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P313. Identification of DNA hypermethylation of SOX9 in association with cervical cancer using CpG microarrays

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Objective: The study was to screen novel candidate methylation markers for cervical cancer detection and then to validate the significantly hypermethylated genes in cervical scrapings.
Methods: MIRA-based array was carried out in dye swap way in a discovery set of 10 pairs of cervical cancer and non-cancer tissues to screen significantly hypermethylated genes in cervical cancer. SOX9, PKLR and DLX4 were selected for further validation by direct bisulfite sequencing. COBRA assay in a test set of cervical cancer(n=15) and non-cancer(n=17) scrapings was conducted to validate the most promising methylation biomarker.
Results: 504 CpG islands, corresponding to 378 genes, were identified to be differentially methylated between cervical cancer and non-cancer tissues. Among them, 30 genes were found to be significantly hypermethylated. SOX9 promoter revealed complete methylation in cervical cancer tissues and complete non-methylation in non-cancer tissues. Methylated SOX9 was detected in 9 of 15 cervical cancer scrapings and in 0 of 17 controls, resulting in a sensitivity and specificity of 60% (9/15) and100% (17/17), respectively. Fisher test showed SOX9 methylation level in cervical cancer scrapings was significantly higher than that in cervical non-cancer scrapings (p=0.0002?.
Conclusion: Methylated SOX9 may be a promising biomarker for early diagnosis of cervical cancer.

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