

### 3. Mapping for a new locus causing hybrid sterility in a China landrace (*Oryza sativa* L.)

D. T. LI<sup>1</sup>, S. S. ZHU<sup>1</sup>, L. JIANG<sup>1</sup> and J. M. WAN<sup>1,2,3</sup>

- 1) State Key Laboratory of Crop Genetics and Germplasm Enhancement, Jiangsu Provincial Center of Plant Gene Engineering, Nanjing Agricultural University, Nanjing, 210095 China
- 2) Institute of Crop Sciences, Chinese Academy of Agricultural Sciences, Beijing, 100081 China
- 3) Corresponding Author, E-mail: [wanjm@njau.edu.cn](mailto:wanjm@njau.edu.cn), Tel & Fax: +86-25-84396516

Semi-sterile panicles of hybrid between *indica* and *japonica* in rice was earlier identified to be due to an allelic interaction at the *S5* locus on chromosome 6, where *S5<sup>i</sup>* and *S5<sup>j</sup>* were carried by *indica* and *japonica*, respectively. *S5<sup>n</sup>*, referred to as wide compatibility gene, existed in some Aus varieties, such as Dular (Ikehashi and Araki 1986). One of parent carrying neutral allele *S5<sup>n</sup>* does not show hybrid sterility when crossed to both *indica* and *japonica*. However, Ketan Nangka, a *javanica* variety carrying neutral alleles at two loci *S5* and *S15* (Wan et al. 1996), showed typical sterility when crossed to Tuanguzao, a landrace of Yunnan province in China.

A mapping population of Tuanguzao/Ketan Nangka//Ketan Nangka was used for detecting the gene(s) controlling hybrid sterility in the hybrid between Tuanguzao and Ketan Nangka. Based on 238 F<sub>1</sub> plants, a linkage map consisting of 123 simple sequence repeat (SSR) markers and an expressed sequence tagged (EST) marker was constructed using MAPMAKER/EXP. A genome-wide analysis was carried out to search for genes conferring significant effects on hybrid sterility using QTL Cartographer soft (version 1.15), at a LOD score of 2.89 (the experiment-wise LOD (log of the odds ratio) threshold significance level was determined by computing 1,000 permutations). Two loci were found to cause the hybrid spikelet sterility via female gamete abortion, designated as *qSS2* and *qSS5* (Table 1). *qSS2* located on chromosome 2 linked closely to RM236 and can explain 18.6% of phenotypic variance. *qSS5* located on chromosome 5 linked tightly to RM413, and can explain 20.1% of phenotypic variance. By further analysis we found that heterozygote genotype of Tuanguzao/Ketan Nangka was the cause of sterility in backcross population and genetic effects of two loci, *qSS2* and *qSS5*, were additive.

Up to date, two sterility loci, *S29(t)* and *S22(t)*, have been reported on chromosome 2. *S29(t)* was detected to confer hybrid sterility between Bai Mi Fen and Ketan Nangka and located on the long arm of chromosome 2 (Zhu et al. 2005). It appeared to be different from *qSS2* detected in this study according to its chromosome location. *S22(t)* was a pollen sterility locus that produce 50% pollen fertility and normal spikelet fertility in the heterozygous condition (Sobrizal et al. 2000), but *qSS2* was a hybrid spikelet semi-sterility locus that caused the hybrid spikelet sterility via female gamete abortion. So *qSS2* would be a new locus controlling hybrid sterility on chromosome 2, designated as *S32(t)* following the hybrid sterility nomenclature. *qSS5* was coincided with *S31(t)* according to the location on chromosome (Zhao et al. 2005).

Three alleles were detected at  $S32(t)$  as follows: Ketan Nangka and Tuanguzao carried  $S32^{kn}(t)$  and  $S32^{ii}(t)$  respectively, an Aus variety, Dular, had a neutral allele  $S32^n(t)$ . The hybrid genotype of  $S32^{kn}(t)/S32^{ii}(t)$  showed sterility due to allelic interaction, such an allelic interaction did not occur in  $S32^n(t)/S32^{ii}(t)$  and  $S32^n(t)/S32^{kn}(t)$  genotypes. The tightest linkage markers detected in this paper will be useful for marker-aided transfer of wide compatibility gene (WCG) in hybrid rice breeding.

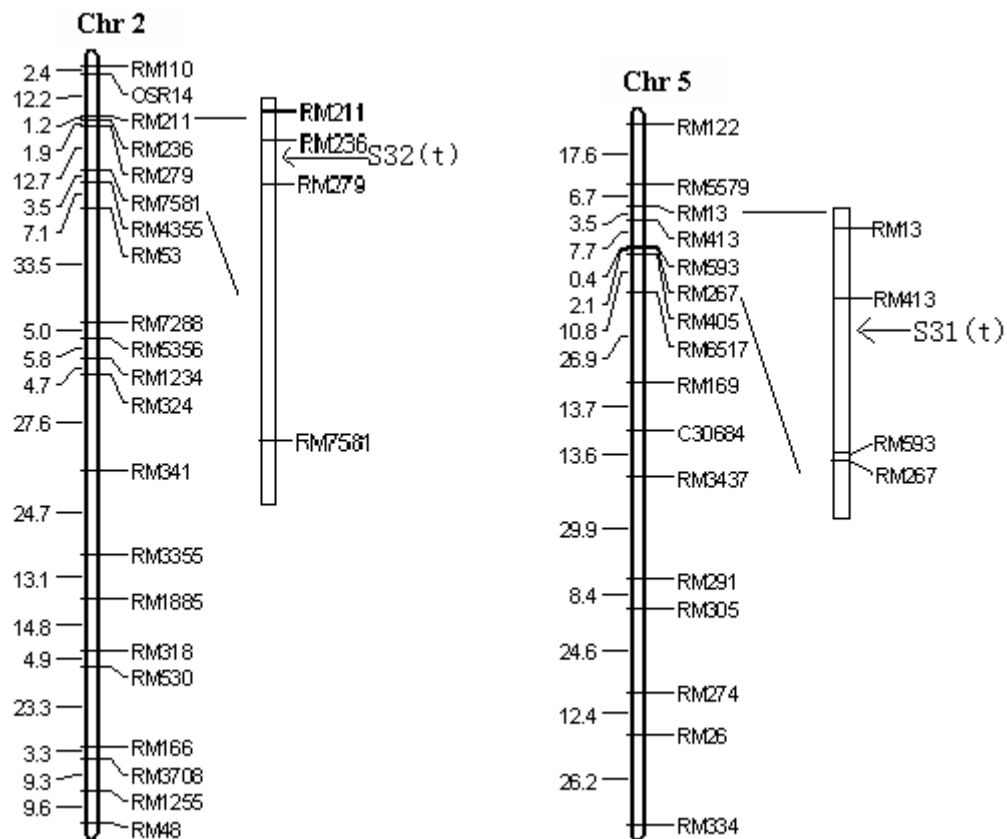


Fig. 1. Chromosome locations of two loci controlling hybrid fertility.

Table 1. QTLs controlling hybrid sterility in the Tuanguzao/Ketan Nangka//Ketan Nangka population detected at LOD 2.89, with composite interval mapping, using QTL Cartographer, version 1.15

QTLs	Chromosome	NML <sup>1</sup>	LOD	Effect	Variance( %)
$qSS2$	2	RM236	14.5	21.5	18.6
$qSS5$	5	RM413	15.1	21.5	20.1

<sup>1</sup> Nearest marker locus of putative QTLs.

## References

Ikehashi, H. and H. Araki, 1986. Genetics of  $F_1$  sterility in remote crosses of rice. In "Rice Genetics",

- IRRI, P.O. Box 933, Manila, Philippines, pp. 119-130.
- Sobrizal, Y. Matsuzaki, P. L. Sanchez, K. Ikeda and A. Yoshimura, 2000. Identification of a gene for male gamete abortion in backcross progeny of *Oryza sativa* and *Oryza glumaepatula*. RGN 17: 59-61.
- Zhu, S. S., C. M. Wang, T. Q. Zheng, Z. G. Zhao, H. Ikehashi and J. M. Wan, 2005. A new gene causing hybrid sterility located on chromosome 2 in a remote cross of rice. Plant Breed 124: 1-6.
- Wan, J. and H. Ikehashi, 1996. List of hybrid sterility gene loci (HSGLi) in cultivated rice (*Oryza sativa* L.). RGN 13: 110-114.
- Zhao, Z. G., C. M. Wang, L. Jiang, S. S. Zhu, H. Ikehashi and J. M. Wan, 2005. Identification of a new hybrid sterility gene in rice (*Oryza sativa* L.). Euphytica (in press).