

The goal of the project is to identify spatial gene expression signatures of currently used antipsychotic drugs, and use them for comparison with two novel drug candidates with antipsychotic potential. Planned research is based on a recently developed approach that permits to spatially map abundances of transcripts using next-generation sequencing. In this way, we expect to identify in a mouse model spatial gene expression signatures induced by clozapine and risperidone, and then compare them with novel antipsychotic drug candidates. Spatial gene expression analyses will also be performed in B6.Del16+/Bdh1-Tfrc genetically modified mice, which have the equivalent of the human 3q29 microdeletion, causing impairments similar to those observed in schizophrenic patients, including impaired social behaviors and cognitive functions ³. Thus, by testing the effects of antipsychotics on spatial gene expression in mutant mice we aim to identify patterns relevant to the clinical benefits.