

Conclusion

Although recent meta-analyses have considered among-population genetic differentiation for molecular and quantitative traits [17], no such study is available on the correlation between measures of molecular versus phenotypic variability within populations, especially following environmental changes. As recently emphasised [18], prior evolutionary history of a species will influence phenotypic evolution during biological invasion. Furthermore, life-history and mating system probably also influence the relationship between the two types of diversity [13]. Genetic monitoring of both molecular and quantitative genetics diversity will provide invaluable information about evolutionary processes during range expansion, but also about the genetic architecture of quantitative traits, as suggested by the recent study of *H. canariense* [12].

Acknowledgements

I thank Benoît Pujol and John Pannell for providing their original data set, and Guillaume Martin, as well as three anonymous reviewers, for helpful comments. I thank the Institut Universitaire de France for lowering my teaching load. This is publication ISEM-2009-39 of the Institut des Sciences de l'Evolution, Montpellier.

References

- Price, T.D. and Sol, D. (2008) Introduction: genetics of colonizing species. *Am. Nat.* 172, S1–S3
- Duckworth, R.A. (2008) Adaptive dispersal strategies and the dynamics of a range expansion. *Am. Nat.* 172, S4–S17
- Sax, D.F. *et al.* (2007) Ecological and evolutionary insights from species invasions. *Trends Ecol. Evol.* 22, 465–471
- Hewitt, G. (2000) The genetic legacy of the quaternary ice ages. *Nature* 405, 907–913
- Naciri-Graven, Y. and Goudet, J. (2003) The additive genetic variance after bottlenecks is affected by the number of loci involved in epistatic interactions. *Evolution Int. J. Org. Evolution* 57, 706–716
- Turelli, M. and Barton, N.H. (2006) Will population bottlenecks and multilocus epistasis increase additive genetic variance? *Evolution Int. J. Org. Evolution* 60, 1763–1776
- Pujol, B. and Pannell, J.R. (2008) Reduced responses to selection after species range expansion. *Science* 321, 96
- Obbard, D.J. *et al.* (2006) Sexual systems and population genetic structure in an annual plant: testing the metapopulation model. *Am. Nat.* 167, 354–366
- Lavergne, S. and Molofsky, J. (2007) Increased genetic variation and evolutionary potential drive the success of an invasive grass. *Proc. Natl. Acad. Sci. U. S. A.* 104, 3883–3888
- Dlugosch, K.M. and Parker, I.M. (2008) Invading populations of an ornamental shrub show rapid life history evolution despite genetic bottlenecks. *Ecol. Lett.* 11, 701–709
- Lavergne, S. and Molofsky, J. (2004) Reed canary grass (*Phalaris arundinacea*) as a biological model in the study of plant invasions. *Crit. Rev. Plant Sci.* 23, 415–429
- Dlugosch, K.M. and Parker, I.M. (2007) Molecular and quantitative trait variation across the native range of the invasive species *Hypericum canariense*: evidence for ancient patterns of colonization via pre-adaptation? *Mol. Ecol.* 16, 4269–4283
- Novak, S.J. and Mack, R.N. (2005) Genetic bottlenecks in alien plant species. Influence of mating systems and introduction dynamics. In *Species Invasions: Insights into Ecology, Evolution, and Biogeography* (Sax, D.F. *et al.*, eds), pp. 201–228, Sinauer Associates
- Latta, R.G. (1998) Differentiation of allelic frequencies at quantitative trait loci affecting locally adaptive traits. *Am. Nat.* 151, 283–292
- Excoffier, L. and Ray, N. (2008) Surfing during population expansions promotes genetic revolutions and structuration. *Trends Ecol. Evol.* 23, 347–351
- Hallatschek, O. and Nelson, D.R. (2008) Gene surfing in expanding populations. *Theor. Popul. Biol.* 73, 158–170
- Leinonen, T. *et al.* (2008) Comparative studies of quantitative trait and neutral marker divergence: a meta-analysis. *J. Evol. Biol.* 21, 1–17
- Keller, S.R. and Taylor, D.R. (2008) History, chance and adaptation during biological invasion: separating stochastic phenotypic evolution from response to selection. *Ecol. Lett.* 11, 852–866
- Hermisson, J. and Wagner, G.P. (2004) The population genetic theory of hidden variation and genetic robustness. *Genetics* 168, 2271–2284
- Martin, G. and Lenormand, T. (2006) The fitness effect of mutations across environments: a survey in light of fitness landscape models. *Evolution Int. J. Org. Evolution* 60, 2413–2427

0169-5347/\$ – see front matter © 2009 Elsevier Ltd. All rights reserved.
doi:10.1016/j.tree.2009.01.015 Available online 4 May 2009

Letters

Evolution education in natural history museums

Janne S. Kotiaho^{1,2}, Petri Ahlroth³, Jari Haimi⁴, Mikko Mönkkönen⁴ and Janne Vilkuna^{2,5}

¹ Centre of Excellence in Evolutionary Research, Department of Biological and Environmental Science, PO Box 35, 40014 University of Jyväskylä, Finland

² Natural History Museum, PO Box 35, 40014 University of Jyväskylä, Finland

³ Finnish Environment Institute, PO Box 140, 00251 Helsinki, Finland

⁴ Department of Biological and Environmental Science, PO Box 35, 40014 University of Jyväskylä, Finland

⁵ Museology, Department of Art and Culture Studies, PO Box 35, 40014 University of Jyväskylä, Finland

During 2009, scientists around the world will celebrate the 200th anniversary of the birth of Charles Darwin, the father of the theory of evolution, and the 150th anniversary of the publication of his main thesis, *On the Origin of Species by Means of Natural Selection*. Today, the theory of evolution is considered to be one of the greatest milestones in the history of science. Despite its undisputed merit in science,

there seems to be constant turmoil around the theory in the public, which might be related to the incomplete understanding of the basic principles of evolution [1,2].

Recently, MacFadden [3] rightly pointed out that natural history museums, which have ca. 100 million visitors annually worldwide, have enormous potential to educate the public about the principles of evolution. In his essay, MacFadden advocates the allocation of resources into novel contents, such as genomics or molecular biology,

Corresponding author: Kotiaho, J.S. (janne.kotiaho@byti.jyu.fi).

in order to increase the public understanding of evolution. We argue that museums should concentrate more on demonstrating the basic principles and outcomes of natural selection, rather than presenting fashionable novel contents such as genomics (which, it seems, even scientists often have a hard time understanding [4]).

It is our intuition that visitors to museums will be taken a long way toward a better understanding of evolution by means of natural selection if museums can get across three often misunderstood principles: variation, selection and constant change. The reason these simple concepts are difficult to grasp is that our everyday observations of nature do not support them, and indeed often deceive us: we perceive all members of a given species to be nearly uniform, or to vary much less than we humans do; we never observe any selection in action; and we seldom observe any natural change in our familiar environment.

Museums are glimpses of the past and present, but frequently exhibits are fairly static, which is a problem if we want to get across a process as dynamic as evolution by means of natural selection. Habitat dioramas are the most popular mode of presentation in natural history museums, even though they have been around for 120 years [5,6]. Indeed, dioramas were (and still are) often crafted into such perfection, with the impeccable cooperation of taxidermists, background painters and foreground artists, that they have become 3D national icons just like the 2D paintings or 3D sculptures of national galleries. This situation constrains museums from removing or changing the dioramas.

If we want to educate the visitors of natural history museums about evolution by means of natural selection, we should aim at delivering the message that across species there is enormous within-species variation, that some of this variation is likely to cause differences among individuals in their lifetime reproductive success and that

these differences will result in a constant change – evolution. In museums, we have a great opportunity to do this; as well as the exhibits open to the public, museums usually have extensive collections containing numerous individuals of each species. A simple illustration of the replacement of one generation by the next generation might work in making the operation of natural selection more tangible. With such an illustration, we can easily see why and how a population can undergo constant change, and thus grasp the basic principles of evolution by means of natural selection.

Natural history museums are our collective memory of the past. Their collections can, and have been, used to study evolution (e.g. [7]). Perhaps even more importantly, however, they could also be used to illustrate to the general public the evolutionary changes that have taken place. We challenge the exhibit designers of natural history museums to emphasize variation within species, and to demonstrate change due to natural selection, rather than stasis in nature.

References

- 1 Pigliucci, M. (2002) *Denying Evolution: Creation, Scientism, and the Nature of Science*. Sinauer Associates
- 2 Dawkins, R. (2006) *The God Delusion*. Bantam Press
- 3 MacFadden, B.J. (2008) Evolution, museums and society. *Trends Ecol. Evol.* 23, 289–291
- 4 Morange, M. (2001) *The Misunderstood Gene*. Harvard University Press
- 5 Wonders, K. (1993) *Habitat Dioramas – Illusions of Wilderness in Museums of Natural History (Acta Universitatis Upsaliensis Figura Nova Vol. 25)*. Coronet Books
- 6 Quinn, S.C. (2006) *Windows on Nature – The Great Habitat Dioramas of the American Museum of Natural History*. Abrams
- 7 Lens, L. *et al.* (2002) Avian persistence in fragmented rainforest. *Science* 298, 1236–1238

0169-5347/\$ – see front matter © 2009 Elsevier Ltd. All rights reserved.
doi:10.1016/j.tree.2009.02.006 Available online 3 May 2009

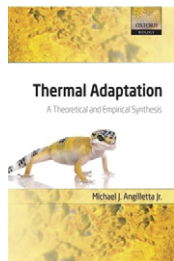
Book Review

Coping with the heat

Thermal Adaptation – A Theoretical and Empirical Synthesis by Michael J. Angilletta Jr. Oxford University Press, 2009. £65.00/£34.95 hbk/pbk (320 pages) ISBN 978 0 19 857087 5/978 0 19 857088 2

David Atkinson

School of Biological Sciences, University of Liverpool, Biosciences Building, Crown Street, Liverpool, L69 7ZB, UK



Many books deal with the adaptation of organisms to their environment, and there are others that focus on thermal biology, but *Thermal Adaptation* brings these two subjects together by tackling adaptive strategies for coping with temperature variation. Pulling this subject together into a coherent account is far from easy, especially as the literature is widely scattered, often with theoretical and empirical studies being unconnected, and with diverse

strategies being used by organisms for coping with thermal variation.

Mike Angilletta imposes order amid this potential messiness first by focusing on a particular type of question. He argues that, despite a ‘vast and venerable literature’ documenting the responses of organisms to temperature, we do not understand why certain species exhibit certain phenotypes. To this end, he draws on models from evolutionary biology to gain insights into thermal adaptation, focusing on mathematical models to ensure that assumptions are made explicit and predictions more precise. Angilletta then tests the predictions against the empirical evidence, which comprises quantification of natural selec-

Corresponding author: Atkinson, D. (david@liv.ac.uk).