IS-94  A prospective study to the association of mannose-binding lectin polymorphisms with Pap smear abnormality and persistent high-risk human papillomavirus infection in southern Taiwan

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Objective: Mannose-binding lectin (MBL) is a serum lectin that mediates phagocytosis and activates complement. We hypothesized that individual carrying the MBL genotypes with reduced functional MBL levels would be associated with persistent high-risk HPV infection and therefore is probably related to the development of cervical cancer. Methods: We used the molecular methods, PCR-SSP and PCR-BFLP, respectively for the determination of the MBL gene polymorphisms in the promoter (-221 X/Y) and the first exon (codon 54 A/B). We analyzed 150 HPV + women (cases) and 277 unrelated HPV—women (controls) recruited from Southern Taiwan. No differences in the demographic characteristics were evident between HPV + and HPV—groups. The mbl-2 polymorphisms in coding region 54, promoter -550 G>C and -221 G>C, were successfully genotyped in all 150 HPV + patients and 277 HPV—controls. All genotype distributions were consistent with the existence of Hardy-Weinberg equilibrium. Results: The major single point polymorphism (G to A) of codon region was ascribed to codon 54. The variant B allele frequencies of two groups were 163% (HPV+) and 152% (HPV—). The frequencies of genotypes A/A, A/B and B/B were very similar in HPV + patients and HPV—controls. The frequencies of the H/H and Y/Y genotypes were significantly high in the HPV+ group (OR = 2.31, 95% CI: 1.42-3.76, p = 0.001) and OR = 1.75, 95% CI: 1.14-2.70, p = 0.011; respectively). The genotype of mbl-2 promoter polymorphisms, HY/HY, was the most significant risk for the HPV + group (OR = 2.31, 95% CI: 1.42-3.76; p = 0.001). Conclusion: Our findings provide evidence that mbl-2 genetic polymorphisms may modulate the susceptibility of women to HPV infection and suggest a potential role of innate immunity in those at high risk of HPV infection.

IS-95  Sexual behavior of Korean young women: preliminary study for the introducing of HPV prophylactic vaccine

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Objective: The decision of optimal age for administration of recently approved prophylactic human papillomavirus (HPV) vaccines depend on the basis of the sexual behavior of each countries. The aim of the study was to survey the age-specific sexual behavior including the sexual debut time and sexual experience in the Korean young women to design the tailored HPV vaccination. Methods: This study was conducted by the Synovate Healthcare in the 6 large city of Korea. By a stratified sampling methods, 2400 women aged 12-29 years old were included. The measures of sexual behavior presented in this report were collected by a Computer—Assisted Self-Interviewing (ACASI). Results: Among women 12-29 years of age, 39 percent of women (934 persons in 2,400 women) were younger than 18 years old. The age of first sexual activity (sexual debut) was 21 years old. The age of partner at the sexual debut was 23 years old. Sexual experience before 15 years old was only 2%. About the condom, 41% did not use or rarely use. Conclusion: Our data demonstrate that the sexual debut time of young Korean women differ from other countries. We conclude that the optimal age for HPV vaccination in Korea would be determined by this situation. Key Words: Sexual behavior, Prophylactic HPV vaccine, Sexual debut

IS-96  Status of HPV 52 and 58 variants on cervical dysplasia in Korean women

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Human papillomavirus (HPV) type 52, 58 are specifically prevalent types in women of Northeastern Asia including Korea. This study examined the status of HPV 52, 58 variants on cervical dysplasia in Korean women. Twenty five HPV 52 and fifty three HPV 58—infected women were included for HPV52, 58 variants analysis: 11 (44.0%), 26 (49.1%) with normal cytology, 7 (28.0%), 20 (37.7%) with low grade intraepithelial lesion (LSIL), 7 (28.0%), 7 (13.2%) with high grade intraepithelial lesion (HSIL), respectively. Genomic DNAs from HPV52, 58 infected women were extracted and HPV 52, 58 L1/E2/E6/E7 specific polymorphism chain reaction (PCR) were amplified and analyzed. At the nucleotide level, HPV52/58 L1: (10/10) position variations, HPV52/58 E2: (0/7) position variations, HPV52/58 E6: (2/1) position variations and HPV52/58 E7: (2/6) position variations were found. At the amino acid levels, HPV 52 showed 1 amino acid change such as E6 A93R and HPV 58 isolates showed 9 types of amino acid changes including L1 L155F, L1 L1550F, L1 L1253M, E2 S279A, E2 V282L, E7 T201, E7 G41R, E7 G65S and E7 G663D. The occurrence of L1 L155P, L1 L1253M, E2 S279A, E2 V282L and E7 T201 variants in HPV 58 showed positive trend associated with the severity of cervical dysplasia (P < 0.05). These results showed the different distribution of HPV52 and 58 variants according to the severity of cervical dysplasia. Information of HPV variants will be used in the epidemiologic basis for geographic locations of variant study.