



Laboratory of Genomics and Bioinformatics

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

Čestmír Vlček

cestmir.vlcek@img.cas.cz

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

Genome sequences are the ultimate source for phylogenomics. To understand the evolution of eukaryotes and the developmental processes that they regulate, it is necessary to analyse their genomes and transcriptomes. We sequenced transcriptomes of two multicellular eukaryotes, both of phylum Radiata, sweet water medusa *Craspedacusta sowerbyi* and cubozoan *Tripedalia cystophora*. The expression of selected developmental genes was characterized in situ. 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, namely *Diplonema papillatum*, *Mastigamoeba balamuthi*, *Andalucia godayi* and *Malawimonas*. Adding genome sequences from diverse protists to currently available eukaryotic genomes enables us to deduce, with a much higher accuracy, details of many steps and processes of the evolution of the eukaryotic cell. A second major topic of our group is directed towards cancer genomics. Using the Illumina microarray technique, we study intracellular interactions in malignant melanoma and identify markers

specific for different cancers. We also analyse the endogenous retroviral elements in human that are associated with cancers and explore the anticancer effects of statin.

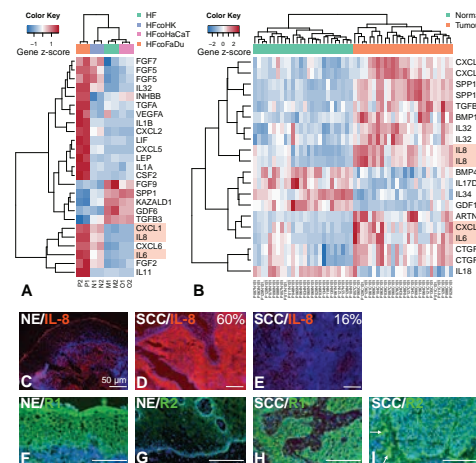


Fig. 1. Expression changes of genes coding for paracrine factors in human fibroblasts cultured with the epithelial cells (A), comparison of tumour and normal tissues of clinical samples of squamous cell carcinoma (B), and expression of selected genes (IL8, CXCL1 and CXCL2) in human tissues visualized by immunofluorescence (C-I).

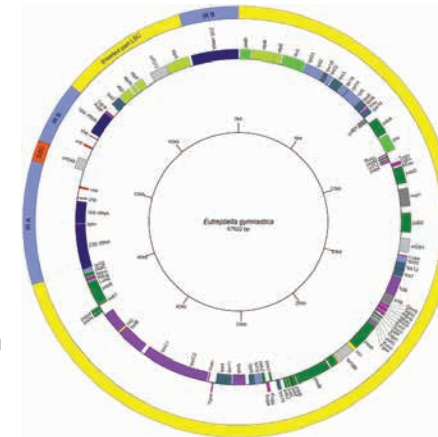


Fig. 2.: Map of the plastid genome of *Eutreptiella gymnastica*.



Fig. 3. Next-generation sequencer GS FLX (Roche).

- Ministry of Education, Youth and Sports of the Czech Republic, 1M0520 - Centre for Applied Genomics, 2005-2011, V. Pačes
- Ministry of Education, Youth and Sports of the Czech Republic, 2B06106 - Novel genomic and biotechnological approaches in molecular oncology: a way to the early diagnostics and targeted therapy, 2006-2011, Č. Vlček
- Ministry of Education, Youth and Sports of the Czech Republic, 2B08031 - Metagenomics and bioinformatics as a basis for preparation of effective approaches, preparation and characterization of microorganisms and their consortia for utilization in bioremediation, 2008-2011, J. Pačes
- GA CR, GCP305/10/J052 - Functional analysis of endogenous retroviral elements in human genome: possible association with cancers, 2010-2012, J. Pačes
- GA CR, GAP506/11/1317 - Diversity and evolution of anaerobic Heterolobosea, 2011-2014, Č. Vlček
- GA CR, GAP305/11/1061 - Evolution of parasitism: analysis of genomes and key physiological functions of free-living *Mastigamoeba balamuthi* and pathogenic *Entamoeba histolytica*, 2011-2015, J. Pačes
- GA CR, GAP506/11/1320 - Establishment of the secondary plastid in euglenids, 2011-2015, Č. Vlček
- Ministry of Health of the Czech Republic, NT13488 - Genomic analysis of tumor-associated fibroblasts in head and neck carcinoma: The basis for new generation of biologic anti-tumor therapy, 2012-2015, H. Strnad
- GA CR, GAP304/12/1333 - Intracellular interactions in malignant melanoma - experimental studies, 2012-2015, H. Strnad
- GA CR, GAP506/12/1010 - Genome sequencing of *Oxymonad* and *Trimastix*, 2012-2014, V. Pačes
- Ministry of Health of the Czech Republic, NT13112 - Studies of anticancer effects of statins, 2012-2015, H. Strnad

1. Hroudová M, Vojta P, Strnad H, Krejčík Z, Řídl J, Pačes J, Vlček Č, Pačes V. Diversity, phylogeny and expression patterns of Pou and Six homeodomain transcription factors in hydrozoan jellyfish *Craspedacusta sowerbyi*. **PLoS One** 2012 7(4): e36420.
2. Hrdá Š, Fousek J, Szabová J, Hampl V, Hampl V, Vlček Č. The plastid genome of *Eutreptiella* provides a window into the process of secondary endosymbiosis of plastid in euglenids. **PLoS One** 2012 7(3): e33746.
3. Vlček Č, Marande W, Teixeira S, Lukeš J, Burger G. Systematically fragmented genes in a multipartite mitochondrial genome. **Nucleic Acids Res** 2011 39(3): 979-988.
4. Melenovský V, Beneš J, Skaroupková P, Sedmera D, Strnad H, Kolář M, Vlček Č, Petrák J, Beneš J, Papoušek F, Oliyarnyk O, Kazdová L, Červenka L. Metabolic characterization of volume overload heart failure due to aorto-caval fistula in rats. **Mol Cell Biochem** 2011 354(1-2): 83-96.
5. Strnad H, Řídl J, Pačes J, Kolář M, Vlček Č, Pačes V. Complete genome sequence of the haloaromatic acid-degrading bacterium *Achromobacter xylosoxidans* A8. **J Bacteriol** 2011 193(3): 791-792.



From the left:
Jan Fousek, PhD / Research Assistant · Miluše Hroudová, PhD / Research Assistant · Čestmír Vlček, PhD / Head of Laboratory · Michal Kolář, PhD / Research Assistant · Jakub Řídl, MSc / PhD Student · Prof Václav Pačes, DSc / Research Fellow · Jan Pačes, PhD / Research Fellow · Šárka Pinkasová / Technician · Hynek Strnad, PhD / Research Fellow

Not in the picture:
Jana Šachová MSc / PhD Student (maternity leave)