

Genetic characterization of hemagglutinin gene of highly pathogenic avian influenza in Malaysia

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ABSTRACT

Introduction: Highly pathogenic avian influenza (HPAI) is a highly contagious disease in poultry which can cause mortality up to 100%. Malaysia has undergone five waves of HPAI H5N1 outbreaks that occurred in 2004, 2006, 2007, 2017 and 2018, involving Peninsular and East Malaysia. The virus's hemagglutinin (HA) protein is responsible for virus attachment to host cell receptor; and mutation in the protein may increase the zoonotic risk of the virus. **Objective:** The objective is to genetically characterize the HA gene of the HPAI viruses in Malaysia. **Materials and Methods:** Five isolates representing Malaysia's five HPAI H5N1 waves were used. HA genes of three viruses were amplified and sequenced. Another two HA nucleotide sequences were obtained from the GenBank. The five nucleotide sequences were then molecularly characterized, aligned and compared with other published sequences. Phylogenetic analysis was constructed using Molecular Evolutionary Genetic Analysis tool. **Results:** Amino acid substitutions were found in all five viruses with the lowest number (6) in the first HPAI wave and the highest (10) in the last wave. These substitutions were associated with phenotypes including increased preferential binding of the virus to the mammalian α -2,6 receptor, decreased virus virulence in mice, as well as enhanced virus replication and transmission via aerosols in ferrets. Despite these, all viruses possessed conserved amino acids at the avian receptor binding sites: glutamine (Q) and glycine (G) at positions 222 and 224 respectively. The phylogenetic analysis revealed that the first HPAI wave belongs to clade 1, the second and third waves to clade 2.3.4.4, and the fourth and fifth waves to clade 2.3.2.1c. **Conclusion:** Though the risk of transmissibility to mammals was found in the HA gene, the zoonotic potential of HPAI viruses should be investigated by analysing the remaining seven gene segments of the virus. In line with this, animal studies should be conducted as well.