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RAPID MAPPING AND CLONING THE CHLORINA MUTANT GENE(VN-A1) IN WHEAT BY BULKED SEGREGANT ANALYSIS AND 660K SNP CHIP

Wheat is one of the most widely grown crops in the world. Induced mutations have been used to generate mutant for genetic improvement and functional genomics in wheat. Recently, huge advances in wheat genome sequencing have contributed to the use of single-nucleotide polymorphism(SNP) in fine mapping and map-based cloning of mutant genes. A chlorina mutant in Triticum aestivum was obtained by treatment with the chemical mutagen sodium azide. Genetic analysis confirmed that the mutant phenotype was controlled by a recessive gene, which was designated as vn-A1. By applying bulked segregant analysis and Wheat 660K SNP chip, 8 KASP makers were developed. Molecular mapping showed that vn-A1 is located in a 1.1-cM genetic region flanking by KASP markers 660K-7A12 and 660K-7A20 corresponded to a physical interval of 3.48 Mb in the Chinese Spring chromosome 7AL containing 61 predicted genes with high confidence. Further analysis showed that a point mutation occurred in the AAA+ conserved region of Magnesium chelatase I subunit(CHLI) generated an amino acid substitution of Aspartic acid to Asparagine, which led to chlorine phenotype of the mutant. The approach using in this study provides a paradigm for the rapid mapping and cloning of the mutant genes underlying the genetic traits in wheat.

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