

ABSTRACT

Thesis title: Genome Sequence Analysis of Human Papillomavirus Type 11 (HPV-11) Infecting Vietnamese Men

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This study aims to conduct a comprehensive whole-genome sequence analysis of Human Papillomavirus type 11 (HPV-11) strains isolated from Vietnamese men to elucidate their genetic diversity, phylogenetic relationships, and mutational characteristics. Clinical samples collected from male patients infected with HPV-11 at Hanoi Medical University Hospital underwent viral DNA extraction and whole-genome sequencing. Specific primer pairs were successfully designed to amplify and sequence the complete viral genome of approximately 8,000 bp. BioEdit, MEGA, and DNASTAR softwares were utilized for sequence assembly and bioinformatics analysis. Comprehensive genomic analysis identified several nucleotide variations leading to amino acid mutations in critical genes, including E6, E7, and L1. The phylogenetic tree constructed based on all genomic regions (E6, E7, E1, E2, E4, E5 α , E5 β , L2, and L1) consistently assigned the HPV-11 strains isolated in Vietnam to sublineage A2. The studied strains exhibited a close evolutionary relationship with strains circulating regionally and globally, such as those in Thailand, China, Slovenia, and Hungary. These findings provide detailed whole-genome characteristics of HPV-11 in Vietnamese men, thereby expanding national and international genetic databases for papillomaviruses. The results contribute to a deeper understanding of viral evolution, support the optimization of local clinical diagnostic assays, and establish a robust molecular foundation for epidemiological surveillance and the improvement of future gender-inclusive HPV vaccination programs in Vietnam.