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**The diagnosis and molecular epidemiology investigation of avian hepatitis E in Shandong province, China**

Kuihao Liu1,#, Yiran Zhao1,#, Jun Zhao1, Ningwei Geng1, Fanliang Meng1, Siqi Wang1, Jing Li1, Zhaobing Zhong2,Liya Zhu3, Sidang Liu1,\*, Ning Li1,\*

1vetlkh@126.com, College of Animal Science and Technology, Shandong Agricultural University, Sino-German Cooperative Research Centre for Zoonosis of Animal Origin Shandong Province, Shandong Provincial Key Laboratory of Animal Biotechnology and Disease Control and Prevention, Shandong Provincial Engineering Technology Research Center of Animal Disease Control and Prevention, 61 Daizong Road, Taian, 271000, Shandong Province, China

2 Taian Daiyue District Administrative Examination and Approval Service Bureau, Taian, 271018, Shandong Province, China

3 Animal Husbandry and Veterinary Service Centre of Linshu, Linyi, 276700, Shandong Province, China

**Abstract:**

**Background/Objective:** Avian hepatitis E virus (HEV) is the pathogenic agent of big liver and spleen disease (BLS) and hepatitis-splenomegaly syndrome (HSS) in chickens, which has caused economic losses to the poultry industry in China. Eighteen samples of BLS chickens were collected in this study to understand the molecular epidemiological characteristics of avian HEV in Shandong province, China.

**Methods:** Gross and microscopic lesions of clinical samples were observed, then virology detection and genetic analysis of avian HEV were performed.

**Results:** The results showed that there were significant swelling and rupture in the liver, and spleen was enlarged. Microscopic lesions demonstrated that obvious hemorrhage in the liver, with infiltration of heterophilic granulocytes, lymphocytes, and macrophages, the reduction of lymphocytes in the spleen. Eleven out of the 18 samples were positive for avian HEV, with a positive rate of 61.11%. More importantly, all avian HEV positive samples were mixed infections. Among them, the mixed infections of avian HEV and chicken infectious anaemia virus (CIAV) and fowl adenovirus (FAdV) were the most common. In addition, the genetic evolution analysis showed that all obtained avian HEV strains did not belong to the reported 4 genotypes, and they constituted a potential novel genotype.

**Conclusion:** These results of this study further enriched the epidemiological data of avian HEV in Shandong province and proved the genetic diversity of avian HEV in China, but also uncovered the complex mixed infections of avian HEV in clinical.

**Keywords:** Avian hepatitis E virus, Mixed infections, Potential novel genotype, Molecular epidemiology