



9 April 2024

OFFLU statement on high pathogenicity avian influenza in dairy cows

Since its inception in 2005, [OFFLU](#) (WOAH-FAO network of expertise on animal influenza) has been closely monitoring the global impacts of high pathogenicity avian influenza (HPAI), including working with multiple countries affected by the current H5N1 HPAI panzootic. Field veterinarians and OFFLU scientists in influenza Reference Centres play a key role in responding to novel outbreaks and characterising avian influenza viruses, including those that spillover to livestock or new and aberrant hosts.

There has been much attention around recent reports of confirmed detection of H5N1 clade 2.3.4.4b in dairy cows in the USA (the first such spillover to bovine species). This virus is a Gs/Gd lineage, clade 2.3.4.4b, 4 gene reassortant with the PB2, PB1, NP and NS segments of North American wild bird-origin. This B3.13 genotype has previously been detected initially in wild and later in domestic birds affected by HPAI but to current knowledge has not been detected outside the USA. The situation is rapidly unfolding; genetic sequences of these viruses from dairy cattle have been shared and further information on these events is being shared and updated daily by the [USDA](#), [FDA](#) and [CDC](#). Answers to [frequently asked questions](#) are also available on their websites.

OFFLU, the WOAHA and FAO are closely monitoring the situation as it unfolds and will share further information through the OFFLU website as it becomes available, especially risk assessments, surveillance and diagnostics advice, guidance for veterinary health professionals. Potential socioeconomic impacts and health and wellbeing of farm workers and veterinarians may be additional considerations as outbreak investigations continue.

OFFLU strives to share information with stakeholders and partners and has created a page specific for the [HPAI detections in livestock](#), where new information will be updated regularly.

OFFLU urges the scientific community to continue to:

1. Monitor HPAI events in animals and report to [WOAH](#).
2. Timely deposit and share genetic sequence data in publicly available databases.
3. Coordinate studies to better understand pathogenesis, transmission and adaptation of virus lineages and share the results with OFFLU.
4. Provide support to national risk managers.

OFFLU (www.offlu.org) will continue to support the activities of its parent organisations (FAO and WOAHA) and partners (WHO) in ensuring that scientifically sound information is available on strains of virus that are detected in poultry and in aberrant hosts.