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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 their assortment of polymerase genes each other between H₉N₂ AIV 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

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