



## Epidemiology, Evolution, and Prevention of Animal Coronaviruses

Guest Editor:

### Dr. Jingfei Wang

Harbin Veterinary Research  
Institute, Chinese Academy of  
Agricultural Sciences, Harbin,  
China

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### Message from the Guest Editor

In the past two decades, the emergence of several coronaviruses, including severe acute respiratory syndrome coronavirus (SARS-CoV) in 2002, Middle East respiratory syndrome coronavirus (MERS-CoV) in 2012, swine acute diarrhea syndrome coronavirus (SADS-CoV) in 2017, and SARS-CoV-2 in 2019, has had a devastating impact on public and veterinary health and socioeconomic stability worldwide. Many different species of animals, especially wildlife and bats, have been identified as natural hosts of diverse coronaviruses, which are the potential agents causing novel infections in both humans and domestic animals. Furthermore, coronaviruses that infect livestock and poultry, such as porcine epidemic diarrhea virus (PEDV), transmissible gastroenteritis virus (TEGV), and infectious bronchitis virus (IBV), have been circulating in many regions around the world and causing huge economic losses to the animal industries. Therefore, investigations on the identification, epidemiology, genetic evolution, and pathogenesis of animal coronaviruses are essential to prevent and control animal coronavirus diseases and eliminate the potential disease risks in humans.





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## Editor-in-Chief

### Prof. Dr. Lawrence S. Young

Warwick Medical School,  
University of Warwick, Coventry  
CV4 7AL, UK

## Message from the Editor-in-Chief

The worldwide impact of infectious disease is incalculable. The consequences for human health in terms of morbidity and mortality are obvious and vast but, when infections of animals and plants are also taken into account, it is hard to imagine any other disease that has such a significant impact on our lives—on healthcare systems, on agriculture and on world economics. *Pathogens* is proud to continue to serve the international community by publishing high quality studies that further our understanding of infection and have meaningful consequences for disease intervention.

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Pathogens Editorial Office  
MDPI, Grosspeteranlage 5  
4052 Basel, Switzerland

Tel: +41 61 683 77 34  
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