



Methylation analysis of *CXCR1* in mammary gland tissue of cows with mastitis induced by *Staphylococcus aureus*

Y.J. Mao^{1,2}, X.R. Zhu¹, R. Li¹, D. Chen¹, S.Y. Xin¹, Y.H. Zhu¹, X.X. Liao¹, X.L. Wang¹, H.M. Zhang¹, Z.P. Yang¹ and L.G. Yang²

¹Key Laboratory for Animal Genetics, Breeding, Reproduction and Molecular Design of Jiangsu Province, College of Animal Science and Technology, Yangzhou University, Yangzhou, China

²College of Animal Science and Technology, Huazhong Agricultural University, Wuhan, China

Corresponding author: L.G. Yang
E-mail: yangliguo2006@qq.com

Genet. Mol. Res. 14 (4): 12606-12615 (2015)

Received February 4, 2015

Accepted May 15, 2015

Published October 19, 2015

DOI <http://dx.doi.org/10.4238/2015.October.19.4>

ABSTRACT. Mastitis is the most important disease in the global dairy industry, and causes large economic losses. *Staphylococcus aureus* is one of most common pathogens that cause bovine mastitis. *CXCR1* has been implicated as a prospective genetic marker for mastitis resistance in dairy cows; *CXCR1* expression significantly increases when cows have mastitis. To investigate the mechanisms involved in its increased expression, bisulfite sequencing polymerase chain reaction (PCR) was used to detect the methylation status of *CXCR1* CpG island, and quantitative fluorescence PCR was used to detect *CXCR1* expression in bovine mammary tissue induced with *S. aureus* in three Chinese Holstein cows. No CpG island was found for bovine *CXCR1* in the upstream 2-kb region, whereas one CpG island that contained 13 CpG sites was found in exon 1 of *CXCR1*. All of the CpG sites were under hypermethylation from 90 to 100% in the mammary tissues. When the

mammary gland mRNA expression of *CXCR1* was 12.10-fold higher in infected cow quarters than in uninfected quarters, the methylation levels of the CpG site at position 519 were significantly lower in the infected quarters than in the uninfected quarters. Pearson correlation analysis showed that the methylation level at position 519 was significantly negatively correlated with the *CXCR1* mRNA expression level ($P < 0.05$). These results indicate that the methylation of the CpG site at position 519 may regulate *CXCR1* expression in cows with mastitis induced by *S. aureus*, but further studies are needed to elucidate the mechanisms involved.

Key words: Cow; *CXCR1*; Methylation; BSP; Mastitis; *Staphylococcus aureus*