



HPAI outbreaks of subtype H5N8

**DG SANTE/G3
16/01/2020**

HPAI H5N8 outbreaks in PL,SK,HU,RO

First 3 outbreaks reported in Poland in 31/12/2019

From 31/12/2019 until 16/01/2020 (**≈2 weeks**) – **16 outbreaks**

Poland -11 = 2 backyards + 9 farms (turkeys, geese, Guinea fowl, laying hens)

Slovakia -1 (backyard)

Hungary – 3 (turkeys, ducks)

Romania – 1 (laying hens)

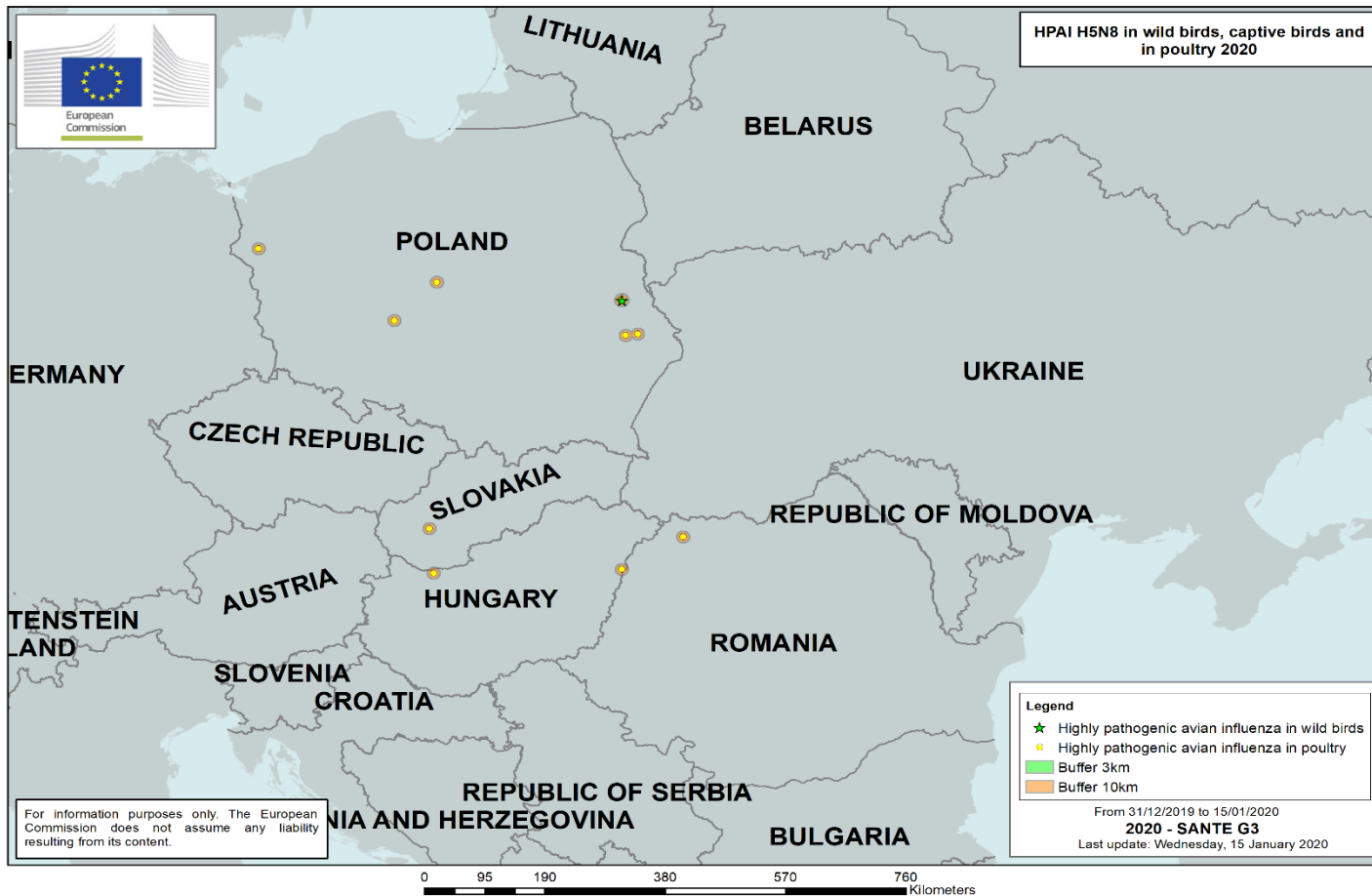
Multiple avian species affected (mainly turkeys, 8 outbreaks)

ONLY ONE CONFIRMATION IN WILD BIRDS (one hawk, in Poland)



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Geographical distribution



Information from EURL (AI)

Phylogenetic analyses of the HPAI H5N8 virus:

- The virus obtained from PL is different from the previous viruses circulate in Europe (similarity with viruses recently circulated in Africa):
 - similarity at HA, NE gene segment with a virus collected in Nigeria in 2019 and with the South African virus A/quail/South Africa/AI5930/2018 (H5N8)
- The virus obtained from HU:
 - high similarity with the HPAI H5N8 virus collected in Poland at the end of 2019 and similarity at HA, NE gene segment with H5N8 virus identified in Nigeria (2019)
- The virus obtained from SK:
 - The partial HA sequence has an identity of 100% with the viruses from Hungary (2020), Poland (2019) and Nigeria (2019)

Phylogenetic analysis by EURL (AI)

- The internal genes of the PL virus is different from the ones identified in the African strains and is the result of a re-assortment event with LPAI viruses identified in wild birds in those areas of Russia (near Kazakhstan)
- PB1 and NP gene segments of the PL virus cluster with viruses collected from wild birds in Russia in 2018, in particular with the H3N8 viruses collected from green sandpipers (Kurgan – Russia 2018) and with the H3N8 and H12N5 viruses collected from a teal and a gadwall (Russia 2017-2018)
- Results suggest this could be a reassortant virus which may have emerged in Russia before reaching the countries which have been affected by this epidemic



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Decision 2018/1136

on risk mitigation and reinforced biosecurity measures and early detection systems

- identify the 'high risk areas' (areas at particular risk for the introduction of HPAI viruses into holdings)
- inform the stakeholders, including small size holdings, about:
the delineation of the 'high risk areas'
risk mitigation and reinforced biosecurity measures
- raise awareness of groups involved in wildlife activities including ornithologists, bird watchers and hunters
- maintain the reinforced biosecurity measures in the 'high risk areas' for the time period during which the heightened risk for HPAI virus introduction and spread persists on the territory
- introduce or reinforce existing early detection systems aimed at rapid reporting by the owners to the competent authority
- **increase surveillance of wild bird populations** and further monitoring for dead or sick birds
- additional temporary measures in the event of confirmation of cases of HPAI in wild birds



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