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Original article

MOLECULAR SURVEILLANCE OF AVIAN INFLUENZA A VIRUSES IN BASRAH AND WASIT, IRAQ

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Summary

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The aim of this study was to detect influenza A virus in broiler chickens and wild ducks in different geographical regions of Basrah and Wasit provinces, Iraq. This study was authenticated by analysing the viral genome and designing a set of universal primers for the detection of all influenza A subtypes in a single enzymatic reaction through the amplification of a highly conserved region of viral M gene. A total of 157 and 155 oropharyngeal and cloacal swabs from broiler chickens and wild ducks, respectively, were analysed. The study shows that influenza A viruses were prevalent in these birds in all study regions with a significantly higher percentage in wild ducks compared to broiler chickens. The results showed that 92/157 samples (54/75 wild ducks and 38/82 broiler chickens) and 96/155 samples (38/75 wild ducks and 58/80 broiler chickens) in Basrah and Wasit, respectively, were positive for the viral M gene. In addition, there was no significant difference in virus prevalence between Basrah and Wasit provinces.

Key words: Basrah, chicken, duck, influenza A virus, RT-PCR, Wasit

INTRODUCTION

Influenza A viruses, which belong to the family *Orthomyxoviridae*, are enveloped with surface glycoprotein spikes and their genome consists of 8 segments of negative-sense single-stranded RNA (Samji, 2009). These viral segments are the polymerase basic 1 and 2 (PB1 and PB2), the polymerase acidic (PA), haemagglutinin (HA), nucleoprotein (NP), neuraminidase (NA), matrix (M), and non-structural (NS) genes (Bouvier & Palese, 2008). Each gene encodes at least one protein to build up the complete virus particle. Influenza A viruses are subdivided into subtypes based on the two types of envelope proteins, haemagglutinin (HA or H) and neuraminidase (NA or N) (Van der Auwera *et al.*, 2014). Currently, there are 18 different HA subtypes (H1 through H18) and 11 different NA subtypes (N1 through N11) (Tong *et al.*, 2013). Avian influenza viruses are further classified into two groups based on the severity of the disease: high pathogenic avian influenza A viruses (HPAI) and low pathogenic