

## 猪 *ATF4* 基因多态性与生产性状的关联及基因表达分析

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**摘要** 为进一步了解和认识 *ATF4* 基因的功能, 揭示 *ATF4* 对猪脂肪代谢的影响, 寻找与肉质性状相关联的分子标记, 文章采用 PCR 方法扩增了 *ATF4* 基因部分序列, 通过序列比对发现在翻译起始密码子 ATG 下游 159 bp 处存在 A159G 转换, 通过 PCR-*Alu* I -RFLP 对大白猪、长白猪、梅山猪和通城猪进行酶切分型, 发现在大白猪和长白猪中均为 AA 基因型, 在梅山猪和通城猪中均为 GG 基因型。进一步对大白猪 × 梅山猪 F<sub>2</sub> 群体资源家系进行了酶切分型, 并分析该位点的多态性与生产性状的关系。结果表明, *ATF4* 的多态性与臀部平均膘厚存在极显著相关 ( $P < 0.01$ ), 与胸腰椎间膘厚、平均膘厚、眼肌高、眼肌面积存在显著相关 ( $P < 0.05$ )。采用 Real-time PCR 分析了 *ATF4* 基因在大白猪与梅山猪背最长肌不同发育阶段的表达模式。结果表明, *ATF4* 基因在大白猪和梅山猪胚胎期 65 d 和出生后 3 d 中的表达水平相对都较低, 且在两品种间无明显差异; 而在出生后 60 d 和 120 d, *ATF4* 基因在大白猪中与梅山猪均出现了上调表达, 并且在梅山猪中的相对表达水平要显著高于大白猪。研究结果为进一步深入研究猪 *ATF4* 基因在脂肪代谢中的分子机理奠定了基础。

**关键词:** 猪 *ATF4* PCR-RFLP 关联分析 表达模式分析

**Abstract:** In order to understand the function of gene *ATF4* and identify new DNA markers involved in pig production traits, the cDNA fragment of porcine *ATF4* was cloned and sequenced. Sequence comparison revealed an A159G substitution downstream of the initiation codon (ATG). We then carried out PCR-*Alu* I -RFLP analysis in Large white, Landrace, Tongcheng and Meishan pigs, followed by association analysis in F<sub>2</sub> "Large white × Meishan" resource family. In all the individuals tested, Large White and Landrace pigs possessed the AA genotype, while Meishan and Tongcheng pigs possessed the GG genotype. Association analysis in F<sub>2</sub> resource family showed that this site was highly associated with buttock fat thickness (*BFT*) ( $P < 0.01$ ) and had significant effect on thorax-waist fat thickness (*TFT*), average backfat thickness (*ABT*), loin eye height (*LEH*), and loin eye area (*LEA*) ( $P < 0.05$ ). Real-time PCR was used to analyze the expression patterns of porcine *ATF4* gene in *longissimus dorsi* at different development stages of Large White and Meishan pigs. The results showed that the gene expression levels of *ATF4* were low 65 days after conception and 3 days after birth, but no significant differences were observed in both breeds. Meanwhile, the expression levels of porcine *ATF4* gene were up-regulated 60 days and 120 days after birth in both breeds and the expression level in Meishan pigs was obviously higher than that in Large White pigs. These data could lay the foundation for further study on the molecular mechanism of porcine *ATF4* gene in lipid metabolism.

**Keywords:** porcine, *ATF4*, PCR-RFLP, association analysis, expression pattern analysis

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