

HUMAN PAPILLOMAVIRUS GENOME VARIANTS IN THE BARRETT'S METAPLASIA-DYSPLASIA-ADENOCARCINOMA SEQUENCE

Mohammad Rabiei

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Poster

Oesophagus

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Phylogenetic analysis of HPV strains from Australian Barrett's metaplasia, dysplasia, and oesophageal adenocarcinoma specimens collected between 2012 and 2014 found HPV-16 predominance with rare HPV-18 presence.

KEY POINTS

- Of the HPV genomes sequenced from Barrett's metaplasia, dysplasia, and adenocarcinoma patients, 31 were closely related to HPV-16 and one to HPV-18.
- HPV-16 was detected across all disease stages: 10 Barrett's metaplasia cases, 10 dysplasia cases, and 11 adenocarcinoma cases, while the single HPV-18 case was from adenocarcinoma.
- Viral DNA was extracted and sequenced using the Sanger method, with phylogenetic analysis conducted using Mega X software and comparison to sequences in public databases.
- The HPV-16 strains clustered with known HPV-16 sequences, and the HPV-18 strain clustered with known HPV-18 sequences, with the predominance of HPV-16 aligning with global epidemiological trends.
- The authors conclude that comprehensive screening should address all high-risk HPV types and suggest the findings could inform vaccination strategies and epidemiological surveillance in high-risk patient groups.

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