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Detection of American lineage low pathogenic avian influenza viruses in *Uria lomvia* in Greenland

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Abstract for oral presentation by Christina Hartby at 9th International Symposium on Avian Influenza. Athens, Georgia, US. April 12-15, 2015.

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Abstract

In early March 2014, unusual high numbers of wild bird Thick-billed Murre (*Uria lomvia*), order Charadriiformes, were found dead at the coast of South Greenland. To investigate the cause of death, 45 birds were submitted for diagnosis at the National Veterinary Institute, Technical University of Denmark. Five birds were randomly selected for diagnostic investigation and samples were taken from the cadavers (pooled oropharyngeal swabs, cloacal swabs, lung/trachea/heart tissues and liver/spleen/kidney tissues, and separate preparation of stomach from a single bird). Avian influenza virus (AIV) with subtype H11N2 was detected in all pools by RT-PCR. Virus was isolated from embryonated chicken-eggs by allantoic inoculation from all pools except the liver/spleen/kidney pool. Full-genome sequencing of AIV isolate revealed American lineage origin of genes.

The remaining 40 birds were subsequently screened for AIV in oropharyngeal and cloacal swab specimens from each bird by RT-PCR. American lineage H11N2 AIV was detected in both oropharyngeal and cloacal swabs from one bird, and American lineage low pathogenic AIV with subtype H5N1 was detected in the cloacal swab from another bird.

The sparse and mixed subtype occurrence of AIV together with an emaciated appearance of the birds, suggests that the Murre die-off may not have been caused by infection with AIV, but that the birds could have died from starvation. However, here we present the first characterization of AIVs from Greenland and our results supports the idea that wild birds in Greenland could be involved in the movement of AIV between North America and Europe.