Complex Microsynteny among Wheat, Rice and Barley at the *Qfhs.ndsu-3BS* Region

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Abstract

A major wheat QTL, *Qfhs.ndsu-3BS*, for resistance to Fusarium head blight (FHB) has been identified and verified by several research groups. The objectives of this study were to construct a high resolution map of the *Qfhs.ndsu-3BS* region, and to examine the microsynteny among wheat, rice and barley at this genomic region. Two SSR markers, gwm533 and gwm493, were used to screen the self-pollinated progeny of a single F_7 plant heterozygous for the *Qfhs.ndsu-3BS* region in Spring and Fall 2003. Among 3155 plants screened, 382 recombinants were identified. Two additional SSR markers and six STS (sequence-tagged site) markers developed from wheat ESTs were used to genotype the 192 recombinants identified in Spring 2003, and a fine genetic map was constructed. An inversion was revealed by comparing the order of STS markers and their counterpart genes on three overlapped rice PAC clones. It was previously reported that the microsynteny at this genomic region between rice and barley was interrupted by insertion of six additional barley genes. Six STS markers were developed from wheat ESTs homologous to each of the six barley genes. One STS marker was placed on the high resolution map, and an inversion between wheat and barley was revealed. Therefore, microsynteny among wheat, rice and barley at the *Qfhs.ndsu-3BS* region is complicated by microrearrangements such as inversions and insertion/deletions, implying that map-based cloning cannot solely depend on the sequence data of rice and barley.

Introduction

Use of genetic resistance to Fusarium head blight (FHB), caused by *Fusarium graminearum*, is an economical and environmentally friendly method to reduce wheat grain and quality losses caused by this disease. A major FHB resistance QTL, *Qfhs.ndsu-3BS*, has been identified and verified by several research groups (Anderson et al., 2001). On the basis of synteny between wheat and rice genomes, STS markers near *Qfhs.nusu-3BS* have been developed (Liu and Anderson, 2003a). These STS markers can be used to construct a fine genetic map of this QTL region, which is of critical importance for map-based cloning of this QTL.

Objectives

- Construct a fine map of the *Qfhs.ndsu-3BS* region.
- Examine the microsynteny among wheat, rice and barley at this genomic region.

Materials and Methods

A FHB resistant recombinant inbred line, RI 63, derived from the cross, Sumai 3 (resistant)/Stoa (susceptible), was hybridized with a FHB susceptible line, MN97448 (Fig. 1). An F_7 plant, 260-1-1-8, heterozygous for the *Qfhs.ndsu-3BS* region, was identified using three SSR markers, gwm533, BARC133 and gwm493. Two SSR markers, gwm533 and gwm493, were used to screen recombinants from the self-pollinated progeny of 260-1-1-8. A total of 3155 plants was screened in Spring and Fall 2003.

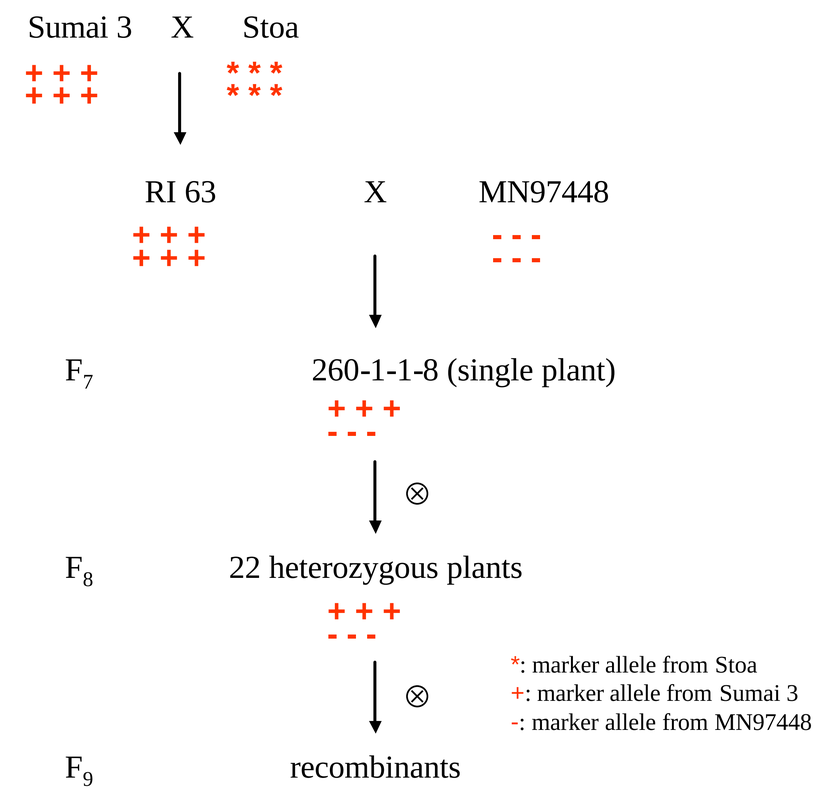

Fig. 1. Selection of recombinants at the *Qfhs.ndsu-3BS* region.

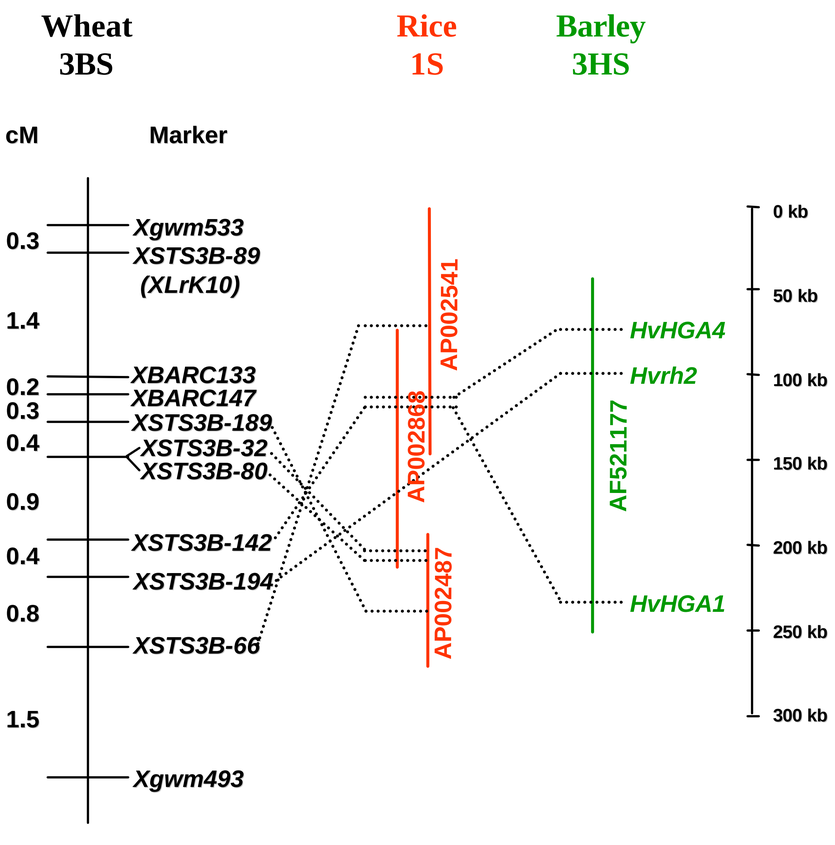

Fig. 2. Complex microsynteny among wheat, rice and barley.
Left: fine map of the *Qfhs.ndsu-3BS* region;
Middle: partial PAC contig of rice chromosome 1S;
Right: physical map of barley chromosome 3HS (Brunner et al. 2003).

Results and Discussion

Two SSR markers, gwm533 and gwm493, were used to screen 1594 plants derived from 260-1-1-8, and 192 recombinants were identified in Spring 2003. Additionally, 1561 plants were screened and 190 recombinants were identified in Fall 2003. The 192 recombinants identified in Spring 2003 were genotyped with two additional SSR markers, BARC133 and BARC147, and six STS markers derived from wheat ESTs (Liu and Anderson, 2003a). A fine genetic map was constructed for the *Qfhs.ndsu-3BS* region (Fig. 2). Except for two STS markers that cosegregate, the genetic distance between adjacent markers ranges from 0.2 to 1.5 cM. An inversion was revealed by comparing the order of STS markers and their counterpart genes on three overlapped rice PAC clones (Fig. 2).

It was previously reported that the microsynteny at this genomic region between rice and barley was interrupted by insertion of six additional barley genes (Brunner et al., 2003). Wheat ESTs that are homologous to the six barley genes were identified using BLAST searches. Six STS markers were designed for the best hits for each of the six barley genes. On the basis of aneuploid analysis, two STS markers were assigned to the deletion bin 3BS 0.78-0.87, the bin containing *Qfhs-ndsu-3BS*. Thus, the counterpart genes of the six barley genes are most likely present in wheat genome too. Only one of the six STS markers, STS3B-194, was polymorphic and was placed on the fine map (Fig. 2). An inversion between wheat and barley was revealed. Therefore, microsynteny among wheat, rice and barley at the *Qfhs.ndsu-3BS* region is complicated by microrearrangements such as inversions and insertion/deletions.

Literature Cited

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