

## Abstract

Grain quality of rice (*Oryza sativa* L.) is a crucial issue for marketing and consumers main preference in Iran. Therefore, Quantitative Trait Loci (QTL) mapping of the traits related to grain quality of rice by using of molecular markers has priority to introduce improved rice varieties. In the present study, in order to QTL mapping for 28 grain quality traits of rice during 2014-2015 were used 157 recombinant inbred lines (F<sub>9</sub>) which derived from cross between two Iranian cultivars (Ali-kazemi and Kadous). To construct of linkage map, parental survey was performed using 300 microsatellite markers which among them 65 showed polymorphism between parents. A genetic linkage map covering 1213 cM of rice was constructed including the distance of 22 cM between polymorphic markers. For cooking and eating quality, 22 QTLs identified by using of QTL NETWORK software. The highest value of F (8.82) calculated for *qwa6* between RM3183-RM461 on chromosome 6. For grain appearance and milling quality related traits detected 19 and 12 QTLs respectively by this software. The highest values of calculated F were belonged to *qlwr7a* (F=10.88) between RM8015-RM20938 on chromosome 7 and *qgw6* in the marker interval of RM217-RM225 on chromosome 6. By using of GenStat software, 16 QTLs identified for cooking and eating quality of rice. The highest phenotypic variation (8.9 & 9% in 2014 and 2015 respectively) was explained by *qwa1* flanking by RM10402 on chromosome 1. The appearance of the grain in paddy, brown and head rice was associated with 27 QTLs which two QTLs on chromosomes 2 and 7 (*qch2* and *qhlhw7*) related to length to width ratio of head rice and chalkiness explained the highest value of phenotypic variance. Small effects on phenotypic variations resulted in identification of minor effect QTLs. Grain appearance of rice were also analyzed by IciMapping software using IM and CIM model and 14 QTLs found for related traits on chromosomes 1, 6, 7, 9 and 12. Presence of pleiotropic QTLs indicated linkage among genes controlling given characteristics. We detected a QTL on chromosome 1 in the marker interval of RM10402-RM246 controlling water absorption (WA) and amylose content (AC) simultaneously. Other QTL on chromosome 2 in the marker interval of RM5390-RM6 was detected for water absorption (WA) and volume expansion (VE). Another QTL on chromosome 6 between RM190-RM13380 controlled WA and gelatinization temperature (GT). Further, we detected one more QTL on this chromosome which control WA and VE. Two different QTLs identified on chromosomes 5 and 8 which each of them affecting grain length of brown and head rice. A QTL found on chromosome 7 which controlled grain length and width, simultaneously. Three QTL clusters located to the interval of RM10402-RM246 and RM431-RM8136 on chromosome 1, RM3183-RM461 and RM190-RM217 on chromosome 6 and RM3555-RM248 and RM7338-RM214 on chromosome 7 were found by QTL Network software. Identified QTLs associated with grain length to width ratio of brown and head rice by GenStat software flanked by two different markers on chromosome 7, indicated a QTL cluster on this chromosome. Our result suggested that MAS of QTLs with pleiotropic effect will be effective and efficient in rice **breeding programs**.



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Mapping Quantitative Trait Loci (QTLs)  
associated with quality of rice using SSR marker

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