

## 建鲤肠型脂肪酸结合蛋白基因的分离及其SNPs与增重的相关分析

夏正龙<sup>1</sup>, 俞菊华<sup>1,2</sup>, 李红霞<sup>2</sup>, 李建林<sup>2</sup>, 唐永凯<sup>2</sup>, 任洪涛<sup>3</sup>, 朱双宁<sup>1</sup>

1. 南京农业大学无锡渔业学院, 无锡 214081 2. 中国水产科学研究院淡水渔业研究中心, 农业部淡水渔业和种质资源利用重点实验室, 无锡 214081 3. 河南科技大学动物科技学院, 洛阳 471003

XIA Zheng-Long<sup>1</sup>, YU Ju-Hua<sup>1,2</sup>, LI Hong-Xia<sup>2</sup>, LI Jian-Lin<sup>2</sup>, TANG Yong-Kai<sup>2</sup>, REN Hong-Tao<sup>3</sup>, ZHU Shuang-Ning<sup>1</sup>

1. Wuxi Fishery College, Nanjing Agricultural University, Wuxi 214081, China 2. Key Laboratory of Freshwater Fisheries and Germplasm Resources Utilization, Ministry of Agriculture, Freshwater Fisheries Research Center, Chinese Academy of Fishery Sciences, Wuxi 214081, China 3. Animal Science and Technology College, Henan University of Science and Technology, Luoyang 471003, China

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**摘要** 文章采用PCR方法从建鲤 (*Cyprinus carpio* var. jian) 基因组分离到2个肠型脂肪酸结合蛋白基因 (Fatty acid binding protein 2, *FABP2*), ORF长度均为399 bp, 相似度为92.2%, 分别记为*jIFABP2a*、*jIFABP2b*, 和斑马鱼 (*Danio rerio*) *FABP2* ORF的相似度分别为88.0%和90.5%。*jIFABP2s*基因结构与*FABPs*家族其他成员一致, 由4个外显子和3个内含子组成, 2a和2b间内含子序列和长度差异明显。系统树显示这2个基因对应斑马鱼的1个*FABP2*基因, 和鲤鱼染色体数是斑马鱼的2倍一致。实时荧光定量PCR结果显示, *jIFABP2a*、*2b*在建鲤肠中的表达量极显著高于脑、肝脏、肌肉、肾脏、心脏、性腺等其他组织 ( $P < 0.01$ ), 且2a表达量显著 (雄鱼,  $P < 0.05$ ) 或极显著 (雌鱼,  $P < 0.01$ ) 高于2b, 但在其他组织则2b表达量稍高, 暗示2a为肠特异性表达, 2b则为广谱表达。通过对比8尾建鲤的2a和2b基因序列, 在2a和2b上分别找到12个和4个SNP, 均位于内含子上。使用PCR-RFLP法检测*jIFABP2a*上4个SNP位点I1-A15G、I1-A99G、I2-C487T和I3-A27T在建鲤选育群体中的基因型分布, 并进行了基因型与个体增重的关联分析, 结果表明, 4个位点与雌、雄成鱼阶段增重分别有极显著或显著相关。同时考虑4个位点的基因型与增重的关系, 结果基因型AGGGCCXX和AGGGXXAT的个体平均增重比其他个体快15%, 这两种基因型个体在选育群中占了9%, 具有较大的选育空间, 可用于建鲤分子育种计划中。

**关键词:** 建鲤 肠型脂肪酸结合蛋白 组织表达 单核苷酸多态性 SNP-增重相关分析

**Abstract:** Two replicate intestine fatty acid binding protein genes (*jIFABP2a* and *jIFABP2b*) were cloned from *Cyprinus carpio* var. jian using PCR. Both ORFs were 399 bp in length sharing 92.2% similarity with each other, and 88.0% and 90.5% with their counterpart in zebrafish, respectively. The gene structure of *jIFABP2s* was same as other *FABPs*, which contained four exons and three introns. Sequences and lengths of introns between 2a and 2b were obviously different. Phylogenetic tree displayed that two *jIFABP2s* corresponded to one zebrafish *FABP2* which matches the fact that the chromosome number of common carp was twice of zebrafish. Real time-PCR showed that *jIFABP2* genes mainly expressed in intestine and the expression level was very significantly higher than other tissues such as brain, liver, muscle, kidney, and gonad ( $P < 0.01$ ). The expression level of *jIFABP2a* was significantly (male,  $P < 0.05$ ) or very significantly (females,  $P < 0.01$ ) higher than 2b in intestine; and 2b was expressed slightly higher than 2a in other tissues. It seemed that 2a expressed specifically in intestine, while 2b expressed ubiquitously. Twelve and four SNP loci were found at *jIFABP2a* and *2b* introns through comparison sequences from 8 individuals, respectively. Genotypes of I1-A15G, I1-A99G, I2-C487T, and I3-A27T on *jIFABP2a* were detected using PCR-RFLP in selection population of *C. carpio* var. jian. The SNP genotypes and individual weight gain correlation indicated that four SNPs were significantly ( $P < 0.05$  or  $P < 0.01$ ) associated with adult weight gain. Diplotype analysis displayed that individuals with genotype AGGGCCXX or AGGGXXAT grew faster than other individuals by 15%. The individuals with these two genotypes only occupied 9% in total selection populations, indicating the presence of large selection space. The 4 SNPs detected in this experiment can be used in *C. carpio* var. Jian growth selection breeding plan.

**Keywords:** *Cyprinus carpio* var. jian, *FABP2*, tissue expression, single nucleotide polymorphisms loci, SNP-weight gain association analysis

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通讯作者 俞菊华 Email: yujh@ffrc.cn

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