5. A new sterile gene from Oryza glaberrima on chromosome 3

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Rice is the staple food for the world and two rice species are cultivated for food production. Oryza sativa originated in Asia but is widely grown. O. glaberrima originated and is cultivated in West Africa. Both species have same genome AA (Chang 1976, Morinaga et al. 1957). Since O. glaberrima is a cultivated species with some useful traits or valuable genes O. sativa lacks, O. glaberrima was supposed to be the first choice of useful gene mining in AA genome species of genus Oryza (Xu et al. 2005). However, a great of crossing experiments dealing with interspecific hybrid between O. sativa and O. glaberrima tell us that the reproductive barrier is main obstruction (Morinaga et al. 1957 Morishima et al. 1962, Morishima et al. 1963, Chu et al. 1969, Jones et al. 1997, Sano et al. 1979, Sano 1983, Tao et al. 1997). And hybrid sterility between two cultivated species is the most common and serious barrier. A series of sterility loci in O. glaberrima, such as gamete eliminator S1, pollen killer S3, S18, S19, S20 and S21, S29(t) located on chromosome 6, 11, 10, 3, 7, 2 respectively (Doi et al. 1998, Doi et al. 1999, Hu et al. 2004, Taguchi et al. 1999), has been determined from advanced backcross populations even hybrid sterility performed quantitative inheritance in preliminary population. But when single sterile gene or pyramiding of several sterile genes were transferred to Asian species of cultivar as a bridge to cross African species again, the F₁ was still high sterile, which means understanding of the nature of interspecific hybrid sterility is far from clear.

In our experiment, 59 accessions of O. glaberrima were used as female parent to make hybridization with Yunnan japonica cultivar Dianjingyou 1. F_1 s were backcrossed using Dianjingyou 1 as male parent. Between BC_1F_1 and BC_3F_1 , 4-5 plants from each were randomly selected to make backcross without selection. From BC_4F_1 , pollen grain fertility was checked and semi-sterility plants were used to make further backcross from each family. At BC_6F_1 , 135 semi-sterility plants selected from 142 families of O. glaberrima/Dianingyou 1/7/Dianjingyou 1 were used to make genotyping. From genotyping and QTL detection results, some plants were used to make BC_7F_1 mapping populations.

An advanced backcross population of BC_7F_1 with 123 individuals, which derived from IRGC103977 (O. glaberrim) as female and donor parent and Dianjingyou 1 (O. sativa) as male and recurrent parent, was raised. And SSR markers were used to map the sterile gene(s).

In the mapping population, pollen grain fertility was clearly segregated into semi-sterile and normal

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two types (Fig. 1). Segregation ratio of the semi-sterile plants and normal plants fitted well with the expected monogenic 1:1 ratio ($x^2=0$, p>0.9). SSR mapping using the population revealed that the semi-sterility locus was located in the region on chromosome 3 closely linked to RM231 and RM251. It was designated as S34(t) (Fig. 2), since no sterile gene from *O. glaberrima* was reported in this region.

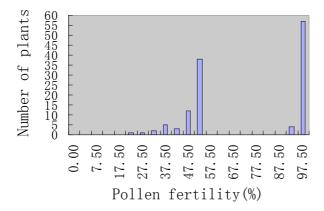


Fig. 1. Frequency distribution of pollen fertility in the BC_7F_1 mapping population of IRGC103977/Dianjingyou 1//Dianjingyou 1/8/Dianjingyou 1.

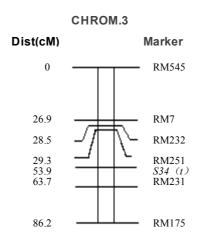


Fig. 2. SSR mapping of sterile gene from Oryza glaberrima on chromosome 3.

This study was supported in part by the Yunnan Natural Science Foundation (2002C0009Z) and Yunnan Department for Science and Technology (2003RC02).

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