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An Update in Clinical Application

Insight On Infection Related Oncology

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Abstract

A13

HPV Genotyping Liner Assay Tests Comparison Among Cervical Cancer Patients in Bandung: Implication for HPV Prevalence and Molecular Epidemiology

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Introduction : Many women are infected with human papillomavirus (HPV), however, only a subset of women infected with persistent high-risk types of HPV will ever develop cervical cancer. Interferon gamma (IFN-γ) is one of the key regulatory cytokines that influence the HPV clearance. The production and the function of IFN-γ may impaired by the defect of the *IFNG* gene, leading to the cervical malignant progression.This study aimed to examine the association between *IFNG* +874 T>A polymorphism and cervical cancer.

Methods : In a case-control study design, consecutive untreated women with cervical cancer who showed for the first time in Hasan Sadikin Hospital Bandung were enrolled (n =98). Their controls were women who came for PAP smear (n = 81), and were not matched in ages and ethnicities. DNA extracted from blood was amplified by amplification refractory mutation system - polymerase chain reaction (ARMS – PCR) to detect *IFNG* +874 T>A polymorphism.

Results : The distribution of *IFNG* genotypes TT, TA and AA for women with cervical cancer who met the inclusion criteria (n = 64) and with negative intraepithelial lesion or malignancy (n = 42) were 14.1%, 50.0%, 35.9% and 7.1%, 52.4%, 40.5%, respectively. No significant differences could be observed between both groups (p= 0.64). Stratifying the cervical cancer women into a group of squamous cell carcinoma (n = 54) revealed no statistical different.

IFNG POLYMORPHISM (+874 T>A) IN CERVICAL CANCER PATIENTS FROM BANDUNG

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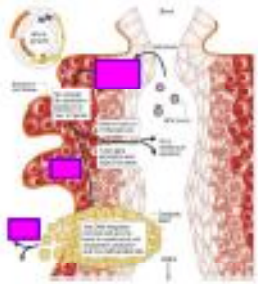
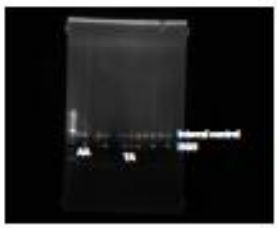
Objective: Persistent infection with human papillomavirus (HPV) may progress in cervical cancer, and host genetic susceptibility may augment disease risk. Interferon gamma is one of the key regulatory cytokines that has a significant effect on immune response, and may influence the HPV clearance and cervical malignant progression. The aim of this study was to examine the relationship between *IFNG* polymorphism in the determination of susceptibility to HPV infection leading to cervical cancer.





Methods: Women with CIN II and CIN III from Bandung were enrolled in this study, and as control women with negative Pap smear were included. DNA was extracted from blood samples and the *IFNG* polymorphism at position +874 was determined by Amlification Refractory Mutation System - Polymerase Chain Reaction (ARMS – PCR).

Discussion: In our study determining polymorphism in *IFNG* +874 T>A, there was more homozygous AA compared to TT in the control group. Therefore, we need to re-analyze the DNA fragment found by sequencing method to confirm the T/A variants introduced by ARMS-PCR. More subjects examined might give a clearer overview regarding the relationship between *IFNG* polymorphism in the determination of susceptibility to HPV infection.

Results: This was an *ad interim* result including 8 patients and 22 healthy women of total subjects of 75 patients and 75 controls. The distribution of IFNG genotypes for patients and controls was as follows: TT(0), TA(6), **AA**(2) and TT(1), TA(5), **AA**(16), respectively. The genotype distribution showed a statistically significant difference (*p value* 0.0018, OR = 8.0, CI = 1.3 – 51.1), however homozygous AA was predominant in control group.

Acknowledgment:

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CERTIFICATE

Bandung Biomolecular Medicine Conference

This certifies that

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