APHIS Identifies Third HPAI Spillover in Dairy Cattle

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On February 13, 2025, the USDA Animal and Plant Health Inspection Service (APHIS) National Veterinary Services Laboratories (NVSL) confirmed by whole genome sequence a detection of highly pathogenic avian influenza (HPAI) H5N1 clade 2.3.4.4b, genotype D1.1 in dairy cattle in Arizona. This confirmation was a result of State tracing and investigation, following an initial detection on silo testing under the USDA's National Milk Testing Strategy (NMTS).

USDA APHIS continues to work with the Arizona Department of Agriculture by conducting additional on-farm investigation, testing, and gathering additional epidemiological information to better understand this detection and limit further disease spread.

The detection of this virus genotype in dairy cattle is not unexpected, because genotype D1.1 represents the predominant genotype in the North American flyways this past fall and winter and has been identified in wild birds, mammals, and spillovers into domestic poultry. Whole genome sequencing indicates that this detection is a separate wild-bird introduction of HPAI to dairy cattle, now the third identified spillover event into dairy cattle. This finding may indicate an increased risk of HPAI introduction into dairies through wild bird exposure. Biosecurity is still key to mitigate the risk of disease introduction or spread between premises; APHIS recommends enhanced biosecurity measures for all dairy farms. Producers should immediately report any livestock with clinical signs, or any unusual sick or dead

wildlife, to their state veterinarian.

The detection does not change USDA’s HPAI eradication strategy and is a testament to the strength of our National Milk Testing Strategy (NTMS). In the interest of sharing information of import to the scientific community, APHIS will publish a technical brief on the findings on our website and post the sequence data on GenBank in the coming week.