



Molecular identification of avian influenza virus A subtypes H5 and H7 in domestic geese and ducks in Basrah, South of Iraq

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Abstract

Waterfowl are the main reservoir for most influenza A virus subtypes, and they can effectively transmit these viruses to other birds and humans. This study aims to identify two influenza virus subtypes, H5 and H7, in domestic geese and ducks in Basrah governorate, Southern Iraq. 310 cloacal swabs were obtained from 150 domestic geese and 160 domestic ducks from different geographical areas. The viruses were first detected by RT-PCR using a pair of universal primers. All positive samples underwent RT-PCR using gene-specific primers to identify H5 and H7 influenza virus subtypes. The results showed that the prevalence of influenza viruses detected through universal primers was 37.7%. Of these, 24.6% and 50% were positive for viruses in domestic geese and ducks, respectively. Regarding virus subtyping in geese, the infection rates with H5 and H7 were 43.2% and 29.7%, respectively, with 27% as a combination of the two, while in domestic ducks, the infection rate with H5 was 27.5%, and with H7 it was 15%. Interestingly, ducks had a high concurrent infection rate for both H5 and H7 subtypes, accounting for 57.5%. The study concluded that the two virus subtypes, individually or simultaneously, were present in domestic waterfowl in regions of Basrah, and they were higher in ducks than in geese.

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Introduction

Avian influenza is a common and widespread disease of birds in many areas worldwide, often resulting in significant economic losses (1). The responsible agent of this disease is influenza virus type A, which belongs to the family of *Orthomyxoviridae* (2). These viruses circulate naturally among wild waterfowl worldwide and can infect poultry and other bird species (3). In addition, the avian influenza virus can be transmitted to domestic animals and humans, causing severe diseases and high mortality rates (4,5). Influenza viruses contain an RNA genome fragmented into eight pieces of different lengths, and each viral segment encodes one or more viral proteins (2). The virus particles have variable shapes ranging from filamentous to spherical depending on the virus's genetic characteristics and the host

type (6). The influenza A virus can be categorized into subtypes based on two types of virus surface glycoproteins: haemagglutinin (H) and neuraminidase (N). Currently, there are 18 and 11 distinct subtypes of haemagglutinin and neuraminidase, respectively, denoted as H1 through H18 and N1 through N11 (7). Regarding disease pathogenicity, avian influenza viruses are further divided into two main types: low-pathogenic and highly pathogenic AIV. Low-pathogenic viruses typically cause mild to moderate infections in domestic poultry, particularly chickens and turkeys, with moderate signs such as decreased egg production and ruffled feathers. In comparison, high-pathogenic viruses often lead to serious infections with a high mortality rate in chicken flocks. They often cause severe disease in poultry, affecting the internal organs with a fatality rate reaching 100% within 48 hours (8). Among the