Laryngeal squamous cell carcinoma (LSCC) belongs to the very heterogeneous group of cancers, namely Head and Neck Cancers (HNSCC). Despite the progress in medical approach the overall 5-year survival rates is still very low, around 60%. Therefore, there is still a need to understand LSCC biology.

The Department of Cancer Genetics expands the knowledge about genetic background of LSCC pathogenesis. In recent years we have described many alternation on DNA, RNA and protein level in this type of cancer.

Our new aim, since 2012, is an investigation of miRNAs involvement in LSCC. It is well known that miRNAs are important players in regulation of crucial cellular processes and every changes of their expression level has an impact in cancer-related parameters such as cell proliferation, apoptosis or migration.

The proposed project is a continuation of our previous study "An attempt to identify microRNA involved in laryngeal cancer pathogenesis". Now we would like to focus on potentially tumor suppressive miRNA in LSCC. Our preliminary results indicate that miR-299-5p is down regulated in LSCC and potentially regulates 14 putative oncogenes (*CALU, MBNL1, PURB, ZNF354A, STX16, PATZ1, EWSR1, MARCKS, KITLG, TFAM, NSMAF, HBP1, PHF20L1, and ZNF800*).

The main aim of this project is to demonstrate the biological function of miR-299-5p in LSCC.

We plan to perform functional analysis which gives us an answer which genes, selected by *in silico* analysis, are the real target gene of miR-299-5p. For this purpose, firstly we will conduct real-time qPCR to confirm overexpression of selected genes in LSCC compared to non-cancerous controls. Next step will be to perform a verification of direct interaction between miR-299-5p and the genes with the highest overexpression in LSCC.

Moreover, we will verify in which cancer-related process miR-299-5p is involved. This step will be conducted using three different functional assays (proliferation, adhesion and migration) on two cell lines transfected by miR-299-5p mimic.

We assume that this approach will give us an answer if miR-299-5p is involved LSCC pathogenesis, as well as it will determine its target genes with putative oncogenic character.

In conclusion, proposed project will expand the knowledge in the field of genetic background of LSCC as well as it will allow to discover new factors engaged in pathogenesis of this cancer.