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### PP066: No association between human papillomavirus infection and oral verrucous lesions

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#### Purpose

Verrucous carcinoma (VC) is a low grade, non-metastasising, slow-growing variant of squamous cell carcinoma (SCC). The aetiology of VC is unknown, and the role of human papillomavirus (HPV) as a causative factor remains contentious. This dubiety can be attributed to varied detection procedures and difficulties in defining 'gold-standard' histological criteria for diagnosing verrucous lesions including VC, Verrucous hyperplasia (VH), and proliferative verrucous leukoplakia (PVL). The rarity of these lesions also makes them difficult to study and investigate, so most previous studies have been made on small numbers of cases. The aim of this study is to analyse oral verrucous lesions (including VC, VH, and PVL cases) for the presence of HPV subtype genomes.

#### Materials and methods

We used a recently developed and validated method, 'next generation sequencing' for the detection of HPV sequences, subtypes, and viral loads from nanogram DNA quantities isolated from formalin-fixed paraffin-embedded tissue. In this present study, we identified a total of 62 oral verrucous cases: 49 OVCs, 12 OVHs, and one PVL. DNA was extracted from all samples and libraries were prepared followed by sequencing at coverage between 2.5% and 13%. Genomic copy number karyograms were produced and all samples were analysed for the presence of all HPV subtypes and for other known human viral genome sequences.

#### Results

HPV sequences were not detected in 61 verrucous cases out of 62 total cases. An HPV type 16 sequence was detected in only one OVH sample [2.24 viral genomes per cell].

#### Conclusions

We confirm that NGS can be used as a precise method for detection of HPV subtypes and loads, and provide genomic copy number karyograms for FFPE verrucous samples in a single test. Furthermore, Our results demonstrate conclusively that HPV involvement is unlikely to be a feature in oral verrucous lesions, nor are any other common human viruses implicated.

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#### Bibliographic information

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