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## Ecology in wild birds

Wild birds are the natural host and reservoir for all type A influenza viruses, especially waterfowl, gulls and shore birds. In these natural hosts the viruses are always evolving. In this process the surface glycoproteins HA and NA have greater genetic diversity in their controlling genes.

For the HA and NA proteins 16 and nine subtypes have been identified. By comparing nucleotide sequences of most of the gene segments of wild bird avian influenza viruses, including within an H and N subtype, a clear separation between Eurasian and American viruses can be seen.

However, this is not seen for the most conserved internal proteins.

For the H7 subtype, further divisions into North American and South American lineages and European, Asian and Australian lineages occur. This fact suggests that transfer of avian influenza virus genes rarely occurs between the American and Eurasian viruses.

However, the recent occurrence in 2014 of European H5N8 HPAI in North America shows that they do occasionally move between these two areas.

As more genetic sequencing is done, more exceptions will appear, for example the H2 subtype follows this geographical divide for poultry and duck isolates, whereas many wild bird isolates from the USA are of the Eurasian lineage.

The complete host range for influenza viruses is not known, but it would appear that Anseriformes (ducks, swans and geese) and Charadriiformes (shore birds such as gulls, plovers and auks) are the most commonly infected.

Their incidence of infection is seasonal, with young birds in autumn showing the highest isolation rates.

Wild bird avian influenza viruses appear to pass easily between different species. Most H13 and H16 isolations are from gulls and there appears to be a possible gull lineage based on some of the internal genes.