# Laboratory of Genomics and Bioinformatics

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


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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. Representative genome sequences are still limited or altogether lacking for a large number of lineages. Using next-generation sequencing platforms we characterize genomes and transcriptomes of many protist species, namely Diplonema papillatum, Mastigamoeba balamuthi, Andalucia godoyi 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 molecular diagnostics and personalized medicine. We study intracellular interactions in malignant melanoma and in tumour-associated fibroblasts using genomics tools.

**Fig. 1.** A protozoan genome project: Mastigamoeba eukaryotic cell photo.

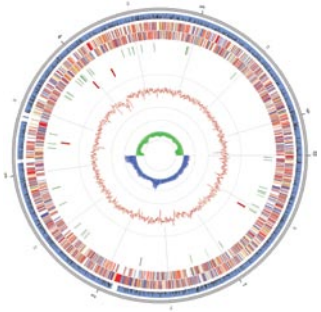

**Fig. 2.** The genome of a phenol derivative-degrading bacterium, Rhodococcus erythropolis strain CCM2595. This bacterium is interesting in the context of bioremediation for its capability to degrade phenol, catechol, resorcinol, hydroxybenzoate, hydroquinone, p-chlorophenol, p-nitrophenol, pyrimidines, and sterols.

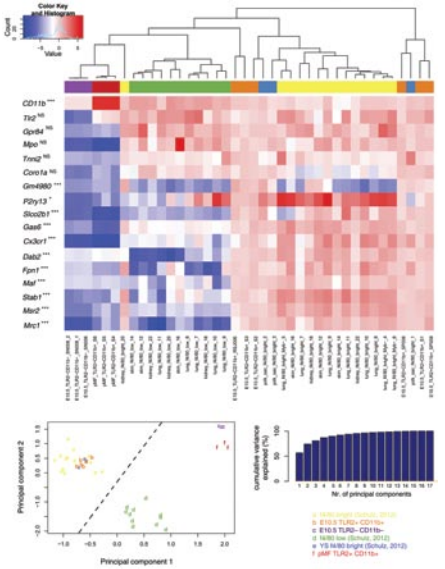

**Fig. 3.** Microarray analysis of E10.5 TLR2+ CD11b+ macrophages. A comparative analysis of gene expression profile of different types of macrophages using two independent microarray datasets.

- GACR, GAP506/11/1317 – Diversity and evolution of anaerobic Heterolobosea, 2011-2014, Č. Vlček
- GACR, 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
- GACR, GAP506/11/1320 – Establishment of the secondary plastid in euglenids, 2011-2015, Č. Vlček
- GACR, GAP304/12/1333 – Intercellular interactions in malignant melanoma – experimental study, 2012-2015, H. Strnad
- GACR, GAP506/12/1010 – Genome sequencing of oxymonad and Trimastix, 2012-2014, V. Pačes
- MH, NT13488 – Genomic analysis of tumour-associated fibroblasts in head and neck carcinoma: the basis for new generation of biologic anti-tumour therapy, 2012-2015, H. Strnad
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- GACR, GA13-28283S – Bridging microbial community ecology and degradation of xenobiotics – the use of metagenomics to investigate microbial degradation potential, 2013-2017, M. Kolář
- MEYS, LG14017 LG-INGO II – Ensuring representation of the Czech scientific community in FEBS, IUBMB, EMBC, EMBO, ESBRA, and relevant organizations, 2014-2016, V. Pačes
- TACR, TE02000058 – Centre of competence for molecular diagnostics and personalized medicine, 2014-2019, V. Pačes, Č. Vlček


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3. Strnad H, Patek M, Fousek J, Szokol J, Ulbrich P, Nesvera J, Pačes V, Vlček Č: Genome Sequence of Rhodococcus erythropolis Strain CCM2595, a phenol derivative-degrading bacterium. **Genome Announc 2014** 2(2).
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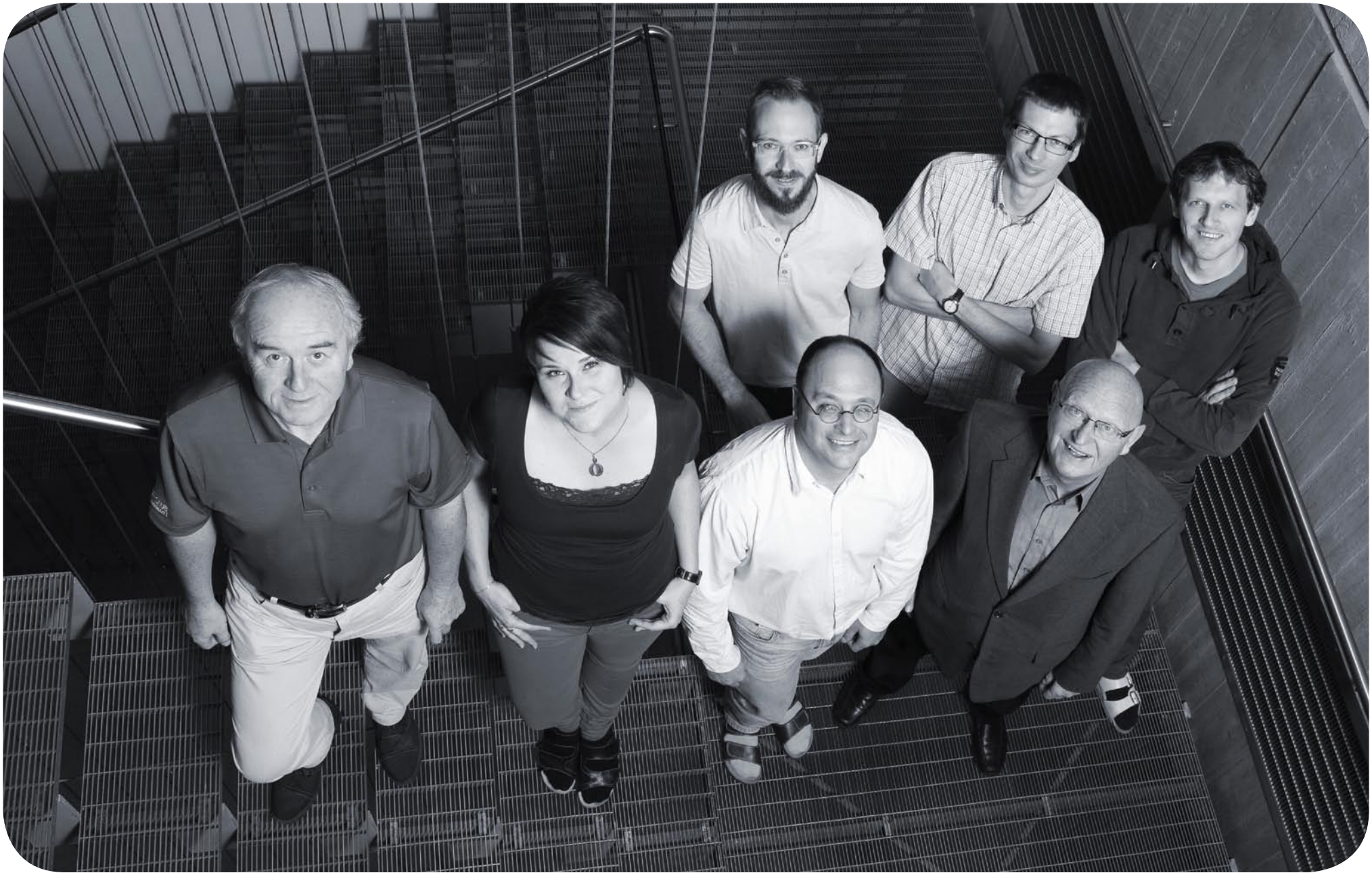

**From the left:** Čestmír Vlček, PhD / Head of Laboratory, Miluše Hroudová, PhD / Postdoctoral Fellow, Jakub Rídl, MSc / PhD Student, Jan Pačes, PhD / Research Fellow, Michal Kolář, PhD / Research Fellow, Prof Václav Pačes, DSc / Research Fellow, Hynek Strnad, PhD / Research Fellow

**Not in the picture:** Šárka Pinkasová / Technician, Jana Šáchová, MSc / PhD Student, Mirka Famfulíková / Diploma Student, Martin Šteffl, MD / PhD Student