

determining the optimal number and frequency of mice to be released. While these issues and questions pose significant challenges to this method of invasive rodent eradication, the seriousness of the biodiversity threat posed by invasive rodents and the potential of transgenic methods as tools for addressing this threat make careful experimental testing of transgenic methods a crucially important research direction.

¹Department of Molecular and Cellular Medicine, Texas A&M University, College Station, TX 77843, USA

²Department of Biological Sciences, North Carolina State University, Raleigh, NC 27695, USA

*Correspondence: kanavy@tamhsc.edu (D. Kanavy).

<http://dx.doi.org/10.1016/j.tree.2017.03.006>

References

1. Piaggio, A.J. *et al.* (2016) Is it time for synthetic biodiversity conservation? *Trends Ecol. Evol.* 32, 97–107
2. Gemmell, N.J. and Tompkins, D.M. (2017) Gene drives and rodent control: response to Piaggio *et al.* *Trends Ecol. Evol.* 32, 314–315
3. Koopman, P. *et al.* (1990) Expression of a candidate sex-determining gene during mouse testis differentiation. *Nature* 348, 450–452
4. Koopman, P. *et al.* (2001) Regulation of male sexual development by Sry and Sox9. *J. Exp. Zool.* 290, 463–474
5. Koopman, P. *et al.* (1991) Male development of chromosomally female mice transgenic for Sry. *Nature* 351, 117–121
6. Petras, M.L. (1967) Studies of natural populations of *Mus*. II. Polymorphism at the T locus. *Evolution* 21, 466–478
7. Lindholm, A.K. *et al.* (2013) Mate choice for genetic compatibility in the house mouse. *Ecol. Evol.* 3, 1231–1247
8. Carroll, L. *et al.* (2004) Fitness effects of a selfish gene (the *Mus* T complex) are revealed in an ecological context. *Evolution* 58, 1318–1328
9. Sugimoto, M. (2014) Developmental genetics of the mouse t-complex. *Genes Genet. Syst.* 89, 109–120
10. Backus, G.A. and Gross, K. (2016) Genetic engineering to eradicate invasive mice on islands: modeling the efficiency and ecological impacts. *Ecosphere* 7, 1–14
11. Gantz, V.M. and Bier, E. (2015) The mutagenic chain reaction: a method for converting heterozygous to homozygous mutations. *Science* 348, 442–444

Spotlight

Schism and Synthesis at the Royal Society

Kevin N. Laland^{1,*}

November 7–9, 2016 witnessed a joint discussion meeting of the

Royal Society and the British Academy (the UK national academies for the sciences and social sciences, respectively) entitled ‘New Trends in Evolutionary Biology: Biological, Philosophical and Social Science Perspectives’. The meeting, anticipated with a mix of feverish enthusiasm and dread, sold out months in advance, the eager audience perhaps expecting radical and traditional evolutionists to go toe to toe, rather than the constructive dialogue among biologists, social scientists, and researchers in the humanities that the academies advertised. One issue under discussion was whether or not the explanatory core of evolutionary biology requires updating in the light on recent advances in evo-devo, epigenetics, ecosystem ecology, and elsewhere.

The topics of the meeting – developmental bias, plasticity, inclusive inheritance, and niche construction – were chosen because they were of interest to both the biological and social sciences. That there should be a confluence between these subjects and those themes emphasized by the extended evolutionary synthesis [1] was no coincidence: it was this mutual interest that motivated the meeting. Such topics might seem an odd assortment to evolutionary biologists aware of other exciting advances, for instance in genomics. However, the focal topics were highlighted precisely because they constitute disputed territory in the evolutionary sciences, which in part was what made the meeting contentious.

This tension was manifest in the discussions where different interpretations of the same findings were voiced. For illustration, the evolutionary developmental researchers, Gerd Müller and Paul Brakefield, respectively described how patterns

of vertebrate digit gain and loss, and butterfly eyespot characteristics across the *Bicyclus* genus, could be predicted with knowledge of their mechanisms of development. For these biologists, a bias in development that produces some morphologies more readily than others can shape the course of adaptive evolution. Douglas Futuyma, by contrast, presented a more traditional standpoint in attributing the adaptive characteristics of organisms solely to selection, with the aforementioned developmental effects being seen as merely imposing constraints. The difference in perspective, while subtle, is crucial. For the former group, sources of bias in phenotypic variation are potentially an important evolutionary process which not only constrains but also facilitates and directs evolution. Bias is a major source of evolvability, and an explanation of its mechanisms, prevalence, and direction is crucial for understanding evolutionary diversification. Conversely, an orthodox view is that developmental bias and constraint are the same, and, because constraint is a well-understood and long-studied phenomenon within the field, it does not motivate any rethinking of evolutionary understanding.

Equivalent differences were manifest in most topics discussed. For instance, Russell Lande and Sonia Sultan disagreed over developmental plasticity – which can be viewed as a genetically specified reaction norm fashioned by past selection, and/or as being reliant on more open-ended (e.g., exploratory) developmental processes that are propagated across generations through epigenetic mechanisms. If the latter, plasticity may be capable of introducing phenotypic novelty and initiating and directing evolutionary change (as described by West-Eberhard [2], see also [3,4]). Similarly, epigenetic inheritance can be characterized as rare, under genetic control, merely another type of ‘gene’ [5], or as an additional major source of adaptive plasticity upon which selection can act, and which can mediate the inheritance of acquired

characteristics [6]. Finally, niche construction fits neatly into established theoretical frameworks when viewed as extended phenotypes [7], but becomes of little explanatory importance. When viewed as an evolutionary process that directs selection along particular pathways, by contrast, niche construction potentially presents a greater challenge [8].

The conference brought home a key point – these debates are not about data but rather about how findings are interpreted and understood. At the heart of the above differences are hidden disparities in how researchers think about development. Seemingly, traditionalists often view features such as plasticity, extragenetic inheritance, and niche construction as being specified by genetic programs that are finely honed by past selection, whereas radicals are more likely to view features of development as being underdetermined by past selection and hence a source of evolutionary novelty.

At least as important are different notions of how the scientific process works, or ought to work. Those speakers at the meeting pushing for change tend to emphasize the role of conceptual frameworks in shaping what questions are asked, what data are collected, and what factors are viewed as causally important. They maintained that alternative ways of addressing problems are of value because they encourage new lines of enquiry, leading to the generation and testing of novel hypotheses. Those defending the status quo, by contrast, tended either to deny that any dominant mindset prevailed or to refute that it imposed a constraint on the field. For these researchers, initiatives such as the extended evolutionary synthesis are simply unnecessary.

There were points of agreement. All parties emphasized that evolutionary biology is a vigorous and progressive field of science. To the chagrin of creationists and some journalists hoping for a fight, no

calls for revolution were heard. Likewise, everyone accepted that the focal phenomena had a long history of investigation within evolutionary biology – they might be ‘new trends’ in the sense that they are currently garnering increased attention, but the ideas go back decades or longer, and their significance has been debated periodically throughout the history of the field. Even so, these phenomena have never completely made it into the mainstream, perhaps (as traditionalists maintain) because they are simply not that important, or possibly (as radicals suggest) because conventional thinking marginalizes them – or because the tools to test them have only recently been devised. For all that, the discussion witnessed little meeting of minds. A schism separated those who championed the extended evolutionary synthesis as an innocent plea for scientific pluralism and those who dismissed it as misguided self-aggrandizement.

There was, however, one non-trivial respect in which the meeting was both synthetic and a source of some excitement. Its original, and indeed primary, objective – to promote dialogue between the biological and social sciences – did appear to succeed. While hardcore evolutionary biologists did not warm to calls to extend the synthesis, time and time again the biological anthropologists, psychologists, and archaeologists present asserted that the plasticity-first hypothesis [2], broadened inheritance, and niche construction are vital to their work. For these social scientists, standard gene-centric selectionist accounts provided less satisfactory explanations. To them, variants of evolutionary theory that bring these phenomena to the center are those to which they could relate, and indeed contribute. This was a potent reminder that the practical implications of differences between standard and expanded evolutionary perspectives amount to more than alternative interpretations, and impact significantly on research programs and on the relationships between

academic fields. It is difficult to ascertain to what extent the speakers and members of the audience were representative of these communities, and hence the generality of such claims remains to be established. Nonetheless, my impression is that the majority of those present left the meeting with a sense of optimism that these particular new trends might in the longer term help to strengthen the use of evolutionary thinking in adjacent fields, and in particular might bring about a richer and more productive brand of evolutionary social science.

¹Centre for Biological Diversity, School of Biology, University of St Andrews, Fife, UK

*Correspondence: knl1@st-and.ac.uk (K.N. Laland).
<http://dx.doi.org/10.1016/j.tree.2017.02.015>

References

1. Laland, K.N. *et al.* (2015) The extended evolutionary synthesis: its structure, assumptions and predictions. *Proc. Biol. Soc.* 282, 20151019
2. West-Eberhard, M.J. (2003) *Developmental Plasticity and Evolution*, Oxford University Press
3. Gilbert, S.F. and Epel, D. (2015) *Ecological Developmental Biology* (2nd edn), Sinauer
4. Sultan, S.E. (2015) *Organism and Environment. Ecological Development, Niche Construction, and Adaptation*, Oxford University Press
5. Dickins, T.E. and Rahman, Q. (2012) The extended evolutionary synthesis and the role of soft inheritance in evolution. *Proc. R. Soc. B* 279, 2913–2921
6. Jablonka, E. and Raz, G. (2009) Transgenerational epigenetic inheritance: prevalence, mechanisms, and implications for the study of heredity and evolution. *Q. Rev. Biol.* 84, 131–176
7. Dawkins, R. (1982) *The Extended Phenotype*, Oxford University Press
8. Odling-Smee, F.J. *et al.* (2003) *Niche Construction: The Neglected Process in Evolution*, Princeton University Press

Spotlight

The Fate of the World's Plants

Stuart L. Pimm^{1,*} and Peter H. Raven²

A recent report assessing the world's plant species finds continuing progress in completing the taxonomic catalog. However,