

研究报告

# 牛 *TLR4* 基因 5' 侧翼区的遗传变异与乳房炎的关联

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## 摘要

*TLR4* 基因通过识别病原体激活免疫细胞, 在天然免疫和适应性免疫防御中起着重要的作用。以中国荷斯坦奶牛、三河牛和中国西门塔尔牛为研究对象, 扩增 477 bp 的目的片段, 测序后发现扩增片段的 245 bp 处 G→C 的转换使得 *Msp* I 酶切位点产生, 形成新的等位基因。因此采用 RFLP-*Msp* I 方法检测该等位基因的多态性, 结果表明, 在 3 个群体中 A、B 两个等位基因均有分布, 处于中度多态。经  $\chi^2$  适合性检验, 三河牛在该位点未达到 Hardy-Weinberg 平衡状态 ( $P < 0.05$ )。利用 SAS 8.2 软件采用最小二乘法拟合线性模型将该基因座不同基因型与奶牛乳房炎进行了关联分析, 结果表明品种和泌乳月效应对乳房炎的影响较大, 各基因型效应差异均不显著 ( $P > 0.05$ )。

关键词 [牛](#) [TLR4 基因](#) [PCR-RFLP](#) [乳房炎](#) [SCC](#) [体细胞评分](#)

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## Genetic Variation in the 5' Flanking Region of Bovine *TLR4* Gene and Correlation with Mastitis

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### Abstract

Toll-like receptor 4 recognizes pathogen ligands and mediates signaling to initiate innate and adaptive immune responses. In this experiment, a 477 bp segment of the 5'-flanking region of *TLR4* gene of Chinese Holstein, Sanhe cattle and Chinese simmental was amplified by polymerase chain reaction. After sequencing, a polymorphic site in amplified production of *TLR4* was identified of having either a G or a C at position 245. This polymorphism in the three populations was detected by digesting the fragment with restriction endonuclease *Msp* I. Results showed that both alleles (A and B) were found in the three populations and the value of polymorphism information content indicated that this was a moderate polymorphism. FONT-FAMILY: Symbol; LETTER-SPACING: 0.1pt; mso-fareast-font-family: 宋体; mso-font-kerning: 1.0pt; mso-ansi-language: EN-US; mso-fareast-language: ZH-CN; mso-bidi-language: AR-SA; mso-bidi-font-family: 'Times New Roman'; test indicated that the polymorphism locus in Sanhe cattle did not fit Hardy-Weinberg equilibrium ( $P < 0.05$ ). In addition, the effect of the *TLR4* polymorphism on somatic cell score was analyzed, and the results indicated that the somatic cell score were significantly affected by lactation month and the type of breeds ( $P < 0.05$ ), but not by different genotypes ( $P > 0.05$ ).

Key words [bovine](#) [TLR4](#) [RFLP-PCR](#) [mastitis](#) [somatic cell count](#) [somatic cell score](#)

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