鸡解偶联蛋白(UCP)基因内含子的克隆与系统发生树的构建 Cloning and Sequencing of the Introns of UCP Gene and Construction of Molecular Phylogenetic Tree in Chicken

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摘要 解偶联蛋白基因是新近发现的能够增加能量的消耗，与脂肪代谢和能量调控密切相关的一组基因。本研究根据小鼠UCP2基因的剪切方式，设计4对引物成功克隆测序了鸡UCP基因的全部5个内含子，发现都是GT-AG类型的内含子，鸡UCP基因的结构和小鼠的UCP2基因结构一致。以不同物种UCP基因的cds 区域序列和内含子2、内含子3序列进行系统发生树的构建，结果表明：以UCP基因cds区域序列构建的系统发生树与物种树是一致的，UCP基因可以作为研究动物群体系统演化研究的有效基因；但以内含子2与内含子3序列构建的系统发生树的结构则完全不是这样，与物种树的差别比较大。

Abstract:The UCP genes were the newly discovered genes that can increase the energy expenditure and involve in the metabolism of fat and regulation of energy. Four pairs of primers in chicken UCP exon region were designed to amplify the introns of chicken UCP gene according to the splice ways of the mouse UCP2 gene (Accession No.AF096288). The sequence results showed that the chicken UCP gene also had five GT-AG type introns. The molecular phylogenetic tree was constructed based on the sequence of cds,intron 2 and intron 3 region,respectively. The phylogenetic tree based on the UCP cds region was consistent with the species phylogenetic tree.This result implicated that UCP gene can be regarded as the useful gene for the study of animal phylogenesis.On the contrast,the phylogenetic tree based on the intron 2 and intron 3 region was different from the species phylogenetic tree,which showed that the evolution of intron and cds region is different.

关键词 鸡 解偶联蛋白基因 分子系统发生树 Key words chicken UCP gene molecular phylogenetic tree

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