

Phylogenetic Study of L1 Protein Human Papillomavirus Type 16 From Cervical Cancer Patients in Bandung

Authors : Fitri Rahmi Fadhilah, Edhyana Sahiratmadja, Ani Melani Maskoen, Ratu Safitri, Supartini Syarif, Herman Susanto

Abstract : Cervical cancer is the second most common cancer in women after breast cancer. In Indonesia, the incidence of cervical cancer cases is estimated at 25-40 per 100,000 women per year. Human papillomavirus (HPV) infection is a major cause of cervical cancer, and HPV-16 is the most common genotype that infects the cervical tissue. The major late protein L1 may be associated with infectivity and pathogenicity and its variation can be used to classify HPV isolates. The aim of this study was to determine the phylogenetic tree of HPV 16 L1 gene from cervical cancer patient isolates in Bandung. After confirming HPV-16 by Linear Array Genotyping Test, L1 gene was amplified using specific primers and subject for sequencing. Phylogenetic analysis revealed that HPV 16 from Bandung was in the subgroup of Asia and East Asia, showing the close host-agent relationship among the Asian type.

Keywords : L1 HPV 16, cervical cancer, bandung, phylogenetic

Conference Title : ICBIR 2014 : International Conference on Biomedical and Interdisciplinary Research

Conference Location : Singapore, Singapore

Conference Dates : March 30-31, 2014