SET Protein Regulates miRNAs Associated with Metastasis and Apoptosis in Oral Squamous Cell Carcinoma

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The SET protein, an oncoprotein involved in multiple activities, is a subunit of a complex that inhibits histone acetylation, contributing to maintaining the DNA hypermethylated and gene silencing. This mechanism plays a potential role in silencing of tumor suppressor microRNAs in cancers, including oral squamous cell carcinoma (OSCC). The modifications of histone acetylation, methylation of DNA and microRNAs levels on cancer must be better understood. Therefore, the present study aimed to investigate the role of SET protein on expression of 84 miRNAs correlated with diagnosis, progression, or prognosis of various tumor types. Two biological models were used: SET protein was i) knocked-down stably in an OSCC cell lineage (shSET HN12) and ii) overexpressed in a human kidney lineage (HEK293T/SET). The miRNA profile was analyzed by real time PCR using the Cancer RT² miRNA PCR Array (SABioscience) and TaqMan miRNA assays to confirm the selected miRNAs. The data showed three miRNAs as significantly responsive in HEK293T/SET cells (2 down-regulated and 1 up-regulated), and 65 in shSET HN12 cells (64 up-regulated and 1 down-regulated). Using Ingenuity Pathway Analysis software for data analysis the miRNAs were grouped as involved in: head and neck cancer (31); apoptosis (24) and metastasis (17). The present study shows that SET protein has important role in the regulation of miRNA level and in OSCC development.

Keywords: SET, miRNA, oral cancer, miRNA expression, apoptosis, metastasis.

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