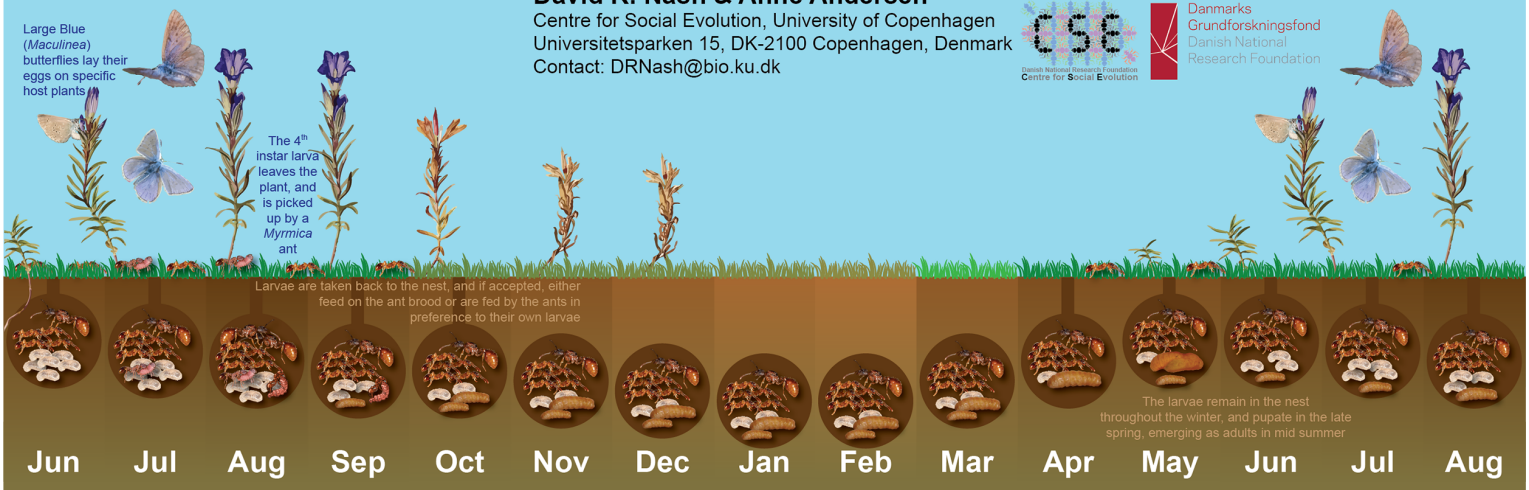
Evolutionary Conservation of Large Blue Butterflies

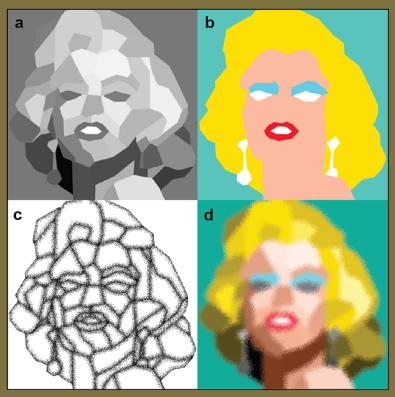
David R. Nash & Anne Andersen
Centre for Social Evolution, University of Copenhagen
Universitetsparken 15, DK-2100 Copenhagen, Denmark
Contact: DRNash@bio.ku.dk

Danmarks Grundforskningsfond
Danish National Research Foundation
Centre for Social Evolution

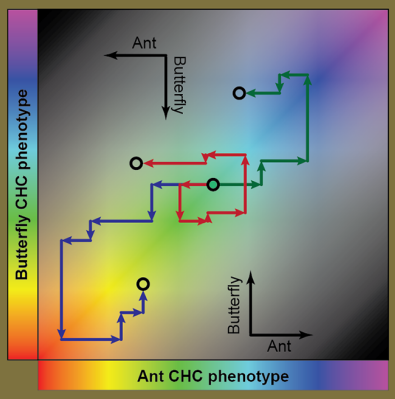


Coevolution between Large Blue butterflies and their hosts

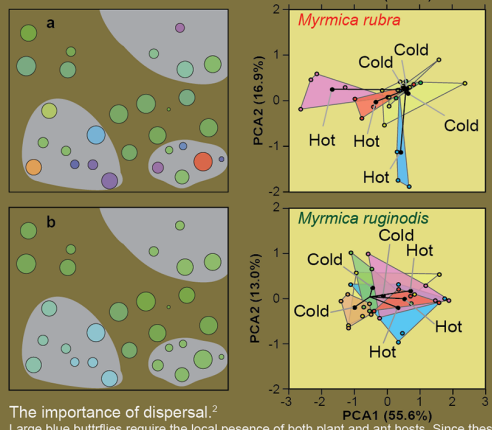
Large Blue butterflies are in an on-going coevolutionary arms race with their host ants (and probaly also their host plants), which is a classic example of the geographic mosaic of coevolution



The three components of the geographic mosaic of coevolution.[1]
a) Populations of interacting species vary in the strength of reciprocal selection from independent evolution (cold spots - light tiles) to hot spots (dark tiles) where coevolutionary selection is intense. b) The outcome of selection varies (different coloured tiles) depending on the interactions between the genotypes of both species and the local environment. c) There is some mixing of genes due to the dispersal of individuals between populations. d) The combination of all three elements leads to a system in which coevolution is a continuous dynamic process that retains ample genetic variation to allow long-term coevolution.

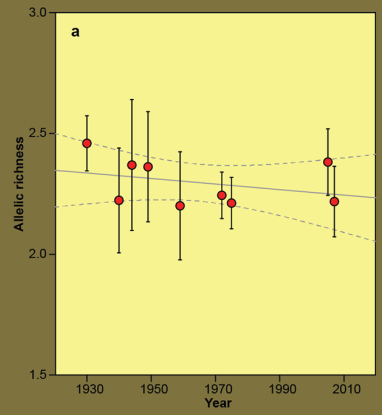


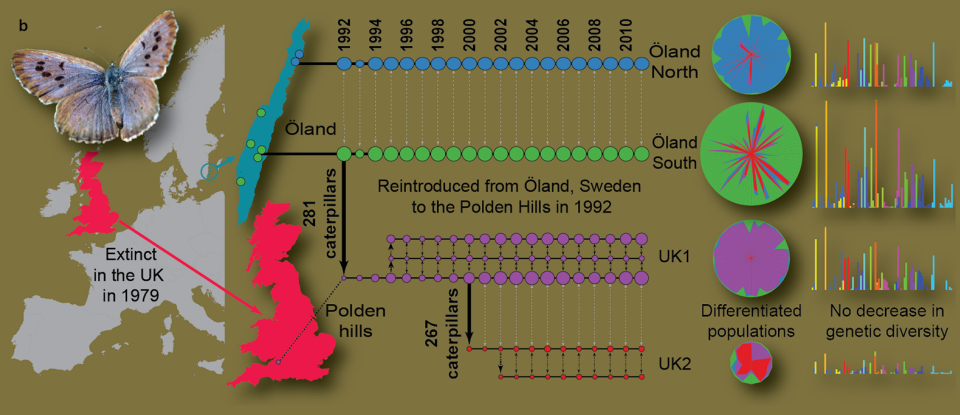
Coevolution based on matching of hydrocarbons.[2]
Large blue butterflies mimic the cuticular hydrocarbons (CHCs) of their *Myrmica* host ants, which are used to recognize colony members. Selection will act of the butterflies to more closely match their hosts' phenotype, while the host will be selected to become more different. The exact trajectory taken will vary between populations (three examples are shown), leading to different outcomes, and will be constantly dynamic.



The importance of dispersal.[2]
Large blue buttrflies require the local pesence of both plant and ant hosts. Since these areas of co-occurrence are patchily distributed (hot spots - grey areas), there are many cold spots where the hosts do not interact with the butterflies and are subject to other selection pressures. If the hosts have lower disersal abilities than the butterflies (a) then local adaptation and coevolution can occur, but if host dispersal is high (b), host local adaption will be swamped by gene-flow from cold spots. These two patterns are shown by the two hosts of *Maculinea alcon* in Denmark, which differ in their social structure and dispersal.

Genetic and evolutionary consequences of the extraordinary life history of Large Blue butterflies

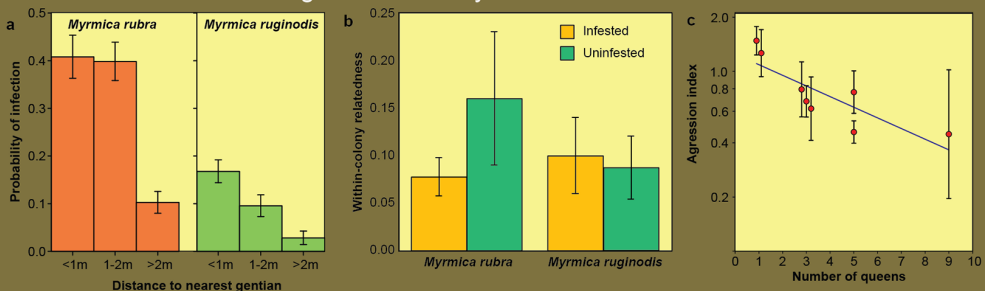




Because of the phenotype matching between butterflies and hosts required for sucessful development, only a very small, non-random fraction of Large Blue butterflies successfully transmit their genes to the next generation. This means that effctive population sizes are small and largely independent of census population size. This in turn has probably lead to the purging of deleterious alleles, which means that although populations are small, they are remarkably stable. The population size of *Maculinea arion* on Møn in Denmark has fluctuated widely over the last century, but its genetic diversity has remained constant (a)[3]. Reintroduced populations of *Maculinea arion* in the U.K. have the same level of genetic diversity as the populations from which they were sourced, despite the bottleneck associated with reintroduction (b), but have become genetically differentiated over distances of only a few kilometers.[4]

Can we predict factors that will increase the chance of Large Blue butterfly survival based on their evolution?

Assessing the CHC phenoype match of potential hosts may increase the success of reintroduction programs, but the highly dynamic nature of the coevolutionary process may mean that this is not as vital as once thought. The importance of dispersal and the nature of cold-spot host populations suggests that hosts surrounding conservation sites should also be examined and maintained. Maintaining the overlap in hosts on a very local scale is also important (a), which also depends on having strong source populations of hosts nearby. The social structure of host ants is also important: For *Maculinea alcon* the chance of being adopted by a host colony of *Mymica rubra* is higher if that colony has lower within-colony relatedness as a result of having multiple queens (b)[5]. This is probably a result of the threshold for differences in CHCs that trigger aggression being higher in colonies with multiple queens (c)[6], as they have to accept more genetically diverse colony-mates.



1. Nash, D. R. (2008) Process rather than pattern: finding pine needles in the coevolutionary haystack. Journal of Biology 7: 14.
2. Nash, D. R., Als, T. D., Maile, R., Jones, G. R. & Boomsma, J. J. (2008) A mosaic of chemical coevolution in a large blue butterfly. Science 319, 88-90.
3. Ugelvig, L. V., Nielsen, P. S., Boomsma, J. J. & Nash, D. R. (2011) Reconstructing eight decades of genetic variation in an isolated Danish population of the large blue butterfly *Maculinea arion*. BMC Evol Biol 11, 201.
4. Andersen, A., Simcox D., Thomas J.A. & Nash, D. R. (in review) Evolutionary potential of reintroduced and source populations of the large blue butterfly (*Maculinea arion*)
5. Nash, D. R. & Boomsma, J. J. (2008) Communication between hosts and social parasites. In Sociobiology of Communication - an interdisciplinary approach (ed. P. d'Ettorre and D. P. Hughes), pp. 55-79. Oxford. Oxford University Press.
6. First, M. A., Duney, M. & Nash, D. R. (2012) Testing the adjustable threshold model for intruder recognition on *Myrmica* ants in the context of a social parasite. Proceedings of the Royal Society of London, Series B: Biological Sciences 279, 516-522.

Aknowledgements: These studies were supported by grants from the Carlsbrg fund and the Danish National Research Foundation to the Centre for Social Evolution (Grant DNRF57)