

SURVEILLANCE OF INFECTIOUS DISEASES

IN ANIMALS AND HUMANS IN SWEDEN 2022

*Chapter excerpt:
Influenza*



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Cover: A cultivation of *Salmonella* at the Public Health Agency of Sweden.
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Reporting guidelines: Reporting guidelines were introduced in 2018 for those chapters related to purely animal pathogens. The guidelines build on experiences from several EU projects, and have been validated by a team of international experts in animal health surveillance. The aim is to develop these guidelines further in collaboration within the global surveillance community and they have therefore been made available in the form of a wiki on the collaborative platform GitHub (<https://github.com/SVA-SE/AHSURED/wiki>). Feel free to contribute!

Layout: The production of this report continues to be accomplished using a primarily open-source toolset. The method allows the source text to be edited independently of the template for the layout which can be modified and reused for future reports. Specifically, the chapter texts, tables and captions are authored in Microsoft Word and then converted to the LaTeX typesetting language using a custom package written in the R software for statistical computing. The package uses the pandoc document conversion software with a filter written in the lua language. Most figures and maps are produced using R and the LaTeX library pgfplots. Development for 2022 has focused on generalising the R package to accommodate conversion into formats other than LaTeX and PDF, with a focus on markdown files which can be published as HTML websites using the Quarto publishing system. The report generation R package and process was designed by Thomas Rosendal, Wiktor Gustafsson and Stefan Widgren.

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Influenza

Influenza viruses are members of the *Orthomyxoviridae* family and are divided into four genera: *Alphainfluenzavirus* (species; influenza A virus [IAV]), *Betainfluenzavirus* (influenza B virus [IBV]), *Gammainfluenzavirus* (influenza C virus [ICV]), and *Deltainfluenzavirus* (influenza D virus [IDV]), which may have numerous animal species (domestic and wild) reservoirs.

Influenza type A is a viral disease affecting both birds and mammals, including humans. The causative agent is an RNA virus with a marked ability to change over time. New strains are created both through accumulation of point mutations (antigenic drift) and through genetic reassortment (antigenic shift). Influenza type A viruses are classified into different subtypes based on the surface glycoproteins:

haemagglutinin (H) and neuraminidase (N). Currently, there are 18 haemagglutinin (H1–H18) and eleven known neuraminidase (N1–N11) subtypes.

There is only one serotype for influenza type B viruses with two evolutionary lineages, the B/Victoria/2/87-like and B/Yamagata/16/88-like lineages. The single serotype of influenza type C virus has six evolutionary lineages.

In 2011, a novel influenza virus was detected in pigs exhibiting influenza-like symptoms. The virus initially identified as a subtype of type C but soon was recognised as a new genus: Influenza type D virus. Although the virus was identified among pigs with respiratory illness, serological evidence indicates presence of influenza D virus in cattle populations around the globe.

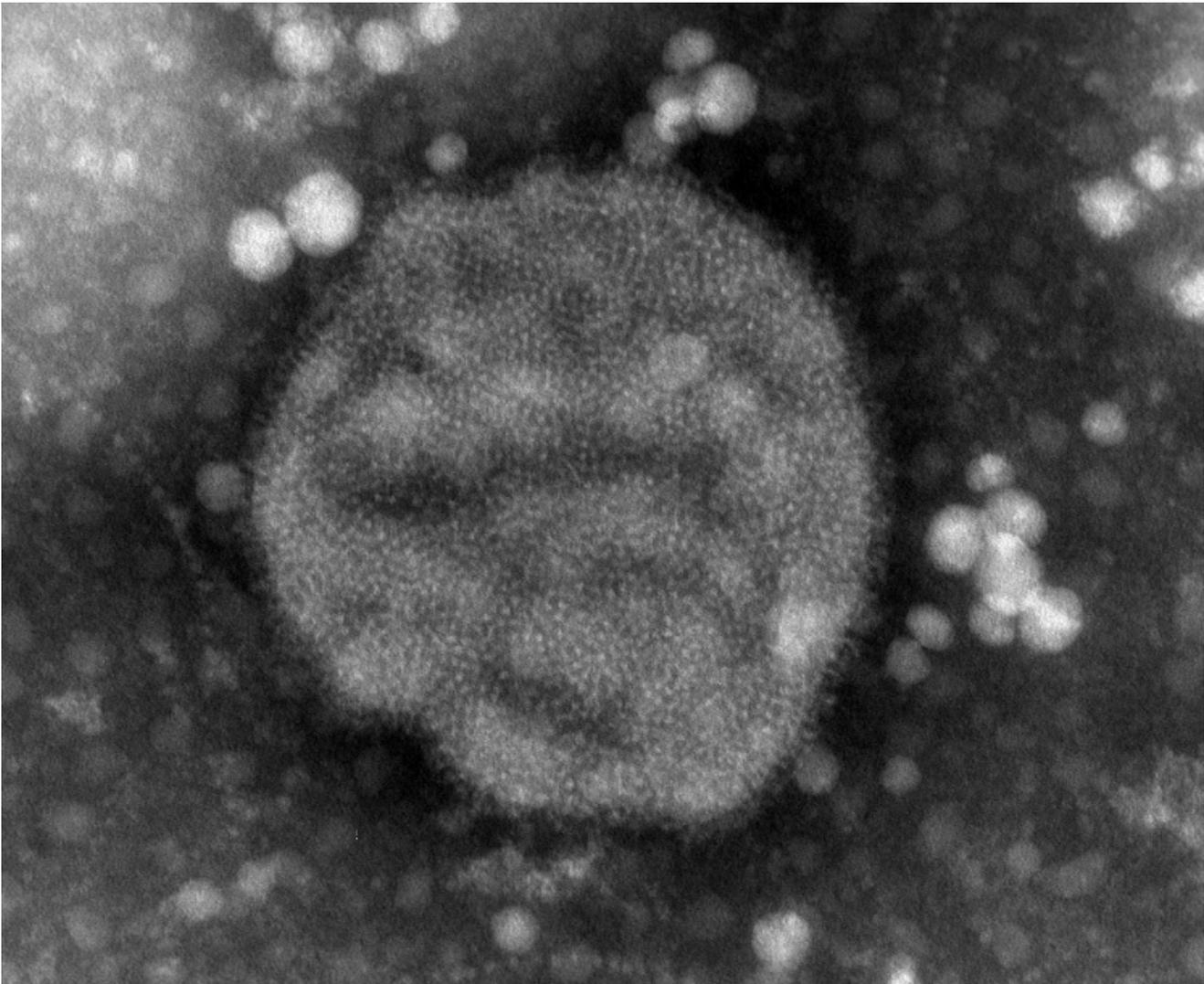


Figure 21: Electron microscopy of low pathogenic H5N2 influenza A virus. Photo: SVA & Public Health Agency of Sweden.