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Investigation of molecular determinants of host tropism of the avian-like swine influenza A (H1N1) lineageU. Wessels¹, O. Stech¹, K. van der Meulen², K. van Reeth², T. C. Mettenleiter¹, J. Stech¹¹Friedrich-Loeffler-Institut, Greifswald- Insel Riems, Germany²University, Ghent, Belgium

In 1979, an unknown avian influenza H1N1 virus crossed the species barrier to swine without reassortment and spread throughout Europe leading to a novel stable swine virus lineage. Remarkably in phylogenetic trees, the hemagglutinin and nucleoprotein sequences of those avian-like swine H1N1 viruses cluster with bird strains and not with the classical swine virus lineage. From that epizootic, the first available isolate is the strain A/Swine/Belgium/1/79 (H1N1) (SwBelg79). The avian virus most closely related is the isolate A/Duck/Bavaria/1/77 (H1N1) (DkBav77) which had been shown to be able to infect pigs. In this study, we aim to reveal the host determinants of avian-like swine H1N1 viruses after the species transmission from avian to swine host by construction of several reassortants in order to test their virulence and replication efficiency in swine respiratory tissue explants and pigs. To obtain those reassortants, we cloned all eight gene segments of both parent viruses and demonstrated the viability of plasmid clones in virus rescue experiments. Overall, this lineage of avian-like swine viruses can be utilized as a model of early evolution in a relevant mammalian host for influenza A viruses.

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