

Biologists call for better choice of model organisms in 'evo-devo'

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Research in evolutionary developmental biology, known as 'evo-devo', is being held back because the dominant model organisms used by scientists are unable to illustrate key questions about evolution, argue biologists in the latest issue of *Nature Reviews Genetics*.

The subject of evo-devo, which became established almost a decade ago, is particularly dependent on the six main model organisms that have been inherited from developmental biology (fruit fly, nematode worm, frog, zebrafish, chick and mouse).

To help understand how developmental change underpins evolution, evo-devo researchers have, over recent years, selected dozens of new model organisms, ranging from sea anemones to dung beetles, to study.

One of the selection criteria deemed most crucial is the phylogenetic position of prospective model organisms, which reflects their evolutionary relationships.

Phylogenetic position is employed in two common, but problematic, ways, either as a guide to plug holes in unexplored regions of the phylogenetic tree, or as a pointer to species with presumed primitive (ancestral) characteristics.

Drs Ronald Jenner and Matthew Wills from the Department of Biology & Biochemistry at the University of Bath (UK), call for a more judicious approach to selecting organisms, based on the evo-devo themes that the

organism can shed light on.

"It is fair to say that, since its inception, some workers feel that evo-devo hasn't quite lived up to its early expectations," said Dr Jenner.

"Partly this is because too much was expected too soon, but we suspect that in terms of its future promise the current choice of new model organisms has not yet been optimised.

Dr Wills said: "Many models to date, in particular the big six, have been chosen because they are easy to keep in the laboratory, select and breed.

"Whilst this is generally fine in the context of development research, the benefits to evo-devo as a subject are limited.

"There are upwards of 35 phyla of animals, and four of our six best models come from just one phylum.

"However, that doesn't mean that simply choosing new models to plug holes in the phylogenetic tree is the best option for further progress in evo-devo."

Dr Jenner added: "The popular advice of choosing new model organisms to maximise phylogenetic spread is nice to show diversity, but it doesn't necessarily lead to new general insights about evolution.

"Choosing new models in this way leaves it entirely a matter of chance whether a new model will illuminate a particular evo-devo theme.

"Instead, we urge workers to select new models specifically to illuminate hitherto neglected general themes within evo-devo."

In other cases, new model organisms are chosen on the basis of how well

they are thought to represent a particular ancestral organism. In connection to this practice, the researchers point to ‘basal bias’ as another way that scientists may get it wrong when choosing new model organisms.

This occurs when scientists choose an organism because it was the first to branch off from its ancestor, rather than because it has known genetic or developmental similarities to it.

"We caution against this widely used rule of thumb, and advise the use of additional criteria, such as molecular branch lengths, to choose species as best representatives of ancestral body plans," said Dr Jenner.

"Just because an organism has sprung from the base of the evolutionary tree does not make it more primitive and representative.

"Equally, those that became separate species further down the evolutionary line are not necessarily increasingly different from that common ancestor.

"Among living species that descended from a particular common ancestor, those designated as ‘basal’ are those that are separated from this ancestor by the smallest number of speciation events.

"Sometimes evolution speeds up in association with speciation – an organism can change a lot in this time.

"However, substantial evolutionary change may also occur in the absence of speciation, so basal species are not necessarily, or even likely a more conserved model of the ancestor.

"We need to make better use of the techniques that allow us to calculate how much an organism’s genome has changed over time, when making

assessments about how much an animal resembles its ancestor, because this information can be helpful in estimating how much an organism's phenotype has changed."

Dr Wills added: "Establishing criteria for choosing model organisms is important in this field, especially given the pressure on available funding sources.

"We encourage evo-devo workers to communicate with funding agents so that the limited resources available will not be disproportionately channelled to the 'big six', which, while important, cannot illuminate all evo-devo's central themes.

"If we want to understand how insects evolved wings or how legs developed from fins, we need to judiciously choose several models from specific parts of the phylogenetic tree.

"There is little point in blindly increasing the diversity of model systems, without some specific goals in mind.

"Our toolkit is too narrow, so as a community we need to clarify our objectives and set the agenda for future studies."

Source: University of Bath

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