miR-1250-5p is hypermethylated in non-Hodgkin's lymphoma

Min Yue Zhang

Lu Qian Wang

James Chim

Video Byte

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Abstract

Non-Hodgkin lymphoma (NHL) is one of the most common cancers worldwide. To better understand factors involved in carcinogenesis, a recent study examined the contribution of one class of proteins. MicroRNAs (miRNAs) are small non-coding RNAs that regulate the expression of target genes. The study focused on one miRNA family member: miR-1250, which is embedded in the second intron of its host gene, apoptosis-associated tyrosine kinase (AATK). Researchers studied the methylation status of AATK/miR-1250 in healthy controls compared to that in lymphoma cell lines and 120 primary lymphoma samples. They found that while AATK/miR-1250 was not methylated in healthy peripheral blood and tonsils, in NHL cell lines and patient samples, methylation was detected, correlating with repression of miR-1250-5p and AATK expression. Restoring miR-1250-5p resulted in decreased cell proliferation as well as enhanced apoptosis and cell death. MAPK and WDR1 were identified as direct targets of miR-1250-5p, and their expression was inversely correlated with miR-1250-5p levels in primary NHL samples. These results suggest that miR-1250-5p acts as a tumor suppressive intronic miRNA that is co-regulated and silenced by methylation of its host gene in NHL. Targeting this pathway may help to develop new treatments, improving the prognosis for those with NHL.