



Avian Influenza

Outbreak experience combined with
multidisciplinary research

Safeguarding human and animal health through veterinary and biomedical research



CENTRAL VETERINARY INSTITUTE
WAGENINGEN **UR**

Your research partner in molecular epidemiology, experimental infections, vaccine development and diagnostics

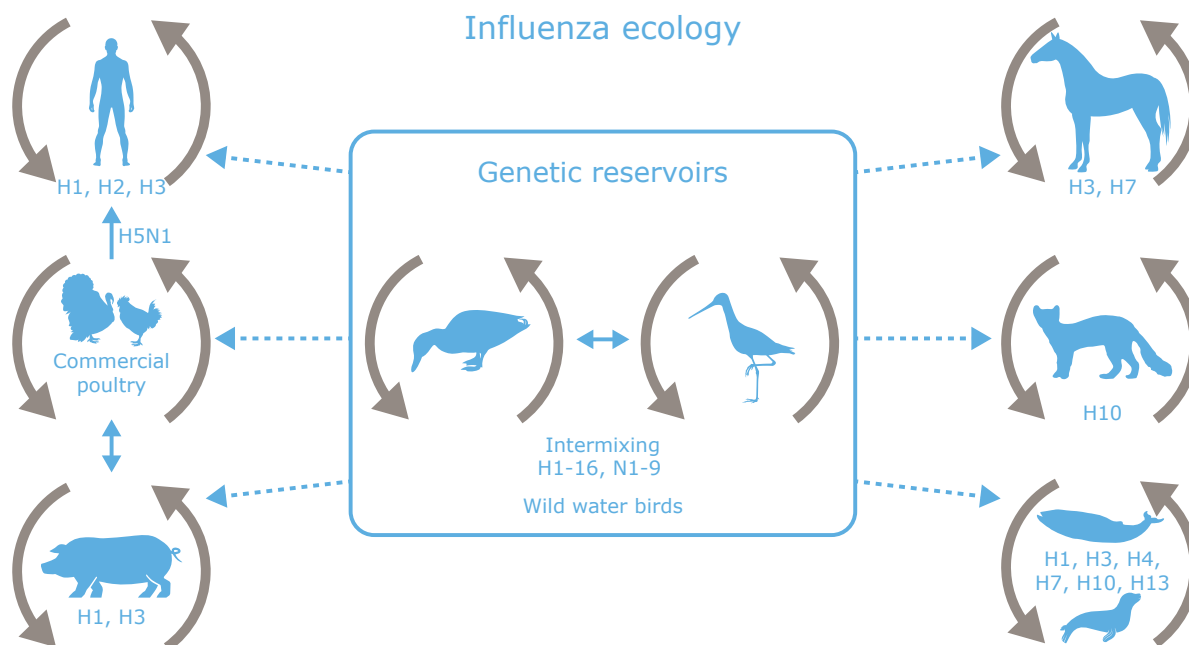
The recent outbreaks of highly pathogenic H5N8 Avian influenza (HPAI) in the Netherlands have demonstrated the need for highly qualified research and diagnostic facilities. CVI has these facilities and during the outbreak it played a key role by performing rapid diagnostics and answering urgent research questions. Not only in the Netherlands but also worldwide AI outbreaks in poultry cause huge economic losses and pose a major threat to public health. Migratory water birds form a natural reservoir of many different AI virus subtypes and pose a risk for the introduction of these viruses into poultry. AI virus infections in reservoir hosts are usually asymptomatic and when introduced in poultry normally cause no or only mild disease, indicated as low pathogenicity avian influenza (LPAI)

AI subtypes are characterised by two envelope proteins, i.e., haemagglutinin (H) and neuraminidase (N). LPAI viruses of the H5 and H7 subtypes, can evolve to high pathogenicity (HPAI) viruses. These viruses can spread rapidly within and between poultry farms and are therefore notifiable. AI is a zoonotic virus meaning that it can cause disease in both animals and humans. Although for veterinary control purposes detection of only H5 and H7 subtypes is required, from a public health point of view it is important to invest in research and diagnostics for all subtypes.

Outbreak experience combined with multidisciplinary research and the AI virus collection makes CVI your research partner for:

- Experimental infections
- Transmission models
- Diagnostic development
- Next generation sequencing
- Bio-informatics
- Molecular and veterinary epidemiology
- Field studies
- Vaccine development

CVI has considerable expertise in diagnostic performance and validation of new tests. Upon the detection of an AI, the virus is isolated and characterised at the molecular level by next-generation sequencing. This sequence information, combined with our bioinformatic pipeline and our extensive knowledge on the epidemiology of influenza infections gives insight into possible transmission routes and zoonotic potential and risks. In addition CVI has experience with the development of veterinary vaccines against AI viruses that optimally combine efficacy with safety. Experimental transmission models and laboratory tests with HPAI viruses are performed in BSL-3 and vBSL-4 containment facilities.



This picture represents an overview of the influenza ecology. Aquatic birds are the reservoirs.

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