

Analyzing SIAH1 and SIAH2 as oncogenic factors in oral squamous cell carcinoma

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Backgrounds: The mortality of oral squamous cell carcinoma (OSCC) is one of the ten leading causes of cancer deaths in Taiwan. Environmental carcinogens such as betel quid chewing, tobacco smoking and alcohol drinking have been identified as major risk factors for OSCC. Our laboratory has found that the SIAH (seven in absentia homolog) family over-expressed due to gene amplification in OSCC. SIAH belongs to the N-terminus Ring-finger E3 family, and the involvement of the N-terminus Ring-finger E3s in crucial signaling pathways implicates in tumorigenesis. This study aimed at investigating the expression and functional significance of SIAH in OSCC. **Materials and Methods:** Real-time PCR were performed to examine the amplification of SIAH1 and SIAH2 gene in clinical specimens of OSCC tissues. Expression of SIAH1 and SIAH2 mRNA and protein was examined by quantitative RT-PCR and immunohistochemical assays respectively. Apoptosis was examined by annexin V staining. **Results:** Levels of SIAH1 and SIAH2 DNA and mRNA were significantly greater in clinical OSCC specimens and in cultured OSCC cells. Knockdown of SIAH1 and SIAH2 led to growth suppression and apoptosis. **Conclusion:** These results revealed a tight correlation of SIAH1 and SIAH2 overexpression with OSCC and suggest an oncogenic role of SIAH1 and SIAH2 in oral cancer.