

Cytological Confirmation of HPV 13 in Lesional Mucosa

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Abstract

The most common causes of the unusual oral mucosa growth disorder known as focal epithelial hyperplasia (FEH) are the HPV strains 13 and 32. Eskimo and Native American children who live in North, South, or Central America are disproportionately affected. Over 90% of patients have HPV, particularly genotypes 13 and 32. Multiple, asymptomatic, 1 to 10 mm flat-topped, verrucous papules that range in colour from white to the neighbouring mucosa are a common presentation. They typically appear on the tongue, lips, gingiva, and oral mucosa. On rare occasions, several distinct papules will combine to produce a bigger lesion that resembles cobblestones. Condyloma is one of the same differential diagnoses for the oral cavity because of the variety in FEH.

Keywords: FEH • Condyloma • Diagnoses • Tongue

Introduction

One of the earliest viruses ever discovered, papillomaviruses have been around for 330 million years. Human papillomaviruses (HPV) have evolved into hijackers of human cells and immunological systems where they proliferate and remain dormant during the course of this lengthy evolution. There are very few systematic researches on oral HPV infections and their consequences. Although oral HPV infections have been associated with sexual behaviour, more recent research suggests that they can spread horizontally from mouth to mouth. The majority of newborn HPV infections are vertically transmitted from the mother during the intrauterine stage, after delivery, or subsequently via saliva. Oral papilloma/condyloma and localised epithelial hyperplasia are the most well-known benign clinical symptoms of HPV infection. There is growing evidence that some oral HPV infections may endure. The malignant transformation caused by HPV is only possible with persistent HPV infection.

A family of tiny, non-enveloped, icosahedral viruses having double-stranded circular DNA is known as the papillomaviridae. Human papillomaviruses (HPVs) come in over 200 different varieties, according to research. A subset of alphapapillomaviruses (alpha HPVs) was referred to as high-risk (HR) HPV types based on epidemiological research. Anogenital cancer and a subgroup of head and neck malignancies are both caused by HR HPVs. The general population has a high prevalence of cutaneous HPV types, primarily from the beta and gamma genera, on the skin's surface. However, there is mounting evidence linking ultraviolet (UV) exposure and betapapillomaviruses (beta HPVs) to the aetiology of non-melanoma skin cancer (NMSC). [1].

Description

Small non-enveloped icosahedral viruses belonging to the Papillomaviridae family range in size from 5,748 base pairs (bp) for the Sparus aurata papillomavirus 1 (SaPV1) to 8,607 bp for the canine papillomavirus type 1 (CaPV1) (CPV1). Basal keratinocytes of the mucosal and cutaneous

epithelia of both animals (reptiles, birds, marsupials, and others) and humans are infected with papillomaviruses (PVs). In 2016, SaPV1, the first PV to be characterised in fish, revealed that this family of viruses is significantly older than previously thought, having emerged 450 million years ago. PVs are thought to be host-restricted; however in extremely rare circumstances cross-species transmission may also take place.

One of the most prevalent viruses of the reproductive system is the human papillomavirus (HPV), which can cause a variety of malignancies and other diseases in both men and women. Cervical cancer, the fourth most prevalent cancer in women, is brought on by HPV. As a result, it plays a significant role in both morbidity and mortality. There are HPVs that infect cutaneous epithelia of the genera beta, gamma, mu, and nu. Some HPV strains, including HPV that colonise human skin are also found in the genus alpha. Only a few HPV kinds are found in the mu and nu genera, whereas the genus beta has over 54 types, which are further classified into five species, and the genus gamma has 98 types, which are further separated into 27 species. These so-called cutaneous HPV varieties cause asymptomatic persistent infections in the immunocompetent population. Gamma, mu, and nu members can cause benign skin lesions, such as cutaneous papillomas or warts. [2].

The HPV genome is divided into three main regions: the long control region (LCR), also known as the upstream regulatory region (URR), which is situated between the L1 and E6 open reading frames (ORFs) and contains the early promoter and regulatory element involved in viral DNA replication and transcription; the early region, which codes for the E1, E2, E4, E5, E6, and E7 proteins involved in viral gene expression, replication, and survival; and the late region, which encodes the late promoter and regulatory (L1 and L2). [3,4]

The oldest viruses still in existence are papillomaviruses, which date back to the late Paleozoic Era, or roughly 330 million years ago. Papillomaviruses have a wide genotypic diversity and tight species-specificity. Around 90 million years ago, the earliest papillomaviruses with mucosal tropism began to evolve. Human papillomaviruses (HPVs) evolved, gaining the ability to employ human cellular proteins for multiplication and to hide by subverting the immune and cellular systems on several levels. A variety of symptoms, including asymptomatic infections, benign warty lesions, possibly malignant lesions, intraepithelial neoplasia, and invasive carcinomas, can be associated with HPV infections. Over 205 distinct HPV genotypes had been identified at the time of writing and were divided into five genera, the largest of which are Alphapapillomavirus, Betapapillomavirus, and Gammapapillomavirus.

The first sexual encounters in early adulthood are when mucosal HPV infections first appear, however non-sexual infection is still a possibility. Despite the fact that the majority of sexually active women will have genital HPV infections, the majority of cervical HPV infections (>90%) are cleared by the host immune system within 1-2 years and only result in silent infections. Only a small percentage of HPV infections, meanwhile, are chronic. The

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chance of acquiring cancer and aberrant epithelial cells then rises. There are several possible explanations for persistent infection. Alcohol use and HR HPV load together elevated women's chance of developing persistent HR HPV infection [5].

Conclusion

The circular, double-stranded DNA of the human papillomavirus has about 8,000 base pairs and is encased in a 55 nm-diameter, non-enveloped icosahedral capsid. The DNA genome's transcription only affects one strand. Nine to ten open reading frames (ORFs) with putative protein coding regions are included in this sequence. The two viral capsid proteins L1 and L2 are encoded in the late (L) region, while the early (E) section comprises ORFs encoding viral regulatory proteins. The lengthy control region, commonly known as the upstream regulatory region or the non-coding region is the third portion of the genome. The lengthy control region has binding sites for viral and cellular host proteins that control viral transcription as well as the origin of DNA replication.

Since this sequence is the most conserved among all HPVs, classification of HPVs is based on the nucleotide sequence of the ORF coding for the capsid protein L1. Less than 60% of the L1 region of the genome homology among human papillomavirus types indicates that they belong to separate genera. Within a genus, different viral species have between 60% and 70% homology. If the homology of the L1 ORF to any other HPV type is less than 90%, the HPV genotype is regarded as new. After the entire genome has been cloned and deposited in the International HPV Reference Center, the novel HPV kinds are labelled in numerical order. Currently, the most potent carcinogenic virus is HPV-16, which is found in species.

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Conflict of Interest

There are no conflicts of interest by author.

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