Abstract

In order to gain more insight into the complex morphogenetical processes that take place during the metamorphosis and their control, differentially expressed transcripts were isolated by means of cDNA-based subtractions developed by Hubank and Schatz (1994). Both, primary polyp specific transcripts as well as such induced by the peptide HeLWamidII being involved in the metamorphose regulation, could be isolated. By the sequential analysis transcripts could be assigned to different functional groups like adhesion proteins, a cell cycle protein, chaperones, proteases, immune relevant proteins and transcription factors. Among them are also proteins which play different roles in the development processes of other organisms. The successive expression analysis of the genes being represented by the isolated transcripts clearly showed that nearly all of them are differentially active.

The metamorphosis is characterized by a dynamic change of temporally and spatially precisely coordinated gene activity. Transient transcription occurred besides a switch on and an up-regulation of the gene expression. Thereby the expression can be either locally restricted or in the form of dynamic waves.

An experimental analysis of the gene expression revealed that a decoupling of morphogenetical as well as molecular control can occur. Thus the metamorphosis does not represent a centrally controlled cascade process, but a locally stirred one, at which a site-directed regulation can occur.

A model for the course of the metamorphosis could be established. A propagation of a first coordinating signal from anterior to posterior takes place shortly after induction (< 1 h), leading already to a complex gene activation. A coordination by a second signal leads to an irreversible induction of the metamorphosis, in the course of which a change in shape occurs. In the case of an absence of the second signal internal regulation mechanisms result in the return to the larval status. Both signals are probably amidated peptides.