

Genetic Characteristics of Chicken Anemia Virus Circulating in Northern Vietnam

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Abstract : Chicken anemia virus (CAV) has a ubiquitous and worldwide distribution in chicken production. Our group previously reported high seroprevalence of CAV in chickens in northern Vietnam. In the present study, 330 tissue samples collected from commercial and breeder chicken farms in eleven provinces in northern Vietnam were tested for the CAV infection. We found that 157 out of 330 (47.58%) chickens were positive with CAV genes by real-time PCR method. Nine CAV strains obtained from the different location and time were forwarded to the full-length sequence of CAV VP1 gene. Phylogenetic analysis of the Vietnamese CAV vp1 gene indicated that the CAVs circulating in northern Vietnam were divided into three distinct genotypes, II, III, and V, but not clustered with the vaccine strains. Among the three genotypes, genotype III was the major one widely spread in Vietnam, and that included three sub-genotypes, IIIa, IIIb, and IIIc. The Vietnamese CAV strains were closely related to the Chinese, Taiwanese, and USA strains. All the CAV isolates had glutamine at amino acid position 394 in the VP1 gene, suggesting that they might be highly pathogenic strains. One strain was defined to be genotype V, which had not been reported for Vietnamese CAVs. Additional studies are required to further evaluate the pathogenicity of CAV strains circulating in Vietnam.

Keywords : chicken anemia virus, genotype, genetic characteristics, Vietnam

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