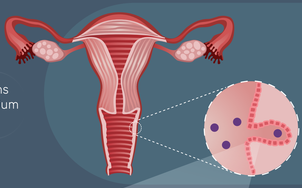
BioTechniques In Focus

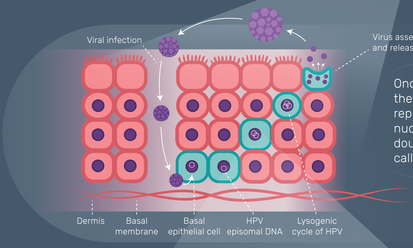
Oxford NANOPORE Technologies

Nanopore sequencing, HPV and cancer

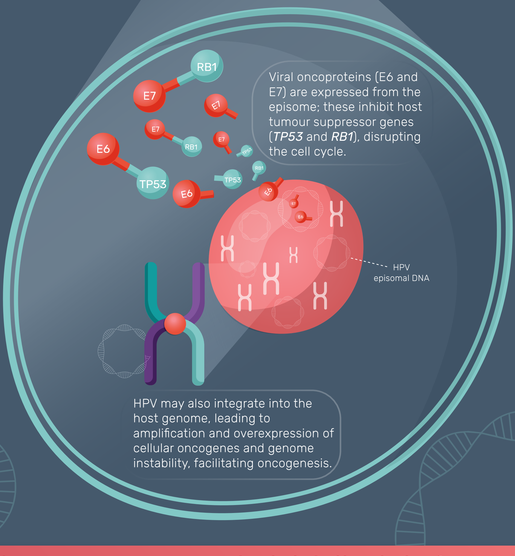
How does HPV cause cervical cancer?



HPV infection begins in the basal epithelium of the cervix.



Once the virus enters the cervical cells, it replicates in the nucleus as a circular double-stranded DNA, called an episome.

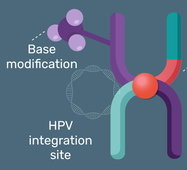


Viral oncoproteins (E6 and E7) are expressed from the episome; these inhibit host tumour suppressor genes (*TP53* and *RB1*), disrupting the cell cycle.

HPV may also integrate into the host genome, leading to amplification and overexpression of cellular oncogenes and genome instability, facilitating oncogenesis.

How can nanopore sequencing help in the study of HPV-driven cervical cancer?

Whole-genome sequencing

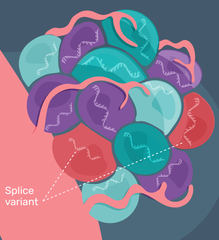


Resolve complex, large-scale structural variants with long and ultra-long nanopore reads

Fully phase integration events into haplotypes

Directly detect methylation - no additional sample prep needed

Single-cell transcriptome sequencing

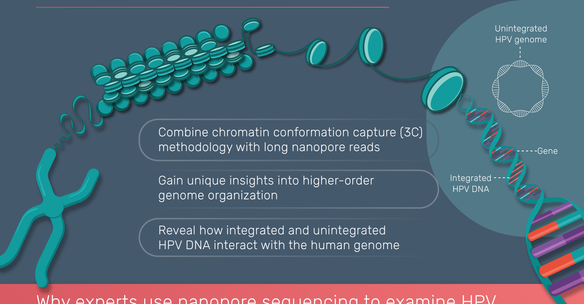


Investigate tumour heterogeneity, which may be associated with cancer development and treatment resistance

Detect full-length transcripts of known and novel genes within a single cell using long nanopore reads

Analyse splice variants and fusion transcripts, and reveal the expression levels of key driver genes

Pore-C



Combine chromatin conformation capture (3C) methodology with long nanopore reads

Gain unique insights into higher-order genome organization

Reveal how integrated and unintegrated HPV DNA interact with the human genome

Why experts use nanopore sequencing to examine HPV and cancer

'Nanopore sequencing gives you highly accurate methylation, but the beauty of this is we can see every CpG site across the HPV genome, on individual viral genomes'

Michael Dean
The National Cancer Institute, USA, speaking at London Calling, 2022

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