

Differential microRNA expression and identification of putative miRNA targets and pathways in head and neck cancers.

ABSTRACT

MicroRNAs (miRNAs) are small noncoding RNAs that involved in various cancer-related cellular processes. Diverse studies on expression profiling of miRNAs have been performed and the data showed that some miRNAs are up-regulated or down-regulated in cancer. Until now, there are no data published on the miRNA expression in head and neck cancers from Malaysia. Hence, this study aimed to investigate potentially crucial miRNAs in head and neck cancer patients from Malaysian populations. A global miRNA profiling was performed on 12 samples of head and neck cancer tissue using microarray analysis followed by validation using real-time RT-PCR. Microarray analysis identified 10 miRNAs that could distinguish malignant head and neck cancer lesions from normal tissues; 7 miRNAs (hsa-miR-181a-2*, hsa-miR-29b-1*, hsa-miR-181a, hsa-miR-181b, hsa-miR-744, hsa-miR-1271 and hsa-miR-221*) were up-regulated while 3 miRNAs (hsa-miR-141, hsa-miR-95 and hsa-miR-101) were down-regulated. These miRNAs may contribute in a simple profiling strategy to identify individuals at higher risk of developing head and neck cancers, thus helping in the elucidation of the molecular mechanisms involved in head and neck cancer pathogenesis.

Keyword: MicroRNA; Head and neck cancers; Microarray; Quanti-tative reverse transcription-PCR; In silico analysis.