Multiple influenza A viruses circulate in growing pigs during epidemic events.

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Key points

- The diversity of influenza A viruses in growing pigs is dynamic
- Influenza A viruses can replicate as a swarm of viruses that are identical, closely related to each other (>99%), or clearly distinct (H1 vs. H3 subtypes)
- Influenza A viruses of the same genotype can re-infect pigs within a short period of time.

Background

Influenza A viruses (IAVs) are commonly found in pigs and are a main cause of respiratory disease. H1N1, H1N2 and H3N2 are the most common subtypes in pigs. However, there are multiple distinct strains of viruses within each subtype. IAV replicates as a swarm of viruses that are identical or contain small genetic differences between them. Furthermore, the genetic and antigenic diversity of swine IAVs is dynamic and may be associated with the virus persistence over time in pig farms. However, the mechanisms that allow the viral population to persist in pigs are not clearly understood. Hence, the objective of this study was to characterize genetic diversity of the complete IAV genome in a cohort of growing pigs.

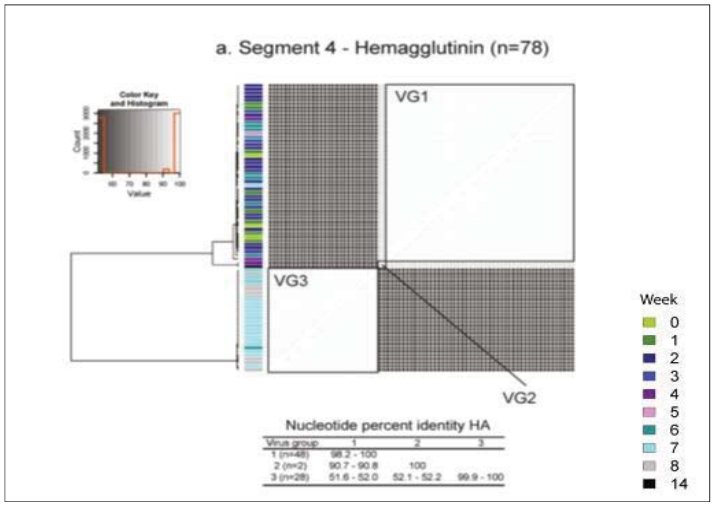
Materials and Methods

132 3-week old piglets selected at weaning and placed in a wean- to-finish farm were sampled weekly for 15 weeks (n=2080 samples). Samples were tested by RT-PCR and the complete genome of influenza was obtained from 93 samples using next generation sequencing. The number of new cases (incident cases) and positive cases (prevalent cases) were calculated per week and compared between weeks as well as the complete gene sequences in order to establish the overall genetic diversity of influenza in the population.

Results and conclusions

Two epidemic waves of IAV infection were detected (Fig 1) with 3 distinct viral groups (VG swarms) found (VG1, VG2 and VG3). An H1 gamma (VG1) dominated the first outbreak, an H3 (VG3) dominated the second outbreak and an H1 beta (VG 2) was only recovered when none of the two other viruses dominated. At the hemagglutinin level VG1 viruses were 98.2% identical or higher, VG2 were 100% identical, and VG3 were 99.9% identical or higher (Fig 2). Most IAV recurrent infections (testing positive twice in non-consecutive weeks) occurred with IAVs from different viral groups (n=19). However, in 5 cases pigs were infected with IAVs of the same viral group.

Our results demonstrate the complex dynamic of the influenza genome in growing pigs under field conditions and demonstrate that pigs can become re-infected, during a short period of time, with IAV that are closely related to each other (99% identical or higher) or clearly distinct (H1 vs. H3 viruses). The complete version of this study can be found online at https://www.nature.com/articles/s41598-017-11272-3



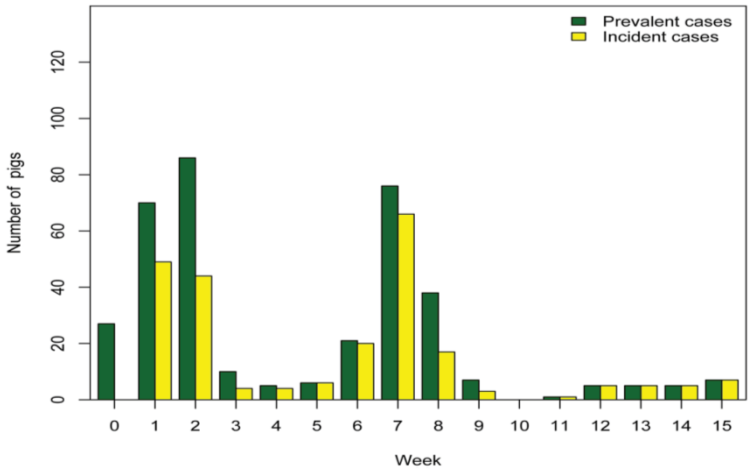


Figure 1. (Top) Number of IAV positive cases (green) and new cases (yellow) per-week

Figure 2. (Bottom) Pairwise sequence identity between IAV found over time. VG1, VG2, and VG3 are indicated. Number of IAV positive cases (green) and new cases (yellow) per-week. Side bar indicates the week at which each IAV was found.