



**Fund “Nauka” Project № 24002 Resume – Special Competition-based Session
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“Analysis of the expression of long non-coding RNA in neurogenic niches of the primate brain”

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Long non-coding RNA are a diverse group of non-coding ribonucleic acids with lengths exceeding 200 nucleotides. They exhibit high tissue and species specificity, and their abundant expression in the brain makes them attractive targets for the diagnosis and treatment of neurological diseases.

Adult neurogenesis is the process of generation of neurons from neuronal stem/progenitor cells in specific regions of the adult brain, known as “neurogenic niches”. These include the subventricular zone of the lateral ventricle (SVZ) and the subgranular zone of the hippocampal dentate gyrus (SGZ). While there are many known protein-coding genes that are expressed in neuronal progenitors and regulate their regenerative potential, little is known about the lncRNA expression in the context of neurogenesis in the primate brain.

The aim of this project is to discover lncRNA transcripts in the transcriptome of the adult primate neurogenic niche SVZ following cerebral ischemia. Cerebral hypoxia induces the expression of transcripts which can promote the proliferation and differentiation of neuronal stem cells. While previous studies have primarily focused on protein-coding gene transcripts, we will investigate the role of lncRNA.

We will utilize an existing next-generation RNA sequencing dataset from our previous study, which demonstrated the transcriptomic changes in protein-coding genes in the primate SVZ following global cerebral ischemia. Through bioinformatics re-analysis of this dataset, we will identify lncRNA candidates, employ histological techniques to visualize their expression in tissue sections, and determine which cell types within the neurogenic niches express specific lncRNA.

Within the framework of the project the team will report for the first time:

1. The long non-coding RNA (lncRNA) genes that selectively alter their expression following ischemia in the adult primate anterior subventricular zone (format: Excel tables and diagrams);
2. The in situ expression of two lncRNA genes in the regions of interest on brain tissue sections from control and ischemic animals (format: micrographs and statistical data regarding the strength of lncRNA gene expression). The images will be publicly

available in the open-access online database MONKEY-NICHE (<http://monkey-niche.org>);

3. The phenotypic characteristics of the cells expressing the selected lncRNA (format: micrographs and data on the percentage breakdown of the different cell types, expressing specific lncRNA, within the regions of interest).