Glioblastoma multiforme (GBM), the most common and aggressive primary brain tumor, is extremely resistant to current treatment paradigms and has a high rate of tumor recurrence. It is not only the most common but also the most malignant tumor of the Central Nervous System (CNS) with the median survival for GBM patients is between 12 and 14 months from diagnosis, and the five-year survival is observed in only 5% of cases. CNS tumors, account for only 2% of all diagnosed primary tumors. However, despite in such a low frequency, they are responsible for nearly 10% of deaths in patients suffering from cancer. Due to the very aggressive and invasive nature of gliomas, a contemporary treatment regimen involving resection of the tumor, radiotherapy and chemotherapy, does not give satisfactory results.

Aggressive growth of GBM tumors and the difficulty of developing an effective treatment regimen moved to the intensive research in order to know and understand the changes occurring at the molecular level, which could become the basis for new therapies. Several studies of gene expression profile showed significant differences between tumors and allowed to divide glioma subtypes, which in traditional histopathological methods are indistinguishable.

The last years of the development of molecular biology have brought success in the human genome sequencing project, followed by the great hopes and expectations in the context of medicine and therapy.

The human genome project provided, on the one hand information on the genome, but on the other hand, pointed out that the part that was considered as the most important- the protein encoding part, constitutes only 2% of the entire genome. Currently, it is believed that many of the molecules affecting e.g. tumor growth, are located within that noncoding part of the genome, where function as regulators of gene expression.

With the changes in the gene expression level t are also directly related the changes in the level of micro RNAs (miRNA) - short, non-coding RNAs, modifying the expression of genetic information.

The presence of multiple molecules, that could be crucial for tumor development as potential therapeutic targets, such as miRNAs was also established in glioma tumor cells. Recently, there were reports of the identification of the so-called miRNA-like molecules and the circular RNAs (circRNA). Both these RNAs are class of non-coding RNAs with potential regulatory capacity, and yet undefined role in the development and progression of brain tumors.

One of the main features that distinguish GBM from other cancers is its extraordinary diversity in terms of its constituent cells- so called heterogeneity of the tumor. It is assumed now that one of the most important cells for the development of GBM are glioma stem cells (GSC). The GSC's characteristic is extremely important, because they determine processes such as: unlimited cell proliferation, the ability to form secondary cancers, and finally resistance to the conventional chemotherapeutic agents. It is now suggested that GSC may be responsible for tumor progression, resistance to treatment and tumor relapse. Therefore, understanding the biologically significant pathways involved in modulating GSC-specific characteristics offers a great promise for development of novel therapeutics, which may improve therapeutic efficacy and overcome present drug resistance.

The main object of the project is the identification and the function characteristics of two new classes of ncRNA: circRNA and sno-miRNA in GBM, but more importantly in glioma stem cells (GSC).

In order to know the function and regulatory mechanisms of ncRNAs of interest to further exclude those that stimulate tumor growth and raise the level of RNA that affect the limitation of its development, nucleic acids-based technologies will be used: sno-miRNA inhibitors (antago-sno-miR (ASO) and synthetic double-stranded RNA (ago-sno-miRNA mimics RNA). To reduce the expression level of circRNA crucial for GBM development, it will be applied modern technology genome editing - the CRISPR / Cas9. The function of the ncRNAs of interest will be evaluated not only in cell line culture, but also *in vivo* in animal model (mouse xenografts).

The use of the above mentioned tools allows to describe and understand the new interaction in GBM biology, and the implemented for realization studies in a mouse model may be used for selection of potential new therapeutic targets in the future.