

Chances and limitations of environmental sample matrices in avian influenza virus surveillance

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The octo-segmented, single-stranded RNA influenza A viruses can be differentiated into 18 HA and 11 NA subtypes. The majority of them can be found in water birds which constitute the natural reservoir of avian influenza viruses (AIV). Based on the type of host protease processing of the viral hemagglutinin glycoprotein, phenotypes of high (HP) and low (LP) pathogenicity can be distinguished among AIV of subtypes H5 and H7. HPAIVs induce excessive mortality in avian hosts and may comprise zoonotic propensity as well. Improved HPAIV surveillance is implicit in early warning strategies to prevent incursions into poultry production and exposure of human hosts. Here, results from field investigations for AIV in different environmental matrices are reported.

Surface water samples of 10 L water were ultrafiltered but enrichment of AIV from spiked samples was limited to a median factor of 15 only. Although AIV genome was detected by RT-qPCR in 60% of surface water but with low viral loads. Similar results were found for sediment samples from the same water bodies. Even less successful were attempts to detect AIV RNA in environmentally deposited avian feces (median 4% positives). In comparison, about 80% of the avian carcasses retrieved in the same region tested positive for HPAIV in the same period.

The use of environmental samples for AIV surveillance cannot be recommended although the matrices, especially sediments, bear potential to inform about deposited influenza virus RNA.

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