



Variability and Genetic Parameter Analysis in F₃ and F₄ Generation of TGMS Rice (*Oryza sativa* L.) Population

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An attempt was made to study variability and genetic parameter analysis in the F₃ and F₄ generation of rice genotypes. The phenotypic variance was higher than the corresponding genotypic variance for all the characters in F₃ and F₄ generation. These differences were indicating greater influence of environment for expression of the traits in F₃ generation and F₄ generations. Considering genetic parameters high genotypic coefficient of variation (GCV) value was observed for number of productive tillers per plant (25.78) and single plant yield (24.578), whereas moderate genotypic coefficient of variation value was exhibited by plant height (10.59). In the present study, all the characters studied recorded generally high heritability estimates in both the generations except panicle length and spikelet sterility in F₄ generation. High heritability with high genetic advance in percent of mean was observed for stigma exertion percentage, plant height, number of productive tillers / plant and single plant yield indicated that these characters were under additive gene control and selection for improvement might be effective. Spikelet fertility percentage and pollen sterility percentage showed high heritability but low genetic advance (%), which indicated that non additive gene effects were involved for phenotypic expression of this character.

Key words: TGMS rice, F₃ and F₄ generation, variability, phenotypic and genotypic parameters

The development of superior high yielding hybrids depends on the choice of parents, which are capable of producing heterotic combinations. Tai (1979) concluded that knowledge of genetic architecture of the genotype is the key to select desirable parents. Availability of more number of TGMS lines with favourable genetic background and desirable features of stable sterility and outcrossing potential will intensify two line breeding programme. Low seed yield in the seed production has been identified as the major limitation to hybrid rice technology. To enhance the hybrid seed yield, the natural outcrossing of sterile lines should be increased which in turn depends upon many floral traits such as panicle exertion, stigma exertion, duration of glume opening etc., The study of genetic variability is a basic requirement in any crop improvement programme for deciding the efficiency of selection. Environmental effects influence the genetic variation of quantitative characters. Hence partitioning of overall variances as genetic and non genetic components becomes necessary for any effective selection programme. The amount of heritable variation is much helpful in the selection process. The extent of genetic variability existing in a crop is of great importance, since greater the diversity widen the scope for selection. Hence, the stable TGMS line TS 29 was crossed with agronomically improved variety CO(R) 49 to transfer

the TGMS trait into cultivated variety. In order to exploit the new gene combination, F₃ and F₄ families were evaluated for yield and desirable floral traits.

Materials and Methods

The stable TGMS parental line, TS 29 was crossed with the improved rice variety CO(R) 49 for synthesis of segregating population. For making cross, parental lines were raised in the summer season (rabi 2006-07) for getting complete sterility in the female line (TS 29). The crossed F₁ seeds were raised along with parents in the next season (kharif 2007) for studying the F₁ plant progenies and single plants were harvested during maturity stage and forwarded to further generations. In F₂ generation the individual plants were raised for studying their pollen and spikelet fertility/sterility level. Unfortunately the climatic condition during spikelet formation stage induced complete or partial fertility alone in the progenies. Hence all the progenies were forwarded to F₃ generation. In the F₃ population, each progeny was raised during sterility inducing environment in paired rows and each row contains 12 plants. During the maturity stage the sterile plants were observed. A total of eighty four homogeneous sterile progenies were identified. The stubbles of sterile plants from the F₃ population were uprooted and planted in the separate field for getting seeds during cool season and each stubble progeny contains nine stubble plants. Pollen fertility was

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observed in all the stubble derived plants. Some of the biometric observations were taken up in the stubble field for selecting desirable sterile lines. Matured seeds were collected after attaining physiological maturity. The F₄ generation were raised during fertility restricting season from the fertile seeds obtained by selfing of the selected sterile stubbles during the fertility favouring environment in the stubble nursery. Pollen fertility was observed in all the families during flowering stage. Complete and uniformly sterile lines were identified with desirable floral traits. These lines are grouped into early and medium duration lines and all the biometrical characters were observed. For biometrical studies the F₃ and F₄ generation were raised in three replications and five plants in each replication were observed and their mean values were used for calculating variances. The mean and

variance of F₃ and F₄ families were estimated for the traits viz., days to 50% flowering, plant height, number of productive tillers per plant, pollen fertility percentage, panicle length, panicle exertion, stigma exertion percentage, spikelet fertility percentage and single plant yield. The estimates of genotypic and phenotypic variance, phenotypic and genotypic coefficient of variation, heritability and genetic advance for different traits were computed according to Lush (1940) and Johnson *et al.* (1955).

Results and Discussion

The analysis of variance and genetic parameters for the important traits in the F₃ and F₄ generations are presented in tables 1 and 2 respectively. The analysis of variance revealed presence of significant differences among the families for TGMS and yield related traits.

Table 1. Genetic variability parameters for different characters in F₃ generation of rice

Characters	Range	Mean	C.D	C.V	P.V	G.V	P.C.V	G.C.V	h ₂ %	G.A	G.A as% of mean
Days to 50% flowering	70.00 - 96.00	80.00	2.63	1.66	33.40	30.73	7.24	6.95	92	10.95	13.74
Pollen fertility percentage	54.70 - 76.20	62.40	3.94	3.19	26.75	20.80	8.29	7.31	78	8.31	13.27
Plant height(cm)	72.00 - 106.33	84.65	2.53	1.51	82.84	80.38	10.75	10.59	97	18.19	21.49
Number of productive tillers per plant	5.67 - 20.33	12.00	1.88	7.95	11.16	9.79	27.52	25.78	88	4.75	49.75
Panicle length(cm)	18.70 - 27.25	22.61	1.69	3.79	5.97	4.87	10.81	9.76	82	4.13	18.15
Panicle exertion percentage	66.94 - 85.31	75.27	2.31	1.56	21.49	19.43	6.15	5.85	90	8.60	11.46
Stigma exertion percentage	54.31-73.76	61.66	0.62	0.51	16.40	16.24	6.57	6.54	99	8.26	13.40
Spikelet fertility percentage	67.13 - 82.47	72.33	2.26	1.58	14.78	12.82	5.32	4.95	87	6.90	9.50
Single plant yield	11.67 - 40.47	25.62	2.51	1.76	42.21	39.59	25.31	24.57	94	12.58	49.12

In F₃ generation, a higher estimate of phenotypic variance (PV- 82.84) and genotypic variance (GV- 80.38) was observed for plant height followed by single plant yield (PV- 42.21 and GV-39.59), days to 50% flowering (PV-33.40 and GV-30.73), and pollen fertility percentage (PV-26.75 and GV-20.80). Spikelet fertility percentage had a phenotypic variance value of 14.78 and genotypic variance value of 12.82. Lowest phenotypic and genotypic variance was recorded by the trait panicle length with 5.97 and 4.87, respectively followed by number of productive tillers per plant which had a phenotypic variance of 11.16 and genotypic variance of 9.79 (Table 1). The values of genotypic and phenotypic variance, their coefficient of variation, heritability and genetic advance for different traits in the F₄ generation are shown in Table 2. The highest level of phenotypic variance (138.81) and genotypic variance (134.31) was recorded for plant height followed by days to 50% flowering (34.88 and 33.35), stigma exertion percentage (28.38 and 25.02), pollen sterility percentage (19.23 and 17.17), panicle exertion percentage (17.51 and 15.52), and spikelet sterility percentage (11.34 and 9.84). The least level of phenotypic variance (3.80) and genotypic variance (1.98) were registered for the traits panicle length followed by number of productive tillers per plant (11.03 and 10.23).

The genotypic coefficient of variation percent was found to be less than phenotypic coefficient of variation for all the traits studied in the F₃

generations. Among the characters, high genotypic coefficient of variation was recorded by the characters viz., Number of productive tillers per plant (25.78) and single plant yield (24.57). Moderate genotypic coefficient of variation value was exhibited in plant height (10.59). The low levels of genotypic coefficient of variations were showed in the characters viz., Panicle length (9.76), pollen fertility percentage (7.31), days to 50% flowering (6.95), stigma exertion percentage (6.54), panicle exertion percentage (5.85) and spikelet fertility percentage (4.95). Phenotypic coefficient of variation was high for number of productive tillers (27.52) and single plant yield (25.31). Moderate PCV values were exhibited by panicle length (10.81) and plant height (10.75). The low level of PCV was observed in characters like pollen fertility percentage (8.29), days to 50% flowering (7.24), stigma exertion percentage (6.57) and spikelet fertility percentage (5.32) (Table 1). The values of the GCV and PCV in the F₄ generation are presented in the Table 2. Lower genotypic coefficient of variation was noticed in all the traits which were studied in the F₄ generation in comparison with phenotypic coefficient of variation. Number of productive tillers per plant had high level of GCV (24.27) in comparison to other traits studied and moderate GCV was recorded in plant height (13.92) and spikelet sterility percentage (10.87). The low level of GCV was shown in the traits viz., Stigma exertion percentage (7.62), days to 50% flowering (7.18), panicle length (6.51), panicle exertion

percentage (5.09) and pollen sterility percentage (4.29). Phenotypic coefficient of variation was high for number of productive tillers per plant (25.16) and moderate level of PCV for plant height (14.15) and spikelet sterility percentage (11.67) in F₄ generation. The low level of PCV was observed for panicle length (9.01), stigma exertion percentage (8.12), days to 50% flowering (7.29), panicle exertion percentage (5.41) and pollen sterility percentage (4.54). The first and foremost criterion to be considered while evaluating a population is the magnitude of genetic variation. Simple measure of variability viz., range, mean and variance were compared for the different generations mentioned above. Phenotypic variance, genotypic variance, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed for all the characters in both the generations. However since the variations are associated with units, the unit free PCV and GCV values are considered more reliable for discussion. Among PCV and GCV estimates comparison of characters based on GCV is more appropriate as it represents the heritable portion of total variability. PCV estimates include environmental effect also (Allard, 1960). Higher magnitude of genotypic variability in terms of GCV of more than 20 per cent was recorded for number of productive tillers per plant in F₃ and F₄ and single plant yield in F₃ generation. The high GCV estimates for number of productive tillers per plant, single plant yield was in accordance with Michael Gomez and Rangasamy (2002), and Nayudu *et al.* (2007). These traits showing high genotypic variability offer greater scope for genetic improvement through selection. Moderate level of variability was observed for plant height and spikelet fertility and sterility percentage in both the generations. This trait was already reported by Mishra and Verma (2002). Low level of GCV estimates were noticed in the present study

Table 2. Genetic variability parameters for different characters in F₄ generation of rice

Characters	Range	Mean	C.D	C.V	P.V	G.V	P.C.V	G.C.V	h ₂ %	G.A	G.A as% of mean
Days to 50% flowering	70.00 - 97.00	80.00	1.04	1.64	34.38	33.35	7.29	7.18	97	11.72	14.56
Pollen sterility percentage	82.80 - 100.00	96.54	1.26	2.32	19.23	17.17	4.54	4.29	89	8.04	8.35
Plant height(cm)	65.33-111.50	83.25	2.08	3.42	138.81	134.31	14.15	13.92	97	23.54	28.21
Number of productive tillers per plant	7.67 - 22.00	13.20	5.51	1.41	11.03	10.23	25.16	24.27	93	6.36	48.23
Panicle length(cm)	18.43 - 25.85	21.64	5.09	2.18	3.80	1.98	9.01	6.51	52	2.11	9.68
Panicle exertion percentage	69.20 - 86.00	77.35	1.51	2.28	17.51	15.52	5.41	5.09	89	7.67	9.88
Stigma exertion percentage	56.15 - 78.81	65.63	2.28	2.95	28.38	25.02	8.12	7.62	88	9.66	14.75
Spikelet sterility percentage	88.33 - 100.00	98.23	2.15	4.17	11.34	9.84	11.67	10.87	87	6.02	20.85

increased heritability for the characters viz., number of production tiller, panicle length, single plant yield was also reported by Suman *et al.* (2005). The floral traits like stigma exertion percentage, panicle exertion percentage, spikelet fertility/ sterility percentage also had high heritability estimates. This result was also confirmed by Seetharamaiah *et al.* (2001) and Ushakumari *et al.* (2002).

Genetic advance was moderate for the character plant height (18.19) followed by single plant yield (12.58) and days to 50 % flowering (10.95) in F₃ generation (Table 1). Characters like panicle

for days to flowering, pollen fertility percentage, panicle length, panicle exertion percentage and stigma exertion percentage. Similar findings were reported earlier for days to 50% flowering by Verma *et al.*, 2000; Suman *et al.* (2005); Paramesha *et al.* (2005); Rita Binse (2006) and for panicle length Mamta singh *et al.* (2007). The influence of environment on each trait could be assessed on the basis of difference between PCV and GCV values. In the present study all the characters showed negligible differences between PCV and GCV, revealing the greater role of genetic factors influencing the expression of these characters. Genetic coefficient of variation alone does not refer to the usefulness of characters for selection. Burton (1952) suggested that get together with heritability estimates would give the best picture of the extent of advance to be expected by selection. The success of genetic advance depends on genetic variability, heritability and selection intensity.

Estimate of heritability were high for all the characters studied in the F₃ generation (Table 3). The highest heritability was noticed for the characters viz., Stigma exertion percentage (99.00 per cent), plant height (97.00 per cent), single plant yield (94.00 per cent), days to 50% flowering (92.00 per cent), panicle exertion percentage (90.00 per cent), number of productive tillers per plant (88.00 per cent), spikelet fertility percentage (87.00 per cent), panicle length (82.00 per cent) and pollen fertility percentage (78.00 per cent). In the present study, all the characters studied recorded generally high heritability estimates in both the generations except panicle length and spikelet sterility in F₄ for broad sense heritability (Table 2). Such a high heritability estimates were reported in the earlier experiments for days to 50% flowering, plant height by Michael Goweze and Rangasamy (2002). The

exertion percentage (8.60), pollen fertility percentage (8.31), stigma exertion percentage (8.26), spikelet fertility percentage (6.90), and panicle length (4.13) recorded low genetic advance. The values of genetic advance as percent of mean were high for the characters like number of productive tillers per plant (49.75 per cent), single plant yield (49.12 per cent) and plant height (21.49 per cent). Moderate genetic advance as percent of mean was recorded for the traits viz., panicle length (18.15 per cent), days to 50% flowering (13.74 per cent), stigma exertion percentage (13.40), pollen fertility

percentage (13.27 per cent), panicle exertion percentage (11.46 per cent) and spikelet fertility percentage (9.50). In the case of F₄ generation, high level of heritability was noticed for days to 50% flowering (97.00 per cent), plant height (97.00 per cent), number of productive tillers per plant (93.00 per cent), pollen sterility percentage (89.00 per cent), panicle exertion, stigma exertion percentage (88.00 per cent) and spikelet sterility percentage (87.00 per cent). Panicle length (52.00 per cent) was observed for moderate heritability percentage. High level of genetic advance was recorded for plant height (23.54) in the F₄ generation and moderate genetic advance for days to 50% flowering (11.72). The traits viz., stigma exertion percentage (9.66), pollen sterility percentage (8.04), panicle exertion percentage (7.67), number of productive tillers per plant (6.36), spikelet sterility percentage (6.02) and panicle length (2.11) had a low level of genetic advance value.

Genetic advance as per cent of mean had high ratio in number of productive tillers per plant (48.23 per cent) and plant height (28.21 per cent) and spikelet sterility percentage (20.85 per cent). These results were also in agreement with the findings of Michael Gomez and Kalamani (2003) and Verma *et al.* (2000). Moderate GA as per cent of mean was recorded in stigma exertion percentage (14.75 per cent) and days to 50% flowering (14.56 per cent). Characters like panicle exertion percentage (9.88 per cent), panicle length (9.68 per cent) and pollen sterility percentage (8.35 per cent) had a low genetic advance as percent of mean (Table 2). The genetic gain that can be expected by selection for a character is given by the estimates of genetic advance. The genetic advance as per cent of mean was found to be high for number of productive tillers per plant, single plant yield and plant height in the F₃ and only number of productive tillers per plant for high genetic advance was observed in F₄ generation. High heritability coupled with high genetic advance observed for these characters indicates the predominance of additive gene action in the inheritance of these characters and suggests their amenability for effective phenotypic selection.

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