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Up-regulated Expression of SNHG6 Predicts Poor Prognosis in Colorectal Cancer

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Abstract

Long non-coding RNAs (lncRNAs) have been shown to play important roles in tumor formation and development. Small nucleolar RNA host gene 6 (SNHG6) is a recently identified cancer-related lncRNA, and its role in colorectal cancer (CRC) remains to be explored. The aim of this study was to evaluate the expression and function of SNHG6 in CRC. The expression of SNHG6 was detected by real time quantitative RT-PCR (qRT-PCR) in 74 CRC tissues and matched noncancerous tissues (NCTs). Relationships between the expression levels of SNHG6 and various clinicopathological features were analyzed by Chi-square test. The Kaplan-Meier method and log-rank test were applied to compare the survival distribution between different groups. CCK8 assay and colony formation assay were used to measure the effect of SNGH6 on cell proliferation. Flow cytometric analysis was performed to measure the effect of SNHG6 on cell cycle and apoptosis. Our results showed that SNHG6 was up-regulated more than 1.5-fold in 50.0% (37/74) of CRC tissues compared with paired NCTs (P<0.0001). High level of SNHG6 expression was strongly associated with advanced tumor stage (P=0.026) and predicted poor prognosis of CRC (P=0.0215). The Cox proportional hazards model demonstrated that SNHG6 expression was an independent prognostic factor for CRC (HR, 2.568; 95% CI, 1.055-6.252; P=0.038). Furthermore, SNHG6 knockdown by siRNA could inhibit cell proliferation, cell cycle progression, and induce apoptosis. Taken together, SNHG6 functions as an oncogene in CRC and appears as a novel prognositic factor for CRC patients.