



News & Comments

Molecular Survey on New Avian Metapneumovirus Subtypes in Wild Birds of Northern- Italy

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Avian metapneumovirus (aMPV), which was first discovered in South Africa in 1978, is a pathogen that mostly affects hens and turkeys. The primary cause of respiratory disease in poultry, which has a significant morbidity but low mortality, is aMPV infection alone. AMPV has high genetic variation, like many other RNA viruses, and various subtypes have been identified using antigenic and genetic traits. The first subtypes identified were A and B. In the 1980s, these subtypes spread to Europe from all over the world. In the US, aMPV subtype C was first discovered in wild birds and then in turkeys. Despite some variations in susceptibility, clinical symptom development, and shedding, all aMPV subtypes were shown to infect Galliformes in experimental settings.

The present work was motivated by the wide range of genetic and biological characteristics of aMPV as well as its wide host range. This study sought to analyze the viral presence and potential viral flux between domestic and wild populations by looking into the existence of the currently circulating aMPV subtypes (A, B, and C) as well as those that have recently been found in wild birds in Northern Italy. The Istituto Zooprofilatico Sperimentale delle Venezie (IZSVe) conducted passive and active avian influenza surveillance activities during which samples were obtained (Legnaro, Padua). To keep track of each sample's location, identification, plate number, and animal signal, a database was set up.

The current study analysed a huge variety of wild birds and benefited from Italy's annual avian influenza surveillance program. Most of the sampled species have not yet been documented in the literature as aMPV hosts, except for mallards, a greylag goose, a European starling, and a cattle egret. The convenience of the sample made it impossible to choose a target species for aMPV research. The bulk of the species are members of the Anatidae family, which might be thought of as potential hosts for an MPV. On the other hand, the recent identification of novel variants in parakeets and gulls demonstrates the significance of extensive monitoring of various species as aMPV reservoirs.

For the Italian poultry industry, which was recently proven to be extremely sensitive to the wild-domestic interface during the previous HPAI outbreak, the absence of A and B subtype findings is encouraging. Without the coordinated efforts, committed resources, and sanctioned project, it would not have been able to sample and examine thousands of wild animals. The direct detection of subtype C in a wild duck underscores the necessity of rigorous monitoring of both this agent and host, notwithstanding the minor role that wild birds play in hosting aMPV-A and B subtypes. The biological



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characteristics of aMPV, such as the short incubation and shedding times, reduce the possibility of detection, which raises the importance of the disease.

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KEYWORDS

Avian metapneumovirus, subtypes, wild birds, mallard, molecular epidemiology

