LETTER

MicroRNA expression in patients with squamous cell carcinoma of the tongue

Dear editor,

Squamous cell carcinoma of the tongue (TSCC) is the most frequent type of oral squamous cell carcinoma and represents the sixth most frequent solid cancer around the world. TSCC is an aggressive malignancy with a propensity for rapid local invasion and metastatic spread[1].

MicroRNAs (miRNA) are a group of endogenous, non-coding, 18-24 nucleotide length single-strand RNA molecules. They influence many diverse biological functions through the repression of the transcription and/or inhibition of the translation of a large number of genes during normal development and pathological responses. It has been shown that miRNA expression profiles change in several pathological conditions, such as cancer[2].

Pairs of primary tongue carcinomas located at the anterior of the tongue and adjacent normal tissues were obtained from 12 patients, who were admitted to the Departments of oral and maxillofacial surgery of Theagenion Anticancer hospital and 'G.Papanikolaou' general hospital of Thessaloniki between April 2010 and May 2011. None of the patients received radiotherapy or chemotherapy. All patients signed a written consent for tissue donation for research purposes. The protocol was approved by the ethics committee of the Aristotle University of Thessaloniki, Greece (no, date).

MiRNA microarray was done in 12 paired samples of TSCC versus matched tongue tissues, in order to analyze differential expression of mature miRNAs. A marked difference in expression was observed in 29 miRNAs between TSCC and normal tongue tissues. Using 2-fold expression difference as a cutoff level, we identified 23 up-regulated miRNAs (20b-5p, 196a-5p, 142-5p, 96-5p, 222-3p, 15a-5p, 205-5p, 20a-5p, 146b-5p, 132-3p, 183-5p, 34c-5p, 138-5p, 135b-5p, 21-5p, 301a-3p, 7-5p, 210, 17-5p, 19a-3p, 18a-5p, 27a-3p, 32-5p) and six down-regulated (133b, 122-5p, 378a-3p, 206, 1, 125b-5p). As we observed there were some miRNAs with a remarkable overexpression in tumor cells compared to matched normal cells such as 196a-5p (37,45), 142-5p (5,94), 96-5p (6,14), 21-5p (5,46), 301a-3p (7,22), 7-5p (4,02), and 18a-5p (4,7). On the other side, five miRNAs were significantly underexpressed in tumor cells. These miRNAs are 133b (-6,82), 122-5p (-4,25), 378-3p (-4,21), 206 (-13,69), 1 (-28,29). MiR-196a is an antiapoptotic agent and performs critical roles such as gene regulation, nuclear architecture, and calcium binding. MiR-96 is targeting the forkhead box protein O1, an important tumor-suppressor that is involved in the regulation of cellular proliferation, differentiation, cell cycle progression, and apoptosis. MiR-21 is an antiapoptotic factor and targets tumor-suppressing genes, TPM1 (tropomyosin 1) and PTEN (phosphatase and tensin homolog). Furthermore, miR-21 is suggested to be an independent prognostic factor and a poor prognosis indicator in tongue squamous cell carcinomas[3]. MiR-133b is reported as a tumor-suppressor miRNA as it inhibits cell proliferation, migration, and invasion by targeting EGFR.

In conclusion, we identified several miRNAs that are dysregulated in tongue cancer and may play an important role both in the pathogenesis, and treatment of the disease. Further identification of dysregulated miRNAs and the clarification of their potential functional roles would be helpful in understanding the pathogenesis of this disease.

Keywords: Tongue squamous cell carcinoma, human genome, microRNAs, regulation, pathways

Conflict of Interest
None declared.

References

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