



The Hypermethylation Characteristics of Tumor Suppressor Genes on Chromosome 3 in Vietnamese Nasopharyngeal Carcinoma Patients

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Abstract

Nasopharyngeal carcinoma (NPC) is a common and malignancies disease in Asia, especially China and Vietnam. Methylation status at CpG islands has been shown to be one of the etiological factors of NPC. Tumor suppressor genes located on chromosome 3, including *ADAMTS9*, *DLEC1*, *RASSF1A* and *ZMYND10* genes, play important roles in tumor initiation, development, and progression. The current study is to evaluate the methylation status of *ADAMTS9*, *DLEC1*, *RASSF1A* and *ZMYND10* genes in Vietnamese NPC patients to find out the potential biomarker for diagnosis and prognosis of NPC. This is the first case-control study of evaluating the hypermethylation characteristics of genes located on chromosome 3 in Vietnamese nasopharyngeal carcinoma patients by Nested-MSP. As the results, the frequency of *ADAMTS9*, *DLEC1*, *RASSF1A* and *ZMYND10* genes methylation were 64.29%, 80.00%, 67.14% and 77.14% in NPC samples and 17.14%, 41.43%, 12.86% and 48.57% in non-NPC samples, respectively. Statistical analysis showed that there was a significant relationship between hypermethylation characteristic genes located on chromosome 3 and Vietnamese NPC patients ($p < 0.05$). The OR results of *ADAMTS9*, *DLEC1*, *RASSF1A* and *ZMYND10* genes were 8.70, 5.66, 13.85 and 3.57, respectively. Those results are consistent with the results achieved by meta-analysis. In conclusion, the current study was the first to provide data of the association between hypermethylation characteristics of *ADAMTS9*, *DLEC1*, *RASSF1A* and *ZMYND10* genes located on chromosome 3 and Vietnamese NPC patients. Those data suggested the prolife of those characteristics could further develop promising biomarker for prognosis, diagnosis and therapy for Vietnamese NPC.

Keywords: Methylation, Nasopharyngeal carcinoma (NPC), *ADAMTS9*, *DLEC1*, *RASSF1A*, *ZMYND10*.