

## INTISARI

**Latar belakang:** *Human papillomavirus* tipe 16 (HPV-16) merupakan penyebab kanker serviks terbanyak pada perempuan di Indonesia. Protein kapsid minor L2 pada HPV sangat penting pada proses infeksi virus dan dapat menjadi kandidat potensial untuk epitop vaksin HPV spektrum luas.

**Tujuan:** Penelitian ini bertujuan untuk menentukan variasi sekuens gen L2 HPV-16 pada spesimen kanker serviks yang tersimpan di Laboratorium Pusat Diagnostik dan Riset Penyakit Infeksi, Fakultas Kedokteran, Universitas Andalas.

**Metode:** Sekuens gen L2 pada 44 sampel DNA HPV-16 dideteksi dan diamplifikasi, lalu dilanjutkan dengan sekuensing gen untuk menganalisis polimorfisme gen L2 dan variasi filogenetik intratipik HPV-16 pada 23 sampel yang berhasil diinterpretasi (9 lengkap dan 14 parsial).

**Hasil:** *Single Nucleotide Polymorphisms* (SNPs) ditemukan sebanyak 18/35 sinonimus (sNSPs) dan 17/35 non-sinonimus (nsSNPs) dengan perubahan asam amino terutama terdapat pada residu 269 (100%) dan residu 330 (43,5%). Varian yang paling prevalen adalah linea A (*European-Asian*) ( $n=22$ ), terutama sub-linea A2 (*European*) ( $n=14$ ), dan satu sampel linea C (*African-2*).

**Kesimpulan:** Variasi sekuens gen L2 HPV-16 ditemukan pada spesimen kanker serviks baik dari segi polimorfisme gen maupun filogenetik. Studi ini diharapkan dapat berkontribusi pada penelitian lanjutan mengenai proses infeksi, onkogenisitas, dan vaksin HPV di Indonesia.

Kata kunci: Human papillomavirus, HPV-16, gen L2, kanker serviks, varian, analisis filogenetik

## ABSTRACT

**Background:** Human papillomavirus type 16 (HPV-16) is the most common etiological cause of cervical cancer in Indonesian women. HPV L2 minor capsid protein is necessary for viral infection and can be a potential candidate for broad-spectrum HPV vaccine epitope.

**Objective:** In this research, we determined the variations in the HPV-16 L2 gene sequence in Indonesian cervical cancer specimens at the laboratory of Center for Infectious Disease Diagnostic and Research, Faculty of Medicine, Universitas Andalas, Padang, Indonesia.

**Method:** L2 gene sequences in 44 HPV-16 DNA samples were detected and amplified, followed by gene sequencing to analyze the presence of L2 gene polymorphisms and intra-typic HPV-16 phylogenetic variations, which led to 23 samples interpreted (9 samples completed and 14 partial).

**Results:** Single Nucleotide Polymorphisms (SNPs) found as many as 18/35 synonymous (sSNPs) and 17/35 non-synonymous (nsSNPs) with amino acid changes mostly located in 269th residue (100%) and 330th residue (43.5%). The most prevalent variant was A lineage (European-Asian) ( $n=22$ ), especially A2 sub-lineage (European) ( $n=14$ ), and one sample belonged to C lineage (African-2).

**Conclusion:** There are variations in the L2 HPV-16 gene sequence in cervical cancer specimens both in terms of gene polymorphism and phylogenetics. This study should contribute to further research on the infection process, oncogenicity, and vaccine of HPV-16 in Indonesia.

**Keywords:** Human papillomavirus, HPV-16, L2 gene, cervical cancer, variants, phylogenetic analysis