

动物遗传学

猪I-FABP基因的分子克隆与组织特异性表达分析

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摘要

小鼠型脂肪结合蛋白对长链脂肪酸具有高度的亲和力, 参与脂肪酸的吸收和细胞内转运。利用cDNA末端快速扩增(RACE)技术并结合同源克隆策略, 克隆到了编码猪小肠型脂肪结合蛋白基因(I-FABP)的全长cDNA序列(GenBank登录号: AY960621), 并对系统发育关系等进行了生物信息学分析。猪I-FABP基因的cDNA序列全长614 bp, 其中包括399 bp的开放阅读框(ORF), 43 bp的5'非翻译区(5' UTR)和122 bp的3'非翻译区(3' UTR), 编码132个氨基酸残基蛋白。在氨基酸水平上与其他物种的I-FABP具有高度的同源性。以鸡绞蛋(Oeaghis jozainae, NJ)为构建的系统发育关系表明, 猪I-FABP与其他物种的I-FABP属于同一类群, 且与人的遗传距离最近。Northern杂交和半定量RT-PCR分析发现, 猪I-FABP在整体组织中均检测到620 bp大小的转录本, 且在整体组织中广泛存在, 但在小肠组织中表达量最为丰富。

关键词

猪; I-FABP; RACE; Northern 杂交; 半定量RT-PCR

分类号

Molecular Cloning and Tissue-specific Expression of Intestinal-type Fatty Acid Binding Protein in Porcine

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Abstract

<P>The intestinal fatty acid-binding protein (I-FABP) shows binding specificity for long-chain fatty acids and is proposed to be involved in the uptake of dietary fatty acids and their intracellular transport. In this study, the full-length cDNA of I-FABP was cloned from pig intestine by homology cloning approach combined with 3' and 5' RACE. Sequence analysis and bioinformatics study showed that this cDNA contained 614 nucleotides, with a 399 bp open reading frame (ORF) flanked by a 43 bp 5' UTR and a 122 bp 3' UTR. The encoded 132 amino acids of pig I-FABP with a molecular weight of approximately 15 kDa shared a high sequence identity of 68%-85% with those of other species. In addition, the phylogenetical analysis also indicated that the pig I-FABP was in the same branch with those of other species. The tissue-specific expression of pig I-FABP was measured by Northern hybridization and semi-quantitative RT-PCR. The results demonstrated that pig I-FABP mRNA was extensively present in various tissues, but I-FABP transcript of approximately 620 bp was more abundant in intestine than in other tissues.</P>

Key words

猪; I-FABP; RACE; Northern hybridization; semi-quantitative RT-PCR

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