Service Priorities and Programmes

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Menstrual blood TAP1 I333V and D637G gene polymorphisms are associated with reduced risk for developing high-grade cervical intraepithelial neoplasia

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Introduction

Recent evidence has shown that single nucleotide polymorphisms (SNPs) in transporter associated with antigen processing 1 (TAP1) gene includes TAP1 I333V and TAP1 D637G may be useful to identify women who are less susceptible to developing high-grade cervical intraepithelial neoplasia (HGCIN) and cervical cancer. Our latest breakthrough in detecting human papillomavirus (HPV) genotypes in the menstrual blood (MB) from patients with CIN and condyloma acuminatum has generated a new era in non-invasive screening.

Objectives

A novel non-invasive method to predict HGCIN risk in patients with CIN or HPV infection using MB was developed to detect TAP1 SNP.

Methodology

Thirty-eight patients with HGCIN (CIN 2 or 3) and 42 patients with low-grade CIN (CIN 1) or HPV infection were recruited. Small piece of the napkin was cut for DNA extraction. Two SNPs in TAP1 gene (I333V and D637G) were genotyped using polymerase chain reaction – restriction fragment length polymorphism technique. Three different genotypes which interpreted as AA (wild type), AG (1 allele showed SNP), and GG (2 alleles showed SNP) were detected at each polymorphic site. Reactions were performed in duplicates and each result was confirmed by DNA sequencing.

Result

Both TAP1 polymorphisms in the MB were successfully detected. Their patterns were summarized as a) 3 genotypes at each polymorphic site were detected; b) the risk to develop HGCIN was significantly reduced for AG and GG genotypes when compared

to AA genotype (TAP1 I333V: chi-square test, p = 0.003, odds ratio (OR) = 0.23, 95% confidence interval (CI) = 0.08 to 0.63; TAP1 D637G: chi-square test, p = 0.01, OR = 0.30, 95% CI = 0.12 to 0.76); c) the risk to develop HGCIN was significantly reduced for carriers with a G allele when compared to those with an A allele (TAP1 I333V: chi-square test, p = 0.001, OR = 0.27, 95% CI = 0.12 to 0.62; TAP1 D637G: chi-square test, p = 0.007, OR = 0.36, 95% CI = 0.17 to 0.76). This study is the first to show that MB TAP1 I333V and D637G gene polymorphisms are significantly associated with reduced risk for developing HGCIN.