

研究报告

藏绵羊GHR基因5'侧翼区序列特征分析

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摘要

对欧拉型藏绵羊生长激素受体(GHR)基因5'侧翼区(包括P1启动子和外显子1A)进行了T-A克隆和序列测定(GenBank accession No. EF116490),在分析其序列结构特征的基础上与GenBank中摩弗伦羊、山羊、普通牛、欧洲野牛进行了比较基因组学和系统进化研究,结果表明:(1)欧拉型藏绵羊GHR基因启动子P1区存在C/EBP、C/EBPb、SP1、Cap、USF、HFH-2、HNF-3b、Oct-1等多个潜在的转录因子结合位点,可能与GHR基因的转录调控和起始以及特异表达有关。在该非编码序列中,重复序列所占比率为2.55%,不存在SINEs、LINEs、LTR类反转录元件和DNA转座子元件,而发现存在一(TG)11微卫星位点;(2)在启动子P1区,藏绵羊与摩弗伦羊、山羊、普通牛、欧洲野牛各物种间同源性大小分别为99.7%、94.2%、85.9%、86.5%;而在外显子1A区段,藏绵羊与摩弗伦羊、山羊、普通牛、欧洲野牛各物种间同源性大小分别为99.0%、97.0%、92.7%、94.6%。物种间欧拉型藏绵羊与摩弗伦羊同源性最高,而欧拉型藏绵羊与普通牛最低。(3)邻接法(即NJ法)构建的分子系统进化树聚类结果表明,欧拉型藏绵羊与摩弗伦羊先聚为一类,再与山羊聚类形成一个分支,而普通牛和欧洲野牛先聚类形成另一大分支,两大分支最后再聚在一起,其聚类结果与线粒体DNA和动物学分类的研究结果一致。

关键词 [欧拉型藏绵羊](#) [GHR基因](#) [克隆](#) [微卫星](#) [启动子](#)

分类号

Sequence characterization of the 5'-Flanking region of the GHR gene in Tibetan sheep

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Abstract

<P>The 5'-Flanking sequence (including the P1 promotor and exon 1A) of the GHR gene in Ours-type Tibetan sheep (*O. aries*) was cloned by T-A method and sequenced (GenBank accession No. EF116490). Characterization and comparison of this sequence with mouflons (*O. musimon*), goat (*C. hircus*), cattle (*B. taurus*) and European bison (*B. bonasus*) orthologues were also conducted. Results showed that: 1) The 5'-flanking region contained many potential transcriptional factor binding sites such as those for C/EBPb, C/EBP, SP1, Cap, USF, HFH-2, HNF-3b, and Oct-1, which might have an important effect on transcription activation and regulation as well as tissue-specific expression. The rate of repetitive sequences was 2.55% and no SINEs, LINEs, LTR anti-transcription elements or DNA transposon elements were found, although one (TG)11 microsatellite was found. 2) In the P1 promotor region, sequence homology between the Tibetan sheep and mouflon, goat, cattle and European bison was 99.7%, 94.2%, 85.9% and 86.5%, respectively, while that for exon 1A was 99.0%, 97.0%, 92.7% and 94.6%, respectively. 3) The molecular phylogenetic tree among these species, constructed by the neighborhood joining method based on the sequences of no-coding region of the GHR genes, placed the two Bovinae species on one branch and the three Caprinae species on the other. Tibetan sheep and mouflons were joined first, followed by the goat, and then the Bovinae species, including the cattle and

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European bison. This result of phylogenetic clustering was not only identical to the taxonomy, but also to the phylogenetic clustering using the mitochondrial DNA of these species.</P>

Key words [Oura-type Tibetan sheep](#) [GHR gene](#) [clone](#) [microsatellite](#) [promotor](#)

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