PP-3-08
Differentially Hypermethylated Genes in Oral Squamous Cell Carcinoma
1Oral Biology Department, Faculty of Dentistry, Universiti Teknologi MARA, Selangor, Malaysia.
2Oral Cancer Research and Coordinating Centre (UM-OCRCC), University of Malaya, Kuala Lumpur 50603, Malaysia.
3Institute of Medical Medicine and Biotechnology, Universiti Teknologi MARA, Selangor, Malaysia.
4Hospital Tengku Ampuan Rahimah, Department of Oral and Maxillofacial Surgery, Klang, Malaysia.
5Institute of Biological Science, Faculty of Science, University of Malaya, Kuala Lumpur, Malaysia.

Purpose: To identify biological, molecular function and cellular component of differentially hypermethylated genes via methylation array analysis of cancer-associated genes of oral squamous cell carcinoma (OSCC).

Methodology: A DNA methylation assay on bisulfite-converted DNA extracted from frozen section tissues of 4 normal subjects and 20 patients OSCC, was carried out using Illumina Infinium Methylation array. Raw data obtained were normalized and filtered using GenomeStudio software. The significant methylated gene list was generated using one-way ANOVA with False Discovery Rate, p-value of less than 0.05 and fold change more than 5 by Partek Genomics Suite 6.5. Gene Set Enrichment analysis was applied for cell biological process, molecular function and cellular component. From these data, we identified few significant hypermethylated genes and further validated with methylation specific polymerase chain reaction (MSPCR).

Results: High quality bisulfite-converted DNA was obtained and the methylation array was successfully run on all samples. In unsupervised cluster analysis of Partek Genome Software, normal subject samples were clustered differently from OSCC cases. A total of 279 hypermethylated genes were generated with fold change more than 5. Gene Set Enrichment analysis revealed that 17 genes were related to cell surface receptor linked signal transduction, 15 in developmental process, 15 in G-protein coupled receptor protein signaling pathway, 12 in signal transduction, 11 in anatomic structure development, and 10 each in transcription factor, cellular process regulation, metal ion transport, cell communication and transmembrane receptor activity. The significant hypermethylated genes were found significantly hypermethylated using MSPCR.

Conclusions: We reported methylation array analysis of 279 hypermethylated genes in the OSCC cases. Most of the differentially hypermethylated genes of OSCC are involved in cell signal transduction, developmental process and G-protein coupled receptor protein signaling pathway.