



Pathogenic *Neisseria*: Genomic Epidemiology, Mechanisms of Antimicrobial Resistance and Infection

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Message from the Guest Editor

The genus *Neisseria* includes several species that are mostly human commensals that colonize the mucosa. However, mostly two of them, *Neisseria meningitidis* and *Neisseria gonorrhoeae*, can cause serious disease in humans. It is included in the World Health Organization priority list of pathogens in need of research and development of new antimicrobials because it has developed or acquired antimicrobial resistance (AMR) to every antibiotic used to treat the disease. Treatment options are scarce and there is not a suitable vaccine, thus posing a current threat to public health worldwide. Genomic approaches are essential to monitor the spread of these pathogens, study outbreaks, transmission chains, detect novel mechanisms of AMR and pathogenicity as well as identify new potential therapeutic targets. The main focus of this Special Issue of Pathogens will be on genetics and genomics of pathogenic *Neisseria* for epidemiological purposes, the investigation of novel mechanisms of AMR and infection. The scope will mainly be on pathogenic *Neisseria*, but we will also welcome relevant work on other commensal *Neisseria* species.





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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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