

OP3.19

The distribution and prevalence of HPV genotype in Maltese women diagnosed with CIN 3 and cervical cancer

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Introduction: The Human papilloma virus (HPV) is the causative agent of cervical carcinoma in women. There is a global variation of HPV genotypes that are highly carcinogenic. The aim of this study was to estimate the prevalence and type-specific distribution of HPV genotype in Maltese patients who were previously diagnosed with cervical intraepithelial neoplasia 3 (CIN 3) or cervical carcinoma.

Methods: 96 formalin fixed paraffin-embedded sections from archival cervical tissue were retrieved from the Pathology Department, Mater Dei Hospital, Malta. HPV genotypes were identified using the Multiplex HPV genotyping kit, which employs the identification of 24 HPV subtypes via PCR-based assay amplification, followed by a hybridisation step and identified via a Luminex analyser. Negative cases were re-analysed with the RTPCR. 92 cases were suitable for data analysis of which 73 cases were positive for HPV (79%). A total of 14 different HPV types were identified; 12 were high-risk HPV and 2 were low-risk HPV genotypes.

Results: The most prevalent HPV genotype in all diagnosis categories was HPV16, followed by HPV 31, 45, 18, 33, 35, 52, 53, 58, 59, 70, 73, 82 and 6. However, in invasive carcinoma cases, the most prevalent was HPV16 followed by 45, 18, 58, 31, 59, 73, 82, and 6.

Conclusion: The present study provided important information about the distribution of individual HPV genotypes in CIN 3 and cervical carcinoma cases in Malta. Although the frequency of HPV16 in the present study is similar to other European studies, the distribution of the other HPV genotypes was different.