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Genome-wide methylation analysis of tissue DNA in oral squamous cell cancer patients

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This study explores the association between the genome-wide DNA methylation status and the occurrence of oral squamous cell cancer (OSCC). A case-control study design was applied to 34 tissue samples from 26 OSCC patients and 8 non-cancer participants. Whole-genome DNA methylation profile of the tissues was measured by Infinium HumanMethylation450 BeadChip, and the methylation levels were presented as β values. Normalization and batch effect adjustment were applied for processing these β values. We defined Δβ as the difference in the mean β values between the cancer and non-cancer groups. Probes with |Δβ| greater than 0.2 were considered for further analysis. The area under Receiver Operating Characteristic curve (AUC) was used to evaluate the discrimination ability of each probe. We also defined the differentially methylated regions (DMRs) of OSCC which may minimize potential artifacts due to random methylation alterations in single probes. Results: Among ~485,000 probes in the BeadChip, ~25,000 probes showed |Δβ| greater than 0.2 and AUC greater than or equal to 0.9. Hierarchical cluster analysis showed that the top 500 most significant probes can correctly distinguish OSCC and normal tissue samples. We identified four genes: BHLHE23, GSX1, MIR124-3, and SVIP with a great accuracy to detect OSCC tissues. We also identified 280 DMRs that included 1,097 hyper-methylated probes with 446 probes located on gene bodies (40.7%). Conclusion: This study shows that there is a strong relationship between OSCC and DNA methylation. DNA methylation can be promising epigenetic biomarkers for the detection of OSCC.

Biography

Chien Kuo Tai completed his PhD from USC Pathology and is currently working as a Professor at National Chung Cheng University, Taiwan.

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