The retroposition process by which processed mRNA of an existing gene (parental gene) is reverse transcribed into cDNA and reintegrated into the genome results in an additional copy (retrocopy). Many retrocopies are nested in the introns of other genes (so-called host genes). Numerous studies show that retrocopies, initially considered transcriptionally inactive, often become functional in the course of evolution - we are talking then about retrogenes. The growing amount of data from high-throughput experiments enables the identification of new functional retrogenes. The relationship between the expression level of retrogenes and the incidence of tumors has been described in the literature. Retrogenes can regulate the expression of other genes, including parental and host genes. This is especially important when parental or host genes are critical to cancer development. Interestingly, the phenomenon of retroposition was especially potent during the evolution of primates. Hence, research hypotheses have been raised that many retrogenes with altered expression in cancer represent important non-coding RNAs regulating other cancer-related genes. We also speculate that the high rate of neoplastic transformation in humans may be due to the presence of a large number of such retrocopies in the human genome.

Our pilot studies have identified retrogenes with altered expression levels in two human cancers, including both primate-specific retrogenes and evolutionary old retrogenes. It has also been shown that genes described in the literature as related to cancer can be regulated by their retrogenes.

The aim of the proposed project is a large-scale analysis of the retrogene expression profile in human tumors to determine if there is any relationship between the high percentage of retrocopy and neoplastic changes in humans. The project will be based on the analysis of bioinformatic transcriptomic data (RNA-Seq) from the repositories, such as The Cancer Genome Atlas, and NCBI GEO, as well as experimental research, to decipher the functional meaning of selected retrogenes. The obtained results will be collected in the form of a database illustrating the retrogene expression profile in human cancer.

The topic of this project, the relationship between a large number of retrocopies and human tumor transformation, has never been studied before. Comprehensive bioinformatics and experimental analyzes of retrogenes and their parental/host genes may allow the evaluation of the role of retrogenes in human cancer. Identification of new, functional retrogenes will be of cognitive importance and possibly provide insight into the pathways regulating already known genes that play a role in cancer cells.