

# 1. Abstrakt

## Gene expression analysis of the cnidarian *Tripedalia cystophora*

In terms of understanding the evolution of metazoan genetic and developmental complexity, the *Cnidaria* are likely to be critically important, as this phylum is regarded as the sister group to the *Bilateria*. To obtain a broader perspective on patterns of gene evolution, we conducted a limited EST analysis on the jellyfish *Tripedalia cystophora* (class *Cubozoa*).

EST library was prepared from the planula larva stage RNA. From 342 characterized ESTs, 44% match human sequences much more strongly than they do to any *Drosophila* or *Caenorhabditis* sequence. Mentioned fact confirms gene conservation between *Cnidaria* and *Vertebrata*. More than 14% of the jellyfish EST with strong metazoan matches to the databases had clear human homologs but were not represented in the *Drosophila* or *Caenorhabditis* genomes. Gene loss has thus been much more extensive in these model invertebrate lineages. We have also determined the expression of several interesting genes using RNA *in situ* hybridization. We determined the expression of *like-glycosyltransferase*, *pirin* and *cyclin I*, genes that were lost in insects and nematodes but were conserved among jellyfish and vertebrates. The complexity of the *Tripedalia* genome is paradoxical, given that this organism contains apparently few tissue types.

Key words: *Cnidaria*, expressed sequence tag, gene set conservation, gene loss, evolution, expression