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Genotyping of avian influenza virus in Tunisia

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The avian influenza virus is the causative agent of several severe influenza pandemics. In Tunisia in 2009, H9N2 strain type A has affected the industrial poultry farms. The samples are collected between 2014, 2015 and 2016 from industrial poultry farms and migratory birds. 500 samples were analyzed, 16 samples were positive by the ELISA-Ag. The samples retained for virological analysis and identified as H9N2 by conventional RT-PCR and real-time (RRT-PCR). Based on the nucleotide sequences of hemagglutinin (HA) and neuraminidase (NA), the phylogenetic study showed that our isolates belong to the G1 sublineage. The cleavage site of their hemagglutinin showed two new motifs 332PSRSSR / GLF341, 332PSKSSR / GLF341, indicating the low pathogenic nature. The isolated strains during this work from migratory birds (Phoenicopterus roseus) and industrial breeding are similar to the Libyan strain about haemagglutinin and close to the Middle East for the neuraminidase. The substitution A333S and R336K, the two newly isolated avian influenza virus cleavage sites possess a pattern different from that observed in the other isolated Tunisian strains in 2010 and 2011, possessing the 332PARSSR/ GLF341 motif. A study in China showed that the A333S substitution increases the virulence of H9N2 strains in mice and chickens, which in turn are accentuated following the deletion induced in the neuraminidase stem. Examination of the hemagglutinin protein sequences shows that strains isolated have in common 3 sites of potential glycosylation which have not been described for strains isolated in previous years: 105NGT107, 298NST300 and 305NIS307. The amino acid sequence of hemagglutinin revealed the presence of Q234L substitution enabling the avian influenza strains to bind to α 2-6 receptors of human cells. The sequencing of the complete genome of the H9N2 influenza viruses is therefore will be done to better predict transmissions. The way in which the disease has been introduced in the country is still not understood and several studies are currently under way.

Biography

Imen Larbi earned her DVM from the Veterinary School of Tunis, and then MS. She completed a PhD degree in Virology from the Faculty of Sciences Tunis. Her research interest includes animal virology, poultry infectious pathogens and their control and epidemiological studies of avian influenza disease. She is involved in the national surveillance of avian influenza research programs at the Institute Pasteur of Tunis.

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