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Genetics and Genomics of HPV and Cervical Cancer

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Message from the Guest Editors

Cervical cancer is the fourth most common cancer amongst female patients worldwide. Infection by high-risk human papilloma virus (HPV) is necessary in most cases, but not sufficient to develop invasive cervical cancer. DNA sequence differences between HPV genomes determine whether an HPV infection has the potential for carcinogenesis. Despite the high frequency of HPV infections, in most cases the virus is cleared by the host immune response and only a small proportion of infected individuals develop persistent infections that can result in malignant transformation, indicating that other biological, genetic and environmental factors may influence individual susceptibility to HPV-associated cancers. Genetic factors contributing to the development of cervical dysplasia and invasive cervical cancer are largely unknown. However, genetic variants that appear to be associated with genes that predispose or protect the host to HPV infections, thereby affecting individual susceptibility, have been reported. The hypothesis of germline predisposition suggested that heritability via genetic factors might contribute to cervical cancer risk variation.

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