Molecular epidemiology and genetic analysis of H9N2 avian influenza viruses comparing with highly pathogenic avian influenza viruses in Korea

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H9N2 avian influenza viruses (AIVs) have become endemic and circulated in poultry industries in Korea since the first outbreak in 1996. We surveyed H9N2 AIVs in Korean chicken farms and live bird markets from 2009 to 2014. A total of 156 H9N2 AIVs was isolated, and we compared the genetic characteristics of the AIV isolates with H5N1 and H5N8 highly pathogenic influenza viruses (HPAIVs) isolated in Korea. Phylogenetic analysis classified the H9N2 AIVs into three categories of genotypes and showed that genetic reassortment had occurred among H9N2 AIVs, HPAIVs and AIVs isolated from wild birds. The first group of H9N2 AIVs were closely related to A/chicken/Korea/01310/2001 H9N2 (01310) which has been used for an H9N2 vaccine strain in Korea. The other two groups showed there assortment of polymerase genes each other between H9N2 AVI and HPAIV. The PB1 genes were similar to H5N8 HPAIV isolated in 2014, and the PB2 genes were closely related to H5N1 HPAIs. The PA genes of the second group were from 01310-like lineage, but those of the third group from HPAIV-like lineage. Considering that many kinds of the similar genetic reassortants of H9N2 AIVs have been reported in the several East Asian countries and H9N2 AIVs are thought as one of the potential pandemic candidates, continuous surveillance and monitorings should be conducted and investigated for the control of further epidemics.

Biography

Jin-Wook Jang is a student in Seoul National University, Seoul, Republic of Korea.

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