

**SURVEILLANCE OF SWINE INFLUENZA VIRUSES (SIV) IN EUROPE 2015-2017 -AN UPDATED.**

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Influenza A virus infections causing economic losses are widely spread among swine populations worldwide. In Europe, over the past decades, four lineages of reassortant viruses between avian and human viruses have formed (H1N1av, H1N2hu, H3N2, H1N1pdm/2009). The emergence of the most recent human pandemic influenza virus (H1N1pdm/2009) from reassortant porcine influenza viruses underlines the importance of swine populations as carriers of influenza lineages with zoonotic and even pandemic potential. However, surprisingly few countries actually embarked on sustained, governmentally driven and publicly controlled monitoring programs. After closure of the EU-financed ESNIP3 program, a passive surveillance program for SIV in selected European countries has been initiated on basis of funding by a veterinary vaccine producer.

The surveillance started in April 2015 and comprised so far up to 18.000 samples. Nasal swab samples or other respiratory tract materials were collected from pigs with apparent respiratory disease. Samples were screened by real time RT-PCR (RT-qPCR) for presence of influenza A viruses (Henritzi et al., 2016). Positive samples were subjected to molecular subtyping, virus isolation, antigenic and phylogenetic characterization.

First results in 2016 confirmed a high incidence of influenza virus infections affecting about one quarter of the examined pigs in a season-independent manner. All four virus lineages and various reassortants between them were detected.

In 2017, increased findings of pandemic H1N1/2009 and co-infections with different H1 subtypes were documented. Prevalences of the different lineages were geographically restricted and incursions of new lineages and/or reassortants were documented for several European countries. In addition, the occurrence of a new spill-over of a recent human seasonal H3-subtype into the swine population was noticed. Furthermore a vast repertoire of at least 32 genotypes, resulting

from reassortment between pandemic H1N1 and previous porcine lineages, was uncovered.