

研究论文

TaMyb2- II 基因在普通小麦 (*Triticum aestivum* L.) 及其近缘种中的单核苷酸多态性分析

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收稿日期 2006-1-26 修回日期 网络版发布日期 2006-11-14 接受日期 2006-5-25

摘要 以39份抗旱性不同的普通小麦、5份A基因组材料、4份拟斯卑尔脱山羊草TaMyb2基因的核苷酸 (*Aegilops speltoides*)、6份粗山羊草 (*Aegilops tauschii*) 和2份四倍体小麦, 分析TaMyb2基因的核苷酸序列长度多态性和单核苷酸多态性, 及其与抗旱性的关系。结果发现, TaMyb2在A基因组材料中无目标片段扩增, 在其他材料中检测到I、II、III 3种类型序列。经详细分析, TaMyb2- II序列长1 606 bp, 在供试材料77 088 bp的核苷酸序列中包括34个单核苷酸变异, 其中26个SNP, 8个InDel, 二者出现的频率分别为1/2 965 bp和1/9 636 bp, 编码区 π 值 (0.00055) 小于非编码区的 π 值 (0.00185), 说明编码区的遗传变异小于非编码区的遗传变异。从SNP水平上分析, 发现普通小麦与其D基因组供体种粗山羊草及四倍体小麦的亲缘关系较近, 与B基因组供体种拟斯卑尔脱山羊草的亲缘关系较远。48份材料的TaMyb2- II序列共分为18个单倍型 (haplotype), 其中haplotype 2、3、5、6、8、9均为旱地栽培的普通小麦品种, 说明普通小麦TaMyb2- II的这几个haplotype结构可能与抗旱性有关。

关键词 TaMyb2- II 单核苷酸多态性 普通小麦 近缘种 抗旱性

分类号 S512

Single Nucleotide Polymorphism of TaMyb2- II Gene in Common Wheat (*Triticum aestivum* L.) and Its Relatives

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Abstract Drought is one of the major elements affecting the yield of wheat, one of the most important crops in arid and semi-arid areas. Mining pivotal drought-resistant genes and probing their polymorphisms are a feasible approach to decipher crops' drought resistance. The genes involved in drought resistance are classified into two classifications, functional genes and regulatory genes, based on their functions responding to water deficient. Much attention has been paid to regulatory genes because of their crucial roles in drought resistance. *AtMyb2* regulates the expression of dehydration-responsive genes *rd22* and *AtADH1* in plants. Recent studies indicate that *TaMyb2* is involved in response to water stress in common wheat, but whether its polymorphisms associated with drought resistance is still unclear. To probe the polymorphisms of *TaMyb2* gene and uncover their functions in drought resistance, a total of fifty-six accessions, including thirty-nine common wheat cultivars with different drought resistance, five species with A genome including three *T. urartu*, one *T. monococcum* and one *T. boeoticum*, four *Aegilops. speltoides*, six *Ae. tauschii* and two tetraploid wheat species, were selected to perform the research. The PCR amplification showed that *TaMyb2* was detectable in all accessions except *A genome* species. Based on the genomic sequences, TaMyb2 was classified into 3 types named as TaMyb2- I, TaMyb2- II and TaMyb2- III, respectively. The full-length sequence of TaMyb- II genomic DNA was 1 606 bp. Twenty-six SNPs (single nucleotide polymorphism) and eight InDels (insertion-deletion) were identified in 77 088 bp nucleotide acid sequence of forty-eight accessions, and the frequencies of SNP and InDel were 1/2 965 bp and 1/9 636 bp, respectively. The frequency of SNP in coding region ($\pi=0.00055$) of TaMyb- II was lower than that in noncoding region ($\pi=0.00185$), the ratio of Ka/Ks was 0.32 which seemed to suggest TaMyb2- II suffered artificial selection pressure and was very conservative. Phylogenetic analysis demonstrated that the relationship between *Ae. tauschii* and common wheat was much closer than that between *Ae. speltoides* and common wheat. Eighteen haplotypes were detected in forty-eight accessions, in which haplotype 2, 3, 5, 6, 8 and 9 were common wheat cultivars with drought resistance, which indicated that these haplotypes might relate to the drought resistance of common wheat.

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Key words [TaMyb2- II](#) [Single nucleotide polymorphism](#) [Common wheat](#) [Relative](#) [Drought resistance](#)

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