

Mapping a Novel Gene of Cold Tolerance at Booting Stage by Using Near-Isogenic Lines in japonica Rice [PDF]

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摘要: Genetic analysis showed that cold tolerance at booting stage of near-isogenic lines (NILs) of Kunmingxiaobaigu was controlled by a gene with large phenotypic variance. One hundred and sixty-four simple sequence repeats (SSR) distributed over 12 chromosomes were used to screen polymorphism between Towata (recurrent parent, RP) and near-isogenic line pool (NILP), and two SSR markers at the long arm of chromosome 5 showed polymorphism in comparison with RP genome. Of the two markers, RM31 was found possibly linked with the cold tolerance gene at booting stage through one-way ANOVA. Twelve SSR markers around RM31 were then used to detect polymorphism between RP and NIL, and only RM7452 had polymorphism. The gene of cold tolerance at booting stage was further mapped on chromosome 5 between RM7452 and RM31 with genetic distances of 4.8 cM and 8.0 cM, respectively. This gene explained 10.50% of phenotypic variance and 5.10% of phenotypic variance of fully filled grains, and was tentatively designated as Ctb(t).

关键词: booting stage; near-isogenic line; simple sequence repeat; genetic analysis; cold tolerance gene

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