DESCRIPTION FOR THE GENERAL PUBLIC

Tumors of hormone-dependent tissues like breast, ovarian and prostate cancers are among women second and fifth as well as among men second cause of death worldwide, respectively. Therefore, it is very important to understand molecular mechanisms associated with progression and disease recurrence. Notch signaling is evolutionarily conserved pathway, which in physiology regulates essential biological processes such as proliferation, differentiation, organogenesis, angiogenesis and participates in epithelial-to-mesenchymal transition in pre- and postnatal life. Recent studies indicate that Notch pathway is also significant participant in tumor biology and its character has not been fully elucidated. Preliminary research based on bioinformatic analyses of correlation of disease recurrence risk and expression profiles of particular Notch pathway members showed that dependently on tissue type and molecular subtype of cancer, Notch genes demonstrate distinct associations with disease-free survival. In prostate cancer, lowered expression of majority of Notch genes correlated with better prognosis, in contrast to ovarian cancer. Moreover, bioinformatic analysis indicated biological differences between favorable and unfavorable prognosis groups. Hence, this proposal assumes deepening the state of knowledge regarding biological processes leading to disease recurrence in ovarian, breast and prostate cancers that are regulated by Notch signaling as well as determination of its predictive potential and identification of potential therapeutic targets. To achieve these aims several bioinformatic algorithms will be employed including Gene Set Enrichment Analysis for determination of biological differentiation, EnrichmentMap and BioLayout Express 3D for visualization of Notch crosstalk with different pathways, ExpressCluster for identification of potential therapeutic targets and Multiple Factor Analysis for determination of predictive potential of Notch genes.