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# Ecology of Influenza A Viruses

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Deadline for manuscript submissions:
**closed (30 June 2022)**

## Message from the Guest Editors

Wild aquatic birds act the major natural reservoir of the influenza A virus (IAV) gene pool from which novel IAVs can emerge to infect other avian and mammalian species. From an ecological aspect, IAVs are natural components of wetland ecosystems in which they occupy trophic niches represented by susceptible hosts while interacting with other biotic and environmental components. But ecosystem interactions underlie possible bidirectional viral flows between natural and anthropogenic habitats.

Natural avian reservoirs enable the perpetuation of low-pathogenic avian influenza viruses (LPAIVs) that, in poultry, can occasionally evolve into highly pathogenic (HP) strains, posing a risk for animal and public health. But the increasing potential involvement of wild birds in HP avian influenza caused by H5 subtype circulation and long-distance spread by migratory populations opens a new scenario.

Our aim is to provide a collection related to IAV ecology and evolutionary adaptation to natural reservoir and spillover hosts. Manuscripts covering all aspects of research relating to IAV–host–environment interactions are welcomed.

Dr. Maria Alessandra De Marco
Dr. Claudia Cotti

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## Message from the Editor-in-Chief

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