

# Human Papillomavirus Genotyping in Histological Sections of Precursor Lesions of Cervical Carcinoma: Its Role as a Possible Adjunct for the Evaluation of the Oncogenic Potential of Specific Human Papillomavirus Genotypes – A Study in a Coastal Region of Southeastern Spain

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**Background:** Human papillomavirus (HPV) genotyping is usually performed on cytological specimens with the aim of discerning between high- and low-risk genotypes. **Methods:** Paraffin-embedded sections (n = 241) comprising 16 normal/benign (N/B) cervical sections, 72 low-grade squamous intraepithelial lesions (LSIL), 133 high-grade SIL (HSIL), 6 invasive carcinomas (cervical cancer), and 14 atypical immature metaplasias (AIMs) were DNA extracted and HPV genotyped.

**Results:** The most frequent HPV genotypes found were 16 and 58. HPV16 was detected in 0% N/B, 18.1% LSIL, 42.9% HSIL ( $p < 0.001$ ), 50% carcinoma, and 35.7% AIM, whilst HPV58 was detected in 25.0, 20.8, 16.5, 0 and 35.7% of these lesions, respectively.

**Discussion:** The high prevalence of HPV58 and the low prevalence of HPV18 suggest the limited effectiveness of HPV vaccination in southeast Spain (prevention of 45.1% HSILs). The HPV genotype distribution profile in AIM suggests that these lesions are more similar to LSIL than HSIL pointing to a low risk of progression to cervical cancer. These results reinforce the necessity of assessing the specific genotype rather than distinguishing between high- or low-risk HPV. The use of histological section instead of cytological specimens for specific HPV genotyping would be very useful in order to ascertain the oncogenic potential of each of the genotypes found in a given area.