长穗偃麦草中E和E1基因组高分子量麦谷蛋白基因启动子部分序列的进 化分析 Evolution of Partial Promoter Region of HMW Glutenin Genes from E and E1 Genome of Agropyron elongatum

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摘要

通过PCR克隆的方法,获得了分别来自二倍体长穗偃麦草的E基因组和四倍体长穗偃麦草的E1基因组的4个高分子量 麦谷蛋白亚基(HMW-GS)基因启动子的部分序列。序列分析表明,它们之间的同源性较高,两个x型亚基启动子序 列之间只有1个碱基的差异,而两个y型亚基启动子序列完全相同,x和y型亚基启动子序列之间的长度和部分碱基 位点都有差异。推测四倍体长穗偃麦草中的E1基因组可能起源于二倍体的E基因组。与来自小麦族的A、B、D和G基 相关文章 因组部分亚基基因的启动子序列比较表明,小麦族的这一区域在进化上是相当保守的,不同基因组来源的序列同 源性都在90%以上。经过对这些序列的聚类分析,表明长穗偃麦草的v型HMW-GS基因与其他亚基基因的进化关系较 远,而x型亚基基因与一个来自小麦1B染色体的亚基基因关系最近。Abstract: The partial promoter regions of HMW glutenin subunit genes were cloned form the genomes E (in diploid Agropyron elongatum) and El (in tetraploid Agropyron elongatum) by PCR approach. There was only one nucleotide acid difference in the promoter sequences of x-type subunits between the two genomes; moreover, the promoter sequences of the two y-type subunits were completely identical. Although these promoter regions were very similar to each other, differences still existed in sequence size and the kind of nucleotide acid between the x-type and y-type subunits. It was speculated that the El genome in tetraploid Agropyron elongatum was probably originated from E genome in diploid species. The comparisons of these subunits with some of those from A, B, D and G genome of Triticeae demonstrated that the sequences of their partial promoter regions were conserved and shared a high homology more than 90%. The phylogenetic analysis based on the sequences in this region indicated that the y-type HMW glutenin subunits of Agropyron elongatum species were different from other subunits, whereas the x-type subunits of them were most closely related to that from the B genome.

关键词 长穗偃麦草 高分子量麦谷蛋白基因 启动子 进化 Key words Agropyron elongatum HMW glutenin gene promoter evolution

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