

Čestmír Vlček

cestmir.vlcek@imq.cas.cz

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www.img.cas.cz/research/cestmir-vlcek



LABORATORY OF

GENOMICS AND BIOINFORMATICS

genome analysis, transcriptome analysis, next-generation sequencing, cancer genomics

In the picture:

1. Václav Pačes | 2. Jakub Rídl | 3. Michal Kolář | 4. Hynek Strnad | 5. Čestmír Vlček | 6. Miluše Hradilová | 7. Šárka Pinkasová | 8. Jan Pačes To understand the evolution of eukaryotes and the developmental processes that they regulate, it is necessary to analyse their genomes and transcriptomes. Genome sequences are the ultimate source for phylogenomics. Single-cell eukaryotes (protists) with their branching close to the root of the evolutionary tree are the best candidates for genome studies. The availability of the genomic sequences will allow inferences to be made about the gene complement of the common eukaryotic ancestor. The main interest is also focused on endosymbiotic origin of two emblematic organelles of the eukaryotic cell, the mitochondrion and the plastid. Using next-generation sequencing platforms we characterize genomes and transcriptomes of many protist species. Adding genome sequences from diverse protists to currently available eukaryotic genomes enables us to deduce, with much higher accuracy, details of many steps and processes of evolution of the eukaryotic cell. A second major topic of our group is directed towards molecular diagnostics and personalized medicine. We study intracellular interactions in malignant melanoma and in tumour-associated fibroblasts using genomics tools. We also participated in characterization of so far the oldest endogenous lentivirus found in the genome of mammalian order Dermoptera. We defined the age of this virus when it infiltrated the Dermoptera lineage and obtained evidence of the coevolution of antiviral factor TRIM5-alpha.

Selected recent papers:

Karnowska A, Vacek V, Zubáčová Z, Treitli S C, Petrželková R, Eme L, Novák L, Žárský V, Barlow L D, Herman E K, Soukal P, <u>Hroudová M</u>, Doležal P, Stairs C W, Roger A J, Eliáš M, Dacks J B, <u>Vlček Č, Hampl V: A Eukaryote without a Mitochondrial Organelle. **Curr Biol 2016**, 26:1274-1284.</u>

Ševčíková T, Klimeš V, Zbránková V, <u>Strnad H, Hroudová M, Vlček Č</u>, Eliáš M: A Comparative Analysis of Mitochondrial Genomes in Eustigmatophyte Algae. **Genome Biol Evol. 2016**, 8:705-722.

Hron T, Farkašová H, Padhi A, <u>Pačes J.</u> Elleder D: Life History of the Oldest Lentivirus: Characterization of ELVgv Integrations in the Dermopteran. **Genome. Mol Biol Evol. 2016**, 33:2659-69.

