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RESEARCH AREA

Over the past decade, an extremely large amount of omics data has become publicly available. Data processing is ongoing, with suboptimal biomedical use. Our research group aims to find answers to unsolved clinical problems using the available data. Our main area of interest is the regulation of gene expression. Over the last few years, several oncologically relevant translocations have been shown to induce tumour cell proliferation by fusion of a cell-specific, highly active super-enhancer with an oncogene. Superenhancers can be identified by bioinformatic methods using chromatin-level markers. The key proteins involved in the function of superenhancers are now being mapped, and small molecules that inhibit their function are available. One such key protein is BRD4, a bromodomain protein with a role in the recognition of acetylated histone and thus the linking of enhancer and promoter regions. Several clinical trials are currently underway to test the efficacy of BRD4 inhibitors in malignancies. Our research aims to understand further details of how superenhancers work. We focus on breast cancer because a significant amount of multi-omics data is available. Significant basic research has already mapped several breast cancer cellular models at the molecular level and these data are freely available for further research. Complemented by the significant number of clinical genomics projects, there is a good chance to better understand the role of super-enhancers in tumorigenesis, stratification and identification of new treatment approaches.

TECHNIQUES AVAILABLE IN THE LAB

In our group, you can learn in vitro and in silico techniques. Our main interest is the study of gene expression and its regulation at the whole genome level in cellular systems. Therefore, students coming to us will learn cell culture techniques, the treatment, manipulation of cell lines, DNA and RNA isolation, quality control of nucleic acids, PCR and QPCR techniques. The entry stage of data analysis techniques is RNA sequencing data analysis on Galaxy platform, later on statistical data processing of genomic data and data visualization will be performed in R programming environment. The use of machine learning methods is

the third stage of data analysis. All these techniques are aimed at dissemination of scientific results and publication, therefore students will also receive expert training in this area.

SELECTED PUBLICATIONS

Bojcsuk, D., Nagy, G., **Bálint, B.L.** (2017) Inducible super-enhancers are organized based on canonical signal-specific transcription factor binding elements. **Nucleic Acids Research** **45**: 3693-3706 Oxford University Press

Ozgyin, L., Horvath, A., Hevessy, Z., **Bálint, B.L.** (2019) Extensive epigenetic and transcriptomic variability between genetically identical human B-lymphoblastoid cells with implications in pharmacogenomics research. **Scientific Reports** **9**: 4889 Nature Publishing Group

Bojcsuk, D., Nagy, G., **Bálint, B.L.** (2020) Alternatively constructed estrogen receptor alpha-driven super-enhancers result in similar gene expression in breast and endometrial cell lines. **Int J Mol Sci** **21**: 1630 Multidisciplinary Digital Publishing Institute

Erdős, E., **Bálint, B.L.** (2020) NR2F2 orphan nuclear receptor is involved in estrogen receptor alpha-mediated transcriptional regulation in luminal a breast cancer cells. **Int J Mol Sci** **21**: 1910, Multidisciplinary Digital Publishing Institute

Gargya, P., **Bálint, B.L.** (2021) Histological Grade of Endometrioid Endometrial Cancer and Relapse Risk Can Be Predicted with Machine Learning from Gene Expression Data. **Cancers** **13**: 4348 Multidisciplinary Digital Publishing Institute