



High methylation of the *SEPT9* gene in Chinese colorectal cancer patients

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ABSTRACT. Methylation of the septin 9 gene (*SEPT9*) occurs in higher frequency in colorectal cancer (CRC) compared to control samples, which suggests that *SEPT9* methylation is a useful biomarker for screening CRC. However, the methylation status of *SEPT9* in Chinese CRC patients is scarcely reported. In the present study, *SEPT9* methylation was tested in CRC tissues obtained from a Chinese population and correlations with pathological characteristics were investigated. The methylation status of *SEPT9* was detected using methylation-specific polymerase chain reaction (PCR)-denaturing high-performance liquid chromatography (MSP-DHPLC) in 234 colorectal tissues (172 cases, 62 controls). Samples were sequenced to confirm the results from MSP-DHPLC. The chi-squared test was used to analyze the correlation of *SEPT9* gene methylation status and pathological characteristics in CRCs. *SEPT9* gene methylation was detected in 152 of 172 (88.4%) cases of verified CRC and in 4 of 62 (6.5%) healthy controls ($\chi^2 = 137.62$, $P < 0.001$). There was no association between the methylation status of *SEPT9* and age, gender,

Duke's stage, TNM stage, differentiation, and site of cancer ($P > 0.05$). Our results suggest that *SEPT9* gene methylation is a valuable biomarker for screening CRC in the Chinese population.

Key words: *SEPT9*; Methylation; Colorectal cancer; Chinese population