

SURVEILLANCE OF AVIAN INFLUENZA VIRUSES IN WILD WATERBIRDS IN LATVIA, 2006-2011

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A total of 2500 waterbirds of three orders – *Charadriiformes*, *Anseriformes* and *Gruiformes* were sampled by cloacal and oropharyngeal swabs in Latvia during the period of 6 years (2006–2011). The sampling was carried out during the breeding period at the Lake Engure and Lake Kaņieris, as well as in small ponds, where artificial nest-sites for Mallard *Anas platyrhynchos* have been erected. Moreover, game birds (ducks *Anatidae* and coot *Fulica atra*) were sampled by surveying the hunter's bag at the opening of the hunting season in mid-August every year at the coastal Lakes Babīte, Engure and Liepāja, as well as at the inland Lake Lubāns and small ponds.

RNA was isolated from collected swabs and tested by using real-time reverse transcriptase polymerase chain reaction (RRT-PCR) targeting avian influenza A type matrix (M) gene and highly pathogenic AI subtypes H5, H7 and N1.

No highly pathogenic avian influenza viruses were identified, however 15% of sampled birds were avian influenza type A matrix gene positive.

Although low pathogenic avian influenza viruses are present in Latvian wild waterfowl, their occurrence is relatively low. Furthermore, the research have to focus on AI subtype identification of positive samples using direct sequencing of AI virus cleavage site H(0).