Abstract

Searching for markers of disease is at the forefront of scientific interest. Biomarker of a specific disease should help in disease management - whether for diagnosing a disease or predicting its progress. We picked microRNAs - short RNAs that regulate mRNA translation, due to their stability and function in the regulation of many cellular processes. Therefore they can be used as a biomarker for many diseases. In our study we focused on neck squamous cell carcinoma (HNSCC), since this type of cancer is widespread and clinically important markers are missing. It is in our interest to seek new kinds of markers, suitable for early diagnosis of the disease and the most accurate assessment of prognosis.

We selected 3 candidate miRNA (miR-29c-3p, miR-200b-5p, miR-375-3p) and used qRT-PCR method to profile their expression in tissues of patients with HNSCC. MiRNA expressions in 42 tumor samples were compared with the miRNA expression in adjacent tissue of the tumor. Adjacent tissue surrounds the tumor and has interesting properties, as it looks like a histological normal tissue, but on closer inspection it is not. It is affected by tumor tissue and may contribute to tumor progression. We managed to distinguish between these two tissues using miR-29c-3p and miR-375-3p. Additional analyzes were focused on miRNA expression and their correlation with clinic-pathological condition of the patient. We found the link between node positivity and expression of miR-200b-5p. MiR-29c-3p and miR-200b-5p were associated with tumor grade. Survival analysis revealed connection between miR-29c-3p and patients prognosis. Overall, these results are useful for assessment of selected miRNAs as diagnostic and prognostic biomarkers of HNSCC.