



Gene action and component of genetic variance analysis in the thermo sensitive genetic male sterile (TGMS) line in rice (*Oryza sativa* L.)

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Received: February 28, 2016; Revised received: August 4, 2016; Accepted: November 4, 2016

Abstract: The field experiment conducted with eighteen TGMS lines, seventy two F_1 's and four checks in randomized complete block design with three replications at the Norman E. Borlaug Crop Research Centre of Govind Ballabh Pant University of Agriculture and Technology, Pantnagar during *Kharif* 2013 and *Kharif* 2014. Estimates of variance of general combining ability were lower than those of variance of specific combining ability for all the traits e.g panicle number per plant (0.54), 1000 grain weight (1.50), harvest index (3.83) and grain yield per plant (17.09) showing preponderance of non-additive gene action except panicle length (1.28) and spikelet number per panicle (522.70) which showed high gca and indicated additive gene action. High estimates of broad sense heritability coupled with high genetic advance in mean percentage for Spikelet number per panicle (98 and 27.23 respectively). For grain yield per plant (98 and 14.38) and grain number per panicle (97 and 19.93) high heritability coupled with moderate genetic advance (98 and 14.38) indicated the scope of getting better recombinants. Selection will be more effective for the traits those have high heritability and high genetic advance.

Keywords: Combing ability, Genetic advance, Heritability, Line×Tester, TGMS

INTRODUCTION

Rice (*Oryza sativa* L.) is belonging to the family of grasses, gramineae (Poaceae). In fact, the hybrid rice research was initiated in 1964 (Yuan, 1966). The genetic tools essential for breeding hybrid rice varieties are as the male sterile line (A-line), maintainer line (B-line) and restorer line (R-line) were developed during 1973 (Yuan and Virmani, 1988). The breeding methodology involves the three approaches (a) Three line method or CMS system which is possible and has been found to be most effective genetic tool for developing hybrids, (b) Two line method or TGMS, PGMS and PTGMS system which is governed by environment and (c) One line system or apomictic system which would enable farmers to use their own seed for the successive crops without experiencing genetic segregation. However, the evolution and wide application of these latter two innovative approaches are not likely to occur in future. Among these, three line approaches is being widely adopted in India and had fruitful resulted in the development of more than thirty five varieties of rice hybrids. The CGMS is essentially CMS with a provision of fertility restoration by nuclear gene(s). Hence, it is also referred to as CMS system. The role of cytoplasm in causing male sterility in rice was reported back in the fifties and the first usable cytoplasmic male sterility-fertility restoration system in rice was developed by substituting genes of *japonica* vari-

ety-Taichung 65 into the cytoplasm of the *indica* variety Chinsurah Boro II (Sampath and Mohanty, 1954). However, this could not be exploited for commercial hybrid seed production probably due to strict self-pollinating nature of the crop. The first commercially usable CMS line was developed in China during 1973 from spontaneous male sterile plant isolated in a population of the wild rice *Oryza sativa* of *spontanea* on Hainan Island. Discovery of the source, designated as wild abortive (WA) type is considered a landmark in the history of hybrid rice. The success of hybrid rice is based on the important findings of some key genes. The wild abortive cytoplasmic male sterility (WA - cms) was found in a spontaneous mutant of wild rice *Oryza sativa* f. *spontanea* in 1970. Its maintainer gene was present in most of the Chinese varieties and restorer gene in most IRRI varieties. These findings led to the development of the first batch of three line hybrids of rice. The WA - cms has become the most employed system in development of rice hybrids (Virmani and Edward, 1983; Jing *et al.*, 2001 and Chen and Liu, 2014). Genetic variability for agronomic characters therefore is a key component of breeding programmes for broadening the gene pool of crops. Heritability and genetic advance are important selection parameter; high genetic advance coupled with high heritability estimates offers the most suitable condition for selection. The limitation of estimating heritability in narrow sense, as

it included both additive and epistatic gene effects, and thereby suggested that heritability estimates in the broad sense will be reliable if accompanied by a high genetic advancement. Heritability is a measure of the phenotypic variance attributable to genetic causes and has predictive function in plant breeding. Genetic advance shows the degree of gain obtained in a character under a particular selection pressure (Tuhina-Khatun *et al.* 2007, Pandey *et al.* 2009 and Akinwale *et al.* 2011). The main objective of the study is to estimate genetic variability of yield and its components and to identify the traits which will be stable in generation after generation.

MATERIALS AND METHODS

The present investigation was carried out at the Borlaug Crop Research Center of G. B. Pant University of Agriculture and Technology, Pantnagar, Uttarakhand (India) in 2014 *kharif* season. The material used for this study consisted of eighteen thermosensitive genetic male sterile (TGMS) lines and four testers (Table 1). The eighteen lines were crossed with four testers during *kharif* season in 2013 using Line X Tester mating design. The resulting 72 cross combinations with 22 parents (lines and testers) grown in randomized complete block design in three replications during the 2014 *kharif* season. Data were collected from five randomized selected plants from each replication. The traits on which data were collected *viz.* Days to 50% flowering, Plant height, Panicle length, Panicle number per plant, Spikelet number per panicle, Grain number per panicle, Per cent spikelet fertility, 1000 grain weight, Harvest index and Grain yield per plant.

Gene action and degree of dominance: Ratio of $\sigma_{ca}^2/\sigma_{sca}^2$ less than 1 was taken as preponderance of non-additive type of gene action, greater than 1 as additive and equal to 1 was taken as equal effects of additive and non-additive type of gene action. Similarly ratio of $\sigma_{ca}^2/\sigma_{sca}^2$ less than 1 was taken as preponderance of non-additive type of gene action, greater than 1, as additive and equal to 1 was taken as equal effects of additive and non-additive type of gene action also. Degree of dominance was calculated by the formula

$$\sqrt{(\frac{(\sigma_{ca}^2)}{(\sigma_{sca}^2)})} \text{ Value of } \sqrt{(\frac{(\sigma_{ca}^2)}{(\sigma_{sca}^2)})}$$

less than 1, was taken as preponderance incomplete dominance, greater than 1, as over-dominance and equal to 1 was taken as equality of complete dominance. All calculations were computed following Singh and Chaudhary (1985).

Heritability in broad sense $h^2_{[b]}$ was calculated for each character as a ratio of genotypic variance to phenotypic variance according to the Allard (1960). Heritability values were categorized according to Johnson, Robinson and Comstock (1955) as: Low = Less than 0.30, Moderate = 0.30 – 0.60 and High = More than 0.60. The expected genetic advance under selec-

tion for different characters under study was estimated according to Allard (1960). The genetic advance as percent of means for each character was calculated as suggested by Johnson, Robinson and Comstock (1955) and range of genetic advance in percentage of mean were Low = less than 10%, moderate = 10-20% and high = more than 20%. Proportional contribution of lines, testers and line \times tester interaction to the total variance were calculated in accordance with Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

Contribution of lines, testers and line \times tester interaction is presented in Table 2. The contribution of lines to the total variance was greater than testers and line \times tester interaction for three parameters. These were days to flowering (49.28%), spikeletes number per panicle (35.51%) and grain yield per plant (51.07%) thus indicating predominant maternal influence for these traits. Contribution of testers was more than lines and line \times tester interactions for two characters *viz.* plant height (46.15%) and panicle length (42.43%) which has been reported by (Rashid *et al.*, 2007). Line \times tester interactions contributed more than lines and testers for five characters *viz.* panicle number per plant (57.86%), grain number per panicle (42.25%), percent spikeletes fertility (58.11%), 1000 grain weight (52.01) and harvest index (55.70).

Component of genetic variance: Estimates of genetic components of variance are presented in (Table 3). Estimates of variance of general combining ability (σ_{gca}^2) was higher than those of variance of specific combining ability (σ_{sca}^2) for plant height, panicle length and spikelets number per panicle, it means these traits governed by additive gene action. Other traits *viz.* days to 50% flowering, number of grain number of panicle, panicles number per plant, spikelets fertility, 1000 grain weight, grain yield per plant and harvest index showing preponderance of non-additive gene action, non additive gene action for these traits have been reported by (Saidaiah *et al.*, 2010, Divyapriya and Kalaiyarasi, 2014 and Ghara *et al.*, 2014). It was supported by ratio of variance of general to specific combining ability ($\sigma_{gca}^2/\sigma_{sca}^2$) which was more than unity plant height, panicle length and spikelet number per panicle. These traits governed by additive gene action. The ratio of dominance to additive variance ($\sigma_{D}^2/\sigma_{A}^2$) indicated the degree of dominance whether the traits showed dominance, incomplete dominance and over dominance. The ratio less than unity for plant height, panicle length, spikeletes number per panicle, grain number per panicle and 1000 grain weight indicated that these traits showed incomplete dominance whereas the ratio ($\sigma_{D}^2/\sigma_{A}^2$)^{1/2} being greater than unity for plant height, panicle length, spikelet number per panicle, grain number per panicle and 1000 grain weight it means these traits showed over-dominance.

Table 1. TGMS lines, testers and their pedigree.

Code No.	TGMS Lines	Parentage
TGMS-1	UPRI-99-70-1	UPRI 95-140 TGMS / UPRI 95-141
TGMS-2	UPRI-99-71-1	UPRI 95-140 TGMS / UPRI 95-150 // UPRI 95-162
TGMS-3	UPRI-99-71-2	UPRI 95-140 TGMS / UPRI 95-150 // UPRI 95-162
TGMS-4	UPRI-99-73-1	UPRI 95-140 TGMS / IR 36 // IR Basmati
TGMS-5	UPRI-99-73-2	UPRI 95-140 TGMS / IR 36 // IR Basmati
TGMS-6	UPRI-99-73-3	UPRI 95-140 TGMS / IR 36 // IR Basmati
TGMS-7	UPRI-99-73-4	UPRI 95-140 TGMS / IR 36 // IR Basmati
TGMS-8	UPRI-99-74-3	UPRI 95-140 TGMS / IR BB 21 // IR Basmati
TGMS-9	UPRI-99-79-1	UPRI 95-140 TGMS / UPRI 95-141 // UPRI 95-162
TGMS-10	UPRI-99-60-1	UPRI 95-140 TGMS / UPRI 95-141
TGMS-11	UPRI-99-72-1	UPRI 95-140 TGMS / UPRI 95-150 // UPRI 95-161
TGMS-12	UPRI-99-72-3	UPRI 95-140 TGMS / UPRI 95-150 // UPRI 95-161
TGMS-13	UPRI-99-72-4	UPRI 95-140 TGMS / UPRI 95-150 // UPRI 95-161
TGMS-14	UPRI-99-74-1	UPRI 95-140 TGMS / IRBB-21 // IR Basmati
TGMS-15	UPRI-99-74-4	UPRI 95-140 TGMS / IR BB 21 // IR Basmati
TGMS-16	UPRI-99-75-1	UPRI 95-140 TGMS / IRBB-21 // UPRI-95-150
TGMS-17	UPRI-99-78-1	UPRI 95-140 TGMS / IR 66159-131-4-3-2
TGMS-18	UPRI-97-60-8	UPRI 95-140 TGMS / UPRI 95-140-1

Table 2. Proportional contribution (%) of lines, testers and L×T interaction variance.

Source	Days to 50% flowering	Plant height	Panicle number per plant	Panicle length	Spikelet number per panicle	Grain number per panicle	Percent spikelet fertility	1000 grain weight	Harvest index	Grain yield per plant
Line	49.28	17.16	38.41	30.12	35.51	27.40	28.33	14.82	42.20	51.07
Tester	4.85	46.15	3.72	42.43	34.66	30.34	13.56	33.16	2.10	5.65
Line × Tester	45.88	36.69	57.86	27.45	29.82	42.25	58.11	52.01	55.70	43.28

Therefore it appeared that the inheritance of days to 50% flowering (Panwar, 2005 and Sharma, 2006) reported non-additive, for other traits different researchers observed the non-additive gene action *viz.* panicle number per plant (Punitha *et al.* 2004 and Sharma, 2006), Percent Spikeletes Fertility (Hossen *et al.* 2005 and Gnanasekaran *et al.* 2006), harvest Index (Hossen *et al.* 2005 and Gnanasekaran *et al.* 2006) and Grain Yield per Plant (Sharma, 2006 and Dorosti and Monajjem, 2014). The traits which are controlled by additive gene action and similar findings found by different observers were plant height (Vanaja *et al.* 2003 and Gnanasekaran *et al.*, 2006), panicle length (Radhidevi *et al.*, 2002), spikeletes number per panicle (Sharma, 2006). Such type of gene action clearly indicated that pure line for additive and heterosis breeding for non-additive gene action would be ideal for their improvement.

Heritability and genetic advance: There was little difference between phenotypic and genotypic variances of all parameters showing negligible effect of environment on the inheritance of these traits. Estimates of broad sense heritability were high and found significant as their absolute values exceeded twice their respective standard errors. The high heritability in broad sense for all the traits in the present study is also reported by (Rita *et al.*, 2009 and Ukaoma *et al.*, 2013) along with genetic advance (low, moderate and high) (Table 3) in term of percentage of mean.

High heritability associated with low genetic advance for different traits *viz.* days to 50% flowering ($h^2=92$, $GA=4.25$) was also observed (Paikhomba *et al.*, 2014 and Agrawal, 2003) for plant height ($h^2=81$, $GA=9.59$) (Ghara *et al.*, 2014 and Paikhomba *et al.*, 2014), for panicle length ($h^2=98$, $GA=8.26$) (Shanthi and Singh, 2002), for panicle number per plant ($h^2=82$, $GA=9.85$), for per cent spikelet fertility ($h^2=86$, $GA=4.67$) and harvest index ($h^2=95$, $GA=4.99$). High heritability associated with moderate genetic advance for grain number per panicle ($h^2=97$, $GA=19.93$) also observed by (Paikhomba *et al.*, 2014), for grain yield per plant ($h^2=98$, $GA=14.38$) similar to results of (Pfunkrei *et al.*, 2011, Toshimenla and Changkija, 2013 and Koli *et al.*, 2013). High genetic advance associated with high heritability was observed only for one trait *viz.* spikeletes number per panicle ($h^2=98$, $GA=27.23$) also reported by (Rita *et al.*, 2009 and Singh *et al.*, 2011). All the traits indicated the high heritability but selection based only on heritability is not efficient, for stable selection both selection parameters e.g. heritability and genetic advance should be high.

Conclusion

On the basis of results as summarized above, it is concluded that the great deal of variability for the important characters studied, high heritability with high genetic advance as per cent of mean for spikeletes

Table 3. Estimates of genetic components of rice TGMS lines.

Parents	Days to 50% flowering	Plant height	Panicle number per plant	Panicle length	Spikelets number per panicle	Grain number per panicle	Percent spikelets fertility	1000 grain weight	harvest index	Grain yield per plant
sl ² Line HS	24.50	6.11	1.93	0.75	438.51	190.86	8.72	0.57	16.50	57.82
sl ² Tester HS	3.00	22.91	0.23	1.40	541.41	268.28	5.41	1.71	1.01	8.04
σ^2_{gca}	6.91	19.85	0.54	1.28	522.70	254.21	6.01	1.50	3.83	17.09
σ^2_{sca}	29.48	16.61	3.86	0.79	484.24	388.73	23.32	2.70	28.68	64.90
sl ² e	1.36	2.80	0.03	0.18	9.45	7.36	1.64	0.15	0.65	0.62
sl ² a(F = 1)	13.82	39.71	1.09	2.56	1045.40	508.41	12.02	3.00	7.65	34.18
sl ² D(F = 1)	29.48	16.61	3.86	0.79	484.24	388.73	23.32	2.70	28.68	64.90
sl ² a / Var.D	0.47	2.39	0.28	3.25	2.16	1.31	0.52	1.11	0.27	0.53
Degree of Dominance (σ^2_D/σ^2_A) ^{1/2}	1.46	0.65	1.89	0.55	0.68	0.87	1.39	0.95	1.94	1.38
$\sigma^2_{gca}/\sigma^2_{sca}$	0.23	1.19	0.14	1.62	1.08	0.65	0.26	0.55	0.13	0.26
sl ² p	44.65	59.12	4.97	3.53	1539.08	904.50	36.99	5.85	36.98	99.70
Heritability (Broad Sense) %	92	81	98	82	98	97	86	90	95	98
Genetic Advance	4.26	10.64	1.00	2.81	54.89	34.82	4.07	2.56	2.59	7.05
Genetic advance in mean percentage	4.25	9.59	8.26	9.85	27.23	19.93	4.67	10.26	4.99	14.38

number per panicle indicates that the characters are largely controlled by additive gene action, which indicating that improvement in this character is possible through hybridization followed by selection with pedigree breeding. The traits which are controlling by non-additive gene action, heterosis breeding would be the ideal for their improvement.

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