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Laboratory of Genomics and Bioinformatics

Genomics, next-generation sequencing, transcriptome analysis

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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.

Using the 454 next-generation sequencing facility (GS FLX/Titanium), we begin to characterize metagenomic samples and genomes of evolutionarily interesting species. To understand the evolution of higher metazoan genomes and the developmental processes that they regulate, it is necessary to make comparisons with appropriate outgroups. 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. Two cnidarian genomes, hydrozoan *Cracpedacusta sowerbyi* and cubozoan *Tripedalia cystophora*, are surveys for genome analysis. Unicellular protozoa, especially their genome content and structure, can unveil where the root of the eukaryotic tree lies. Genome sequencing of several protozoan species is planned. The metagenomic approach to the environmental samples and unculturable microbes is under way, too.

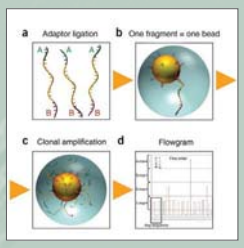
A second major project of our group is directed towards identification of specific markers in cancer tissue with potential applications in medical diagnosis. We use Illumina microarray chip analysis for detection of appropriate gene sets.

Current grant support

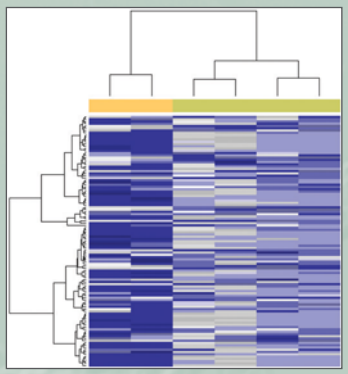
Ministry of Education, Youth and Sports (Center for Applied Genomics, 1M0520; NPV II, project 1M0833)

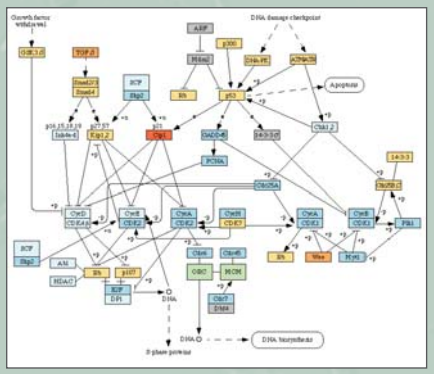
Selected recent papers

1. Kozmik Z, Růžičková J, Jonášová K, Matsumoto Y, Vopálenský P, Kozmiková I, Strnad H, Kawamura S, Piatigorsky J, Pačes V, Vlček Č. Assembly of the cnidarian camera-type eye from vertebrate-like components. **Proc Natl Acad Sci USA.** 2008;105:8989-8993.
2. Jenčová V, Strnad H, Chodora Z, Ulbrich P, Vlček Č, Hickey WJ, Pačes V. Nucleotide sequence, organization and characterization of the (halo)aromatic acid catabolic plasmid pA81 from Achromobacter xylosoxidans A8. **Res Microbiol.** 2008;159:118-127.
3. Kozmik Z, Swamynathan SK, Růžičková J, Jonášová K, Pačes V, Vlček Č, Piatigorsky J. Cubozoan crystallins: evidence for convergent evolution of pax regulatory sequences. **Evol Dev.** 2008;10:52-61.

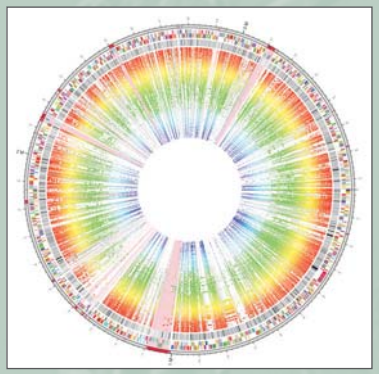


The Genome Sequencer FLX supports a number of formats, allowing users to customize the number of samples per instrument run and the number of reads per sample.
Genome Sequencer process: A and B adaptors are appended to each fragment (a) to allow binding to DNA capture beads (b). Fragments are amplified on the beads in emulsion (c). When sequenced in the Genome Sequencer FLX, each clonally amplified fragment generates its own unique sequence read (d).





Arrest of the cell cycle after exposure of human cell lines to statins. [a] The cell cycle network is suppressed by up-regulation of p53 and TGF-β pathways (up-regulated genes in orange, down-regulated in blue). [b] Expression profiles of cell cycle-related transcripts show the same pattern in several biological and technical replicates (two leftmost columns: no statins administered, the other four columns: replicated samples exposed to statins).



Rhodobacter genome - homologues in bacterial genomes: genes on forward and reverse strand are coloured according to their function, more inside is similarity heatmap with homologues in selected bacterial genomes.