

Background

There are six different coronaviruses infecting pigs with four from the genus *Alphacoronavirus* (transmissible gastroenteritis coronavirus (TGEV), porcine respiratory coronavirus (PRCV), porcine epidemic diarrhea virus (PEDV) and swine acute diarrhea syndrome coronavirus (SADS-CoV); one from the genus *Betacoronavirus* (porcine hemagglutinating encephalomyelitis virus (PHEV) and one from the genus *Deltacoronavirus* Porcine Deltacoronavirus (PDCoV)¹. TGEV, PEDV, PDCoV are enteropathogenic coronaviruses and cause acute gastroenteritis in all age group of pigs. PHEV induces vomiting and/or encephalomyelitis¹. PRCV affects tonsils, the upper respiratory tract or lungs. Unlike other swine coronaviruses, PRCV does not cause substantial problems. PEDV, PDCoV and SADS-CoV are considered newly emerging coronaviruses. Pigs are known to be intermediate/amplifying hosts for zoonotic viruses with pandemic potential. These zoonotic viruses include influenza, Japanese encephalitis, Nipah and coronaviruses². In 2009, pigs facilitated the emergence of a novel reassortment influenza A strain virus which later triggered a pandemic. Pigs are described as “mixing vessels” since they are susceptible to avian, swine and human influenza which facilitates genetic recombination and mutation events². Active surveillance for swine coronavirus monitors the mutation of swine coronaviruses and informs of any possible spill over events between pigs and humans.

Objectives

1. Report the prevalence rate of swine coronavirus among livestock pigs between 2018 to 2023
2. Understand the diversity of swine coronavirus among positive samples
3. Report the prevalence rate of newly emerging swine coronavirus

Methods

Our team visits the largest slaughterhouse in Hong Kong every month to sample livestock pigs imported from Mainland China (figure 1). We sample livestock pigs from Fujian, Guangdong, Hubei, Jiangxi, Guangxi, Guizhou, Hunan, Henan and Hong Kong. Our team collects 80 blood samples and nasopharyngeal swabs at midnight right before livestock pigs are slaughtered and sold in markets the next day (figure 3). Nasopharyngeal swab specimens are extracted to RNA using QiAMP Viral Kit. These samples are tested for coronavirus RNA-dependent RNA polymerase (RdRp) using PCR methods. Gel electrophoresis showing a band size of 440bp undergoes Sanger sequencing to indicate the type of swine coronaviruses detected.



Figure 1 Our team visits the Sheung Shui Slaughterhouse at midnight



Figure 2 Our team members are dressed in personal protective equipment and helmets for safety



Figure 3 Viral transport medium in screw cap vials and clotted blood tubes are prepared for sampling

Results

To date, 3234 samples were screened for swine coronaviruses and 28% of the samples were positive for swine coronaviruses. The swine coronaviruses positive rate for each year follows 30% (2018), 30% (2019), 26% (2021 December and 2022), and 18% (2023). We detected swine coronaviruses in Fujian, Guangdong, Hubei, Jiangxi, Guangxi, Guizhou, Hunan, Henan and Hong Kong. We also noticed co-infections in pigs with H1N1 and swine coronavirus. Our results reflect transmission potential such that 70% of the samples collected in February 2022 tested positive for swine coronavirus while over half were PDCoV (figure 5). We occasionally observed a high prevalence of PEDV, PDCoV and PRCV in the studied period especially during winter and spring (figure 5). Major wide circulations of these viruses were likely occurring in different provinces in the specified periods. Furthermore, most of these positive pigs were infected during transportation.

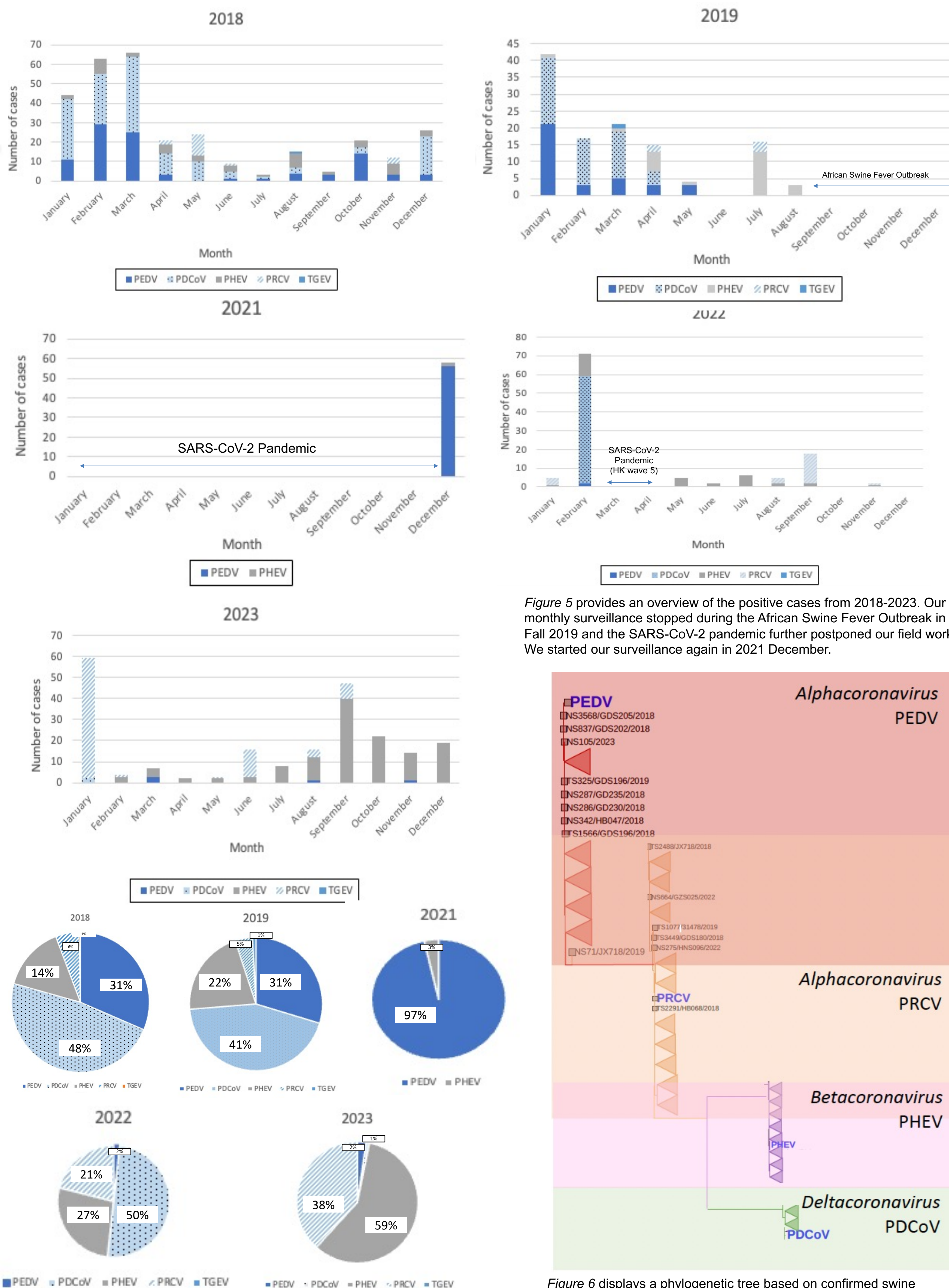


Figure 5 provides an overview of the positive cases from 2018-2023. Our monthly surveillance stopped during the African Swine Fever Outbreak in Fall 2019 and the SARS-CoV-2 pandemic further postponed our field work. We started our surveillance again in 2021 December.

Figure 6 displays a phylogenetic tree based on confirmed swine coronavirus samples. Samples were collapsed (triangle shape) if the average branch tree length was less than 0.005.

Another potential factor in facilitating virus transmission is the crowded environment and poor hygiene in the slaughterhouse. All coronaviruses detected in our samples are previously known. We did not detect SARS-CoV-2 in our samples, suggesting that pigs are not susceptible to SARS-CoV-2. We also did not detect swine acute diarrhea syndrome coronavirus (SADS-CoV) in our study. We also noticed co-infections in pigs with influenza A and swine coronaviruses.

Conclusion

Swine coronavirus transmission in pigs is rapid and detrimental to agriculture. Recent global detection of highly pathogenic variants of PDCoV and PEDV and the emergence of novel swine coronaviruses emphasize the importance of One Health. Active surveillance and next-generation sequencing methods identifies mutation events in swine coronaviruses and transmission patterns among pigs.

References

- 1 Porcine Coronaviruses: Overview of the State of the Art - PMC [Internet]. [cited 2023 May 4]. Available from: <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC795>
- 2 McLean RK, Graham SP. The pig as an amplifying host for new and emerging zoonotic viruses. *One Health*. 2022 Jun 1;14:100384.

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