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PROFILING KARYOTYPE-DEPENDENT PATTERNS OF miRNA EXPRESSION IN ACUTE PROMYELOCYTIC LEUKEMIA

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Acute promyelocytic leukemia (APL) is a subtype of acute myeloid leukemia (AML), with a balanced reciprocal translocation t(15; 17) (q24.1; q21.1) detected in most cases. Acute leukemia progression is accompanied by the occurrence of genetic and epigenetic modifications, including microRNA. The aim of the work is to analyze the role of differential miRNA expression in APL, depending on the cytogenetic properties of tumor cells. The study used cytological specimens containing bone marrow smears: APL with t(15; 17) (q24.1; q21.1) ($n = 7$), normal-karyotype APL ($n = 8$) and benign tumors (BT) ($n = 20$). Analysis of expression levels of miR-128, miR-150, miR-155, miR-26a, miR-181b, miR-29b, miR-20a, miR-223, miR-92a, miR-100, miR-126, miR-451, miR-103a, miR-191, and miR-378 was performed by RT-qPCR. The markers differentiating between BT and APL, no matter which karyotype, are miR-150, miR-26a, miR-29b, miR-20a, miR-223, miR-126, and miR-451a ($P < 0.05$). Expression levels of miR-128 ($P = 0.020513$) and miR-155 ($P = 0.013986$) are statistically different between APL with t(15; 17) (q24.1; q21.1) and normal-karyotype APL. The results obtained confirm the epigenetic regulation of APL; however, the miRNAs in question lie beyond t(15; 17) (q24.1; q21.1), suggesting the presence of more complex, staged regulatory pathways underlying APL.

Keywords: microRNA, acute promyelocytic leukemia, acute myeloid leukemia, t(15, 17) (q24.1, q21.1), *PML-RARα*