

High Grade Cervical Lesions are Caused Preferentially by non-European Variants of HPVs 16 and 18

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Infections by non-European variants of HPVs 16 and 18 have been associated with risk of HSIL. Our aim was to correlate nucleotide variability of both types and risk of persistent infection and clinical outcome in a cohort study that is being conducted in Brazil. Data presented encloses four years of follow-up. We characterized molecular variants of both types by sequencing a fragment of the LCR, as well as E6 and L1 genes for HPV-16 variants only. For both types, European variants composed the most prevalent and diverse group. European variants of HPV-18 tended to lead to persistent infections more frequently than non-European ones. We did observe association between persistence of a given variant and the racial ancestry of the host. Furthermore, risk of HSIL was higher in women harboring non-European variants of HPV-16. The same trend was observed with HSIL detected during follow-up. This study confirms the association between non-European variants of HPVs 16 and 18 and risk of cervical neoplasia, and highlights the importance of their geographic distribution for cervical cancer risk assessment. Support: FAPESP and NIH

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