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Molecular Epidemiology of Human Papillomavirus Infection

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Deadline for manuscript submissions:
closed (22 August 2025)

Message from the Guest Editors

Human papillomavirus (HPV) is an important sexually transmitted infectious agent. HPV belongs to the *Papillomaviridae* family, which is formed by more than 200 viral genotypes. Among them are structural differences that allow the epidemiological classification into high-risk, probable high-risk, and low-risk for developing cancer.

In addition, studies have observed the potential for oncological risk among variants of high-risk HPV types, based on the clinical analysis of patients associated with molecular diagnosis. The variants have shown a set of polymorphisms that point to distinct risks for the development of high-risk lesions and cancer, since different variant strains can present different oncogenic potentials, especially when taking into account the different geographic origins and evolutionary modifications of the virus and the host, creating a different clinical profile among populations.

We welcome submissions of research and review articles on any relevant topics that involve the epidemiological aspects of HPV infection, HPV infection control, and the genetic diversity of high-risk HPV types and their respective oncogenic potentials.

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Special Issue