Fine Mapping of Quantitative Trait Loci for Grain Weight in Rice (Oryza sativa L.): a review

Mohammad Noroozi¹ and Ali Sattari²*

1. Iranian Rice Research Institute, Deputy of Mazandaran, Amol, Iran
2. Phd. student of Dept. of Agronomy and Plant Breeding, Faculty of Agriculture, Zabol University, Iran

Corresponding author: Ali Sattari

ABSTRACT: Rice is staple food for more than half of the world's population. Along with improvements in the standard of living, the demand for superior grain quality with high grain yield is increasingly becoming a priority issue in many rice producing areas of the world. As one of the most important yield components, grain weight plays an important role in the formation of rice yield; an increase in 1000-grain weight (TGW) will increase the rice yield. 1000-grain weight (TGW) is one of the three component traits of the grain yield in rice (Oryza sativa L.). Grain weight is a major determinant of crop grain yield and is controlled by naturally occurring quantitative trait loci (QTLs). For grain weight which is well-known as the yield trait having the highest heritability, about 300 QTLs have been documented, but only a few QTLs have been cloned. Results indicate that the effects of minor QTLs could be steadily detected in a highly isogenic background and suggest that such QTLs could be utilized in the breeding of high-yielding rice varieties.

Keywords: Quantitative Trait Loci, Rice, Grain Weight

INTRODUCTION

Rice is staple food for more than half of the world's population. Number of panicles per plant, number of grains per panicle and 1000-grain weight (TGW) are the three component traits determining grain yield in rice (Oryza sativa L.), all of which are controlled by multiple genes termed as quantitative trait loci (QTLs). In the past decade, fine-mapping and cloning of QTLs for agronomically important traits in rice have attracted more and more attentions, in which TGW is the yield trait achieving the greatest progress. To date, seven QTLs for TGW have been cloned, among which GS3, TGW6 and GL3.1/OsPPKL1 are mainly responsible for grain weight and grain length, and GW2, qSW5/GW5, GS5 and GW8 for grain weight and grain width (Qi et al., 2012; Zhang, 2012; Huang, 2013; Ishimaru, 2013). 2015 Enhancing grain yield has always been a primary objective of the rice breeding. In the past two decades, mapping of quantitative trait loci (QTLs) has provided a promising way to facilitate our understanding of the genetic control of yield traits in rice. A huge number of QTLs for these traits have been detected in primary populations and documented in open resources such as the Gramene (Bai, 2012). For grain weight which is well-known as the yield trait having the highest heritability, about 300 QTLs have been documented, but only a few QTLs have been cloned (Bai, 2012; Huang, 2013). 2015 Xie (2006, 2008) identified two QTLs for GW, gw8.1 and gw9.1, in a 308- and 37.4-kb region on rice chromosomes 8 and 9, respectively, and the O.rufipogon allele contributed to an increase in GW. Meanwhile, Li (2004) fine mapped gw3.1 to a pericentromeric region of 93.8 kb on chromosome 3, with the O.rufipogon allele being dominant for small grain size. Subsequently, a major gene for grain length and weight in this same region, GS3, was cloned (Fan, 2006). As one of the most important yield components, grain weight plays an important role in the formation of rice yield; an increase in 1000-grain weight (TGW) will increase the rice yield (Bai, 2011). Percentage of grains with chalkiness (PGWC) is an important quality component of rice, as it has a profound influence on eating and milling qualities (Cheng2005; Yamakawa2007).
**digenic epistatic effects and QE interaction effects QTL controlling GW in rice**

Considering the sensitivity of kilo-grain weight to environments, Lu (1997) and Zhuang (1997) compared the differential detection of QTL across environments to determine whether or not QTL environment (QE) interaction existed. However, the foregoing studies did not estimate epistatic effects between QTL, as well as predict QE interaction effects simultaneously. Wang (1999) proposed a QTL mapping strategy that can estimate QTL epistatic effects of additive x additive and predict their interaction with environments. The methodology was used in a recent QTL mapping investigation (Liao, 2000; Cao, 2001 a; 2001b; Li, 2001; Luo, 2001; Xing, 2002).

**Fine mapping of a grain weight QTL on rice chromosome 8 using near-isogenic lines**

Grain or seed weight is an important trait in rice. It is directly associated with yield, and indirectly correlated with the cooking quality and the physical appearance of rice, which is important both aesthetically and commercially (Takeda and Saito, 1980; Webb, 1991). With the progress of molecular genetic maps, many quantitative trait loci (QTLs) for GW/size have been identified in populations from crosses between divergent cultivars or accessions of rice (Lin, 1996; Zhuang, 1997; Li, 1998; Cui, 2003; Ishimaru, 2003). A total of 26 QTLs for GW have been detected in populations derived from crosses between the wild rice Oryza rufipogon (IRGC 105491) and diverse cultivars. While the seed of O. rufipogon small in size, it is interesting to note that 58% of the QTLs reported in these interspecific crosses identify O. rufipogon alleles as contributing to an increase in seed or GW (Xiao, 1998; Moncada, 2001; Thomson, 2003; Septiningsih, 2003). A quantitative trait locus (QTL) for grain weight (GW) was detected near SSR marker RM210 on chromosome 8 in backcross populations derived from a cross between the Korean japonica cultivar Hwaseongbyeo and Oryza rufipogon (IRGC 105491). The O. rufipogon allele increased GW in the Hwaseongbyeo background despite the fact that O. rufipogon was the small-seeded parent. Using sister BC3F3 near-isogenic lines (NILs), gw8.1 was validated and mapped to a 6.1 cM region in the interval between RM42 and RM210 (P·0.0001) (Xie, 2006).

**Seed-specific silencing of OsMRP5 reduces seed phytic acid and weight in rice**

Myo-inositol 1,2,3,4,5,6-hexakisphosphate, known as phytic acid (PA), is the major storage form of phosphorous (P) in cereal and legume seeds, existing as mixed salts (phytates) of mineral cations, including minor amounts of Zn $^{2+}$ and Fe $^{3+}$ (Lott, 2000; Raboy, 2001). Most of the P and minerals in these salts are not utilized for monogastric animals. A number of genes have been identified to be involved in PA metabolism, and mutations of these genes are known to cause LPA phenotypes in various crops (Raboy, 2009). Among them are the Ins(3)P1 synthase (MIPS) gene (Hitz, 2002; Yuan, 2007), which catalyze the cyclization of D-glucose-6-phosphate to 1D-myoinositol-3-phosphate [Ins(3)P1] (Loewus and Murthy, 2000), the myo-inositol kinase (MIK) gene (Shi, 2005; Kim, 2008b), the inositol polyphosphate kinase (IPK) gene (Shi, 2003; Stevenson-Paulik, 2005; Yuan, 2012), and the multi-drug resistance-associated protein (MRP) ATP-binding cassette (ABC) transporter gene (Maroof, 2009; Nagy, 2009; Panzeri, 2011; Shi, 2007; Xu, 2009). Furthermore, Suzuki (2007) and Josefsen (2007) demonstrated that a diverse range of enzymes, some of which might be multifunctional, catalyze the intermediate steps in seed phytate metabolism in rice. The OsMRP5gene, of which mutations are known to reduce seed PA as well as seed yield and viability, was down-regulated specifically in rice seeds by using an artificial microRNA driven by the rice seed specific promoterOle18. (Li, 2014).

**qTGW1.1, a QTL for 1000-Grain Weight in Rice (Oryza sativaL.)**

Number of panicles per plant, number of grains per panicle and 1000-grain weight (TGW) are the three component traits determining grain yield in rice (Oryza sativaL.), all of which are controlled by multiple genes termed as quantitative trait loci (QTLs). To date, seven QTLs for TGW have been cloned, among which GS3, TGW6 and L3.1/OsPPKL1 are mainly responsible for grain weight and grain length, and GW2, qSW5/GW5, GSSand GW8for grain weight and grain width (Qi, 2012; Zhang, 2012; Huang, 2013; Ishimaru, 2013). In the map-based cloning studies, these QTLs were verified to have large additive effects for TGW, ranging from 0.80 g to 5.57 g. In addition, they were consistently detected across different genetic backgrounds and environments, with one QTL explaining 12.1%−28.0% of the phenotypic variance in a primary population (Yu, 1997; Li, 2000; Hua, 2002; Xing, 2002; Zhang, 2012; Ishimaru, 2013). Based on comparison among the five NILs on the segregating regions and the results of QTL analysis, qTGW1.1 was delimited to a 376.9-kb region flanked by DNA markers Wn28382 and RM11554. Our results indicate that the effects of minor QTLs could be steadily detected in a highly isogenic background and suggest that such QTLs could be utilized in the breeding of high-yielding rice varieties. (Hong-wei, 2015).

*Previously unidentified histone H4 acetyltransferase enhances grain weight*
Grain weight is an important crop yield component; however, its underlying regulatory mechanisms are largely unknown. Grain-weight quantitative trait locus (QTL) encoding a new-type GNAT-like protein that harbors intrinsic histone acetyltransferase activity (OsglHAT1). Genetic and molecular evidences pinpointed the QTL-OsglHAT1’s allelic variations to a 1.2-kb region upstream of the gene body, which is consistent with its function as a positive regulator of the traits. Elevated OsglHAT1 expression enhances grain weight and yield by enlarging spikelet hulls via increasing cell number and accelerating grain filling, and increases global acetylation levels of histone H4. OsglHAT1 localizes to the nucleus, where it likely functions through the regulation of transcription. Despite its positive agronomical effects on grain weight, yield, and plant biomass, the rare allele elevating OsglHAT1 expression has so far escaped human selection. Our findings reveal the first example, to our knowledge, of a QTL for a yield component trait being due to a chromatin modifier that has the potential to improve crop high-yield breeding (Jun Song, 2015).

REFERENCES


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