

动物遗传学

牛 *FABGL* 基因的克隆及其与牛生物经济学性状的相关分析

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摘要

运用同源序列克隆技术结合反转录PCR技术和3', 5' cDNA末端快速扩增技术得到了牛*FABGL*基因的完整CDS, 3' 非翻译区和部分5' 非翻译区。序列分析和生物信息学研究表明, 所获得的牛*FABGL*基因的cDNA包含994个核苷酸和780 bp的开放阅读框及198 bp的完整的3' 非翻译区。该基因编码260个氨基酸残基蛋白, 在氨基酸水平上与人的同源基因具有高度的相似性(88%)。采用PCR-SSCP方法, 在递交的包含完整CDS的长为1 925 bp的该基因的基因组DNA序列(GenBank接受号: DQ409814)1 065 bp和1 792 bp处, 分别发现了两个单核苷酸碱基突变: Y=C/T, R=A/G; 它们分别位于该基因第五和第八内含子。对包含这两个多态位点的3个品种(安格斯、海福特和西门塔尔)牛的共179个个体等位基因频率与部分肉质及生长性状进行了关联分析, 结果发现, 在第八内含子内具有GG基因型的个体的肉用性能指数(4.283±0.475 kg/cm)较具有AA基因型个体的(4.008±0.465 kg/cm)高(P≤0.01); 而且同一位点具有GG基因型的个体的眼肌面积(73.380±13.005 cm²)显著高于具有AA基因型的个体(67.744±12.777 cm²)(P≤0.05)。在第五内含子内, 具有CC、CT、TT 3种不同基因型的个体之间, 平均日增重差异均达到极显著水平(P≤0.01), 以具有TT基因型的个体平均日增重最高(0.652±0.330 kg/d), CC基因型的最低(0.421±0.178 kg/d)。

关键词 [牛; 单核苷酸多态性; beta-酮酰基酰基转运蛋白还原酶基因; SSCP; 相关; 肉用性能指数; 眼肌面积; 平均日增重](#)

分类号

Molecular Cloning of Bovine *FABGL* Gene and Its Effects on Bovine Bioeconomic Traits

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Abstract

The complete CDS sequence of the bovine FABGL gene was determined by homology cloning approach combined with RT-PCR and 3'- and 5'-RACE. The results of sequence analysis and bioinformatics study showed that this cDNA contained 994 nucleotides, with a 780 bp open reading frame (ORF) flanked by a 16 bp 5'-UTR (incompletely) and a 198 bp 3'-UTR. The deduced amino acid sequence (260 AA) shows 88% identity with the corresponding sequence in humans. Two single nucleotide substitutions, one located in intron 5 (I5) at position 1 065 bp (Y = C/T) (GenBank: DQ409814) and the other in intron 8 (I8) at position 1 792 bp (R = A/G), were detected using the PCR-SSCP method. Analysis of the allele frequencies of the two polymorphic sites in three different cattle breeds (Angus, Hereford, and Simmental) with different genotypes showed large differences: in locus I8, cattle with the GG genotype showed higher beef performance index (BPI) (4.283 ± 0.475 kg/cm) in comparison with cattle with the AA genotype (4.008 ± 0.465 kg/cm) ($P \leq 0.01$). Regarding the ribeye area, cattle with the GG genotype showed significantly higher ribeye area (73.380 ± 13.005 cm²) compared with cattle with the AA genotype (67.744 ± 12.777 cm²) ($P \leq 0.05$). In locus I5, some associations for the average daily gain (ADG) were found at the significance level of 0.01 between three different genotypes (CC, CT, TT): cattle with the TT genotype showed the highest ADG (0.652 ± 0.330 kg/d), whereas cattle with the CC genotype showed the lowest ADG value (0.421 ± 0.178 kg/d).

Key words [cattle](#) [SNPs](#) [FABGL gene](#) [SSCP relationship](#) [BPI](#) [ribeye area](#) [ADG](#)

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