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# Lab Times

News  
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Evo-Devo

Wanted:

New Model Organisms

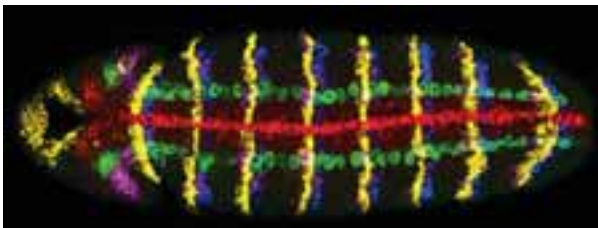
Evolutionary developmental  
biology (evo-devo)

# New Models, Please

The amalgamation of developmental and evolutionary biology, called evolutionary development (evo-devo), revealed a wealth of new data on how animal and plant forms are made and how they evolved. More, new model organisms promise new insights. However, how does one choose the right ones for research?

**X**enopus, the chick, the mouse, the zebrafish, *Drosophila*, *Caenorhabditis elegans* and *Arabidopsis thaliana* are the classic representatives of higher organisms in life sciences, ranging from genomics via physiology to developmental research. These models also dominate evo-devo, the science of understanding evolution via the comparative analysis of early animal or plant development. In the past 15 or so years the “big six” animal models did a good job for evo-devo.

To begin with research on myriads of flies followed by mice, worms, frogs and chicks revealed that the development of body parts such as limbs, wings, eyes or hearts, though very different in structure among animals, is governed by the same genes in different animals. The animals



The analysis of the expression of homoeotic genes opened the door to evo-devo research.

share a common “tool kit”, common “master genes” that guide their development and the formation of their bodies. That insight, at the same time, was a breakthrough for understanding how body structures evolved during evolution – how fins were modified into limbs, how mouthparts, claws, swimming and feeding appendages, wings and – in the case of plants – how flowers or trichomes have evolved.

Now that genome sequences of these model organisms as well as from many other species are available and new high throughput technologies have been developed, lots of new data are rapidly being collected. Certainly people also expect

a wealth of new insights about how biological diversity was and is still formed.

However, missing is the very basis for evo-devo studies – more model animals and plants. This year Ronald Jenner and Matthew Wills at the University of Bath (UK) lobbied in *Nature Review Genetics* for new model organisms for evo-devo research.

“The choice of new model organisms has not been optimal”, write Jenner and Wills. It’s true, the “big six” model organisms have been chosen because they are easy to keep in the laboratory, select and breed – and because it was assumed that biological phenomena uncovered in them could be transferred to humans. While these arguments generally turned out to be correct and useful in the context of developmental research, the benefits to evo-devo as a subject are limited.

Limited?? Those six were very true treasure troves, allowing for one of the most fascinating discoveries in recent biology, the identification of homoeotic genes that form body plans and body parts in animals (and plants – see page 20). Their analysis finally led to the discovery of some law-like generalities of development and evolution. However, flies, mice, frogs, worms, zebrafish and chicks cover only 3 of more than 35 phyla of animals. “By far not enough,” says Jenner adding in the same breath that simply selecting new model animals by maximising phylogenetic spread, or by plugging holes in the phylogenetic tree is not the best option of choice.

## How to choose a model organism?

In times of spare money and spare time one should give some thoughts to how to choose a new evo-devo model. Those who are familiar with the history of biology know that it can take umpteen years of

work to fully exploit a new model system, giving scientists a hard time. On top of everything, such model (re)search results appear if at all in only a few publications that are not likely to attract a great deal of attention. Basic research on new creatures typically doesn’t get you to the top of citation lists, it doesn’t grab overwhelming attention of colleagues and editors – leaving us with the sobering question: How can one develop new evo-devo models and which animals or plants should one choose?

## Questions count

Jenner and Wills suggest that an organism is picked by its suitability to answer a specific evo-devo question. “Maximising phylogenetic spread is good to show diversity but it doesn’t necessarily lead to new general insights about evolution,” says Jenner. This position is supported by other evo-devo scientists, as for example Frietson Galis (Leiden University, The Netherlands) who heads the brand new European Society for Evolutionary Developmental Biology (EED). She says, “I fully support Jenner and Wills. However, I also think that we put too much emphasis on model systems. We should not forget that we need to study biodiversity.” Scrupling that focusing on model organisms limits the scope of science. She says that, “for any question raised one should choose a suitable subject, irrespective of whether it is a model system or not. It’s really important that science managers understand that we need to do research not only on model systems.”

Armin Moczek from the Indiana Molecular Biology Institute who is working with the horned dung beetle of the genus *Onthophagus*, stated, “The choice of model systems should primarily be motivated by the exact question(s) one is trying to answer, and not all questions require particular phylogenetic considerations. For example, many people would argue that some of





the greatest frontiers in evolutionary biology include the following three issues: (i) the origin of life, (ii) the origin of multicellularity, and (iii) the origin of major evolutionary novelties. I would argue that to address issues (i) + (ii) phylogenetics is critical, for (iii) it is largely irrelevant.”

Also Michel Milinkovitch and Athanasia Tzika argue in a recently published paper (Escaping the Mouse Trap, *J. Exp. Zool.* 2007, 308B, 337-346) that “the phylogenetic-distance criterion is limited by at least two parameters: (i) the rate of phenotypic transformation is highly variable among lineages and (ii) variation worth investigation exists at multiple phylogenetic levels.”

### The genome pipeline is full

Can it be true? Is phylogenetics really not so relevant for the analysis of evolutionary novelties as generally thought? Scientists often assume that the position in the evolutionary tree correlates with basal or more advanced developmental stages, respectively. Accordingly, among species that descend from the same common ancestor

those are designated as basal that are separated from this ancestor by the smallest number of speciation events. That’s the reason why biologists chose the zebrafish as a “canonical vertebrate” – the common ancestor of all vertebrates was a fish.

However, what is the zebrafish a model for? For chordates, for vertebrates, for bony fish, for ray-finned fish, for teleost fish or for the family Cyprinidae? “The answer heavily depends on what characters one is interested in,” argue Milinkovitch and Tzika. They are right.

One should keep that in mind when sequencing the genomes of representatives of possibly the deepest nodes of major clades like the South American opossum (*Monodelphis domestica*), the African elephant (*Loxodonta africana*), the European common shrew (*Sorex araneus*), the European hedgehog (*Erinaceus europeaus*), the guinea pig (*Cavia porcellus*) and the nine-banded armadillo (*Dasypus novemcinctus*).

The choice of these species for future evo-devo research was made on the assumption that each of these species represents a

non-overlapping subset of mammalian phylogenetic and morphological diversity. Also, the Plant Genome Comparative Sequencing Program (PGCSP) funded by the American National Science Foundation looks out for “key nodes or groups of plants in the Tree of Life that would enable researchers to answer specific biological questions relevant to the goals of the PGRP”

### The problem of true novelties

However, the correlation of putative key nodes and the evolution of genome sequence leading to evolutionary novelties isn’t stringent. Speciation can be accompanied with increased evolutionary change and vice versa, evolutionary change can occur without speciation. Simplicity must not be ancestral, it can also be the result of a subsequent reduction of the body plan. As Jenner says, “Just because an organism has sprung from the base of the evolutionary tree this does not make it more primitive or representative. Knowledge of phylogenetic position is essential for studying the origins of novelties which is an important



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goal of evo-devo studies.” In fact, nobody can predict which of the species is the least modified in the evolutionary tree or which one is closest to the origin of a novelty. “For example, the snake-like body has evolved multiple times independently in squamate reptiles. Is there a most primitive snake-like animal?” explains Jenner,

Therefore, you can be sure that calling your attention to a specific animal or plant because you think that it will answer specific evo-devo questions leads to a certain, if not heavy, bias and insight into the general laws of development may be limited. That outspoken critique is made often. “[Model organisms] are all somehow a little odd and not mainstream. [...] If we want to understand evolution through Evo-Devo studies we need to look at a broad range of species

because we can't build out an evolutionary pathway by looking at extreme organisms,” said Janet Rossant (Hospital for Sick Children, Toronto) in an interview with *Nature Review Genetics*. To be honest, there's no other way. One can study the development of wings and winglessness only in insects, the development of limbs only in tetrapods. Anyway, Jenner doesn't judge bias to be a big problem. “Bias is just another word for focus”, he says.

### A strong voice for evo-devo

Bias, phylogenetic spread – can we really predict what experimental animal or plant may ultimately prove a special evo-devo concept or provide us with the most informative answers? Didn't scientific breakthroughs often come from unexpect-

ed places? Galis doesn't want to give any specific advice concerning the criteria for how to choose a model system. Jenner says that one should not develop new models from scratch but “perhaps search the literature for appropriate organisms that scientists from other disciplines have already worked on”.

Whatever you choose as a new organism, evo-devo is about comparing species or taxa so there's no other way than working with more than a handful of animals or plants. Also, given the importance of better understanding the basic mechanisms underlying biological diversity, evo-devoists should play an energetic, proactive role in the scientific community when it comes to singling out new model species.

KARIN HOLLRICHER

## Candidates on the Catwalk

For a while now, the impressive horns of beetles of the genus *Onthophagus* (1) have been challenging any audacious scientists to figure out just how those head satellites evolved. Yet, evo-devo research on these beetles commenced only recently. Armin Moczek from the Indiana Molecular Biology Institute wrote in an email, “If you define evo-devo more narrowly as evolutionary developmental genetics, then horned beetles are a much more recent phenomenon.”

An ideal new model animal for evo-devo research could be the water flea *Daphnia pulex* (2), suggests Ronald Jenner. The tiny freshwater crustacean has been the subject of ecological, evolutionary and toxicological studies for decades. Five years ago, the *Daphnia* Genomics Consortium started to develop genomic tools; the *D. pulex* genome is currently being annotated. Its distantly related congener *D. magna* is also on board; a sequencing project is on its starting block. Studying close relatives – so-called satellite species – allows insights into micro-evolution.

The choice of the starlet sea anemone *Nematostella vectensis* (3) as a model for evo-devo was motivated by the remarkable amenability to laboratory manipulation. That has already made it a productive system for exploring cnidarian development and a proliferation of molecular and genomic tools, including the currently ongoing *Nematostella* genome.

For studying segmentation and body patterning, Nipam Patel, from the Center for Integrative Genomics (University of Berkeley), has a new crustacean in his lab known as *Parhyale hawaiiensis* (4). As he reports, embryos of the easy-and-quick-to-grow animal survive injections; transposon-induced mutagenesis and RNAi also seem to work.

A research team led by Bernie Degnan (University of Queensland, Australia) focuses on the sea sponge *Amphimedon queenslandica* (5). This animal belonging to the earliest metazoans has no Hox genes

that in flies, worms, mice, elephants and even humans are responsible for the head-tail-axis. Body-organising functions are governed by NK-homeobox-like genes.

Mathieu Joron (University of Edinburgh) is promoting *Heliconius* (6) butterflies as promising models for studying micro-evolution, especially for investigating the adaptive changes of colour-patterns on the wings. Studying *Heliconius* species could shed light onto the mechanisms underlying colour-pattern changes and the longstanding question whether adaptive convergence between unrelated species is driven by natural selection or occasional phenotypic leaps facilitated by conserved developmental pathways.

Yet another group of interesting evo-devo candidates are *cichlid fish* (7). Hundreds of extremely young and genetically almost identical, though phenotypically diverse, species offer a kind of “natural experiment” and can be seen as “natural mutants”. Work on the development and evolution of colorational differences, that play an important role in sexual selection and speciation, as well as evo-devo studies on tooth shape difference, that are crucial for trophic adaptations, are ongoing in several labs around the world. Also, work on the evolution of *swordtail*

*fishes'* swords, which are in fact modified caudal fins and which have arisen through sexual selection, should not be forgotten. Genomic resources exist and a genome project is in the planning stage.

*Platynereis dumerilii* (8), a marine annelid exhibiting many ancient features in its lifestyle, anatomy, development and gene inventory could also become a new evo-devo model. Though there are a mere 41 entries in PubMed documents about this tiny animal, the oldest dating from 1951, recent work in Detlev Arendt's lab (EMBL, Heidelberg, Germany) raises hope that *P. dumerilii* will serve us with an answer to the question: How did the central nervous system come into existence?

