

**2017-2020 – project No S-MIP-17-108 "The prognostic value of miRNA classifier as a novel tool for prediction of glioma patient outcome and response to therapy", funded by the Research Council of Lithuania, dr. P. Vaitkienė**

Acronym: GREAT (Glioma RNA Expression Answer for Therapy)

Glioma is one of the most common brain tumors with the characteristic feature of poor treatment response, short survival, significant functional impairment and high risk of disease progression. Prediction of outcomes after brain surgery is critical for treatment guidance and optimized use of healthcare resources. Molecular markers are able to complete the gap between surgery and individualized treatment of disease. The most promising molecular markers are small non-coding micro-RNAs which were largely described as bio-markers for the disease prognostication and treatment guidance. Scientific studies generated numbers of the data about miRNAs expression as a promising marker for gliomas. However, the data about the expression of individual miRNA hardly ever can be applied as a marker for evaluation of such heterogeneous disease as glioma. For this purpose, we will analyze expression of 15 miRNAs as a complex, which enables to prognosticate glioma progression and response to treatment. Uniqueness and novelty of the miRNAs set comes from several points: the analysis will include low and high grade astrocytomas for a deeper understanding of miRNA in gliomagenesis to set more reasonable markers for tumor prognosis and response to therapy. The second unique point of the project also comes from its multidisciplinary approach to patients' functional status assessment. During the project, we will gather comprehensive information about patient health status, psychological and neuropsychological functioning, and quality of life. This approach will allow us to analyze the clinical importance of miRNA expression information in much broader clinical and psychological contexts. Such multidisciplinary approach to set up molecular biomarker is highly novel in Lithuania as well as worldwide. Moreover, evaluation of miRNA level in patient blood serum will give important information about the application of circulating miRNA as biomarker using minimal interventions. The prognostic value of miRNA set will be compared with the hallmarks for glioma signature - MGMT methylation and IDH mutation. Finally, all the molecular findings and collected patient data will be used together for the establishment of an algorithm to prognosticate and choose a suitable strategy of therapy using miRNAs set expression data.