

研究论文

水稻RIL群体苗期耐冷性QTL分析

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摘要 水稻苗期冷害是影响早春季节和高纬度地区水稻成苗和秧苗生长的重要限制因素之一。为了鉴定控制水稻苗期耐冷性的QTL,研究采用了1个水稻“粳籼交”重组自交系(RIL)群体,结合1张高密度分子遗传图谱,对3叶期幼苗经过10℃冷处理3d、恢复培养2d和4d时的秧苗存活率进行复合区间作图。亲本Lemont和特青的苗期耐冷性具有极显著差异,Lemont的苗期耐冷性很强,而特青对低温敏感。在重组自交系群体中,苗期耐冷性表现为连续变异,在两个方向上均出现大量超亲分离。共检测到5个水稻苗期耐冷性QTL,分别位于水稻1、3、8和11号染色体上,单个QTL对性状的贡献率为7%~21%。其中,4个QTL的增效基因来源于亲本Lemont,另1个QTL的增效基因来源于亲本特青。2个主效QTL(qSCT-3和qSCT-8)分别位于3号染色体标记区间RM282-RM156和8号染色体标记区间RM230-RM264,对性状的贡献率达到或接近20%,被检测到的LOD值显著较高,其增效基因均来自于耐冷性亲本Lemont。研究结果进一步揭示了水稻苗期耐冷性QTL具有丰富的位点多样性,表明耐冷性普遍较强的粳稻是发掘苗期耐冷性优异基因的主要稻种资源。

关键词 [水稻\(Oryza sativa L.\)](#); [重组自交系\(RIL\)](#); [耐冷性](#); [数量性状基因座位\(QTL\)](#)

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Mapping of QTL Controlling Seedling Cold Tolerance Using Recombinant Inbred Lines of Rice (*Oryza sativa* L.)

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Abstract Low temperature stress is common for seedlings of rice (*Oryza sativa* L.) in early-spring and high-elevation environments. With an objective to identify QTL for seedling cold tolerance, a new recombinant inbred line (RIL) population was used to conduct QTL mapping study. Seedling cold tolerance of the RILs and their both parents was assessed based on survival rates of seedlings at 3-leaf stage which was exposed to cold treatment of 3 d at a low-temperature of 10°C. A marked difference between both parents in seedling cold tolerance was observed. The japonica parent Lemont was tolerant to the cold while the indica parent Teqing sensitive to the cold. The RILs displayed approximately continuous trait variations and transgressive segregation was observed in both directions. Composite interval mapping was carried out using a high-density linkage map. Totally, five QTL for seedling cold tolerance were mapped to chromosomes 1, 3, 8 and 11, respectively, each explaining 7%-21% of the phenotypic variation. Among these QTL, four had their positive alleles from Lemont and the other one from Teqing. Two major QTL for the trait were identified on chromosomes 3 and 8, respectively, with much higher LOD scores. They individually accounted approximately for 20% of the phenotypic variation. The Lemont alleles at the two major QTL increased the trait values. These results showed the genetic diversity of QTL for seedling cold tolerance and indicated that japonica tolerant to cold was the major germplasm resource carrying favorable genes conferring seedling cold tolerance in rice.

Key words [Rice \(*Oryza sativa* L.\)](#); [Recombinant inbred line \(RIL\)](#); [Cold tolerance](#); [Quantitative trait loci \(QTL\)](#)

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