Uncovering of naturally occurring variations in flowering time in rice

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Abstract

In order to dissect genetic factors controlling naturally occurring variations in rice flowering, we have performed a QTL analysis using 15 populations derived from a cross between japonica cultivar, Koshihikari, and cultivars and lines originated from various regions in Asia. Based on the QTL mapping, several QTLs were detected on 5 rice chromosomes in cross combination and some of QTLs were shared among combinations. Chromosomal location of these QTLs was well corresponding with those detected in Nipponbare and Kasalath. Allelic effects of those QTLs varied among combination used, suggesting that a large portion of the wide range of phenotypic variations in flowering time could be generated by the combination of different allele of these QTLs. In addition, we analyzed closely related cultivars, Nipponbare and Koshihikari from the QTL analysis of flowering time. Even these cultivars are closely related, two QTLs have been detected on chromosome 3 and chr.6. It was demonstrated that one of QTLs on chromosome 3 was novel one from previously detected based on the chromosomal location. QTL analyses using multiple crosses revealed that comprehensive series of loci involving in natural variation in flowering time.

Media summary

Understanding of genetic basis of flowering time will result in a fine tuning of regional and seasonal adaptability in rice.

Key Words

Flowering time, natural variation, quantitative trait loci, rice

Introduction

Flowering time (heading date) is one of crucial factors determining regional and seasonal adaptation in rice and has been major target trait to be selected in breeding program. Heading date is a complex trait that is governed by multiple genes and environmental factors, such as day-length, temperature, and soil conditions. A wide range of variation in flowering time was observed among rice cultivars. During the last decade, genetic studies using DNA markers have facilitated the genetic dissection of heading date and many quantitative trait loci (QTLs) for heading date have been identified using several mapping populations
(reviewed by Yano et al. 2001; Uga et al. 2007; Nonoue et al. 2008). Furthermore, four QTLs for heading date (Hd1, Hd6, Hd3a, and Ehd1) were isolated using a map-based strategy (reviewed by Yamamoto and Yano 2008). These studies have markedly improved our understanding of the genetic control mechanisms underlying flowering in rice. Although rapid accumulation of knowledge about a genetic basis of rice flowering time, the genetic mechanisms underlying the wide range of flowering time variation still remain to be clarified. In this study, to clarify what factors are involved in this wide range of variation, we performed a comprehensive genetic dissection of flowering time using more than 10 F2 populations and advanced backcross progeny derived from a cross between Asian rice cultivars.

Methods

To detect quantitative trait loci controlling flowering time, we produced F2 populations derived from a cross between Japanese cultivars and world rice collection (Kojima et al. 2005). These plant materials were raised in the field of National Institute of Agrobiological Sciences, Tsukuba, Japan. Days to heading (DTH), the number of days required from seeding to emergence of first panicle from leaf sheath, were monitored. QTL analyses were performed using composite interval mapping (Zeng 1994) as implemented by the program Zmapqtl (model 6) of the software package QTL Cartographer version 2.5.

Results

DTH ranged from 91 to 202 among 10 cultivars used in this study. Range of DTH in F2 populations showed a large and continuous variations. Transgressive segregants towards late flowering were observed in most of F2 populations. Based on the QTL mapping, several QTLs were detected on 5 rice chromosomes in 10 cross combinations and some of QTLs were shared among combinations (Figure 1). It should be noted that several QTLs were detected in the region of Hd6 (chromosome 3: chr3), Hd3a (chr6), Hd1 (chr6) and Hd5 (chr8). It was likely that these QTLs were involved in generation of a large variation in flowering time in Asian rice cultivars. Chromosomal location of these QTLs was well corresponding with those detected in Nipponbare and Kasalath (Yano et al. 2001). Allelic effects of those QTLs varied among combination used. For example, for the QTLs detected in the region of Hd1 and Hd5, additive effect of some Asian cultivars showed opposite direction, increasing and decreasing days-to heading. It was also note that a relatively large allelic difference at Hd7 in some crosses combinations, compared with that between Nipponbare and Kasalath. This allowed us to explore novel allele at QTL previously detected. These results suggested that a large portion of the wide range of phenotypic variations in flowering time could be generated by the combination of different allele of these QTLs. In addition, we analyzed closely related cultivars, Nipponbare and Koshihikari from the QTL analysis of flowering time. Even these cultivar are closely related, two QTLs have been detected on chromosome 3 and 6. Fine mapping of these two QTLs were performed using advanced backcross progeny, suggesting that one of QTLs on chromosome 3 was novel one from previously detected based on the chromosomal location.

In previous studies it was clearly demonstrated that QTLs with minor effect could not be detected using primary mapping population, such as F2 and recombinant inbred lines (Ebitani et al. 2005, Uga et al. 2007, Takai et al. 2007). In order to identify additional QTLs with minor effects, we are now developing
chromosome segment substitution lines of same series of cross combinations (Yamamoto and Yano 2008). More comprehensive understanding of genetic factors generating natural variation will allow to perform fine-tuning of flowering time in rice.

Figure 1. Flowering time QTLs detected by using F2 population derived from crosses between Japanese cultivar, Koshihikari, and 10 cultivars from different areas in Asia. *Hd1* – *Hd14* are QTLs detected by using progenies form a cross between Nipponbare and Kasalath (Yano et al. 2001).

**Conclusion**

QTL analyses using multiple crosses revealed that comprehensive series of loci involving in natural variation in flowering time in rice. Because of Japanese cultivar, Koshihikari, was used as common parental line, we could compare allele effects of the QTL detected in same chromosome regions. Based on the result obtained, major part of natural variations in flowering time are likely to be generated by a combination of several type of alleles, presumably including loss of function allele, in a series of QTLs detected in this study.

**References**


