ANALYSIS OF GENE ENCODING E6 PROTEIN OF THE HUMAN PAPILLOMAVIRUS TYPE 16 FROM CERVICAL CARCINOMA PATIENTS

Rina Amtarina

ABSTRACT

Background: Human Papilloma virus (HPV) infection has been known as the major cause of cervical cancer which represent the leading causes of morbidity among women worldwide. E6 and E7 ORFs contain the transforming ability of HPV and was the first indication of an important role for these genes in HPV associated tumorigenesis. Some of the changes in E6 may alter biological properties and protein function.

The aim of this study is to analyze the sequence of the gene encoding E6 protein of HPV 16 from Cervical Carcinoma patients at Dr. Sardjito Hospital Yogyakarta period October 2007-February 2008.

Methods: Thirty one cervical cancer patients were studied. The viral DNA were isolated from the cervical tissue using standard method. The viral type were determined by PCR using specific primers for HPV 16. The gene encoding E6 protein of HPV 16 were amplified using specific primers and sequenced using automated DNA sequencer machine.

Results: after HPV typing, the entire HPV 16-E6 coding region was amplified and sequenced in all samples. We detected total 13 variants of nucleotide from all sequence samples that caused a base substitution in the E6 coding region, resulting in amino acid changes namely T109C, C116A, G124A, G132T, C143G, A144G, A276G, T286A, A289G, C335T, A403G, G489C, G491T. Compared to another sequence from whole world, we detected the same nucleotide changes especially on Africa type 1, Africa type 2 and Australian strain.

Conclusion: The entire HPV 16-E6 coding region had been amplified and sequenced successfully. There were nucleotide changes that caused polymorphisms of amino acid sequence.

Keywords: HPV type 16, Cervical Carcinoma, protein E6, nucleotide, amino acid, polymorphisms.