



Genetic divergence of elite *indica* thermosensitive genic male sterile lines in rice (*Oryza sativa* L.)

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The knowledge of available genetic diversity in elite thermosensitive genic male sterile (TGMS) lines has great significance in two-line system of hybrid rice (*Oryza sativa* L.) breeding programme of the tropics. In this investigation, genetic diversity was determined in 34 genotypes comprising 30 *indica* TGMS lines developed locally at Pantnagar and four cultivars viz., Pant Dhan 4 and Ajaya (*indica*), Taichung 65 (*japonica*) and IR 65598-112-2 (tropical *japonica*) aimed to develop two-line intra- and inter-subspecific rice hybrids of different maturity groups.

The experiment was conducted during kharif 2000 in the RBD with two replications. Each genotype had four-row plot of 4 m length with the inter- and intra-row spacing of 20 × 15 cm. Observations on 11 characters viz., days to 50% flowering, plant height, panicle number/plant, panicle length, spikelet number/panicle, grain number/panicle, per cent spikelet fertility, total dry matter/plant, 1000-grain weight, harvest index and grain yield/plant, were recorded on five competitive and randomly selected plants except 50% flowering days which was taken on plot basis. The divergence analysis was carried out using Mahalanobis D^2 statistics [1]. The genotypes were grouped into clusters following the Tocher's method [2].

The significant mean squares indicated potent variability among the genotypes for all the characters. Genotypes were grouped into three clusters (Table 1). Cluster I was the largest having 31 genotypes while clusters II and III had two and one genotype(s), respectively. All the *indica* genotypes (30 TGMS lines and Pant Dhan 4) except Ajaya fell into cluster I which formed cluster III. Low magnitude of genetic divergence among TGMS lines is also reported earlier [3, 4]. Taichung 65 and IR 65598-112-2 constituted cluster II. Results amply confirmed the genetic dissimilarity of *indica* subspecies to *japonica* and tropical *japonica*, the later two being more similar among them. Despite belonging to the same geographic region, Ajaya fell

into cluster III, different from cluster I grouping all *indica* TGMS lines and Pant Dhan 4. This type of genetic diversity among genotypes of the same geographic region might be due to differential adaptation, selection criteria, selection pressure and environments [5]. This indicated the role of genetic drift and selection in different environments to produce greater diversity than the geographic diversity [5]. 30 *indica* TGMS lines formed single cluster and this might be due to similarity in their pedigree (Table 1) and identical selection pressure and adaptation.

Cluster II contained only Taichung 65, a *japonica* and IR 65598-112-2, a derived tropical *japonica*, but revealed the maximum intra-cluster distance (16.70) as these genotypes originated in two different breeding programmes of Taiwan (temperate) and the Philippines (tropical). The reason for their grouping into the same cluster might primarily be due to its pedigree where introgression of *japonica* genes occurred in the finally selected line(s) after hybridization. Thus, Taichung 65 and IR 65598-112-2 were diverse enough and the cluster II was the best for both between and within group hybridization view points. Cluster I possessing 31 genotypes had also high intra-cluster distance (15.80). As regards inter-cluster distance, cluster I showed maximum genetic distance from cluster II ($d = 39.77$) suggesting maximum diversity between genotypes of these two clusters. Hybridization between such diverse lines selected as male/female from the respective clusters is likely to produce heterotic two-line hybrids. This assumption was proved true as some of the most heterotic two-line hybrids ($L_5 \times T_2$, $L_{11} \times T_3$ and $L_6 \times T_2$) had female TGMS parents from cluster I and male parent from cluster II (data not shown).

The genetic divergence among clusters was well reflected in cluster means of various characters (data not shown). The cluster III revealed the highest means for days to 50% flowering, panicle length, spikelet number/panicle, grain number/panicle, total dry

Table 1. Clustering pattern of genotypes and their agronomic features under Pantnagar conditions

Genotype	Code	Parentage	DF#	PH# (cm)
Cluster I : 31 Genotypes				
24/34-11-2 BS	L ₁	FP*/FP/UPRI 95-117	97.8	87.2
69-15 S	L ₂	FP/UPRI 95-117	103.5	72.1
359-1 S	L ₃	FP/UPRI 95-124//BPH-RI2	150.0	86.1
365-2 S	L ₄	FP/UPRI 95-150//UPRI 95-162	102.5	77.5
365-8 S	L ₅	FP/UPRI 95-150//UPRI 95-162	100.7	93.4
369-1 S	L ₆	FP/UPRI 95-141//IR 29723	108.7	84.8
396-3 S	L ₇	FP/UPRI 95 141//IR 29723	94.5	85.9
369-15 S	L ₈	FP/UPRI 95-141//IR 29723	100.5	81.9
370-3 S	L ₉	FP/UPRI 95-141//FP/IR 29723	102.5	78.3
370-5 S	L ₁₀	FP/UPRI 95-141//FP/IR 29723	99.0	81.5
381-4 S	L ₁₁	IR Bas.//FP/IR29723	106.0	119.2
24/34-12 BS	L ₁₂	FP//FP/UPRI 95-117	97.2	75.9
69-1 S	L ₁₃	FP/UPRI 95-117	101.0	97.2
206-8 S	L ₁₄	FP/UPRI 95-141	103.7	75.8
206-12 S	L ₁₅	FP/UPRI 95-141	106.2	73.6
307-4-6 S	L ₁₆	FP/UPRI 95-141	108.7	77.6
307-4-12 S	L ₁₇	FP/UPRI 95-141	103.2	76.1
307-4-13 S	L ₁₈	FP/UPRI 95-141	99.0	78.3
307-5-1 S	L ₁₉	FP/UPRI 95-141	99.7	92.1
307-5-2 S	L ₂₀	FP/UPRI 95-141	102.0	86.9
307-5-4 S	L ₂₁	FP/UPRI 95-141	102.0	82.1
307-5-7 S	L ₂₂	FP/UPRI 95-141	97.5	78.9
307-5-9 S	L ₂₃	FP/UPRI 95-141	99.5	84.9
308 13 S	L ₂₄	FP/UPRI 95-124	96.0	79.6
UPRI	L ₂₅	FP/UPRI 95-150	95.0	90.1
97-53TGMS				
UPRI	L ₂₆	FP/UPRI 95-150	97.5	75.7
97-54TGMS				
UPRI	L ₂₇	UPRI 95-150	97.0	82.5
97-56TGMS				
UPRI	L ₂₈	FP/UPRI 95-141	100.7	71.1
97-61-3S				
TGMS				
UPRI	L ₂₉	FP/UPRI 95-141	104.0	74.2
97-61-8S				
TGMS				
UPRI	L ₃₀	FP/UPRI 95-141	108.0	72.9
97-61-10S				
TGMS				
Pant Dhan-4	T ₁	IR 262/Remadja	104.2	118.1
Cluster II: Two Genotypes				
Taichung 65	T ₂	Kameji/Shinriki	84.2	121.3
IR	T ₃	Shen Nung	76.2	110.0
65598-112-2		89-366/Genjah wangkal		
Cluster III: One genotype				
Ajaya	T ₄	IET 4141/CR 98-7216	115.5	107.5

*FP: UPRI 95-140, #DF: days to 50% flowering; PH: plant height

matter/plant, grain yield/plant, 1000-grain weight and harvest index while the cluster I exhibited the highest mean for spikelet fertility. The maximum means for plant height and panicle number/plant were expressed in cluster II. These results indicate none of the clusters containing genotypes with all the desirable characteristics for direct selection and exploitation. Hybridization between genotypes of cluster I with cluster II and III was, therefore, suggested for development of desirable intra- and inter-subspecific hybrids.

Results on the relative contribution of different characters towards genetic divergence revealed 1000-grain weight (49.19%) and grain number/panicle (25.49%) contributing the maximum. These characters together influence grain yield profoundly and presence of wide diversity for them among parental lines is of paramount significance in development of the most heterotic hybrids. Plant height and spikelet number/panicle also contributed to genetic divergence.

The study, therefore suggested importance of 1000-grain weight, grain number/panicle, plant height and spikelet number/panicle for selection of TGMS lines and their male parents for hybridization among distantly related clusters I & II and I & III - keeping in view their yield potential, to obtain higher magnitude of heterosis in two-line rice hybrids.

References

1. **Mahalanobis P.C.** 1936. On the generalized distance in statistics. Proc. Nat. Inst. Sci., India, **2**: 49-55.
2. **Rao C.R.** 1952. Advanced statistical methods in biometrical research. John Wiley & Sons, New York, USA.
3. **Naghia P., Malik J.P.S., Pandey M.P. and Singh N.K.** 2002. Application of RAPD markers for genetic distance analysis of hybrid rice parental lines. Indian J. Genet., **62**: 1-4.
4. **Rongbai L. and Pandey M.P.** 2002. Genetic improvements of features for hybrid seed production and self seed multiplication of thermosensitive genic male sterile lines in rice. J. Genet & Breed, **56**: 89-97.
5. **Murty B.R. and Arunachalam V.** 1966. The nature of genetic divergence in relation to breeding system in some crop plants. Indian J. Genet., **26**: 188-198.