



STUDY OF GENETIC PARAMETERS IN THERMO-SENSITIVE GENIC MALE STERILE LINES (TGMS) OF RICE (*Oryza sativa* L.)

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ABSTRACT

Twenty eight suspected TGMS lines in rice developed from various sources were evaluated for genetic variability and heritability parameters along with correlation coefficients based on morphological traits and pollen fertility studies. Highest PCV and GCV were observed for pollen fertility, spikelet fertility and number of productive tillers suggesting that these characters are under the influence of genetic control. High heritability was recorded for stigma length and panicle length. High heritability coupled with high genetic advance as per cent of mean was observed for panicle length. Pollen fertility was positively and significantly associated with panicle exertion, spikelet fertility, number of seeds per panicle and single plant yield at genotypic level. Emphasis may be given on characters like stigma length, panicle length and single plant yield for improvement of these lines, since majority of other traits are environment dependant.

KEY WORDS: Correlation, Genetic advance, Heritability, Rice, TGMS lines, Variability

INTRODUCTION

Today, rice is synonymous with food security in most parts of the Asia. Recent progress in plant breeding research indicated that a significant shift in the yield frontier could be made possible through hybrid rice. Three-line breeding utilizing the Cytoplasmic Genic Male Sterility (CMS) system has been found to be effective in the development of commercial hybrids, but this system has some constraints such as a yield plateau in rice hybrids, dependency on a single CMS source, restriction on the choice of male parents due to problems associated with fertility restoration, complex seed production procedures, and high seed cost (Yuan, 1998). To overcome these problems, the two-line system of hybrid breeding utilizing Environment Sensitive Genetic Male Sterility (EGMS) especially the Thermo Sensitive Genetic Male Sterile lines (TGMS) is considered as an alternative to CGMS system. Use of the thermo sensitive genic male sterility system in two line breeding is simple, inexpensive, efficient and eliminates the limitations associated with the cytoplasmic-genetic male sterility (CGMS) system in rice due to the different weather conditions prevailing in India. Hence, an understanding of genetic variability, heritability and correlation of pollen fertility with other traits will help in the effective selection of parents to exploit the maximum heterosis.

MATERIAL AND METHODS

A total of 28 medium and late maturing TGMS lines were selected for the present study. They were evaluated at Paddy Breeding Station, Tamil Nadu Agricultural University, Coimbatore during *Rabi*, 2009-10, in a randomized block design with three replications. The data was recorded for twelve traits *viz.*, days to first flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), spikelet fertility (%), grain yield per plant (g), angle of glume opening, stigma exertion (%), stigma length (cm), pollen fertility (%), panicle exertion (%) and no. of spikelets per primary panicle in five randomly selected plants of each genotype.

The analysis of variance was carried out statistically utilizing the mean values (Panse and Sukhatme, 1995) for the twelve characters studied in selected 28 TGMS lines. GCV and PCV were calculated using the formula suggested by Burton (1952). The heritability estimate in the broad sense was calculated by the method proposed by Lush (1940).

RESULTS AND DISCUSSION

The analysis of variance revealed the significant difference among 28 TGMS lines for the twelve characters studied, indicating sufficient scope for further

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improvement. The mean, GCV, PCV, heritability (broad sense) and genetic advance as percentage of mean worked out for twelve characters are presented in Table 1. The mean values of panicle exertion (50.94%), panicle length (20.90) and stigma length (2.27) were good, indicating that the genotypes were of superior quality for executing the hybrid breeding in rice. To have more outcrossing rate in male sterile lines of rice, in turn for more hybrid seed set, the traits panicle exertion, angle of glume opening, stigma exertion and stigma length are important. PCV was higher than GCV for all the characters studied. PCV ranged from 9.94 (panicle length) to 127.98 per cent (number of productive tillers) and GCV ranged from 3.07 (angle of glume opening) to 59.39 (pollen fertility). GCV was found to be moderate (10-20%) for plant height, stigma length, panicle exertion, panicle length and number of seeds per panicle. Similar findings of moderate GCV was reported earlier for plant height and panicle length (Umadevi *et al.*, 2009). Difference between the PCV and GCV was low for panicle length and stigma length indicating the less influence of environment. The quantitative traits, viz., pollen fertility (109.67), spikelet fertility (106.02), number of spikelets per panicle (82.86), plant height (82.14), number of productive tillers (127.98) and days to first flowering (78.21) expressed high variability at phenotypic level and low variability at genotypic level. This shows the high influence of environment for the expression of these traits in the TGMS lines studied.

The heritability and genetic advance estimates were interpreted as low, medium and high as per the classification of Johnson *et al.* (1955). Broad sense heritability ranged from 0.206 (angle of glume opening) to 88.55 per cent (stigma length). As heritability alone cannot serve as an indication of the expected genetic improvement, the genetic advance is also taken into consideration. High heritability estimates coupled with high genetic advance was observed for stigma length and panicle length. This indicated the lesser influence of environment in expression of these characters and prevalence of additive gene action in their inheritance which is amenable for direct selection. It was earlier reported for panicle length by Ushakumari *et al.* (2002) and Umadevi *et al.* (2009). High heritability coupled with very low genetic advance as per cent of mean was recorded for single plant yield indicating the non additive gene action hence, selection for this trait may not be rewarding. Low heritability with low genetic advance observed for days to first flowering, plant height, panicle exertion, angle

of glume opening and number of spikelets per panicle indicated the high influence of environment in the expression of these traits.

The genotypic correlations were of higher magnitude than the corresponding phenotypic correlation coefficients for the majority of trait combinations observed (Table 2). This is due to the predominant role of heritable factors. This study revealed that the pollen fertility had significant and positive correlation with panicle exertion, spikelet fertility, number of seeds per panicle and single plant yield at genotypic level. The observation supports earlier findings by Borbora *et al.* (2005) and Panwar and Mashiat Ali (2007) for number of filled grains per panicle. Highly significant and negative correlation of pollen fertility was observed with plant height, stigma exertion and stigma length at genotypic level. This indicates the traits panicle exertion, spikelet fertility, number of seeds per panicle and single plant yield are to be concentrated for the selection of plants while improving the TGMS lines.

Path coefficient analysis was worked out to get an insight into the direct and indirect effects of different characters on pollen fertility and the results are presented in Table 3. The moderate residual effect of 0.4551 in the present study indicated that some more characters are to be included for accounting purpose. Spikelet fertility (0.6482), panicle exertion (0.4456), number of seeds per panicle (0.1573) and single plant yield (0.1385) had the positive direct effect on the expression of pollen fertility. Days to fifty per cent flowering is having the highest negative direct effect on the expression of pollen fertility. The traits number of productive tillers, panicle exertion, stigma exertion, stigma length and single plant yield are having both positive direct and indirect effects on pollen fertility. Though plant height (-0.1849), angle of glume opening (-0.1625) and panicle length (-0.0164) are having negative direct effect on pollen fertility, these traits are having the positive indirect effect through majority of other traits studied. Similarly, number of seeds per panicle and spikelet fertility are having negative indirect effect, though the traits are having positive direct effect on the expression of pollen fertility.

The materials used for this study are the thermo sensitive genic male sterile lines, where majority of the reproductive traits are determined by environment. This study suggested that due emphasis may be given on characters like stigma length, panicle length and single plant yield for improvement of these lines, since majority of other traits are environment dependant.

Table 1. Estimates of genetic components for quantitative characters of rice TGMs lines

Traits	Mean	PCV	GCV	H ₂ (BS)	GA	GA (% over mean)
Days to first flowering (DFF)	68.45	78.21	4.57	0.341	0.376	0.549
Plant height (PH)	94.1 cm	82.14	19.57	5.67	9.03	9.60
No. of productive tillers (NPT)	14.35	127.98	36.14	18.45	10.43	48.97
Pollen fertility (PF)	29.48%	109.67	59.39	29.33	19.53	66.26
Stigma exertion (SE)	19.28%	70.36	27.14	14.88	4.16	21.57
Stigma length (SL)	2.27 mm	13.87	13.06	88.55	57.48	85.01
Angle of glume opening (AGO)	14.33°	67.68	3.07	0.206	4.12	0.29
Panicle exertion (PE)	50.94%	74.81	13.3	3.16	2.48	4.87
Panicle length (PL)	20.90 cm	9.94	8.89	80.09	82.79	93.78
Spikelet fertility (SF)	27.14%	106.02	55.94	27.85	16.51	60.82
No. of seeds / panicle (NSP)	81.28	82.86	10.00	1.46	2.02	2.49
Single plant yield (SPY)	21 g	47.97	43.56	82.45	1.43	28.97

PCV : Phenotypic coefficient of variance

GCV : Genotypic coefficient of variance

H₂(BS) : Heritability in broadsense

GA : Genetic advance

Table 2. Genotypic and phenotypic correlations of rice TGMS lines

Traits	DFE	PH	NPT	SE	SL	AGO	PE	PL	SF	NSP	SPY	PF
DFE	G	1.000	-0.172	0.195	-0.236	-0.123	-0.017	-0.464	0.122	0.451	0.103	-0.004
	P		-0.132	0.128	-0.148	-0.073	0.030	-0.267	0.074	0.320	0.142	-0.026
PH	G	1.000	-0.132	0.256	0.180	-0.061	-0.115	-0.051	0.305	-0.180	0.533	-0.526**
	P		-0.014	0.166	0.076	0.018	-0.073	-0.007	0.203	-0.095	0.313	-0.149*
NPT	G	1.000	1.000	-0.190	0.153	0.082	-0.189	-0.105	-0.212	-0.115	-0.290	-0.264*
	P			-0.178	0.150	0.077	-0.170	-0.097	-0.191	-0.114	-0.246	-0.052
SE	G	1.000	1.000	1.000	0.058	-0.100	0.159	-0.154	0.986	0.132	0.249	-0.628**
	P				0.051	-0.095	0.154	-0.140	0.959	0.127	0.228	-0.289*
SL	G	1.000	1.000	1.000	1.000	0.117	0.239	0.056	0.061	0.239	0.295	-0.867**
	P					0.078	0.192	0.047	0.039	0.208	0.240	-0.235*
AGO	G	1.000	1.000	1.000	1.000	1.000	-0.048	0.390	-0.025	-0.040	0.005	-0.052
	P						-0.050	0.325	-0.024	-0.021	0.027	-0.013
PE	G	1.000	1.000	1.000	1.000	1.000	1.000	0.157	0.208	0.044	0.263	0.154*
	P							0.151	0.196	0.044	0.240	0.043
PL	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	-0.122	-0.283	0.104	-0.199
	P								-0.119	-0.242	0.095	-0.137
SF	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.081	0.259	0.646**
	P									0.074	0.245	0.271*
NSP	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.191	0.454**
	P										0.177	0.159
SPY	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	0.404**
	P											0.150
PF	G	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000	1.000
	P											1.000

* Significant at 5% level, ** Significant at 1% level

Table 3. Path coefficient analysis of pollen fertility and contributing characters in TGMS lines of rice

Traits	DFE	PH	NPT	PE	AGO	SE	SL	SF	NSP	PL	SPY	Genotypic correlation
DFE	-0.4696	0.0602	0.0350	0.0012	0.4371	0.0339	0.0462	-0.0035	-0.0533	0.1568	0.0235	0.2675
PH	-0.1529	-0.1849	0.0672	0.0798	0.1122	0.0442	0.0324	-0.0072	-0.0890	0.2618	0.0254	0.5587
NPT	-0.1912	0.1447	0.0859	0.0860	0.1379	0.0555	0.0510	-0.0080	-0.0948	0.2828	0.0313	0.5811
PE	-0.0037	0.0938	0.0469	0.4456	-0.0393	0.0301	0.0437	-0.0026	-0.0408	0.0735	0.0355	0.3944
AGO	-0.4607	0.0466	0.0266	-0.0139	-0.1625	0.0268	0.0428	-0.0032	-0.0466	0.1034	0.0180	0.1854
SE	-0.1843	0.0946	0.0552	0.0549	0.1382	0.0863	0.1237	-0.0116	-0.1501	0.5171	0.0683	0.7923
SL	-0.1444	0.0399	0.0291	0.0458	0.1269	0.0710	0.1503	-0.0099	-0.1342	0.4092	0.0522	0.6359
SF	-0.1007	0.0812	0.0415	0.0247	0.0869	0.0609	0.0904	0.6482	-0.1248	0.4146	0.0425	0.6009
NSP	-0.1540	0.1013	0.0501	0.0395	0.1277	0.0797	0.1242	-0.0126	0.1573	0.5182	0.0735	0.7850
PL	-0.1136	0.0747	0.0375	0.0178	0.0711	0.0689	0.0949	-0.0105	-0.1299	-0.0164	0.0555	0.8145
SPY	-0.0796	0.0339	0.0194	0.0403	0.0579	0.0425	0.0566	-0.0050	-0.0863	0.2595	0.1385	0.4778

Residual effect = 0.4551

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