



Epidemiology, Evolution, and Prevention of Animal Coronaviruses

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Deadline for manuscript
submissions:

closed (1 September 2023)

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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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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Journal Rank: JCR - Q2 (*Microbiology*) / CiteScore - Q2 (*General Immunology and Microbiology*)

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