

Identification and utilization of QTLs underlying yield and yield stability from wild relatives of rice

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Abstract

The nearly isogenic nature of introgression lines (ILs) provides a relative advantage over other segregating populations in the rapid implementation of pyramiding approach through crosses and marker analysis. A set of 126 ILs carrying various introgressed wild-genome segments from *Oryza rufipogon* Griff. in the genetic background of an elite Korea *japonica* rice cultivar (*O. sativa* L.), Hwayeongbyeo, was developed using the marker assisted selection (MAS) technique combined with repeated backcrosses. The 126 ILs have different size and frequency of wild genome segments introgression on each of 12 chromosomes. A total of 51 quantitative trait locus (QTLs) for agronomic and domestication-related trait and two qualitative loci associated with pericarp coloration were identified. The number of QTLs per trait ranged from 2 to 6. Proportion of phenotypic variation associated with QTLs varied from 8.6% to 52.2%. Ten (21.3%) of the *O. rufipogon*-derived alleles contributed the desirable effect on agronomic traits. Favorable introgressed alleles from *O. rufipogon* were identified in QTLs traits including panicle number and days to heading.

Media summary

Development and application of Introgression Lines in QTL mapping and cultivar development

Key Words

Oryza rufipogon, QTL, introgression lines (ILs), rice

Introduction

The advent of the molecular marker, maps and the sequence of the entire rice genome make it possible to identify individual QTLs associated with the agronomic trait, stress tolerance and quality traits, and analyze the function of these QTLs. Recently, several QTLs regulating agriculturally important traits have been cloned (Lippman et al. 2007). These include QTLs related to the heading date, grain number, grain size, regeneration ability and shattering. These QTLs contribute not only contribute to the breeding

program directly, but also to efforts to elucidate the mechanism of rice domestication. For QTL analysis, the use of Introgression Lines (ILs) should be more effective in identifying target QTLs, compared with the F₂ population, recombinant inbred lines (RILs), backcross inbred lines (BILs) (Yano & Sasaki 1997). Eshed and Zamir (1994) constructed the first complete set of substitution lines in tomato carrying a single *Lycopersicon pennellii* chromosome segment in a homogeneous background of *Lycopersicon esculentum*, representing the entire wild tomato genome. In rice, introgression lines carrying *O. glaberrima* (Doi et al. 1997), and common wild rice (*O. rufipogon* Griff.) segments (Tian et al. 2005) were constructed.

In the present research, introgression lines have been constructed through successive backcrosses and MAS, and the ILs have been used to dissect QTLs related to agronomic traits.

Materials and Methods

For construction of the introgression lines carrying the wild segments in the Hwayeongbyeo background, 14 representative RILs were selected from 120 RILs (BC₁F₇) based on the genotypes (Lee et al. 2005). Using Hwayeongbyeo as the recurrent parent, two successive backcrosses were made. After two generations of selfing, 960 BC₃F₂ plants were harvested and planted to produce BC₃F₃ populations. The respective target segments were checked by the corresponding SSR markers and 126 BC₃F₃ lines were selected to construct the ILs. 126 ILs and the recurrent parent were grown in the field during the summer of 2006 at Chungnam National University, Daejeon, Korea. Each line was represented by a single row of 22 plants planted with 15 cm between plants and 30 cm between rows at a completely randomized block design with two replications.

Domestication-related and agronomic traits were evaluated in the BC₃F₄ families, with one qualitative trait, pericarp coloration (*pc*). Twelve quantitative traits were evaluated: days to heading (DTH), culm length (CL), panicle length (PL), panicle number per plant (PN), seed shattering (SH), spikelets per panicle (SPP), percentage seed set (PSS), awn (AWN), primary branches per panicle (PB), secondary branches per panicle (SB), 1,000 grain weight (GW), and grain yield (YP). The linkage map was built with 124 SSR markers, and the order and distance between markers were based on the previously developed SSR maps (McCouch et al. 2002). The chromosome location of QTLs was determined by single-point analysis (SPA) and interval mapping (IM) using QGENE 3.06. QTLs were detected if the phenotype was associated with a marker or interval locus at P<0.0001 which was equal to an average LOD value > 3.0, while the level of P < 0.005 corresponded to an average LOD>2.4.

Results and Discussion

126 introgression lines were selected and genotyped using 124 SSR markers. Genotype analysis showed that the ILs population harbor 384 homozygous and 293 heterozygous segments of the common wild rice (*O. rufipogon*) in which the segment size ranged from 0.5 cM to 85.5 cM. The average size of the segments was 18.6 cM and 18.2 cM of homozygous and heterozygous segments. Most introgressed segments were detected by a single SSR marker, and these results agree with those reported by Tian et al. (2005).

Significant QTLs were detected for thirteen traits as summarized in Fig. 1. A total of 51 QTLs and two loci controlling pericarp coloration were detected. They were distributed on all of the 12 chromosomes and showed co-localization in several chromosomal regions (Fig. 1). The number of QTLs per trait ranged from 2 to 6. As was reported in other studies, the IL population was more effective in detecting QTLs than an RIL population mainly due to the nearly isogenic nature of the ILs. For the same 12 traits, 47 and 32 QTLs were detected in the ILs and RILs populations from the same cross, respectively (Lee et al. 2005).

QTLs associated with the same agronomic or domestication traits were detected in the same or similar regions of the chromosome in different populations or *Oryza* species. These include the QTLs for shattering, awn and grain weight. In this study, the QTL related to seed shattering, *sh4* was identified on chromosome 4. Several studies report the shattering QTL in the same chromosomal region (Li et al. 2006; Xiong et al. 1999). The QTL for 1,000-grain weight, *gw5* detected in this study was identified in a similar chromosomal location in *O. rufipogon* (W1944). Some QTLs for grain quality and cold tolerance traits have not been reported in previous QTL studies in rice suggesting potentially new genes in this wild accession (data not shown).

The availability of introgression lines in an agronomically acceptable background will not only facilitate more rapid utilization of valuable genes from the wild parent, but also provide a powerful tool for the identification and fine mapping of genes underlying QTLs associated with a wide variety of phenotypes. Also, because the recurrent cultivar, Hwayeongbyeon is a leading cultivar, the derived IL population might represent a significant improvement and a basis for the development of a new cultivar.

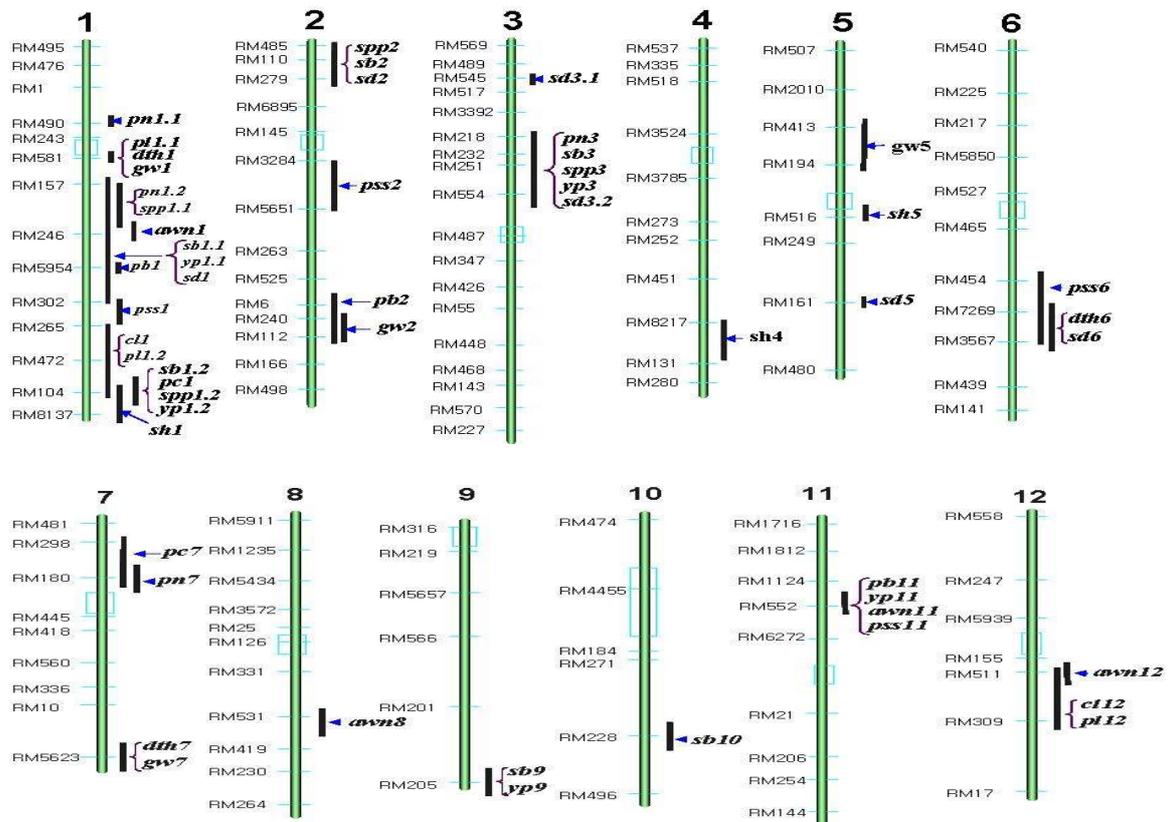


Fig. 1. Map location of the QTLs for agronomic and domestication-related traits detected using 126 ILs. QTLs detected by single point analysis were represented to the right of the chromosomes.

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