

ORAL ABSTRACTS

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DETECTION OF HIGHLY PATHOGENIC AVIAN INFLUENZA H5N1 IN MARINE MAMMALS FROM SOUTH AMERICA

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Background

Since its emergence in China in 1996, high pathogenicity avian influenza (HPAI), caused by H5N1, has evolved into a global panzootic. In addition to birds and poultry, H5N1 viruses have spread to wild and domestic mammals, as well as humans. Since 2021, unprecedented deaths in South American wild birds, poultry, and marine mammals have been reported.

Materials & Methods

Formalin-fixed, paraffin-embedded tissue (FFPE) samples (central nervous system (CNS), lung, pulmonary lymph node, heart, spleen, intestine, kidney, liver and placenta, upon availability in each animal) from 11 marine mammals found dead in coastal areas of South America in 2023 were collected for molecular diagnosis, histopathology, and immunohistochemistry (IHC).

Results

Histologically, lesions that could be attributable to HPAI were more frequently detected in the CNS and after correlation with IHC results, which typically consisted in neuronal and glial necrosis, gliosis, vasculitis, hemorrhages, spongiosis and lymphoplasmacytic and neutrophilic meningoencephalitis with perivascular cuffing. Avian Influenza Virus (AIV) -positive immunostaining was mostly detected in neurons, glial cells and ependymal cells. However, a positive correlation between RT-qPCR and IHC assessment were not found in all the animals, since in some cases, the infection by AIV was only confirmed by molecular methods.

Conclusion

The neurotropism of these H5N1 viruses in marine mammals was confirmed since the virus were systematically detected in the CNS of all evaluated animals by PCR. This was also supported by the presence of microscopic lesions and the presence of abundant AIV antigen by IHC in most of the analyzed specimens.