Quantification and genotyping of human papillomavirus by real-time pcr and hpv DNA chip in cervical samples

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목적: Cervical cancer is the second-most frequent cancer in women around the world. Infection with high-risk human papillomavirus types (HR-HPV) is closely connected to this cancer. Although Papanicolaou (Pap) smear and Hybrid capture II (HC-II) are commonly used for detection of HPV, these methods have limitation because the correlation between cytology lesion, HPV types and viral loads per cell are not completely reflected. We introduce improved useful method based on Real-time PCR (RT-PCR) and Microarray HPV genotyping.

방법: We tested novel primer sets (GPM7 Forward/Reverse) that target in the conserved L1 region of HPV genome to detect the broad range HPV types, at least 36 types, and evaluation of viral loads per cell. Generated RT-PCR products that are Cy-5 labeled in reverse primers are directly used to screen genotype on microarray.

결과: This assay applied on 150 genital samples that were presented cytological abnormality, and were HC II positive in 64% (n=96) and negative in 36% (n=54). In our results, when RT-PCR negative range was adjusted at below 100 copy, RT-PCR Positive was 80% (n=120) and negative was 20% (n=30). Genotyping was sequently performed with RT-PCR Positive samples by microarray. 85.5% of 55 ASC-US (Atypical Squamous Cells of Undetermined Significance) classified samples were identified genotype, mainly type 16 (16.4%), and 14.5% of them were negative. Each HPV positive ratio was 85.5%, 86.7%, 96.9% and 100% in ASC-US, LSIL, HSIL and Cancer.

결론: Although the relation of statistical significance between viral load and cytology was not cleared, we verified its increased pattern in high grade lesion. We will study with more clinical samples for precise statistical significance test. Quantification and identification of HPV by connected methods with RT-PCR and DNA chip will be helpful to predict the progression of cervical cancer.

Chance of Hereditary Risk with Sequential Endometrial and Colon cancer with regard to Lynch syndrome: A pilot study

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목적: Two common cancer types related with Lynch syndrome are colon and endometrium. Several mismatch repair genes (MLH1, MSH2, and MSH6) are reported to be associated with hereditary nature of Lynch syndrome. The aim of our study was to estimate the frequency of Lynch syndrome in sequential tumor patients.

방법: Women who have been treated for 2 primary colorectal/endometrial cancers were identified from Samsung Medical Center. Patients' information about age at cancer diagnosis, order of cancer development and other characteristics were obtained. Immunohistochemistry of MLH1, MSH2, and MSH6 were done for two tumor sites. And other genetic tests (microsatellite instability, gene sequencing) were done.

결과: A total of 15 women with dual primary cancers were identified. In 2 women, colon cancer and endometrial cancer were diagnosed simultaneously. Of the remaining 13 women, 6 (46%) women had an endometrial diagnosed first. Fifty four (54%) women had a colon cancer diagnosed first. Mean age at diagnosis and median time to second cancer for endometrial / colon cancer were 54/51.7 and 5.3/2.9 years. Patients with a family history of cancer were 9(60%). Suspicious immunohistochemistry of MLH1/MSH2/MSH6 were 3/3/3(20/20/20%). Microsatellite unstable population were 5(33%). There were 3 Lynch syndrome/HNPCC patients after gene sequencing tests.

결론: After reviewing cases of women with dual cancer patients, preceding endometrial cancer patients including synchronous tumor were above half of the cases. Therefore, careful consideration of gynecologic oncologist for selecting Lynch syndrome should be provided to suspicious patients.