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QTL Mapping of Yield, Yield Components, and Morphological Traits in Rice (Oryza sativa L.) Using SSR Marker

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ABSTRACT

The experiment was aimed at identifying QTL (quantitative trait loci) controlling ten traits of yield, yield component and plant morphology of rice based on BC_1F_1 of IR75862-206-2-8-3-B-B-B//IR64 mapping population consisted of 115 plants. It was arranged in Completely Randomized Design with three replicates. Ninety three SSR markers spread across the twelve rice chromosomes were used to map the QTL. These markers were mostly segregated according to Mendel Law except for fourteen markers. There were eleven QTL detected in eight traits, i.e., heading date, flag leaf length, plant height, panicle length, panicle weight, seed set, weight of 100 grains, and grain weight per plant, meaning that one or two QTL were detected in each trait. These QTL were located at chromosome 2, 3, 4, 6, 11, and 12. Some QTL were located at the same chromosome even at the same location indicating the close association of the traits. It also indicated that there were common QTL which were found across genetic background and specific QTL which were found at specific genetic background. Further study was prospective for the molecular marker application in rice improvement.

Key words: QTL, agronomic traits, SSR, rice

INTRODUCTON

Important traits of plant such as yield and yield related traits are mostly quantitative traits which have continuous phenotypic distribution. It implied that many genes with relatively small effect termed as QTL (quantitative trait loci) controlling the traits. The ability of molecular marker technique to dissect quantitative trait into Mendelian loci (Tanksley, 1993) opens the chance to identify and locate QTL. In turn it will be very useful for plant improvement (Septiningsih et al., 2003).

Yield and yield related traits have been the major goal of rice breeding and remain important in the future. Studies on agronomic traits have been done and yielded promising result (Jing-hong et al., 2008). Some agronomic traits such as heading date, panicle characteristics, spikelet fertility, grain size as well as the yield have become the focus in some studies (Vergara et al., 1996; Moncada et al., 2001; Septiningsih et al., 2003; Thomson et al., 2003; Cui et al., 2004; Linh et al., 2006; Jing-hong et al., 2008). On the other hand, flag leaf characteristic may significantly contribute to the yield, but less study was done on this particular trait. QTL study of those agronomic traits will be useful for the application of molecular marker in breeding for the particular agronomic traits and yield as well.

Simple Sequence Repeats (SSR) or micro satellite marker is a marker of choise for rice study and is increasingly used in the recent studies. SSR marker is simple and relatively cheap (PCR based marker), accurate (work into the DNA), could be used for high throughput application (Panaud et al., 1995), also is a co-dominant marker that can detect multi allele in a locus (Powell et al., 1996). A lot of SSR markers have been developed for rice study. McCouch et al. (2002) reported that there were 2240 unique marker loci validated in rice, or approximately one SSR at every 157 kb of rice genome. More SSR could be searched especially after the completion of rice genome sequencing (IRGSP, 2005; Yu et al., 2002). Zhang et al. (2007) reported the availability of another 52,845 SSR markers.

This study was aimed at identifying QTL controlling yield, yield components, and morphological traits using SSR marker.

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