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Association mapping for grain size traits in rice

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Abstract

Introduction

Grain size, an important quality trait of rice is affected by length, breadth and length-breadth ratio influenced by multiple genes. Association mapping is a powerful tool for genetically dissecting complex traits controlled by multiple quantitative trait loci (QTLs). In the present study, an attempt was made to identify markers associated with kernel size, kernel weight, grain size and grain weight by candidate gene based association mapping.

Methodology

In all, 96 rice genotypes were used for recording grain size traits *viz.,* length (L), breadth (B), L/B ratio and grain weight for both kernel and polished rice and for screening with molecular markers associated with the grain size QTLs/genes from previous reports. Association mapping was done using GLM and MLM models of TASSEL 2.1.

Results

Of the markers used, the locus RM18616 explained maximum phenotypic variance (14.6%) followed by RM430 (10.42%). The locus RM18582 linked to the major QTL for grain size on chromosome 5 was found to be associated with all the grain size traits and grain weight both in kernel and polished form of rice with a phenotypic variance range of 2-10%. The markers linked to the known genes viz., GW5, qSS7, qGW8 and SRS5 also showed association with the majority of the grain size traits but with low phenotypic variance ranging from 2.0-8.44%.

Discussion and Conclusion

From the present study, RM18582 and RM18616 loci found to be strongly associated with grain size and have the potential to be used in marker assisted breeding of grain size traits.