

奶牛产奶性状与乳房炎相关基因CpG含量及分布特征的比较分析

解小莉^{1,2,3}, 俞英², 袁志发¹, 杨洁², 马裴裴², 李迪超¹, 尉守科¹, 安峰¹, 封晓静⁴, 张沅²

1. 西北农林科技大学理学院, 杨凌 712100 2. 中国农业大学动物科技学院, 北京 100193 3. 西北农林科技大学动物科技学院, 杨凌 712100 4. 西北农林科技大学信息工程学院, 杨凌 712100

XIE Xiao-Li^{1,2,3}, YU Ying², YUAN Zhi-Fa¹, YANG Jie², MA Pei-Pei², LI Di-Chao¹, YU Shou-Ke¹, AN Feng¹, FENG Xiao-Jing⁴, ZHANG Yuan²

1. College of Sciences, Northwest A F University, Yangling 712100, China 2. College of Animal Science Technology, China Agricultural University, Beijing 100193, China 3. College of Animal Science and Technology, Northwest A F University, Yangling 712100, China 4. College of Information Engineering, Northwest A F University, Yangling 712100, China

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摘要 DNA甲基化是表观遗传学的重要组成部分, 基因启动子区及第一外显子区的CpG甲基化通常抑制该基因的表达, 而去甲基化则促进基因表达。已有的研究发现荷斯坦牛的乳房炎指标SCC(Somatic cell count)与产奶量呈较强负相关。文章分析并比较了这两类性状的相关基因的启动子区、第一外显子、下游2 000 bp序列中CpG含量及分布特征。结果表明, 乳房炎相关基因的启动子、第一外显子中CpG含量显著低于产奶性状相关基因, 而两类性状基因下游2 000 bp序列中CpG含量无显著性差异。另外, 文中提出了两个量化基因序列中CpG特征的指标, 一个是CpG平均距离, 用来衡量序列中的CpG分布; 另一个是条件概率 $p(G|C)$, 用以量化序列中二核苷酸CpG随碱基C出现的可能性, 并对两类基因的启动子和第一外显子区域的这两个指标做了统计检验。研究结果对产奶性状与乳房炎相关基因的DNA甲基化调控研究奠定了基础。

关键词: 产奶性状相关基因 乳房炎相关基因 CpG座位 DNA甲基化 条件概率

Abstract: DNA methylation is a major part of epigenetics. DNA methylation on the CpG sites in gene promoter and the first exon often represses gene expression, but demethylation activates gene expression. Previous research has shown that a negative correlation was found between mastitis index (somatic cell count, SCC) and milk production traits in Holsteins. The content and distribution of CpG dinucleotide sites in different regions of the candidate genes related to milk production traits and mastitis were studied in the present study. The regions contained promoter (2000 bp upstream of transcriptional start site), exon 1, and 2000 bp downstream of transcriptional end site. The CpG number of promoter and exon 1 in the mastitis-related genes was significantly less than that of the milk production-associated genes. However, the CpG number of 2000 bp downstream of the genes for the two traits was not significantly different. Two new index quantified CpG characterizations were proposed. One is the CpG distance, which can measure the distribution of CpG. The other is the conditional probability $p(G|C)$, which is used to quantify the probability of CpG in a nucleotide sequence along with C. The two indexes of promoter and exon 1 in the two types of genes and their statistic analysis were carried out. This study sets the basis for DNA methylation regulation of milk production traits- and mastitis-related genes.

Keywords: milk production traits-associated genes, mastitis-related genes, CpG site, DNA methylation, conditional probability

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通讯作者 俞英 Email: yuying@cau.edu.cn

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- [1] Bird A. DNA methylation patterns and epigenetic memory. *Genes Dev*, 2002, 16(1): 6-21. 
- [2] Tycko B. Epigenetic gene silencing in cancer. *J Clin Invest*, 2000, 105(4): 401-407.
- [3] Vanselow J, Yang W, Herrmann J, Zerbe H, Schuberth HJ, Petzl W, Tomek W, Seyfert HM. DNA-remethylation around a STAT5-binding enhancer in the α S1-casein pro-moter is associated with abrupt shutdown of α S1-casein synthesis during acute mastitis. *J Mol Endocrinol*, 2006, 37(3): 463-477. 
- [4] Yu Y, Zhang HM, Tian F, Zhang WS, Fang HB, Song JZ. An integrated epigenetic and genetic analysis of DNA methyltransferase genes (*DNMTs*) in tumor resistant and susceptible chicken lines. *PLoS One*, 2008, 3(7): e2672.
- [5] Koivula M, Mantysaari E A, Negussie E, Serenius T. Genetic and phenotypic relationships among milk yield and somatic cell count before and after clinical mastitis. *J Dairy Sci*, 2005, 88(5): 827-833. 
- [6] Schutz MM. Genetic evaluation of somatic cell scores for United States dairy cattle. *J Dairy Sci*, 1994, 77(7): 2113-2129. 
- [7] 马裴裴, 俞英, 张沅, 张勤, 王雅春, 孙东晓, 张毅. 中国荷斯坦牛SCC变化规律及其与产奶性状之间的关系. 畜牧兽医学报, 2010, 41(12): 1529-1535.
- [8] Halasa T, Nielen M, De Roos APW, van Hoorne R, de Jong G, Lam TJGM, van Werven T, Hogeveen H. Production loss due to new subclinical mastitis in Dutch dairy cows estimated with a test-day model. *J Dairy Sci*, 2009, 92(2): 599-606. 
- [9] Jiang L, Liu JF, Sun DX, Ma PP, Ding XD, Yu Y, Zhang Q. Genome wide association studies for milk production traits in Chinese Holstein population. *PLoS One*, 2010, 5(10): e13661.
- [10] Ogorevc J, Kunej T, Dov? P. An integrated map of cattle candidate genes for mastitis: a step forward to new genetic markers. *Acta Agric Slovenica*, 2008, (Supl. 2): 85-91.
- [11] Whelehan CJ, Meade KG, Eckersall PD, Young FJ, O'Far-relly C. Experimental *Staphylococcus aureus* in-fecton of the mammary gland induces region-specific changes in innate immune gene expression. *Vet Immu-nol Immunopathol*, 2011, 140(3-4): 181-189. 
- [12] Moyes KM, Drackley JK, Morin DE, Looor JJ. Greater expression of TLR2, TLR4, and IL6 due to negative energy balance is associated with lower expression of HLA-DRA and HLA-A in bovine blood neutrophils after intramam-mary mastitis challenge with *Streptococcus uberis*. *Funct Integr Genomics*, 2010, 10(1): 53-61. 
- [13] He YH, Chu Q, Ma PP, Wang YC, Zhang Q, Sun DX, Zhang Y, Yu Y, Zhang Y. Association of bovine CD4 and STAT5b single nucleotide polymorphisms with somatic cell scores and milk production traits in Chinese Holsteins. *J Dairy Res*, 2011, 78(2): 242-249. 
- [14] Pryce JE, Bolormaa S, Chamberlain AJ, Bowman PJ, Savin K, Goddard ME, Hayes BJ. A validated genome-wide association study in 2 dairy cattle breeds for milk production and fertility traits using variable length haplotypes. *J Dairy Sci*, 2010, 93(7): 3331-3345. 
- [15] Gardiner-Garden M, Frommer M. CpG islands in verte-brate genomes. *J Mol Biol*, 1987, 196(2): 261-282. 
- [16] Yamada Y, Watanabe H, Miura F, Soejima H, Uchiyama M, Iwasaka T, Mukai T, Sakaki Y, Ito T. A comprehensive analysis of allelic methylation status of CpG islands on human chromosome 21q. *Genome Res*, 2004, 14(2): 247-266. 
- [17] 凡时财, 邹见效, 徐红兵, 张学工. 人类基因组CpG岛甲基化概况的预测. 科学通报, 2010, 55(14): 1329-1334.
- [18] Pålmeke N, Santacruz D, Walter J. Comprehensive analysis of DNA-methylation in mammalian tissues using MeDIP-chip. *Methods*, 2011, 53(2): 175-184.
- [19] Irizarry RA, Ladd-Acosta C, Wen B, Wu Z, Montano C, Onyango P, Cui H, Gabo K, Rongione M, Webster M, Ji H, Potash JB, Sabunciyani S, Feinberg AP. The human colon cancer methylome shows similar hypo- and hypermethylation at conserved tissue-specific CpG island shores. *Nat Genet*, 2009, 41(2): 178-186. 
- [20] Li QH, Li N, Hu XX, Li JX, Du Z, Chen L, Yin GL, Duan JJ, Zhang HC, Zhao YF, Wang J, Li N. Genome-wide mapping of DNA methylation in chicken. *PLoS One*, 2011, 6(5): e19428.
- [21] 凡时财, 张学工. DNA甲基化的生物信息学研究进展. 生物化学与生物物理进展, 2009, 36(2): 143-150. 

- [1] 曹家雪 张红平 杜立新.环境因素对DNA甲基化的影响[J]. 遗传, 2013,35(7): 839-846
- [2] 王庭璋 单泉 徐建红 薛庆中.基因组规模DNA甲基化测序数据预处理及表观遗传分析[J]. 遗传, 2013,35(6): 685-684
- [3] 杨晓丹, 韩威, 刘峰.DNA甲基化与脊椎动物胚胎发育[J]. 遗传, 2012,34(9): 1108-1113
- [4] 许飞, 王慧君, 马端.表观遗传学——耳聋研究的新视野[J]. 遗传, 2012,34(3): 253-259
- [5] 吴新刚, 彭姝彬, 黄谦.乳腺癌耐药蛋白基因的转录调控机制[J]. 遗传, 2012,34(12): 1529-1536
- [6] 郭广平, 顾小平, 袁金玲, 吴晓丽.不同生理年龄毛竹DNA甲基化的MSAP分析[J]. 遗传, 2011,33(7): 794-800
- [7] 郭欣欣, 叶海燕, 张敏.果蝇DNA甲基化研究进展[J]. 遗传, 2011,33(7): 713-719
- [8] 苏建民, 许文兵, 李艳艳, 王丽君, 王勇胜, 张涌.转基因克隆牛胎盘中印迹基因*PEG10*的DNA甲基化水平[J]. 遗传, 2011,33(5): 533-538
- [9] 郭磊, 李慧, 韩之明.DNA甲基化和组蛋白修饰在克隆动物发育过程中的作用[J]. 遗传, 2010,32(8): 762-768
- [10] .牛的体外受精胚与克隆胚中多能性相关基因5' 端的甲基化模式[J]. 遗传, 2010,37(5): 297-304
- [11] 付胜杰, 王晖, 冯丽娜, 孙一, 杨文香, 刘大群 .叶锈菌胁迫下的小麦基因组MSAP分析[J]. 遗传, 2009,31(3): 297-304
- [12] 于红.表观遗传学: 生物细胞非编码RNA调控的研究进展[J]. 遗传, 2009,31(11): 1077-1086
- [13] 苏玉, 王溪, 朱卫国.DNA甲基转移酶的表达调控及主要生物学功能[J]. 遗传, 2009,31(11): 1087-1093

[14] 谭建新, 孙玉洁. 表观基因组学研究方法与评价[J]. 遗传, 2009,31(1): 3-12

[15] 刘景河, 梁兴伟, 朱家桥, 魏亮, 侯毅, 陈大元, 孙青原. 克隆牛流产胎儿DNA甲基转移酶基因5'端的异常甲基化[J]. 遗传, 2008,35(9): 559-568