

Diagnostic Methods

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Monitoring and characterization of swine influenza virus (swIAV) in Europe since 2015: Newly developed hemagglutinin- and neuraminidase-specific multiplex RT-qPCR

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Introduction: Influenza A virus infections causing economic losses are widely spread among swine populations worldwide. Swine can be infected by avian as well as human influenza viruses and hence, can act as so-called mixing-vessels. In Europe, over the last decade, three stable lineages of reassortant viruses between avian and human viruses have formed. The human pandemic H1N1/2009 virus as a fourth player in this field is currently disturbing the balance of previously established European porcine influenza virus lineages. The emergence of the most recent human pandemic influenza virus (H1N1/2009) from reassortant porcine influenza viruses underlines the importance of swine populations as carriers of influenza lineages with zoonotic and even pandemic potential. In view of the OneHealth concept a more intense surveillance of these populations therefore is mandatory. Meaningful surveillance calls for subtype-specific, sensitive and rapid diagnostic tools.

In line of these demands hemagglutinin- (HA) and neuraminidase (NA) -specific multiplex RT-qPCRs have been developed that are suitable to detect and characterize Eurasian swIAV directly in clinical samples.

Methods: Primers and Taqman probes were selected from alignments of full length HA and NA sequences of Eurasian origin swIAV. Analytical and diagnostic validation was carried out on a representative set of IAV (subtypes H1, H3, N1, N2) of avian, porcine and human origin. Established lineage-specific RT-qPCRs were used to screen porcine nasal swab samples obtained from herds with respiratory disease. Rt-qPCR subtyping results were compared to conservative Sanger-sequencing data.

Results: A diagnostic algorithm for detection and subtyping of swIAV in clinical samples was established that was entirely based on RT-qPCRs.

Conclusion: The newly developed multiplex RT-qPCRs based algorithm proved extremely useful for monitoring swIAV in swine herds in several European countries.

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