

ABSTRACT

The incidence of cervical uterine cancer tends to increase and is becoming a serious health problem in Indonesia. Data from the National Cancer Registry in 1996, showed that cervical uterine cancer is at the first rank, related to morbidity and mortality among cancer patients. More than 4000 new cases were detected annually, and a large portion came in a very late stage, causing treatment unsuccessful and increasing mortality.

Much effort towards prevention through early detection, and improvement of treatment has been a particular interest and research among many centers, but unfortunately without substantial results. Early detection followed by appropriate intervention on cervical cancer patients is a matter of importance, because of the well documented facts, that the effectiveness of treatment will then be much more successful. Diagnosis of cervical uterine cancer up to these days is mostly performed through clinical and confirmed by histopathological measures. This is not an early diagnosis! Another problem is according to many references and clinician experiences there are some discrepancies between histopathological grading and clinical outcome. There is becoming a strong acceptance that the pathogenesis of cancer is based on a genetical and molecular basis, and for this reason a molecular approach should be developed for more accurate and early diagnostic.

This research using molecular diagnostic tools within the field of pathobiology, is intended to explore the role of two tumor suppressor genes namely p53 and pRb on one side, and one oncogene, namely c-myc on other side, in relation to cellular proliferation activities, within the concept of the carcinogenesis of cervical uterine cancer. Immunohistochemistry investigation using some basic molecular diagnostic tools among others PCR, Blotting, SSCP as well as routine histopathological testing has been performed. In this study the genetic and molecular aspect of cervical cancer induced by Human Papilloma Virus was determined using the Dual Wave Length Thin Layer Chromatoscanner CS-930, and immunohistochemical measurement through monoclonal antibodies. Multivariate analysis was used to show the differences between the gene proteins, expressed by the three above mentioned genes, in cases with infection by HPV 16 and HPV 18 subtypes, in comparison with cases without infection by the HPV 16 and HPV 18 subtypes. Discriminant statistical analysis was used to detect the discriminator, and furthermore the functional contribution of this discriminator was calculated, using multiple ratio statistic based on the Fisher discriminant coefficient. These statistical results, have shown a significant difference between the two cancer groups. It came out strongly that the p53 and the c-myc protein are the dominant discriminators.