



Human Papillomavirus Infections in Public Health and Pathology

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Message from the Guest Editors

Dear Colleagues,

It is widely understood that the human papillomavirus (HPV) is a major cause of cervical cancer, resulting in a serious disease burden worldwide in terms of public health. Many previous reports have suggested that HPVs be classified into numerous genotypes based on the phylogenetic analyses. They may be further distinguished by the distinct carcinogenic pathogenicities exhibited in cervical tissues, although the reason for this occurrence is not known. Moreover, longitudinally pathological/cytopathological findings have suggested that HPV infections can induce various morphologically benign and malignant changes in cervical and vaginal cells. However, these changes have not been adequately elucidated. Advanced molecular epidemiological and cytopathological findings may contribute to solving these unknown issues. In light of these circumstances, and in order to gain a better understanding of HPV infections, pathology, and public health, this Special Issue will publish research molecular epidemiology/evolution and pathology/cytopathology based on the application of advanced technologies to sophisticated genomics, bioinformatics, and molecular biology.





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Message from the Editor-in-Chief

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