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Detection of four human polyomaviruses (MCPyV, HPyV6, HPyV7 and TSPyV) in cervical specimens from HIV-infected and HIV-uninfected women

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Abstract**Objectives**

To investigate the presence of recently discovered human polyomaviruses in cervical specimens collected from African and French women, in relation to HIV serostatus, high-risk human papillomavirus infection (HR-HPV), and cervical disease.

Methods

Cervical specimens were collected from 140 HIV-1-seropositive African women and 50 HIV-seronegative French women. Presence of Merkel cell polyomavirus (MCPyV), human polyomavirus 6 (HPyV6), human polyomavirus 7 (HPyV7) and Trichodysplasia spinulosa-associated polyomavirus (TSPyV) was detected by real-time PCR, and presence of HR-HPV DNA by Hybrid Capture 2 assay with subsequent HPV genotyping using the INNO-LiPA HPV Genotyping Extra assay. Cervical biopsies were analysed by histopathology.

Results

The detection rates were 55.3%, 3.2%, 2.1% and 0% for MCPyV, HPyV6, HPyV7 and TSPyV, respectively, with no significant difference by population. The MCPyV viral load ranged from 14 to 210 DNA copies/ 10^6 cells (median, 80 DNA copies/ 10^6 cells). There was no association between detection of human polyomaviruses in cervical specimens and geographic origin/HIV serostatus, HR-HPV co-infection or precancerous cervical lesions.

Conclusions

These observations argue against a possible role of MCPyV as a cofactor in HPV-induced carcinogenesis. MCPyV and, to a lesser extent, HPyV6 and HPyV7 might belong to the female genital tract microbiota.