



## Čestmír Vlček

vlcek@img.cas.cz

### Laboratory of Genomics and Bioinformatics

Genomics, transcriptome analysis, expression profiling

## Research topics

Our laboratory was amongst the first to complete genome projects. Information generated in these projects was used in evolutionary studies and recently also in biotechnological applications.

The genome project of *Rhodobacter capsulatus* has been completed. The tools of bioinformatics were developed in order to analyse nucleotide sequences generated in the lab as well as those available in the international databases.

We now begin to characterize genomes and genes of at least three different cnidarian species, hydrozoan *Craspedacusta sowerbyi*, cubozoan *Tripedalia cystophora* and anthozoan *Aiptasia pulchella*. To understand the evolution of higher metazoan genomes and the developmental processes that they regulate, it is necessary to make comparisons with an appropriate outgroup. Cnidaria, a group of lower Metazoa, are the natural outgroup for comparative genomics and developmental studies. The availability of the model animal genomic sequences will allow inferences to be made about the gene complement of the common bilaterian ancestor. Cnidarian genomes are a potential key to understanding many aspects of animal evolution.

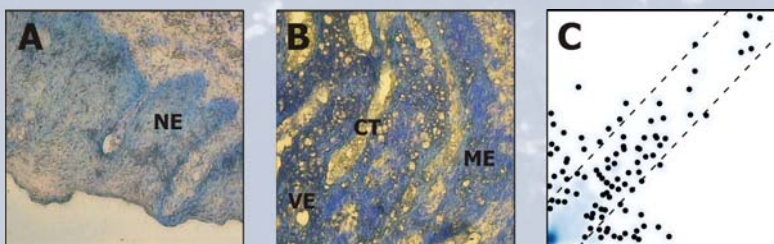
A second major project of our group is directed towards identification of specific markers in cancer tissue with potential applications in medical diagnosis. We use Illumina microarray chip analysis for detection of appropriate gene sets.

### Current grant support

Ministry of Education, Youth and Sports (Center for Applied Genomics, 1M0520; NPV II, project No.: 1M0520)

### Selected recent papers

1. Bukovská G, Klučar L, Vlček Č, Adamovič J, Turňa J, Timko J. Complete nucleotide sequence and genome analysis of bacteriophage BFK20 - A lytic phage of the industrial producer *Brevibacterium flavum*. *Virology*. 2006;348:57-71.
2. Pavlíček A, Gentles AJ, Pačes J, Pačes V, Jurka J. Retroposition of processed pseudogenes: the impact of RNA stability and translational control. *Trends Genet*. 2006;22:69-73.
3. Drábková L, Vlček Č. The phylogenetic position of *Oxychloe* (Juncaceae): evidence from morphology, nuclear and plastid DNA regions. *Taxon*. 2007;56:95-102.
4. Fujimura N, Vacík T, Machoň O, Vlček Č, Scalabrin S, Speth M, Diep D, Krauss S, Kozmik Z. Wnt-mediated down-regulation of Sp1 target genes by a transcriptional repressor Sp5. *J Biol Chem*. 2007;282:1225-1237.



Oral cancer (B) is believed to have developed through a progression of pre-malignant histopathological changes in normal epithelium (A, NE). Like other cancers, oral cancers have heterogeneous cell population in addition to the malignant epithelium (ME): connective tissue / fibroblasts (CT) and vascular epithelium (VE). Comparison of transcription profiles (C) can help find genes that are specific for cancer progression.



Čestmír Vlček, PhD / Head of Laboratory

Jan Pačes, PhD / Research Scientist

Hynek Strnad, MSc / Research Scientist

Lenka Drábková, PhD / Research Scientist

Michal Kolář, PhD / Research Scientist

Pavel Urbánek, PhD / Research Scientist

Šárka Pinkasová / Technician

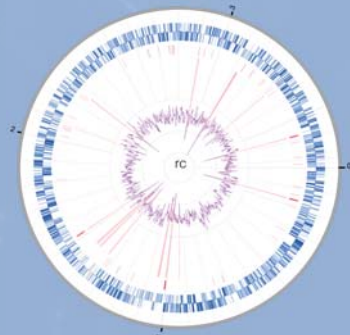
Václav Pačes, Prof, DSc / Associated with the group

Zdeněk Krejčík, MSc / PhD Student

Radek Zíka, MSc / PhD Student

Miluše Hroudová, MSc / PhD Student

Daniel Panchártek / Diploma Student



*Rhodobacter* chromosome: [a] blue and gray: predicted genes in forward and reverse orientation [b] red: t-rna, [c] violet: gc content (window 5kb); [d] light red: highlights denote gc < 50%



Hydrozoan medusa *Craspedacusta sowerbyi* is a genomic model important for the study of metazoan