Description for the general public

Among gliomas, the most common aggressive primary brain tumor is glioblastoma, which accounts for more than half of the tumors that originate from glial or glial precursors. Therefore, it is extremely important to understand the molecular mechanisms involved in this pathological condition. One of the unusual suppressor genes, the function of which has not been fully understood in glioblastoma, especially at the molecular level, is the *WWOX* gene. Studies show that the level of its expression in glioblastoma is reduced compared to normal tissue or tissues with a lower degree of malignancy. It has been observed that congenital mutations of the *WWOX* gene cause loss of protein functionality, and thus serious neurological defects such as spinocerebellar ataxia-12 (SCAR12) or WWOX-related epileptic encephalopathy (WOREE). In addition, the *WWOX* gene also plays a role in the development of the Central Nervous System (CNS), being responsible for preventing neuronal damage or neurodegeneration by limiting pathological protein aggregation. Preliminary results based on bioinformatics analysis of the risk of disease recurrence and survival depending on the level of *WWOX* expression indicate a lower risk of disease recurrence and longer survival of patients with high level of the examined gene. Moreover, *in silico* analysis shows that *WWOX* regulates other genes. The results obtained from *in vitro* tests also indicate that the high expression of *WWOX* has a positive effect on the inhibition of the studied tumor growth. Therefore, the project aims to perform a global analysis of gene expression at the transcriptome and promoterome level and biological tests in the created research models to assess basement membrane migration, proliferation, apoptosis and cytoskeleton rearrangement. In addition, the analysis of WWOX protein co-localization with proteins selected on the basis of sequencing results will allow to understand their interactions in specific cell compartments.