

Methylation array analysis of tissue DNA in oral squamous cell cancer patients in Taiwan

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Purpose: The aim of this study is to perform a genome-wide methylation profile of 1,505 CpG sites of 807 cancer-associated genes and search for diagnosis and screening biomarkers for oral squamous cell cancer (OSCC).

Methods: Buccal tissue samples of 40 OSCC patients obtained from the tissue bank of China Medical University Hospital were served as the case group. A total of 15 normal samples composed the control group. Specificity, sensitivity, and the area under the Receiver Operating Characteristic curve (AUC) were calculated along with 5-fold cross validation to evaluate the accuracy of a predictive model.

Results: Thirty-four single CpG sites with both the sensitivity and specificity higher than 70% were selected as the classifier. A total of 8 panels consisted of two or three CpG sites showed a perfect specificity and a high sensitivity (85%~90%). The panel of genes ASCL1 and FLT4 represented the best combination with a perfect specificity, 90% of sensitivity, AUC=95%, and 92.6% (standard error 0.1%) of the mean correct classification rate in 5,000 times of the 5-fold cross validation.

Conclusions: In the present study we found the methylation status of the selected CpG sites might have a great potential to serve as the diagnostic biomarkers for OSCC. These promising candidate CpG sites deserve for further study in the early diagnosis and screening of OSCC.

Biography

Yu-Fen Li has completed her Ph.D in 2004 at University of Southern California. She has published more than 25 papers in reputed journals.

Chien-Kuo Tai has completed his Ph.D from University of Southern California and postdoctoral studies from UCLA. He is an associate professor at National Chung Cheng University.