

NEWS AND VIEWS

PERSPECTIVE

Functional genomics opens doors to understanding metamorphosis in nonmodel invertebrate organisms

MÓNICA MEDINA

School of Natural Sciences, University of California, Merced, CA 95338, USA

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Metamorphosis can be described as the period in the life cycle of an animal in which an immature individual undergoes drastic anatomical and physiological changes to develop into an adult. Usually these transitions are accompanied by a change of habitat or behaviour. Because it is present in a large number of animal phyla, we can infer that metamorphosis is an important evolutionary and developmental transition. Metamorphosis is a remarkable example of modularity in life cycles, in that a single genome can produce highly distinctive phenotypes occupying different niches. For instance, many marine invertebrates are characterized by a distinct larval stage, often pelagic, that metamorphoses into a benthic, often sessile, adult.

Although metamorphosis is known to have evolved multiple times independently throughout the animal tree, there are a few similarities across phyla in how this developmental transition takes place. One striking similarity in marine invertebrates is the concept of metamorphic competence. Metamorphic competence refers to the ability of a developing larva to complete metamorphosis into the adult benthic stage upon induction by external settlement cues. These cues are represented by a broad range of stimuli on the benthos such as the presence of bacterial biofilms, diverse algal species, or animal prey among others. In most cases, however, each species has only one or few corresponding specific cues that are highly effective in inducing settlement. In this issue, Williams *et al.* present findings from a molluscan species on how the transcriptome varies throughout metamorphosis after induction of settlement.

Studying the molecular underpinnings of how metamorphosis takes place in diverse species has been revamped by insight from genomic data. While overall gene expression profiles have been assessed during life cycle of insects (Arbeitman *et al.* 2002) and vertebrates (Baldessari *et al.* 2005), little information is available for the diverse lophotrochozoan phyla (Heyland & Moroz 2006). In their manuscript, Williams *et al.* (2009) address this gap by describing the changes in transcriptional profiles in the tropical abalone *Haliotis asinina* (Mollusca: Gastropoda) from mid-late larval development through to metamorphosis following induction of settlement (Fig. 1). Once abalone larvae are exposed to a coralline alga known to effectively induce meta-

morphosis in this gastropod, the transcriptome deviates significantly from that of unexposed larvae.

At least five distinct temporal gene expression profiles can be observed throughout the metamorphic transition. Although it was previously thought that competent larvae exhibit reduced transcriptional activity (Hadfield *et al.* 2001), this new study points in a new direction. The abalone data set unveils the complexity of the larval transcriptome at the competent stage, during which several spatio-temporal programs are running simultaneously. One of the interesting findings in this study is the support for anticipatory development in abalone larvae (i.e. older larvae have more similar transcription profiles to induced post-larvae than to young larvae). Additionally, it appears that some transcripts known to suppress metamorphosis may be involved in the maintenance of competence. This is an important larval strategy given the degree of randomness associated with finding a suitable habitat to settle when suspended in the water column. Finally, an equally important finding is the fact that although conserved metazoan signalling pathways are expressed during development, these pathways appear to be regulating a suite of abalone specific genes during metamorphosis.

Some of the technical aspects of this manuscript are also worth mentioning. The authors used a blind-spotted cDNA array, of which the cDNA collection encompassed a broad range of transcripts from multiple developmental stages and tissue types. Once transcriptome changes were assessed, only the differentially expressed genes were subsequently sequenced. A blind approach reduces costs significantly, making a similar type of analysis accessible to laboratories working with nonmodel species.

While this study is pioneering in the field of marine genomics and was carried out when sequencing costs were still high for large expressed sequence tags (EST) projects, new technological developments have made these tools even more inexpensive. Next generation sequencing technologies (e.g. pyrosequencing) can generate larger amounts of EST data of similar read length as Sanger sequencing at significantly lower costs. This price reduction, coupled with a decrease in cost of commercial oligonucleotide arrays, can make functional genomics studies a standard practice in molecular ecology and evolutionary biology laboratories (reviewed in Wheat 2008). It can therefore be argued that given the, until recently, unimaginable ease with which we can now develop genomic tools for nonmodel organisms, examining similar developmental processes in multiple species will be a powerful tool to understand whether similar or divergent transcriptional networks drive these processes throughout Metazoa. The transition of comparing a few genes in few species to whole transcriptomes in an even wider range of species will enhance our understanding of the evolution of animal diversity.

Given that external cues are often needed to trigger metamorphosis and settlement, genomic approaches combined with environmental technology (reviewed by Hofmann & Gaines 2008) have the potential for facilitating the integration of marine ecology, population biology and evo–devo studies. As stated by West-Eberhard (2003), the evolutionary significance

Correspondence: Mónica Medina, Fax: +1-209-228-4053; E-mail: mmedina@ucmerced.edu

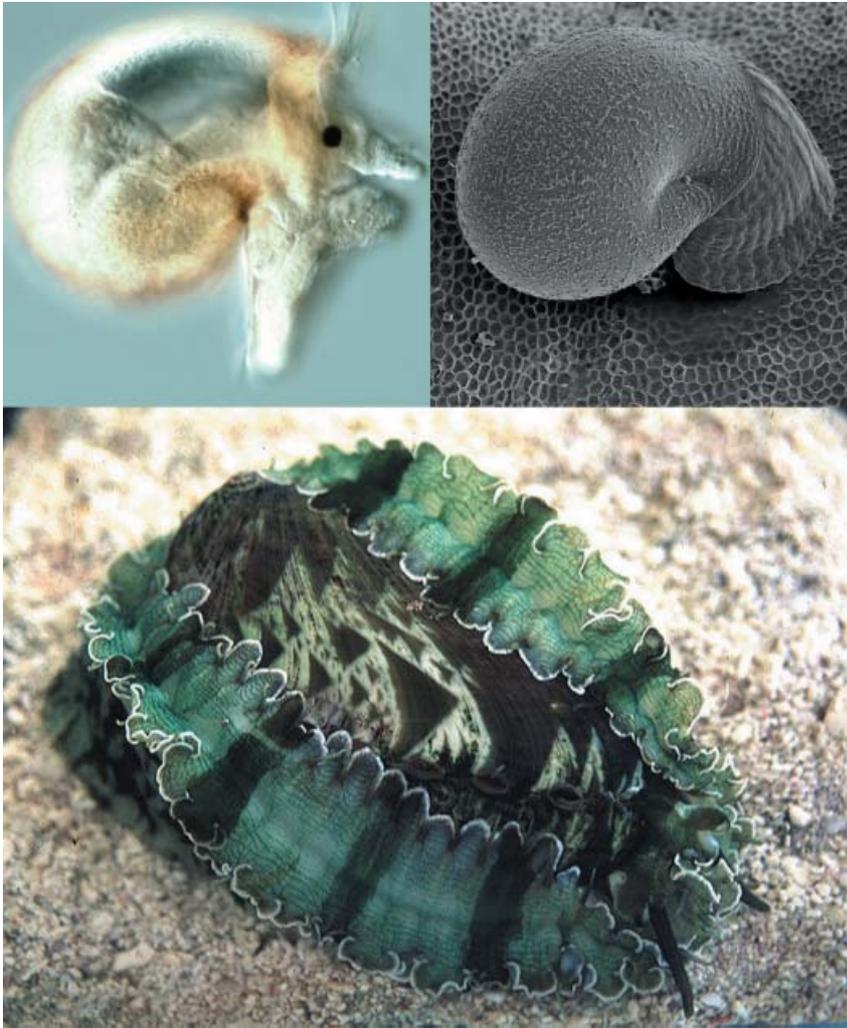


Fig. 1 Williams *et al.* present insights on how the transcriptome varies throughout metamorphosis in the abalone *Haliotis asinina*. Upper left panel, pelagic veliger larva, photo credit: Helen Gunter. Upper right panel, settled metamorphic larva, photo credit: Erica Lovas. Bottom panel, sessile adult individual, photo credit: Elizabeth O'Brien.

of metamorphosis is that it allows selection to produce extreme diversification of the morphological, physiological and behavioural traits produced by a single genome. It is an exciting time for those interested in the evolution of life cycles, as genomic tools will likely provide new answers on how different genomes are encoding information for metamorphic transitions. Nonmodel organisms can finally step into the spotlight!

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Mónica Medina is a marine biologist at the University of California at Merced. Her research interests include comparative and ecological genomics, and their use in the study of coral reef biology and invertebrate evolution.

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