

**Genetic characterization of variants of HPV-16, HPV-18 and HPV-52 circulating in Italy among general and high-risk populations.**

**Fрати ER(1), Bianchi S(1), Amendola A(1), Colzani D(1), Petrelli F(2), Zehender G(3), Tanzi E(1).**

(1)Department of Biomedical Sciences for Health, University of Milan, I-20133 Milan, Italy.

(2)School of Medicinal and Health Products Sciences, University of Camerino, I-62032 Camerino, Italy.

(3)Coordinated Research Centre 'EpiSoMI', University of Milan, I-20133 Milan, Italy.

**ABSTRACT**

Viral factors, such as high-risk human papillomavirus variants, can increase the risk of viral persistence and influence the progression to cancer. In the present study, the long control region (LCR) of human papillomavirus (HPV)-16 and HPV-52, and the L1 region of HPV-16 and HPV-18, identified from subjects belonging to both general and high-risk populations (migrants, HIV+ subjects and adolescent/young people) residing in Italy, were characterized using molecular and phylogenetic techniques. To the best of our knowledge, this is the first Italian study to analyze a large number of sequences (n=458) and report phylogenetic data on the HPV-52 variants. The phylogenetic analysis showed that 90% of the LCR variants of HPV-16 and HPV-52 clustered within lineage A (European lineage) and only sequences identified from subjects belonging to high-risk populations fell into the non-European lineages. Analysis of the LCRs revealed a high genomic diversity with a large number of changes. Several mutations in the binding sites for viral and cellular transcription factors characterized the HPV-16 LCR variants belonging to the African lineages B and C, were observed in subjects with cytological abnormalities (high squamous intraepithelial lesions). The HPV-16 and HPV-18 L1 molecular characterization identified 30% of changes in the immune-dominant epitope loops. These data give a clear picture of the situation in Italy, and a starting point for understanding the molecular pathogenesis and developing molecular diagnostics for HPV, vaccines and other therapeutic approaches in order to control and/or eliminate virus-induced diseases.

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