

Abstract

Acute myeloid leukemia (AML) is a very heterogeneous disease associated with cytogenetic aberrations and genetic mutations. Many of these changes have been revealed and their detection became usual part of the diagnostic process today. However, changes of expression profiles of small, noncoding RNAs, so called microRNAs (miRNAs), are less known and not used for diagnostics yet. These RNAs, 19-24 nucleotides long, take part in the regulation of expression of different genes through complementary base pairing to the 3' non-translated region (3'UTR) of the target messenger RNA (mRNA). They can influence key processes of the cell, like differentiation, proliferation or apoptosis.

The changes in expression of different miRNAs are known from different types of cancers. In solid tumors, they are usually detected from bioptic samples; but also plasma samples are now in the center of attention as so called liquid biopsies providing the information about molecular genetic events in the organism. Many studies have revealed deregulated miRNAs in the bone marrow, full blood or isolated progenitor cells (CD34+) of AML patients, only four of them have analyzed plasma samples. We focused on the plasma samples and we targeted on such miRNAs, which levels differ at AML diagnosis and after the chemotherapy. Out of more than 750 examined miRNAs, we have found and validated 6 miRNAs differently expressed between the AML patients at diagnosis and healthy controls; their levels also correlated with the disease development.

As a part of study of possible mechanisms of AML pathogenesis, target genes of miRNAs found in microvesicles released by cancer cells and able to fuse with macrophages and theoretical possibility of influencing the macrophages by these miRNAs were also investigated.

Keywords:

Acute myeloid leukemia (AML), microRNA (miRNA), plasma, chemotherapy