

# Non-model heuristics to be used in the struggle

[Environment](#), [Ecology](#)



non-model organisms, organoids, genome sequencing, proteomics, or even biofilms – could push aside conventional model organisms as they have long existed. Rine (2014) is quick to note that, even as new technologies have forced a reappraisal of what a model organism is, research advances in the more traditional model organisms offer vibrant and vigorous new opportunities for young scientists and for future generations.

There seems little question, as Rine (2014) proposes, that new advances in translational research will expand opportunities in the realm of basic research. Thus, even as the possibility exists of more and more organisms becoming model organisms as time passes, the new technology and fresh insights also promise to expand the areas wherein model organisms can furnish us with exciting new advances. Hunter (2008) stresses that model organisms – such as *Caenorhabditis elegans* and *Drosophila* – became the invaluable tools of fundamental biological and clinical research by the middle of the twentieth century. But there have emerged occasions wherein clinical trials employing the model organisms have shown poor predictive power. Moreover, there has been the steady growth in interest vis-a-vis the use of human stem-cell lines in clinical trials in lieu of conventional model organisms. Additionally, it may occur – especially as our tinkering with sub-cellular and genomic processes become more advanced and esoteric – that some commonplace model organisms may fall from grace simply because they cannot handle or tolerate the insertion of novel DNA to anywhere the extent required (Hunter 2008). At the present time, however, it seems most accurate to argue that the old model organisms will not so much be swept aside as will be – at least for the immediate future – augmented or

accompanied by the growing usage of other non-conventional model organisms that offer fresh insights into vertebrate aging (the turquoise killifish), or that allow us to better understand how biological systems regenerate (axolotls), or that allow us to understand biological organisms adapt to, and survive, environmental extremes (tardigrades) (Russell et al 2017). The reality is that new models are surely going to eclipse the heavy reliance that science has historically had upon a select few organisms.

But, instead of pushing those conventional organisms aside, it is entirely possible that these new non-model model organisms will become merely additional heuristics to be used in the struggle to secure greater knowledge of human biological processes. In a society that values youth, the possibility that the turquoise killifish could present us with a profound segue into new advances in combating aging is – in and of itself – a remarkably exciting prospect.

One matter of continuing interest is how advances in genomic research will reshape the catalogue of model organisms used by researchers to gain insight into biological processes. Spradling et al (2006) contend that the genomics revolution could eventually lead to the use of a wide array of “genetically tractable” organisms to delineate human pathogenesis – from birth defects to neurological dysfunction, to reproductive failure to aging in biological systems.

The genomics revolution has the distinct potential to use a wide array of organisms to decipher gene-gene and gene-environment interactions while also giving us the capacity (though perhaps not just yet) to provide prophylactic and curative interventions that are designed on a customized

and individualized manner (please see Spradling et al 2006). As genomics grow, it is possible that other organisms will assert themselves as superior to the traditional models. But, even if this should prove the case, the increasing expertise and knowledge we accrue about genetic and genomic materials will also give us a chance to use conventional model organisms in new ways to learn even more about how we can combat the ills, diseases and disorders that undermine human life.

In that regard, the future prospects most certainly seem bright. Fields and Johnston (2005) are among a number of experts who are wholly convinced that model organisms like the yeast, worm and fruit fly will not be consigned to the dustbin of history any time soon. It does seem unwise to dismiss their strong faith. Last of all, as pointed out by Alfred and Baldwin (2015), the emergence of inexpensive short-read sequencing methods have made it possible for scientists to engage in reverse ecology over the past decade or more. Without getting into the esoteric finer points, the new tools and praxes which have come into view since the early 2000s have allowed for scientists to more clearly see the genomic imprints left behind by past selection pressures, and to shine a light on the trait evolution of model organisms. What emerges out of all of this is a new appreciation for the fact that, in some cases, the relationships between model organisms and humans is actually more intimate than supposed.

Furthermore, it is becoming clear that there is a greater array of diversity in model organisms that we previously recognized - which means that we have still more to learn about them and about what they can tell us about sundry

biological processes (Alfred & Baldwin 2015). Again, even though model organisms have been used for generations, new technologies and new knowledge are revealing that we still have very much more to learn about them. In that regard, their usefulness as model organisms is not at all exhausted. 5. Final Conclusions As the preceding several pages make quite plain, there can no longer be any question about the the vital importance of the model organism in facilitating medical research.

The salutary features of these organisms should pass beyond dispute at this point, and have been lengthily discussed above, but they do reveal a common trend: some organisms, because of their life cycle and developmental curves, because of the ease with which they can be harvested, and because of their general low maintenance, are simply well-suited to the exigencies and demands of molecular and sub-cellular research. As new advances are made, it is likely that these models will see become part of a growing roster of other model organisms that provide especial insights into esoteric areas – such as vertebrate aging – that are still quite a mystery to researchers. But the model organisms that have been so important for so long are not likely to fade away into irrelevance any time soon, largely because they are foundational building blocks for building upon pre-existing knowledge in a host of research areas. While it is possible that old-time model organisms will gradually become less important, they will not fade away simply because they offer too many attractive benefits that excite cost-conscious researchers.

The model organism is not dead, but will instead assume a more diverse array of forms in the decades to come.