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Identification of a Notched Kernel Gene Associated with Pre-Harvest Sprouting Using Oryza glumaepatula Introgression Lines in Rice

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ABSTRACT

Pre-harvest sprouting in rice is related to the lack of a normal dormancy level during seed development and maturation. The prominent effects of pre-harvest sprouting are lower yield due to harvest losses and end-product quality reduction. A single novel gene (nk2) for notched kernel was identified at backcross segregating population (BC4F2) of Oryza glumaepatula to Oryza sativa cv. Taichung 65 as recurrent parent. The nk2 gene was closely associated to pre-harvest sprouting character, and mapped on the long arm of chromosome 5 with 3.5 cM and 3.6 cM distance to G1103 and R521 RFLP markers, respectively.

Key words : Notched kernel, pre-harvest sprouting, genetic map, rice

INTRODUCTION

Precocious germination of cereal grain is a serious problem in crop production. Pre-harvest sprouting is the condition where germination of grains occurs in the spike before harvest. Prolonged rainfall and high humidity contribute to premature germination of grains before harvest. In south-east Asia, due the long spell of rainy weather in early summer and autumn, pre-harvest sprouting frequently happens and leads to great loss of yield and low quality in rice. Lack of adequate seed dormancy is the major reason for pre-harvest sprouting in the field especially under wet weather conditions (Seshu and Sorrells, 1986; Li, Ni et al., 2004).

In many cereal crops, such as wheat, barley, pre-harvest sprouting is usually controlled by multiple genes. Although this trait is governed by multiple genes it is also highly heritable. The recent development of molecular markers has made it possible to identify individual genetic factors controlling such traits. Several QTLs conferring pre-harvest sprouting have been identified in wheat (Kulwal et al., 2004, 2005; Gross et al., 2002), in barley (Li, Ni et al., 2004).

In rice, however, no information for pre-harvest sprouting has been reported. Recently, several rice molecular linkage maps have been developed by independent research groups (McCouch et al., 1988; 2002; Causse et al., 1994; Harushima et al., 1998). These linkage maps have facilitated analyses of genetic controlling several traits, such as heading date (Yamamoto et al., 2000; Yano et al., 2000), grain quality (Aluko, 2004; Li, Xiao et al., 2004), blast resistance (Zenbayashi et al., 2002; Fjellstrom et. al., 2004). By backcrossing and marker assisted selection methods, a series of O. glumaepatula introgression lines with O. sativa, cv. Taichung 65 genetic back-ground was developed (Sobrizal et al., 1999). A single novel gene for pre-harvest sprouting in rice found during the development of this introgression lines was reported in this paper.

MATERIALS AND METHODS

Plant materials

A cultivated rice Oryza sativa L. cv. Taichung 65 as a female and a wild rice O. glumaepatula Steud. (Acc. IRGC 105668) as a male were used as the parents in the original cross. The resultant F_1 plants served as female parents and were continuously backcrossed with Taichung 65 to generate BC_4F_1 populations. One hundred eighty four BC_4F_1 plants were genotyped using 106 RFLP markers distributed evenly on the rice genome in order to select the candidate plants for a series of O. glumaepatula introgression lines (Sobrizal et al., 1999). Based on these data, the plant BC_4F_1 274-3 carried heterozygous alleles at R2289, R1553 and C246 on chromosome 5 (Fig. 1). The self progenies of this plant (BC_4F_2 population) consisted of 59 plats segregated for notched kernels. This BC_4F_2 population was employed for genetic analysis.

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