

Hydra – a simple *in vivo* model allowing cellular analysis at *in vitro* depth

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For years, cnidarians drew researcher's attention due to important phylogenetic position – as a basal Metazoan and sister group to Bilateria. Moreover significant ecological and economical role of corals stimulated research on this group of invertebrates. At the same time corals turned out to be quite difficult to be investigated at cellular level, and up to now laboratory culture of Anthozoa is still a challenge. This limitation led an easy-to-culture freshwater hydrozoan *Hydra* to become a «lab rat» among cnidarians, and an extensive toolkit of methods was developed to use this model in research at cellular and molecular levels.

Short-term cell cultures, transplantation and reaggregation procedures as well as different labeling techniques made possible the identification of all cell lineages in *Hydra*, which was not yet achieved in any other cnidarians. Recently emerged complete genome sequencing of *H. magnipapillata* and lineage-specific transcriptome sequencing data (www.compagen.org) provided insight into the identification of key molecules for stem cell maintenance, commitment and differentiation. Finally, transgenesis technique became available for *Hydra*, thus offering unlimited potential for detailed analysis of gene function by stable up- or down-regulation of gene of interest.

Altogether, this toolkit allows addressing in *Hydra* model a plenty of questions, which are currently being under investigation worldwide. The evolution of signaling networks and patterning processes in development, the complexity of stem cell regulation and cell fate determination, the evolution of innate immunity and host-microbe interactions – that is just a bare list of question in focus of research today. In applied biotechnology, *Hydra* took its place as well – as a novel source of potential bioactive molecules (e.g. antimicrobial peptides) and a bioreactor for cheap production of recombinant proteins.

In summary, *Hydra*, being a relatively simple model organism, allows performing *in vivo* cellular analysis at the level comparable with that of *in vitro* cell culture-based systems.