Pituitary adenomas are common intracranial tumors representing up to 15% tumors of brain location. Different subtypes of PAs are classified based on WHO recommendations. Gonadotroph adenomas are one of the most common subtypes of pituitary tumors that are developed from cells type of pituitary gland. Gonadotroph tumors, just as pituitary tumors in general are commonly considered as benign, however, tumor invasive growth is observed in large proportions of patients. It's one of most important prognostic factor and is believed as cause of inability of complete tumor surgical resection, aggressive growth and local recurrence.

Efforts are made to reveal the biological background of invasiveness of pituitary tumors and identify the particular protein, genes and other biological factors on cell level involved in invasive growth. Such molecules could potentially serve as indicators for clinical decisions regarding additional treatment and observation of patients. Additionally they could serve as a target for novel rational therapeutic approach.

We recently identified one of microRNA particles hsa-mir-184 as related to invasive growth in gonadotroph PAs. MicroRNA represent a class of regulatory molecules that regulate protein synthesis and as a consequence cell functionality. Abnormalities of microRNA molecules affect the balance of protein levels in the cell and disturb cell's proper functions. This can contribute to neoplastic transformation and a number of microRNA particles have been identified to play a role in development of cancer.

**The aim of the project is to evaluate the role of hsa-mir-184 in pathogenesis and invasive growth of gonadptroph pituitary adenoma (PA).**

**We hypothesize that disturbed regulation of expression of gene encoding *MIR184* result in increased expression of this microRNA and contribute to the invasive growth of pituitary tumor through unknown mechanism.**

DNA methylation is a process of adding methyl groups to DNA in cells. It is a key process in regulation of gene expression and as a consequence plays an important role in functioning of cells. Our previous studies suggest that the abnormal regulation of *MIR184* gene found in our study is due to disrupted DNA methylation process. Therefore, our project includes the assessment of DNA methylation of *MIR184* gene in patients.

To investigate the functional role of miR184 in pituitary tumor growth and explain possible mechanism, we also need to conduct some experiments on cells. Two different types of rat cells, which were derived from pituitary adenomas, will serve as a model. We will transiently elevate natural level of miR184 in these cells and afterwards observe and measure selected cell properties.

Such project design will let us confirm if the aberrant regulation process of miR184 is due to disrupted DNA methylation and describe possible role of this miRNA in more aggressive growth of pituitary tumor cells.