Molecular characterisation and phylogenetic analysis of H3N8 virus isolated from imported waterfowl at animal quarantine station

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ABSTRACT

Introduction: Wild aquatic birds are natural reservoirs of influenza A viruses and H3 subtype is one of the most prevalent subtypes in waterfowl. Fecal swabs samples from imported barnacle goose and paradise shelduck at the animal quarantine station were sent to VRI for routine screening for Avian Influenza virus (AIV). **Objective:** To identify and genetically characterize the eight genomic RNA segments of AIV. **Materials and methods:** Virus was cultivated by chicken embryonated eggs. The eight segments (HA, NA, M, NP, NS, PB2, PB1 and PA) were amplified, sequenced, molecular characterized and phylogenetically analyzed. **Results and conclusion:** The viruses were identified as AI subtype H3N8 virus. The viruses were highly similar to the H3 virus from Netherlands and N8 viruses from Belgium with 99% and 100% nucleotide identity respectively. The phylogenetic analysis revealed that all eight segments were grouped in the Eurasian lineage. The cleavage motif PEKQTR in the HA gene showed that the viruses were of low pathogenic AI strains. In the HA gene, though four amino acid substitution were seen, the viruses retained avian-type receptor binding preference. No deletion in the NA stalk region was observed and the viruses were predicted sensitive to the antiviral drugs. No E627K mutation was detected in the PB2 protein. D622G and N383D mutations associated with increased polymerase activity were identified in PB1 and PA gene respectively. In NP gene, M105V and A184K related with enhanced viral replication and increased AIV virulence in chicken were noticed. V149A corresponding to the decreased host antiviral response in the NS gene was recognized. N30D, I43M and T215A in M gene that were linked to increased virulence in mice were seen. As H3 poses potential threats to both human and animals, and with the increase in international trade of birds; strict quarantine practice at the entry point and good laboratory capabilities is crucial to prevent the introduction of new AIV into our country.