

ABSTRACT

Background: Condyloma acuminata is a sexually transmitted disease caused by Human Papilloma Virus (HPV). High-risk HPV has the ability to develop into malignancy, whereas low-risk HPV is very rarely cause malignancy. The p16^{ink4a} examination is used to detect potentially malignant HPV. Detection of HPV genotype by using PCR has a very high sensitivity.

Purpose: This study is to determine the expression of p16^{INK4a} in condyloma acuminata lesions with low risk HPV infection, high risk HPV infection, and multiple HPV infection infections

Methods: This is cross sectional study conducted at Sexual Transmitted Infection Division of Outpatient Clinic, Dr. Soetomo General Hospital Surabaya. 13 patients with condyloma acuminata were examined genotyping by PCR and p16^{INK4a} by immunohistochemistry. Sample was taken from the lesion of condyloma acuminata by biopsy.

Results: There were 5 patients with diffuse p16^{ink4a}. The results of diffuse p16^{ink4a} indicate that in these patients have the ability to develop into malignancy.

Conclusions: Further study (cohort prospective) in condyloma acuminata patients with diffuse p16 features to determine the probability of malignancy in patients

Key words: Condyloma acuminata, genotyping, p16^{INK4a}, pcr