

**Aberrant Methylation of *HLTF* Gene in Human Esophageal Cancer**

Liang Wang<sup>1,3\*</sup>, Xiaojing Zhang<sup>1\*</sup>, Peng Yin<sup>1\*</sup>, Yan Gao<sup>5</sup>, Yuan Zhang<sup>1</sup>, Xianling Feng<sup>1</sup>,  
Si Chen<sup>1</sup>, Huimin Yu<sup>1</sup>, Weiling Huang<sup>1</sup>, Yong Huang<sup>1</sup>, Qianhe Jian<sup>1</sup>, Zhenfu Zhao<sup>1</sup>,  
Xinmin Fan<sup>1</sup> and Zhe Jin<sup>1,2,3,4</sup>

<sup>1</sup>*Department of Pathology, The Shenzhen University School of Medicine, Shenzhen, Guangdong, People's Republic of China, 518 060*

<sup>2</sup>*Shenzhen Key Laboratory of Micromolecule Innovational Drugs, The Shenzhen University School of Medicine, Shenzhen, Guangdong, People's Republic of China, 518 060*

<sup>3</sup>*Shenzhen Key Laboratory of translational Medicine of Tumor, School of Medicine, Shenzhen University, Shenzhen, Guangdong, People's Republic of China, 518 060*

<sup>4</sup>*Laboratory of Chemical Genomics, School of Chemical Biology and Biotechnology, Peking University Shenzhen Graduate School, Shenzhen, Guangdong, P.R. of China, 518 055*

<sup>5</sup>*Nanshan Hospital, Guangdong Medical College, Shenzhen, Guangdong, P.R. of China, 518 052*

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**ABSTRACT** The aim of this study was to investigate whether and at which neoplastic stage promoter hypermethylation of Helicase-like Transcription Factor (*HLTF*) is involved in human esophageal carcinogenesis. The researchers examined *HLTF* promoter hypermethylation using real-time quantitative methylation-specific PCR in 229 primary human esophageal tissues of contrasting histological types. Both *HLTF* mean normalized methylation value (NMV) and hypermethylation frequency were significantly higher in dysplastic Barrett's esophagus (Dy0.0303 and 10.0%), and esophageal adenocarcinomas (EAC, 0.0079 and 10.4%) than in normal esophagus (NE, 0.0006 and 0.0%;  $p < 0.05$  and  $p < 0.05$ , respectively). Incremental increases in the frequency of *HLTF* hypermethylation were observed during progression from NE (0.0%) to Barrett's esophagus (BE, 3.3%), D (10.0%), and EAC (10.4%). Meanwhile, *HLTF* mean NMV was significantly higher in esophageal squamous cell carcinoma (ESCC, 0.0102) than in NE ( $p < 0.05$ ). Also, *HLTF* was hypermethylated in 7.7% ESCCs. Furthermore, mean NMV of *HLTF* was significantly higher in current alcohol drinking EAC patients (0.0194) than in non-current ones (0.0066,  $p < 0.05$ ). *HLTF* hypermethylation is an uncommon event in human esophageal cancer, but occurs early in a subset of EAC, and is related to the alcohol drinking status of EAC patients.