研究报告

鸭脂联素基因单核苷酸多态性检测及群体遗传分析

董飚 $^{1, 2}$, 龚道清 2 , 孟和 3 , 郁建锋 1 , 赵旭庭 4 , 段修军 4 , 顾志良 1

- 1. 常熟理工学院生物系, 常熟 215500;
- 2. 扬州大学动物科学与技术学院, 扬州 225009:
- 3. 上海交通大学农业与生物学院, 上海 200240;
- 4. 江苏畜牧兽医职业技术学院, 泰州 225300

收稿日期 2006-12-4 修回日期 2007-1-19 网络版发布日期 2007-8-2 接受日期

以昆山麻鸭、樱桃谷鸭、高邮鸭、荆江麻鸭、金定鸭,山麻鸭、龙白鸭和白羽番鸭8个鸭品种为实验材料,根据鸭 脂联素基因开放阅读框序列设计5对引物,用PCR-SSCP方法进行单核苷酸多态性分析,并对不同品种群体进行群体 遗传学分析。结果发现引物4扩增片段上共存有7个单碱基突变,第430、457、523处的G-A 、A-G、T-C单碱基突变▶文章反馈 导致第144、153、175个氨基酸分别由丙氨酸(A)变为苏氨酸(T)、异亮氨酸(I)变为缬氨酸(V)、酪氨酸(Y) 变为组氨酸(H);而C507T,T540C,C576T和C597T 4个单碱基突变为沉默突变。鸭群中表现出*AA、AB、AC、BB*、 BC、CC、DD、DE 8种基因型。8种基因型在8个鸭品种间分布存在极显著的差异(PC0.01)。除金定鸭外,其他品种 均处于Hardy-Weinberg平衡状态。群体遗传分析表明金定鸭的纯合度最高,高邮鸭最低,其他各群体的纯合度较 相近;金定鸭为低度多态,高邮鸭为高度多态,其他品种为中度多态。表明鸭脂联素基因不同品种中具有丰富的 单核苷酸多态性,可以进一步作为候选基因来分析其与脂肪性状的相关性。

关键词 脂联素基因 单核苷酸多态性 遗传分析 脂肪性状 分类号

Identification and genetic analysis of SNPs in duck adiponectin gene

DONG Biao^{1,2}, GONG Dao-Qing², MENG He³, YU Jian-Feng¹, ZHAO Xu-Ting⁴, DUAN Xiu-Jun⁴, GU Zhi-Liang¹

- 1. Department of Biology, Changshu Institute of Technology, Changshu 215500, China;
- 2. College of Animal Science and Technology, Yangzhou University, Yangzhou 225009, China;
- 3. College of Agriculture and Biology, Shanghai Jiaotong University, Shanghai 200240, China;
- 4. Jiangsu Animal Science and Veterinary Medicine College, Taizhou 225300, China

Abstract

<P>Single nucleotide polymorphisms (SNPs) within the duck adiponectin gene were detected by single strand conformation polymorphism (SSCP) using 5 pairs of primers to amplify an area spanning the open reading frame. Eight duck breeds, including Kunshan Sheldrake, Cherry Valley Meat duck, Gaoyou duck, Shanma duck, Jinding duck, Longbai duck, Jingjiang Sheldrake and White feather Muscovy duck, were used. Seven nucleotide variations were found, of which G430A, A457G, and T523C resulted in amino acid changes of A144T, I153V, and Y175H, respectively. The remaining 4 SNPs were C507T, T540C, C576T and C597T. Eight genotypes (AA, AB,AC,BB,BC, CC, DD, and DE) were detected in the 8 breeds. c2 analysis showed that the distribution of the eight genotypes was very different among the different breeds (P<0.01). Ex-cept for the Jingding duck, all breeds were in accordance with the Hardy-Weinberg equilibrium. Genetic analysis indicated that homozygosity was highest in the Jinding duck, lowest in the Gaoyou duck and similar in other breeds. Polymorphism information content (PIC) was low in the Jinding, high in the Gaoyou and intermediate in other breeds. These results showed that the adiponectin gene had a high level of polymorphism in different duck breeds, and could be used as a candi-date gene to analyze the correlation between its polymorphism and fat traits in duck.</P>

扩展功能

本文信息

- ▶ Supporting info
- **PDF**(0KB)
- ▶[HTML全文](0KB)
- ▶参考文献

服务与反馈

- ▶把本文推荐给朋友
- ▶加入我的书架
- ▶加入引用管理器
- ▶复制索引
- Email Alert
- ▶浏览反馈信息

相关信息

▶ 本刊中 包含"鸭"的 相关文章

▶本文作者相关文章

- 董飚
- 龚道清
- 孟和
- 郁建锋
- 赵旭庭
- 段修军
- 顾志良

Key words <u>duck</u> <u>adiponectin gene</u> <u>SNPs</u> <u>genetic analyses</u> <u>fattiness trait</u>

DOI: 10.1360/yc-007-0995

通讯作者 顾志良 zhilianggu88@hotmail.com