

研究论文

牛科动物HSL基因序列分析及其分子进化研究

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收稿日期 2005-8-22 修回日期 2005-12-21 网络版发布日期 2007-1-9 接受日期

摘要

在对牛科中4种动物即牦牛、瘤牛、普通牛和水牛HSL基因外显子 I 部分核苷酸序列进行测定的基础上, 与Gen-Bank中其他物种相应基因核苷酸序列、氨基酸序列进行了比对分析, 并构建了牦牛与其他物种间分子系统进化树。结果表明: 牦牛与普通牛、瘤牛、水牛、猪、人、小鼠、大鼠7个物种HSL基因外显子 I 部分核苷酸序列间保守性较高, 同源性大小依次为99.8%、99.6%、97.4%、90.6%、88.4%、83.5%、82.3%。相应氨基酸序列间保守性更高, 同源性分别为100%、100%、98.2%、94.0%、92.2%、89.8%、89.8%。牦牛与各物种该基因部分核苷酸序列间碱基变异类型主要表现为碱基转换和颠换, 无碱基插入和缺失发生, 碱基转换的频率高于颠换的频率; 在核苷酸水平上的多数碱基替换都是同义替换; 序列间单碱基变异位点大多出现在同一位点, 多发生在密码子第3位, 其次是第1位, 最少发生在第2位, 符合分子进化的中性学说。HSL基因外显子 I 部分核苷酸序列进行多序列对位排列构建的各物种间分子系统进化树结果表明, 普通牛和瘤牛首先聚为一类, 再分别与牦牛、水牛、猪、人聚类, 最后与小鼠、大鼠聚为一类。该聚类结果与动物学上的分类结果一致, 表明HSL基因外显子 I 部分核苷酸序列适合于构建物种间分子系统进化树。研究表明, 牦牛、普通牛和瘤牛3个物种间的遗传距离大小相近, 牦牛和水牛间的遗传距离与普通牛、瘤牛和水牛间的遗传距离大小相当。牦牛、普通牛和瘤牛3个物种间的遗传距离远小于它们各自与水牛这一物种的遗传距离, 它们三者之间的亲缘关系也相对于它们各自与水牛间的亲缘关系都较近, 故将牦牛、普通牛和瘤牛划分在同一个属——牛属(Bos)更为合理。

关键词 [牛科](#); [HSL基因](#); [系统](#); [进化](#)

分类号

Sequence Variation and Molecular Evolution of Hormone-Sensitive Lipase Genes in Species of Bovidae

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Abstract

<P>The partial sequences of exon I of hormone-sensitive lipase (HSL) genes in yak (*Bos grunniens*), cattle (*Bos taurus*), zebu (*Bos indicus*), and buffalo (*Bubalus bubalis*) were analyzed. Comparisons of these sequences and the deduced amino acid sequences with the homologous HSL gene and protein sequences in other mammalian species including pig (*Sus scrofa*), human (*Homo sapiens*), mouse (*Mus musculus*), and rat (*Rattus sp.*) retrieved from the GenBank were carried out and finally a phylogenetic tree was constructed using the partial DNA sequences of the HSL genes in all species. The results showed that the homologies of the partial exon I sequences of the HSL genes between yak and cattle, zebu, buffalo, pig, human, mouse, and rat were as high as 99.8%, 99.6%, 97.4%, 90.6%, 88.4%, 83.5%, and 82.3%, respectively. This was accompanied by highly homologous amino acid sequences of the HSLs: 100%, 100%, 98.2%, 94.0%, 92.2%, 89.8%, and 89.8% identity, respectively. There are more transitions, less transversions, and no insertion or deletion in variable nucleotides of the HSL genes between the yak and other species. The majority of the variable mutations was synonymous and was found most frequently at the third codon, followed by the first and second

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codons, a finding that was in accordance with the neutralism hypothesis for molecular evolution. In the phylogenetic tree, the cattle and zebu were clustered together first, followed by the yak, buffalo, pig, human, mouse, and rat. This was in agreement with taxonomy suggesting that the partial sequences of exon I of the HSL genes were useful in constructing the phylogenetic tree of mammalian species. Among the four species of Bovidae, genetic differentiation in the HSL genes between yak and buffalo is equivalent to that between buffalo and cattle and between buffalo and zebu. Furthermore, the genetic distances in the HSL genes are much smaller between yak, cattle, and zebu than those between each of the three species and the buffalo. Therefore, it is reasonable to consider yak as an independent species of the genus *Bos*.

Key words [Bovidae](#); [HSL gene](#); [phylogeny](#); [evolution](#)

DOI:

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