

Genetic diversity studies in thermosensitive genic male sterile lines in rice (*Oryza sativa* L.)

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ABSTRACT

Genetic divergence of twenty eight Thermo-sensitive Genic Male Sterile lines in rice was studied for twelve characteristics. Among the traits studied, panicle exertion contributed the most for the genetic diversity of TGMS lines followed by spikelet fertility and stigma length. The TGMS lines were grouped into twelve clusters, of which cluster VII with five genotypes was the largest and cluster XII was the smallest with one genotype. The intra cluster distance ranged from 0.00 (cluster XII) to 15.51 (cluster VII). The inter cluster distance was found to be the highest between clusters III and XII (28.16). When the cluster mean was compared for twelve traits observed, cluster II and X expressed low pollen fertility of less than 1.0 per cent and spikelet fertility of less than 4.0 per cent. The clusters I, VI and XII recorded the pollen fertility of less than 90 per cent, whereas the clusters VIII, III and IX expressed pollen fertility of 80 per cent and above. The entries in cluster X had more than 80% of panicle exertion with more than 20° as angle of glume opening. The stigma length was high with moderate number of spikelets per panicle and panicle length. Since the TGMS lines in cluster X had more number of desirable traits, they can be effectively utilized for heterosis breeding in rice.

Key words: diversity, rice, TGMS lines

Rice is the most important crop in the world, and used as the staple food by more than half of the world population. The green revolution in many rice producing countries enabled global rice production to meet the demand of the world's increasing population. However, by 2025, the world must increase rice production to 880 million tonnes from the present 560 million tonnes. Recent progress in plant breeding research indicated that a significant shift in the yield frontiers could be possible through hybrid rice. Utilization of hybrid vigour has played an important role in increasing rice yield, since its success in the 1970s in China.

In the tropics, the cytoplasmic genic male sterility (CMS) and the thermosensitive genic male sterility (TGMS) are the two male sterility systems that can be used (Virmani, 2006). The CMS with wild abortive (WA) cytoplasm is the method used most extensively, although studies have shown that the TGMS was more effective in increasing seed production efficiency and grain yield (Virmani and Kumar, 2004). Two line hybrids derived from TGMS lines showed a higher frequency of heterotic

combinations than the three line hybrids derived from CMS lines (Lopez and Virmani, 2000). Apart from this, unitary source of male sterility causes the genetic vulnerability in the hybrids. For the successful utilization of male sterility system in heterosis breeding, more TGMS lines in different genetic background need to be developed and utilised. Many workers have stressed the importance of genetic divergence for the selection of desirable parents (Murthy and Arunachalam, 1996 and Rahman, 1997) so as to exploit the heterosis. Keeping in view of the importance of TGMS in hybrid rice, the present study was taken up to assess the genetic divergence of twenty eight TGMS lines for twelve traits.

MATERIALS AND METHODS

The experimental material consisted of twenty eight TGMS lines in rice developed by pedigree and mutation breeding of the line TS 29. The lines were grown in randomized block design with a spacing of 20 x 20 cm in three replications at Paddy Breeding Station, Tamil Nadu Agricultural University, and Coimbatore during Rabi 2009-10. Need based plant protection measures were given.

Observations on twelve characters *viz.*, days to fifty percent flowering, plant height (cm), pollen fertility (%), panicle exertion (%), angle of glume opening, stigma exertion (%), spikelet fertility (%), number of seeds per panicle, panicle length (cm), stigma length (mm), number of productive tillers and single plant yield (g) were recorded in five random plants of each TGMS line of all the three replications. The data was subjected to Mahalanobis D^2 statistics to measure the genetic divergence and the grouping of TGMS lines was done following the Tocher's method as given by Rao (1952).

RESULTS AND DISCUSSION

The analysis of variance revealed that there was significant variation between the twenty eight TGMS lines studied. Hence the observations on twelve characters in the TGMS lines of rice were analysed for genetic diversity. Among the different traits studied, panicle exertion contributed 28.04 per cent as shown in Table 1. This was followed by spikelet fertility (16.14 per cent), stigma length (14.29 per cent) and single plant yield (13.23 per cent).

Table 1. Independent character contribution towards divergence in twelve characters of 28 rice TGMS lines

Character	Times ranked	% contribution
DFP	0	0.0000
Plant height	0	0.0000
Pollen fertility	18	4.7619
Panicle exertion	106	28.0423
Angle of glume opening	2	0.5291
Stigma exertion	23	6.0847
Spikelet fertility	61	16.1376
No. of seeds/panicle	25	6.6138
Panicle length	1	0.2646
Stigma length	54	14.2857
No. of prod. Tillers	38	10.0529
Single plant yield	50	13.2275
Total	378	100

The other characters contributed comparatively less percentage for the expression of genetic divergence. The traits like days to first flowering and plant height had not contributed for the genetic divergence in the 28 lines evaluated. The

TGMS lines were grouped into twelve clusters based on relative magnitude of diversity present in the material studied (Table 2). The clustering pattern revealed that the distribution of TGMS lines were at random with regard to their origin. Among the different clusters, it was observed that the cluster VII was the largest which had five TGMS lines followed by cluster V with four lines. The TGMS lines coming under one cluster represent the overall genetic similarity among them for different characteristics observed. Clusters I, II, III, IV, VI, VIII, IX, X and XI contained two lines and the cluster XII had only one TGMS line.

Table 2. Clustering pattern of 28 rice TGMS lines on D2 statistics

Cluster	No. of genotypes	Name of genotypes
I	2	TNAU 14S, TNAU 30S
II	2	TNAU 64S, CBGD 05-02
III	2	TS 06-812-1, TNAU 62S
IV	2	CBTS 0282-27-4-7-2, CBTS 0282-27-1-1
V	4	TS 29 IVT 1705-1, CBTS 0282-27-4-12-5, CBTS-0282-5, CBTS 0282-75-2-4
VI	2	TNAU 50S, TNAU 60S
VII	5	CBTS 0282-06-27-1, CBTS 0282-151-6, CBTS 0282-27-4-1, TNAU 21S, TS 20 IVT J 1705-1
VIII	2	TNAU 67S, CD 98049-2-10
IX	2	TNAU 38S, TNAU 68S
X	2	TNAU 61S, CBCD 05-02
XI	2	TNAU 27S, TNAU 28S
XII	1	TNAU 20S

The estimates of intra and inter cluster D2 and D values for twelve characters have been presented in Table 3. The intra cluster distance ranged from 0.00 for cluster XII to 15.51 for cluster VII. The inter cluster distance was observed to be the highest (28.16) between cluster III and XII, indicating that the genotypes of these two clusters were genetically more diverse. The minimum diversity was observed between the clusters I and VI (9.22) followed by clusters I and X (10.27), which are found to be lesser than the intra cluster distance.

Table 3. Inter and intra cluster D^2 values and cluster distances

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	36.05 (6.004)	119.48 (10.93)	557.14 (23.60)	236.96 (15.39)	109.99 (10.49)	84.95 (9.22)	494.84 (22.25)	702.44 (26.50)	526.30 (22.94)	105.48 (10.27)	407.90 (20.20)	286.99 (16.94)
II		37.96 (6.16)	737.72 (27.16)	404.04 (20.10)	196.21 (14.01)	186.62 (13.66)	597.97 (24.45)	752.38 (27.43)	581.49 (24.11)	106.25 (10.31)	498.72 (22.33)	401.84 (20.05)
III			48.92 (6.99)	182.51 (13.51)	519.78 (22.80)	532.31 (23.07)	217.61 (14.75)	166.42 (12.90)	124.64 (11.16)	672.62 (25.94)	182.73 (13.52)	792.87 (28.16)
IV				62.36 (7.90)	256.09 (16.00)	199.01 (14.11)	265.88 (16.31)	259.10 (16.10)	251.74 (15.87)	288.46 (16.98)	144.87 (12.04)	461.41 (21.48)
V					184.05 (13.57)	155.28 (12.46)	508.22 (22.54)	653.39 (25.56)	497.96 (22.32)	179.15 (13.39)	343.17 (18.53)	394.51 (19.86)
VI						72.85 (8.54)	512.55 (22.64)	618.63 (24.87)	479.98 (21.91)	152.69 (12.36)	315.57 (17.76)	246.34 (15.70)
VII							240.61 (15.51)	224.20 (14.97)	207.30 (14.40)	570.74 (23.89)	327.80 (18.11)	563.77 (23.74)
VIII								86.52 (9.30)	134.78 (11.61)	694.19 (26.35)	225.10 (15.00)	775.35 (27.86)
IX									109.52 (10.47)	618.30 (24.87)	188.73 (13.74)	642.98 (25.36)
X										143.75 (11.99)	448.14 (21.17)	406.85 (20.17)
XI											167.93 (12.96)	631.52 (25.13)
XII												0.00 (0.00)

Table 4. Cluster means for different characters of 28 rice TGMS lines

Cluster	DFE	PH(cm.)	PT	PF(%)	PE(%)	AGO(°)	SE (%)	SL (mm.)	SF (%)	SPP	PL(cm.)	SPY (g.)
I	113.67	159.05	15.17	2.68	83.61	17.92	24.19	2.85	5.61	150.92	19.42	0.016
II	112.83	146.70	18.08	0.63	77.66	18.68	15.71	2.68	3.24	92.83	18.26	0.013
III	114.17	167.95	14.92	88.76	89.25	18.75	33.70	2.60	81.92	151.00	21.60	0.050
IV	111.83	149.93	11.25	44.84	84.21	20.42	27.01	2.65	50.60	152.17	21.91	0.015
V	112.08	155.23	15.54	14.23	85.11	17.88	27.68	3.21	12.72	130.29	21.55	0.023
VI	117.67	155.32	12.42	2.65	79.46	18.17	30.47	2.64	3.39	122.25	19.44	0.006
VII	118.60	163.27	14.63	76.64	80.74	17.00	21.10	2.64	62.87	150.03	22.28	0.024
VIII	116.00	178.08	12.33	90.39	79.39	18.83	20.63	2.76	81.69	105.67	21.12	0.019
IX	113.33	158.83	15.75	79.63	80.32	15.83	29.13	2.70	72.64	124.42	17.91	0.018
X	116.67	164.30	14.67	0.79	83.17	20.83	15.74	2.87	2.20	103.67	20.94	0.008
XI	113.17	143.23	13.08	60.01	80.94	19.17	35.21	3.07	53.85	100.58	21.93	0.018
XII	117.00	157.63	11.17	5.97	76.37	11.67	21.77	2.27	4.95	119.83	22.62	0.015

DFE – Days to 50% flowering; PH - Plant Height; PT - No. of prod. Tillers; PF – Pollen Fertility; PE - Panicle exertion; AGO - Angle of glume opening; SE - Stigma exertion; SL - Stigma length; SF - Spikelet fertility; SPP - No. of spikelets /panicle; PL - Panicle length; SPY - Single plant yield

The greater the distance between two clusters, wider is the genetic diversity among the TGMS lines studied. The cluster mean (Table 4) for different characters studied reveal that the clusters II and X had less than one per cent of pollen fertility, less than four per cent spikelet fertility and less number of spikelets per panicle. The TGMS lines coming under the clusters I, II, VI, X expressed more than 95 per cent pollen sterility, but the inter cluster distance between them are lesser and hence

they are not genetically diverse. The lines coming under the clusters VIII, III and IX expressed pollen fertility of 80 per cent and above during the experimental condition. The entries in cluster X were 99.21 per cent pollen sterile and had 97.80 per cent spikelet sterility with 83.17 per cent panicle exertion with more than 20° as angle of glume opening (20.83°). The stigma length was high (2.87mm) with moderate number of spikelets per panicle (103.67) and panicle length (20.94). The

cluster III was fertile (88.76%) with good panicle exertion (89.25%), stigma exertion (33.70%), high spikelet fertility (81.92%), number of spikelets per panicle (151.0) panicle length (21.60 cm) and so higher single plant yield (0.05g). A critical appraisal of the observations is that none of the TGMS lines had all the favourable traits, so that the line can be directly utilized for our hybrid breeding programme. The desirable means for twelve traits studied are distributed relatively in different clusters obtained. This was already reported by Bose and Pradhan (2005), Monika *et al.* (2008) and Saraswathi *et al.* (2012).

CONCLUSION

From this study, it is found that the entries present in cluster X such as TNAU 61S, CBCD 05-02 were pollen sterile with good panicle exertion with more than 20° as angle of glume opening. The stigma length was high, produced sterile spikelets with moderate number of spikelets per panicle and panicle length. Hence the genotypes TNAU 61S, CBCD 05-02 could be utilized for hybrid breeding in rice.

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