

DESCRIPTION FOR THE GENERAL PUBLIC (IN ENGLISH)

According to Central Dogma of Molecular Biology, the genetic information flows in the following processes: i) transcription, where RNA is synthesized from DNA (deoxyribonucleic acid) template and ii) translation, in which the information from RNA is used to produce a protein. Long noncoding RNAs (lncRNAs) are a special class of RNA molecules, playing a role in a number of significant processes, either in the cytoplasm or in the nucleus. Increasing studies indicate that they are implicated in human diseases, especially in cancers. Despite the large number of studies identifying nuclear lncRNAs, to date only a handful of them have been functionally characterized. It is known, that nuclear-retained lncRNAs can be involved in alternative splicing process, which provides a protein diversity as well as in chromatin remodeling that leads to changes in gene transcription. More and more research indicate a change of lncRNAs expression level in cancer. Furthermore, the alterations of alternative splicing and chromatin structure modifications are also observed in tumour cells. Thus, it can be speculated that lncRNAs are associated with carcinogenesis by regulating the above mentioned processes.

The aim of the project is to investigate the role of preselected lncRNAs, associated with carcinogenesis, in two nuclear processes: alternative splicing regulation and chromatin structure modulation. The research conducted by us includes identification of interactions between lncRNAs and proteins, being involved in the processes. All the experiments will be performed on HEK293T cells, derived from human kidney tissue, using novel molecular techniques and bioinformatics approaches.

As long noncoding RNAs included in this project show deregulated expression level in different cancers, they constitute promising candidates for further study. Our own research has already shown that one of these lncRNAs affects activity of a known oncogene. Deciphering the acting way of lncRNA in basic cellular mechanisms will bring us closer to understanding their action mechanisms in cancer development and progression.