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RESEARCH AREA

The main projects of our research group: 1. Genetic regulation in various viral families: We have been assembling the transcriptome atlases of various viruses using short- and long-read sequencing technologies. We have currently been investigating the following viruses: herpes simplex virus, pseudorabies virus, varicella-zoster virus, human cytomegalovirus, Epstein-Barr virus, vaccinia virus, influenza virus, a baculovirus, an endogenous retrovirus, a circovirus, various RNA viruses, etc. Additionally, we have been examining how the transcriptions as well as the transcription and the DNA replication are interrelated with each other. We have put forward two hypotheses for assuming a genome-wide interplay among the transcription and replication machineries, which are the Transcription Interference Network (TIN) hypothesis and the Transcription and replication Network (TRIN) hypothesis, respectively. 2. Generation of intelligent viral vectors for brain research: Application of genetically modified pseudorabies virus for tansneuronal tract-tracing, as well as analysis of neural activity using optical methods. 3. Examination of the genetic basis of major depression and suicide: high-coverage whole-exome analysis of depression. 4. Various microbiome research projects since 2019 have been launched.

TECHNIQUES AVAILABLE IN THE LAB

1. Long-read and short-read sequencing: Illumina next generation sequencing; Oxford Nanopore Technologies and Pacific Bioscience third-generation sequencing platforms. We have tested various methods using these platforms, including Cap-selection, direct RNA sequencing, targeted sequencing, etc. 2. Molecular cloning: application of restriction endonucleases and CRISPR-Cas9 technology, recombinant virus technology, etc. 3. PCR and real-time RT PCR: These techniques are used for quantitative analysis of gene expression. 4. Microscopy: light microscopy, as well as, confocal and fluorescence microscopy.

SELECTED PUBLICATIONS

Tombácz, D., Prazsák, I., Szűcs, A., Dénes, B., Snyder, M., **Boldogkői, Z.** (2018) Analysis of the transcriptome of Vaccinia virus using long-read sequencing techniques. **GigaScience 7:** 139.

Tombácz, D., Prazsák, I., Moldován, N., Szűcs, A., **Boldogkői, Z.** (2018) Lytic Transcriptome Dataset of Varicella Zoster Virus Generated by Long-read Sequencing. **Front Genet 9:** 460.

Balázs, Z., Tombácz, D., Szűcs, A., Snyder, M., **Boldogkői, Z.** (2017) Long-read sequencing of the human cytomegalovirus transcriptome with the Pacific Biosciences RSII platform. **Sci Data 4**: 170194.

Tombácz, D., Maróti, Z., Kalmár, T., Csabai, Z., Balázs, Z., Takahashi, S., Palkovits, M., Snyder, M., **Boldogkői, Z.** (2017) High-coverage whole-exome sequencing identifies candidate genes for suicide in victims with major depressive disorder. **Sci Rep 7:** 7106.

Fekete, R., Cserép, C., Orsolits, B., Martinecz, B., Lénárt, N., Tóth, K., Méhes, E., Szabó, B., Németh, V., Gönci, B., Sperlágh, B., **Boldogkői, Z.,** Kittel, Á., Baranyi, M., Ferenczi, S., Kovács, K.J., Szalay, G., Rózsa, B., Webb, C., Hortobágyi, T., West, B.L., Környei, Z., Dénes, Á*. (2018) Microglia control neurotropic virus infection via P2Y12-mediated recruitment and phagocytosis. **Acta Neuropathologica 136:** 461-482.