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 Atplasia 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.

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Selected recent papers


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.