

HIGHLIGHTED ARTICLES

Phylogeography of red deer in Europe revealed by mitochondrial DNA markers

Red deer (*Cervus elaphus*) is one of the most important and widespread game species throughout Europe, with an estimated population size exceeding half a million. The current distribution of red deer is assumed to be strongly influenced by human activities in addition to the colonization history and the last glaciation event. Due to the stationary habits of female social groups, the establishment of new populations by human translocations has often been reported. There are even historical data describing such translocations from the Viking sagas.



Worldwide, red deer has a circumboreal distribution, and genetic investigations have pointed to a central Asian origin. Despite its prominence as a big game animal, a detailed investigation of the genetic

relationships of red deer populations in Europe has not been performed until now. As a consequence, the large (geographic) scale impacts of human translocations have not been known. In an article published in *Journal of Biogeography*, Anna Skog and co-workers report on the mitochondrial phylogeography of red deer in Europe.

Skog *et al.* analysed two regions within the mitochondrial genome from most European populations and by phylogenetic analyses of the gene sequences found that there are three main evolutionary lineages in Europe. The southern lineage is the most ancient. This genetic lineage is found in Africa in Sardinia/Corsica and at one site in Spain. The rest of Europe is populated by two genetically distinct red deer lineages, showing a western/northern and an eastern distribution, respectively.

Within each main lineage there are several variants, and the diversity and distribution of these variants give indications about putative glacial refugia. Skog and co-workers suggest that such refugia have existed in Spain (the Iberian Peninsula) and in the Balkans. Thus, the Western and Eastern clades have survived during the last

glaciation in these regions and subsequently repopulated Europe from their respective refugia. This is further substantiated by calculations of how old the Western and Eastern clades are. Using the mutations separating the clades and estimated mutation rates for the genes, they calculated the split between the Western and Eastern clades to date at least 150,000 years ago, thus pre-dating the last glaciation.

Somewhat surprisingly, the analysis revealed no obvious signs of long-distance human translocations. While there is little doubt that this has happened in the past, the data of Skog *et al.* indicate that translocations have predominantly been short distance, or involved animals being translocated between regions where animals belong to the same main clade.

[Read the article online >>>](#)

Source paper: Skog, A., Zachos, F.E., Rueness, E.K., Feulner, P.G.D., Mysterud, A., Langvatn, R., Lorenzini, R., Hmwe, S.S., Lehoczky, I., Hartl, G.B., Stenseth, N.C. & Jakobsen, K.S. (2008) Phylogeography of red deer (*Cervus elaphus*) in Europe. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.01986.x

Image: Dortmund, Tierpark, Hirschkuh (*Cervus elaphus*). Courtesy of Mathias Bigge.

High-altitude small mammals of the North American Great Basin are not completely isolated

The term “sky islands” sounds intriguing, but it may be more lyrical than useful when discussing mammal distributions, according to new research from Eric Waltari of the Sackler Institute of Comparative Genomics at the American Museum of Natural History and Robert Guralnick from the University of Colorado at Boulder. The team used an emerging technique, ecological niche modeling, to show that the populations of small mammals living on mountaintops in the Great Basin—on islands in the sky—are not as isolated as previously thought.

In the new paper published in the *Journal of Biogeography*, Waltari and Guralnick test the concept of geographic isolation on thirteen species of small mammals. The species chosen were mapped with current and past climate data to “backcast” the distribution of each species at the height of the last ice age 21,000 years ago. The predictions of the model are calibrated with

known fossil records. Backcasting allows researchers to test whether species had different distributions in the past; the current study, for example, found that most of the species (12 of 13) lived at lower elevations 21,000 years ago and that the average distribution of each species was larger than it is now.

Determining the area that species inhabited in the past helps researchers understand current population distribution within the Great Basin and potential linkages between “sky islands.” Many of the species in this study (9 of 13) had suitable habitat below their current range that could link different populations. This surprising result can be further tested with molecular research. Waltari and Guralnick also found that not all species were widespread across the basin 21,000 years ago, highlighting the idiosyncratic nature of species’ responses to climate change.



“Niche modeling is a quick and straightforward approach to addressing problems that molecular data will eventually solve,” says Waltari.

[Read the article online >>>](#)

Source paper: Waltari, E. & Guralnick, R.P. (2008) Ecological niche modelling of montane mammals in the Great Basin, North America: examining past and present connectivity of species across basins and ranges. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.01959.x

Image: Great Basin National Park (Nevada). Courtesy of the National Park Service .

Macroevolutionary mosaics – revealing the history for complex host–parasite systems

An emerging synthesis linking biogeography, ecology and coevolution provides a new framework to explore the structure and history of intricate biological associations such as those represented by host and parasite systems. A general model, established by Dr. Eric Hoberg from the US National Parasite Collection, USDA and Dr. Daniel Brooks from the University of Toronto, for the evolution of parasite biotas emerges from empirical evidence describing a complex mosaic in which host switching and geographic colonization have served as determinants of diversity.

Complex assemblages of hosts and parasites are explained through coevolution and colonization and by integrating aspects of three hypotheses – ecological fitting, oscillation (episodes of increasing host range alternating with isolation on particular hosts) and taxon pulses (cyclical episodes of geographical expansion of ancestral species followed by isolation of populations producing descendant species, occasionally accompanied by ecological

divergence, setting the stage for the next episode of expansion) – to establish a context for host and geographical distribution across varying temporal and spatial scales. Concepts are examined and framed by equating colonization with a breakdown in mechanisms for ecological isolation such as those driven by periodic global extinction, or episodic and cyclical climate fluctuation and environmental perturbation that have characterized marine and terrestrial systems in evolutionary and ecological time. Major radiations for assemblages of hosts and parasites, across nearly all taxa, have their roots in episodic events of extinction and biotic expansion in Earth history.

The synthesis signifies a conceptual shift from a mechanistically simplistic view of diversification through long-term mutual association and mutual modification of lineages to one involving an intricate historical mosaic involving host switches resulting from change in ecological context and geographic distribution. This

view suggests that major episodes of climate change can trigger multiple rapid host switches, including those we call emerging diseases. This provides an appropriate ecological and evolutionary dimension for understanding patterns of introduction and dissemination of invasive species, and emergence of pathogens, parasites and disease in the current regime of global climate change with attendant disruption of ecological continuity.

[Read the article online >>>](#)

Source paper: Hoberg, E.P. & Brooks, D.R. (2008) A macroevolutionary mosaic: episodic host-switching, geographical colonization and diversification in complex host–parasite systems. *Journal of Biogeography*, doi: 10.1111/j.1365-2699-2008-01951.x.

More information about *Journal of Biogeography*



Edited by: Robert J. Whittaker

ISI Journal Citation Reports® Ranking: 2007: 3/31 (Geography, Physical); 20/116 (Ecology)

Impact Factor: 3.539

The mission of the journal is to contribute to the growth and societal relevance of the discipline of biogeography through its role in the dissemination of biogeographical research. To that end, the editorial policy is that the journal seeks to be representative of the discipline of biogeography, to be global in scope, and to be inclusive of major traditions and viewpoints within the discipline.

Visit www.blackwellpublishing.com/jbi for more journal information