Laboratory of Genomics and Bioinformatics

Genomics, next-generation sequencing, genome, microarray transcriptional profiling, cancer

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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. Using the 454 next-generation sequencing facility (GS FLX/Titanium), we characterize genomes of different species and metagenomic samples. To understand the evolution of eukaryotes and the developmental processes that they regulate, it is necessary to analyse their genomes. Single-cell eukaryotes 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 genome projects under way are that of *Mastigamoeba balamuthi* and *Diplonema papillatum*. The metagenomic analyses of environmental samples and unculturable microbes are under way, too.

A second major project of our group is directed towards identification of markers specific for head and neck cancer tissue with potential applications in medical diagnosis. We use the Illumina microarray chip technique for detection of appropriate gene sets that are upregulated in this cancer disease. The found markers could identify the disease subtype and so help to aim the treatment.

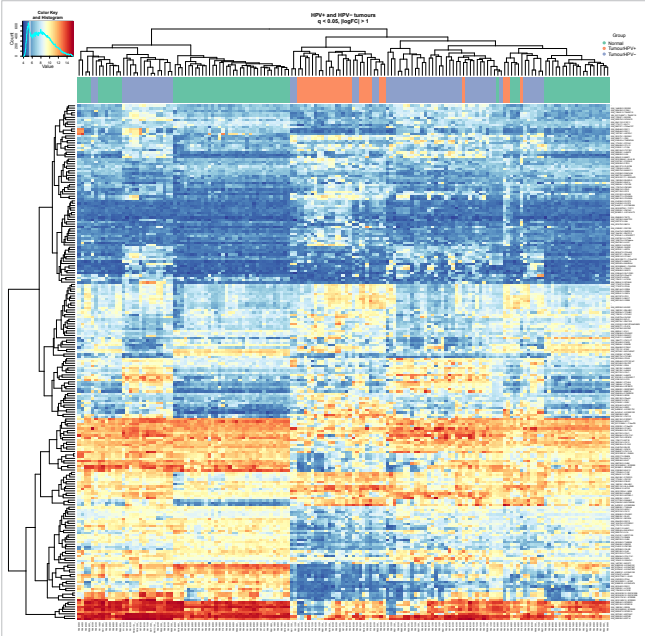

Fig. 1. Graphical presentation of differences in expression of genes. The samples have been taken from head and neck squamous cell cancer patients with and without human papilloma virus infection.

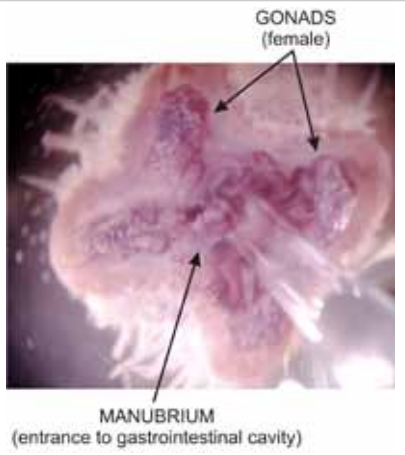

Fig. 2. Tissue-specific expression pattern of csSix4/5A transcription factor visualized (dark violet) by whole-amount *in situ* hybridization of adult jellyfish *Craspedacusta sowerbyi* (freshwater hydrozoan cnidarian). Expression is localized in gonads (germ cells, production of oocytes) and at the margin of manubrium (nerve cells – mechanosensors, feeding).

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

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- GA CR, GCP305/10/J052 – Functional analysis of endogenous retroviral elements in human genome: possible association with cancers, 2010-2012, J. Pačes

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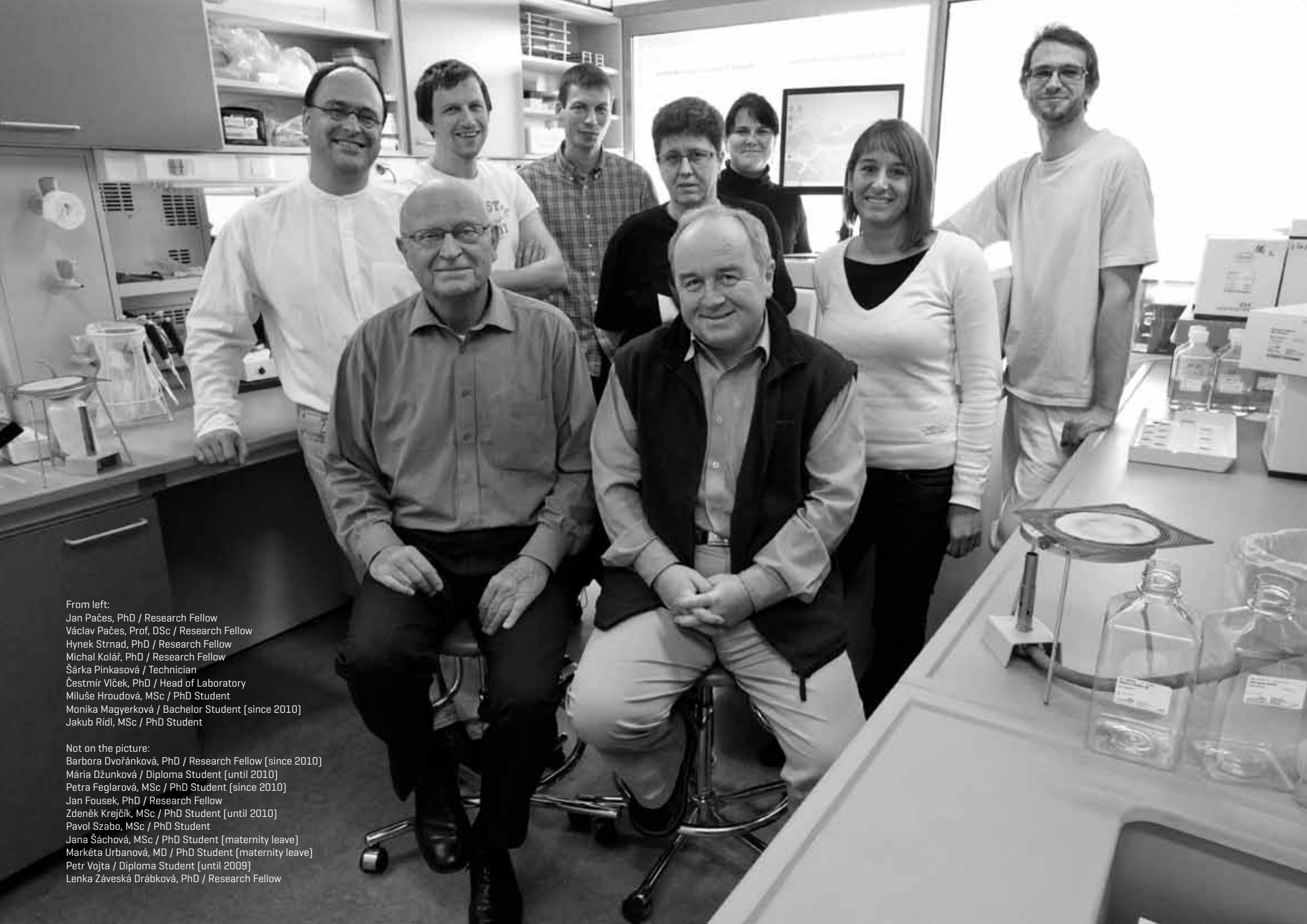

From left:
Jan Pačes, PhD / Research Fellow
Václav Pačes, Prof, DSc / Research Fellow
Hynek Strnad, PhD / Research Fellow
Michal Kolář, PhD / Research Fellow
Šárka Pinkasová / Technician
Čestmír Vlček, PhD / Head of Laboratory
Miluše Hroudová, MSc / PhD Student
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Barbora Dvořánková, PhD / Research Fellow (since 2010)
Mária Džunková / Diploma Student (until 2010)
Petra Feglarová, MSc / PhD Student (since 2010)
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