Molecular characterisation of low pathogenic avian influenza H9N2 virus from imported violet turaco

Shohaimi SA, Leow BL, Mohd Yusop FF, Sidik MR, Mohd Saeid FH

Veterinary Research Institute (VRI), 59, Jalan Sultan Azlan Shah, Ipoh, Perak, Malaysia

ABSTRACT

Introduction: Avian influenza (AI) H9N2 is an economical and public health threat. It has become a major problem in the poultry industry in many countries. Although H9N2 viruses are considered low pathogenic avian influenza (LPAI), they pose a significant threat to public health as they are considered viruses with pandemic potential. In 2021, H9N2 viruses were isolated from tracheal swabs of violet turaco (Musophaga violacea) that had been imported from Mali to Malaysia. Objective: In this study, we described the molecular characterization of H9N2 viruses based on hemagglutinin (HA) gene. Materials and methods: Reverse Transcription - Polymerase Chain Reaction (RT-PCR), DNA sequencing and phylogenetic analysis were used to characterize the H9N2 virus. Results and conclusion: The HA sequence of the isolate showed >97% nucleotide identity with those of H9N2 viruses isolated from chickens in African countries in 2017. The amino acids in the HA cleavage site showed a typical motif of the LPAI (PARSSR/GLF). Notably, the isolate had leucine (L) at position 226 at the receptor binding site, indicating that this isolate has the potential to infect mammals including humans. Phylogenetic studies showed that this H9N2 isolate belonged to lineage G1 and was very similar to viruses isolated from an outbreak in chickens in Senegal and Morocco. The isolate in this study was found to belong to the G1 lineage and this is the first time this lineage is reported in Malaysia. Previously, lineage Y-280 and Korean have been reported. In conclusion, the international trade of birds carrying AI viruses may pose a serious threat not only to the poultry industry but also to humans. Thus, the most important step in avoiding the spread of this disease is to screen imported birds for infections. Furthermore, effective quarantine system and diagnostic capabilities are critical in preventing the entry of foreign AI strains.