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滨麦HMW GS启动子和编码区基因的分离与序列分析

Isolation and Sequence Analysis of the HMW GS Promoter and ORF Genes from *Leymus mollis*

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英文关键词: *Leymus mollis* HMW GS Promoter Coding region Sequence analysis

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中文摘要:

为了深入了解滨麦 (*Leymus mollis*) HMW GS基因的结构特征,采用PCR方法,从滨麦基因组中分离出HMW GS基因启动子序列(Genbank登录号:FJ600498)和编码区序列(Genbank登录号:GQ169797)。启动子序列(FJ600498)从5'至3'方向依次有E box、N box、G box、HMW谷蛋白特异增强子和TATA box等麦谷蛋白特异调控元件,推断其为滨麦HMW GS启动子基因。编码区序列(GQ169797)具有单一完整的开放阅读框(ORF),编码396个氨基酸残基,依次包含信号肽、N末端区、中部重复区和C末端区等HMW GS的典型结构区域;中部重复区主要重复单元为6肽(PQQGQQ)和9肽(GYYPTSPQQ);有6个半胱氨酸残基(Cys),分布在N末端区(5个)和C末端区(1个),第3、4个相邻。推断其为滨麦的 γ 型HMW GS编码区基因。系统进化分析表明,启动子序列(FJ600498)与异形花草(*He. piliferum*)和冰草(*Ag. cristatum*)的HMW GS启动子基因序列具有相对较近的同源关系;编码区序列(GQ169797)与纤毛鹅观草(*Elymus ciliaris*)和披碱草(*E. glaucus*)的HMW GS编码区基因序列具有相对较近的同源关系。

英文摘要:

HMW GS promoter sequence (FJ600498) and coding region sequence (GQ169797) were isolated from the genome of *L.mollis* by the method of PCR. The HMW GS promoter sequence of *L.mollis* from 5' to 3' flanking in turn contained E box, N box, G box, 38bp HMW glutenin specific enhancer and TATA box, which were the promoter regulatory elements of typical HMW GS gene. The HMW GS coding region sequence had a single complete open reading frame (ORF), which encoding 396 amino acids. The deduced amino acid sequence contained the signal peptides, N terminal region, the central repeat region, and C terminal region. In repeat domains, hexapeptide (PQQGQQ) and nonapeptide (GYYPTSPQQ) were the main repeating unit. The sequence had six cysteine residues, five within N terminal and one within C terminal domains, and the 3rd and the 4th cysteine neighboring. These structure characteristics suggested that GQ169797 is a γ type HMW GS gene of *L.mollis*. Phylogenetic analysis showed that the promoter (FJ600498) was closely related with the HMW GS promoter sequence of *Heterantherium piliferum* and *Agropyron cristatum* and the ORF sequence has a relatively close homology with γ type HMW GS gene of *Elymus ciliaris* and *Elymus glaucus*.

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