fertility (14.46%) and pollen fertility (9.93%) exhibited maximum contribution towards total divergence among the genotypes studied. Hence, these characters could be given importance for selection of genotypes for further crop improvement program.

#### Key words

*Genetic diversity, Rice, temperature sensitive Genetic Male Sterility.*

Rice (*Oryza sativa L.*), is the most important crop among cereals which is a staple food for 90 per cent of the population in Asia. In India, rice is cultivated in an area of 44 m.ha with a production of 103.41 million tons of paddy and an average productivity of 2.35 t/ha milled rice or 3.52 t/ha rough rice (India Stat, 2012). The present population of 1.22 billion Indians is expected to reach 1.30 to 1.53 billion by 2020 and 2030. So, to support such a huge population, rice production has to be increased by at least 70 per cent over next three decades to meet growing demand Balkunde et al., (2013). With the dwindling cum stagnant agricultural land and water resources, the sought after increase in population will therefore be attained mainly through the enhancement of crop productivity under efficient crop production systems. A plateauing trend in the productivity of the high yielding varieties of rice is a most disturbing trend noticed in recent years. Hybrid rice technology showed the possibilities to increase the productivity with a yield advantage over the best inbred varieties, which in turn generating considerable interest in the adoption of this technology in tropical and subtropical regions of the country (Virmani, 2006). Being a self-pollinated crop, requires the use of a male sterility system to develop commercial rice hybrids mainly based on cytoplasmic male sterility, environment sensitive genetic male sterility and chemically induced male sterility. Currently, CMS is the most

widely used method for hybrid rice production with the help of three lines (A, B and R). Even though this system is more viable and reliable, due to its dependence on single source for male sterility (wild abortive) and its cumbersome process, environmental genetic male sterility (EGMS) system has advantage over it, where the male sterility is influenced by environmental conditions (photoperiod/temperature) and the maintainer line is not required. Among the EGMS, temperature sensitive genetic male sterility (TGMS) serves as an efficient and successive tool in development of hybrid rice at tropical conditions (Lopez & Virmani, 2000). TGMS lines have complete pollen sterility at a temperature (>30 °C/ >24 °C) at day and night. They revert back to partial to normal pollen fertility at a lower temperature (<24 °C/>16 °C). In order to meet the increasing demand of rice, it is important to develop hybrid with high yield potential. The genetic diversity plays an important role to the plant breeder in choosing the right parent (Murty & Arunachalam, 1966). The present investigation was made to study the genetic divergence and clustering pattern in rice TGMS lines for selection of suitable parents for its use in hybridization program and to get better knowledge about the traits contributed for diversity and choice of traits in selection of parents.

The experiment was conducted in fertile phase at Hybrid Rice Evaluation Centre (HREC), Gudalur during *Kharif* 2017 comprised of 119 TGMS lines

(Table 1) collected from Hybrid Rice Evaluation Centre (HREC), Gudalur and Paddy Breeding Station (PBS), Coimbatore. The experiment was laid out in Randomized Block Design with three replication at a spacing of 20 x 20 cm in a single row of 4m each. Normal cultural practices were followed as per standard recommendations to get a good crop stand. Ten yield components such as days to 50 per cent flowering, plant height (cm), number of productive tillers per plant, flag leaf length (cm), panicle length (cm), panicle exertion per cent, pollen fertility per cent, spikelet fertility per cent, number of grains per panicle and single plant yield (g) were recorded from five randomly selected plants in each replication and the mean values were taken for statistical analysis. Genetic diversity between the genotype can be better estimated using  $D^2$  statistics given by Mahalanobis (1936). Grouping of genotypes into different cluster was done by using Tocher's method (Rao, 1952).

The 119 TGMS lines were grouped into nine clusters based on the yield traits using Torcher's method such that the genotypes belonging to same cluster had an average smaller  $D^2$  values than those belonging to different clusters. This result is in accordance with the findings with Sowmiya and Venkatesan (2017). Out of nine clusters, maximum number of lines were grouped in cluster I consisting of 85 lines followed by cluster II (15 lines), clusters III and V consisting of eleven and three lines. The clusters IV, VI, VII, VIII, and IX were found to be solitary. The lines grouped into clusters were given in the Table 2. The pattern of distribution of genotypes into various clusters was at random indicating that geographical region and genetic diversity were not related. This is in agreement with findings of Ranjith *et al.*, (2018).

Average intra and inter cluster distances for yield traits of TGMS lines are presented in Table 3. The cluster III recorded maximum intra cluster distance (22.08) followed by cluster II (19.44), cluster V (19.42) and cluster I (17.54). The lines within these clusters were genetically divergent; hence cross between them could produce desirable segregants. The maximum inter cluster distance was observed between the clusters V and IX (78.69) followed by cluster V and VIII (63.62), cluster III and V (56.06), suggesting that the crosses involving lines from these clusters would give wider and desirable recombination. The clusters IV, VI, VII, VIII, and IX as these clusters were represented by single genotypes namely TNAU 92S, TNAU 139S, GDR 54S, GDR 9S and TNAU 112S respectively indicating high degree of heterogeneity among the genotypes. The lowest divergence was noticed

between the clusters IV and VII (18.26) followed by clusters IV and VI (18.78), clusters VII and VIII (21.49).

The above result shows that the greater the diversity between two cluster, the wider the genetic diversity between genotypes. Keeping this in view, it indicated that hybridization between the genotypes in clusters IV, VI, VII, VIII, and IX would produce lines with desirable traits. The genotype of these clusters may be used as parents in the crossing programme to generate breeding material with high diversity.

The cluster means for each characters are presented in Table 4. It indicated that the cluster VI had minimum number of days to 50 per cent flowering (57.67 days) and cluster VII with maximum number of days to 50 per cent flowering (83.33 days). Tall (92.45 cm) and dwarf (75.34 cm) plant height was observed in the cluster IX and VI respectively. The long panicle length was observed in cluster VII (24.33 cm) and short in cluster IX (19.83 cm). The cluster VIII recorded high panicle exertion (69.71 per cent) whereas cluster IV had minimum per cent of panicle exertion (57.95 per cent). The cluster VIII had long flag leaf length (31.87cm) where as it is short in cluster VII (25.62 cm). The number of productive tillers was more in cluster III (19.65) and less in cluster IV (10.09). The maximum per cent of pollen fertility was observed in cluster VII (81.98 per cent) and minimum in cluster VI (32.71 per cent). The spikelet fertility was more in cluster IX (69.33 per cent) and less in cluster VIII (35.27 per cent). More number of grains per panicle was recorded in cluster V (318.67) and less in cluster IX (34.00). The cluster III had maximum single plant yield (36.45 g) and cluster IV with minimum single plant yield (10 g). The genotypes from these clusters with high mean values may be directly used for adaptation or may be used a parents in future hybridization programme.

The number of times that each character appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 5. Number of grains per panicle (49.76 per cent) contributed maximum toward divergence followed by number of productive tillers (23.43 per cent), spikelet fertility (14.46 per cent), pollen fertility (9.93 per cent), days to 50 per cent flowering (1.44 per cent), plant height (0.14 per cent), panicle length (0.13 per cent), panicle exertion (0.01 per cent) and the trait flag leaf length had not contributed to divergence hence, it indicates all the lines have homogeneity with flag leaf length. The results were found to be similar with Pragnya



*et.al.*,(2018). Hence, the analysis shows that the traits number of grains per panicle, number of productive tillers, spikelet fertility and pollen fertility contributed maximum toward divergence and revealed that these characters should be taken into consideration while selecting parents for hybridization.

## References

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**Table 1. Clusters based on yield traits of rice TGMS lines**

Cluster	Entries
I	GT 4/14, GT27/14,GT48/14,GDR 3S,GDR 5S,GDR 15S,GDR 17S,GDR 18S,GDR 21S,GDR 22S,GDR 23S,GDR 24S,GDR 27S,GDR 29S-1,GDR 34S,GDR 35S,GDR 36S,GDR 38S,GDR 39S,GDR 40S,GDR 42S,GDR 43S,GDR 46S,GDR 47S,GDR 48S, GDR 52S,GDR 53S, GDR 55S,GDR 58S, GDR 68S,GDR 70S,GDR71S,GDR,72S,GDR 73S,TS29-100-GY(g),TNAU 1S,TNAU 2S, TNAU 14S,TNAU16S,TNAU 19S,TNAU 23S,TNAU 26S,TNAU 38S , TNAU 34,S,TNAU 37S,TNAU 39 S,TNAU 42 S, TNAU 51S, TNAU 59 S-1,TNAU 59 S-2,TNAU 60S,TNAU 67S,TNAU 71S,F4 17S,TNAU 82 S,TNAU 83S,TNAU 84 S,TNAU 86 S,TNAU 95 S,TNAU 97S,TNAU 98S,TNAU 100S,TNAU 102 S,TNAU 103 S, TNAU 106 S,TNAU 107 S,TNAU 116 S,TNAU 118 STNAU 119 S,TNAU 120 S, TNAU 124 S, TNAU 126 S,TNAU 129 S,TNAU 131 S,TNAU 132 S,TNAU 135 S,TNAU 136 S, TNAU 143 S,TNAU 147 S-1,TNAU 151 S,TS 29-100GY, TNAU 101 S,TNAU 111 S,TNAU 115 S,TNAU 137 S, ADT 39-300 GY-300-GY
II	GDR 1S,GDR 10S,GDR 44S,GDR 61S,TNAU 50S,TNAU 53S,TNAU 4S,TNAU 18S,TNAU 123S,TNAU 145S,TNAU 147S,TNAU 142S,TNAU 15 S,TNAU 46S
III	GDR 4S,GDR 16S,GDR 28S,GDR 19S,GDR 29S,GDR 50S,TNAU 4S-1,TNAU 30S,TNAU 31S,TNAU 104 S,TNAU 93S
IV	TNAU 92S
V	TNAU 45S,TNAU 113S,TNAU 114S
VI	TNAU 139S
VII	GDR 54S
VIII	GDR 9S
IX	TNAU 112S

**Table 2. Average intra (in bold) and inter cluster D<sup>2</sup> distance for yield traits in rice TGMS lines**

CLUSTERS	I	II	III	IV	V	VI	VII	VIII	IX
I	<b>17.54</b>	26.15	24.76	25.04	46.87	22.24	24.63	28.55	37.93
II		<b>19.44</b>	35.07	25.89	31.36	25.73	34.03	43.35	55.09
III			<b>22.08</b>	39.34	56.06	32.35	34.99	29.40	31.59
IV				<b>0.00</b>	38.00	18.78	18.26	35.81	53.23
V					<b>19.42</b>	40.21	50.80	63.62	78.69
VI						<b>0.00</b>	28.08	36.57	44.60
VII							<b>0.00</b>	21.49	45.10
VIII								<b>0.00</b>	31.46
IX									<b>0.00</b>

**Table 3. Cluster mean values for yield traits in rice TGMS lines**

Clusters	DFF	PH	NPT	FLL	PL	PE	PF	SF	NGP	SPY
<b>I</b>	76.71	82.91	15.09	27.89	21.35	64.07	69.50	56.44	155.80	25.60
<b>II</b>	78.38	84.58	16.20	28.91	21.48	63.41	70.62	59.31	226.00	29.96
<b>III</b>	77.47	84.08	19.65	29.69	22.42	69.35	48.55	65.04	122.70	36.45
<b>IV</b>	71.00	81.87	10.09	28.25	22.60	57.95	76.79	35.27	202.00	10.00
<b>V</b>	71.56	85.78	16.52	28.27	21.49	61.04	50.17	49.50	318.67	35.56
<b>VI</b>	57.67	75.34	11.34	30.42	20.30	63.80	32.71	50.68	191.00	25.33
<b>VII</b>	83.33	85.06	12.80	25.62	24.33	59.88	81.98	27.26	141.00	19.83
<b>VIII</b>	60.00	87.23	17.55	31.87	23.87	69.71	75.00	35.27	81.00	36.17
<b>IX</b>	62.33	92.45	15.91	29.50	19.83	68.51	45.35	69.33	34.00	21.83

<b>DFF</b>	:	Days to 50% flowering	<b>FLL</b>	:	Flag leaf length (cm)
<b>PH</b>	:	Plant height (cm)	<b>PF</b>	:	Pollen fertility (%)
<b>NPT</b>	:	Number of productive tillers	<b>SF</b>	:	Spikelet fertility (%)
<b>PL</b>	:	Panicle length(cm)	<b>NGP</b>	:	Number of grains per panicle
<b>PE</b>	:	Panicle exertion (%)	<b>SPY</b>	:	Single plant yield (g)

**Table 4. Contribution of yield traits to divergence in rice TGMS lines**

Si. No	Characters	Times Ranked 1st	Contribution (%)
1	Days to 50 flowering	101	1.44
2	Plant height (cm)	10	0.14
3	Number of productive tillers	1645	23.43
4	Flagleaf length (cm)	0	0.00
5	Panicle length (cm)	9	0.13
6	Panicle exertion (%) )	1	0.01
7	Pollen fertility (%)	697	9.93
8	Spikelet fertility (%)	1015	14.46
9	Number of grains per panicle	3494	49.76
10	Single plant yield (g)	49	0.70