ABSTRACT

Breast cancer is the most frequent cancer in women and is prognostically very heterogeneous. Early breast cancer has an excellent overall prognosis with long-term survival above 90%. In this group we can also find patients with highly unfavourable progress with a risk of future disease relapse. Due to effective anticancer treatment is a main task of precise clinical decision to determine risk of an individual patient in the term of cancer relapse. We can use clinical (tumor diameter, lymph nodes) and pathological markers (grade, ER, PgR, HER2, and Ki-67), all of them have low individual sensitivity and specificity. Molecular tests based on multigene DNA or RNA assays have higher sensitivity and specificity but their interrelated concordance is low. One of the main scientific task is to find almost specific and sensitive prognostic biomarkers.

microRNAs are small, highly stable, non-coding RNAs, which regulate tens of mRNAs and proteins inside cells. In cancerogenesis, they could act as oncogenes or tumor supressors as well and affect main steps of initiation and progression of cancer. One of the scientific directions is to determine their prognostic significance. Many experimental and clinical studies defining prognostic significance of miRs in early breast cancer was published but their data were very different.

Our project analyzed expression of miR-155, miR-24, miR-181b a miR-19a in sera of patients with early breast cancer. All miRs were significantly over-expressed in time of diagnosis in comparison to healthy controls. After surgical tumor removal and adjuvant therapy declined and normalized expression of all miRs with different dynamics. High-risk patients had significantly higher expression of miRs in comparison with low-risk group. Patients in high-risk group had slower and less profound decline of miRs after anticancer treatment. Low-risk patients normalized miRNAs expression after anticancer treatment, but this wasn't visible in high-risk group. Serum expression of miR-155 and miR-24 improved prediction of cancer relapse independently of the other parameters. Only expression of Ki-67>20% specified relapse probability along with expression of miR-155 and miR-24. In multivariate analysis we confirmed that neither of chemotherapy, radiotherapy and hormonal therapy were able to significantly change expression of miR-24, miR-155 and affect disease relapse. Serum expression of miR-24 and miR-155 could act as independent prognostic biomarkers.