

Abstract

Atypical Porcine Pestivirus Molecular Evolution within a Persistently Infected Swine Farm [†]

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Atypical porcine pestivirus (APPV) is a single stranded RNA virus from the family Flaviviridae. It has been identified as the possible causative agent of congenital tremor (CT) type A-II in newborn piglets. To date, APPV has been reported in several countries in North and South America, Europe, and Asia, showing a worldwide distribution. Although clinical signs are only present in piglets born from gilts and occasionally in piglets born from high parity sows, adult pigs can also be carriers and persistently shed the virus.

In this study, we retrospectively investigated the molecular evolution of APPV in one endemically infected farm between the first outbreak in 2013 and 2019. Monitoring was done consistently over time in a controlled environment with no viral introduction from the outside. During the monitoring period, clinical outbreaks were observed in 2013, 2015, and 2016. Samples from clinically trembling piglets at the time of these outbreaks, as well as from persistent carriers detected during regular monitoring, were used for viral sequence analysis.

This field case study provides new insights into the genetic evolution of this novel pathogen circulating within a farm. With this study, we aimed to provide new information regarding nucleotide and amino acid variability of APPV over time, phylogenetic analysis on complete genome sequences and partial regions, and to evaluate their potential role into the escape from the host-immune system. These findings are essential for future vaccine design strategies against APPV as well as for understanding the genetic variation patterns of other (novel) pestiviruses.

Keywords: pestivirus; APPV; atypical porcine pestivirus; persistent infection; purifying selection



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