

## Detection QTLs for grain quality traits and yield in two BILs population of rice

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**Abstract.** Rice, the second most important crop after wheat, has been cultivated in Iran. Marketing conditions and quality traits after yield are the most important factors to adopt of new varieties. Therefore in recent years Iranian scientists decided to training on breeding improved high yield varieties with good grain quality. Quantitative trait loci (QTLs) yield and grain quality traits of rice (*Oryza sativa* L.) with additive, epistatic, and QTL × environment (QE) interaction effects were studied using a mixed-model-based composite interval mapping (MCIM) method and two populations of Back cross inbred lines (BILs) with a common maternal parent. In each of the populations two or three main effects of QTLs were detected for yield, amylose content, gel consistency and gelatinization temperature. Some identified QTL clusters suggested pleiotropic effects could control these traits. The phenotypic variation of AAE and AA QTLs effects were smaller than main QTLs. We conclude that the major genes and some minor and modifier genes controlled rice grain quality and yield components. The information obtained in this study have used to manipulating the QTLs for these traits by molecular marker-assisted selection and the best lines with excellent quality and high yield recognized.

**Key words:** Rice, grain quality, QTL, epistasis

### Introduction

Iranian consumers preferred long, slender and no chalked grains that produce dry, fluffy and separated grains, aromatic, good appearance and soft texture after cooked. Marketing conditions and quality traits after yield are the most important factors to adopt of new varieties. Therefore in recent years Iranian scientists decided to training on breeding improved high yield varieties with good grain quality. Studies on the genetic basis of grain quality traits and yield are necessary because of the complexity of their inheritance and the effect of environmental and other conditions. Studies on the genetic basis of grain quality traits and yield are necessary because of the complexity of their inheritance and the effect of environmental and other conditions. This complexity inheritance genes and negative correlation of quality traits with yield have led to the failure of breeding efforts to improve the good quality rice varieties that have high yield. Elucidation of their genetic basis would greatly help to improve the above-mentioned traits.

Wada et al. (2006) mapped four QTLs for AC on chromosomes three, seven, nine and 12. One QTL for texture was identified on chromosome three. Yong et al. (2006) reported that a major QTL for AC, qAC-6 was located on chromosome six. Using 110 polymorphic SSR markers and 209 recombinant inbred lines Amarawathi et al. (2008) mapped QTLs related to AC, GC and GT on seven different chromosomes. A number of independent studies have reported the incidence of QTLs for yield and yield components (Moncada et al. 2001; Thomson et al. 2003). In the present study, two BILs populations were used to conduct a QTL study on some grain quality traits and yield in rice at three environments. This could provide essential information to better understand the genetic control of grain quality traits and yield to identify the potential target of stable QTLs, epistasis and QE interactions.

### Materials and Methods

#### **Plant materials and trait measurements**

In this study Two rice BILs (Hashemi/ IR67418-110-32222 and Hashemi/ Neda with a common maternal parent) genetic populations derived from advanced back cross were examined. Hashemi is a local Iranian rice cultivar that is adapted to the northern region of Iran with excellent grain quality and aromatic. IR67418-110-32222 was a line from IRRI introduction with high yield and poor grain quality traits. Neda was an improved Iranian variety from (IR24/Hasansaraiee//Sangetarom) crosses, that have high yield and poor

grain quality. The two BILs genetic populations were planted in the rice-growing seasons for 3 years in the experimental farm of the Rice Research Institute of Iran (RRII). Inbred lines of the two genetic populations were grown as spaced plants and transplanted at (1×6) m<sup>2</sup> plots with six rows. There was a distance of 25 cm between plants on a row and the rows were 25 cm apart. Only four rows in the middle plot were used for measuring yield. Field management followed the normal agricultural practice. Three grain quality traits (AC, GC and GT) measured in quality lab of RRII with IRRI standard methods. Molecular markers that polymorphic between parents, evaluated in BILs populations.

#### **Data and QTL analysis**

The main-effect QTLs (A), epistatic QTLs (AA) and the QTLs environment interactions (AE and AAE) in the two BILs populations were mapped using the QTLNetwork ver. 2.0 software (Yang and Zhu. 2005) based on a mixed linear model. Composite interval analysis was undertaken using a forward-backward stepwise multiple linear regression with a probability into and out of the model of 0.05 and window size set at 1 CM. Significant thresholds for QTL detection were calculated for each data set using 1000 permutations and a genome-wide error rate 0.05 (significant).

#### **Results and Discussion**

A significant ( $P < 0.01$ ) F-value of ANOVA for lines, a comparison of the parents, and an analysis of the parents versus population lines in each genetic population in separate and combining analysis of the three years revealed high variation between the populations lines of the two BILs for the studied traits. From approximately 350 SSR markers which screened on parental genotypes of the two genetic populations, 61 and 65 primers generated clearly scorable polymorphisms between the Hashemi and IR67418-110-32222, and Hashemi and Neda respectively. The parental polymorphic primers of each population were applied to assay their lines. The total genetic maps lengths of the Hashemi\IR67418-110-32222 and Hashemi\Neda were 1003.45cM and 1210.53cM respectively.

We were able to identify 3 significant QTLs with main effect for yield in each population. These QTLs were y6, y7 and y8 in Hashemi\IR67418-110-32222 and y3, y7, y8 in Hashemi\Neda populations. Two QTLs of these were modified by environment (AE). Two QTLs (y7 and y8) were similar in populations. The QTLs with largest effect y8 was located on chromosome 8. Also we identified 4 and 3 pairs of epistasis QTLs for yield in two populations, 1 pairs of these QTLs had significant AAE interactions in each of these populations. The results confirm that the genetics of yield in rice is complex in nature as reported before (Kwon et al. 2008); and their QTLs may have only main effects and/or may involved in epistatic (AA) or environmental (AE, AAE) interactions. The main effect QTLs explained 24.31% and 24.93% variation in phenotypic traits in two populations respectively. The range of additive effects were 0.803 to 2.370 (ton per ha) in yield. Alleles from Neda and IR-22 at y3, y6 and y7 increased and At locus y8 alleles from Hashemi decreased yield.

For AC, GC and GT 3, 2 and 2 putative QTLs with significant additive effects were identified in Ha\IR population. The ac6, gc6 and gt6 which lies in the marker interval RM190-RM225, explained the largest phenotypic variation in these traits indicating that this QTL played a main role for quality traits in these BIL populations and were a QTL cluster on this located of chromosome 6. The favorable alleles from Hashemi in this QTL cluster decrease AC and GT. In Ha\Ne population, a QTL cluster on chromosomes 6 which lies in the marker interval RM217-RM225 explained largest phenotypic variation and common in these traits too. Interestingly a QTL cluster localized on chromosome 6, flanked by RM190-RM225 in Ha\IR and by RM217-RM225 in Ha\Ne, is in the Wx gene region, or a region very close to it. RM190 was designed based on the genomic sequence of waxy gene (Temnykh et al., 2000). The Wx gene region was influenced in AC, GC and GT in both the populations. Other previous research also detected QTLs that were located in Wx gene region, or a region very close to it on chromosome 6, that controlled AC, Gc and GT (Shen et al, 2005; Tian et al. 2005). QTLs (ac8) in Ha\IR-22 and (ac8-1 and gc8) in Ha\Ne were modified by environment and had significant (AE) effects. Also we identified 4 and 2 pairs of epistasis QTLs for AC in two populations, 1 pairs of these QTLs had significant AAE interactions. For GT recognized 2 and 2 pairs of epistasis QTLs in 2 BILs population with no significant AAE interactions. For GC identified 2 and 2 pairs of epistasis QTLs in 2 BILs

population. In all traits the Phenotypic variation of AE and AAE smaller than the main(A) effects.

### Conclusions

We conclude that the major genes and some minor and modifier genes controlled rice grain quality and yield components. The information obtained in this study have used to manipulating the QTLs for these traits by molecular marker-assisted selection and the best lines with excellent quality and high yield recognized.

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