



Changes in methylation of genomic DNA from chicken immune organs in response to H5N1 influenza virus infection

Y.H. Zhang¹, J.L. Meng¹, Y. Gao¹, J.Y. Zhang¹, S.L. Niu¹, X.Z. Yu²,
Y.B. Li³, Y.T. Guan³, B.X. Sun¹ and Z.H. Zhao¹

¹College of Animal Science, Jilin University, Changchun, China

²College of Agriculture, Forestry and Life Sciences, Clemson University,
Clemson, SC, USA

³The Harbin Veterinary Research Institute,
Chinese Academy of Agricultural Sciences, Harbin, China

Corresponding authors: B.X. Sun / Z.H. Zhao

E-mail: sunpathing@sohu.com / zhzhao@jlu.edu.cn

Genet. Mol. Res. 15 (3): gmr.15037382

Received January 4, 2016

Accepted August 4, 2016

Published September 16, 2016

DOI <http://dx.doi.org/10.4238/gmr.15037382>

Copyright © 2016 The Authors. This is an open-access article distributed under the terms of the Creative Commons Attribution ShareAlike (CC BY-SA) 4.0 License.

ABSTRACT. DNA methylation is an important epigenetic modification in eukaryotes, which plays a significant role in regulating gene expression. When the host is invaded by the influenza virus, gene expression is regulated via changes in DNA methylation levels or patterns, leading to the activation or suppression of relevant signaling pathways or networks, triggering a series of immune responses against viral invasion. Here, we investigated the changes in genomic DNA methylation in the immune organs of chicken infected with H5N1 influenza virus. Genome-wide DNA methylation levels in the spleen, thymus, and bursa of Fabricius of specific pathogen-free (SPF) chicken infected with the Guangdong (G-H5N1) and Anhui (A-H5N1) H5N1

strains, and water (control) were analyzed by fluorescence-labeled methylation-sensitive amplified polymorphism (F-MSAP). The results indicated that total DNA methylation levels did not differ between spleen genomic DNA in chicken treated with different viral strains and the control ($P > 0.05$). However, the total DNA methylation levels were significantly upregulated in the thymus ($P < 0.01$) and bursa ($P < 0.05$) of chicken in the A-H5N1 group compared to those in the G-H5N1 and control groups. These results provide a basis for the screening of avian influenza-resistance genes or methylation markers, analyzing the epigenetic regulation mechanisms of avian influenza, and performing selective breeding for disease resistance.

Key words: Avian influenza; H5N1; Immune organs; DNA methylation; F-MSAP