

HIGHLIGHTED ARTICLES

December 2008

This edition of 'Editor's Choice' includes 6 articles recently published in *Journal of Biogeography*. Please click on the links below to read the article summary:

- Azorean arthropods do it fast in dark caves
- Comparing present and past expansion processes in a desert bird
- Past climate transition explains penguin genetic diversity
- Do migratory pathways affect regional abundance of wintering birds? A test in northern Spain
- Venomous snakes illuminate ancient speciation patterns in Middle American highlands
- The Hawaiian Archipelago is a stepping stone for dispersal in the Pacific

Azorean arthropods do it fast in dark caves

Azorean arthropods have diversified according to the age, area and relative isolation of each island within the archipelago. However, each group experiences these factors differently; hence their patterns of diversification differ according to their particular life histories. This is the main finding of a study conducted by Joaquín Hortal from the NERC Centre of Population Biology of the Imperial College, and Paulo Borges from the Azorean Biodiversity Group (CITA-A) of the University of the Azores, recently published in the *Journal of Biogeography*. The authors show that although the shape of the relationship between diversification and time is in general the same, different groups show different rhythms of evolution. They reach these conclusions within the first independent evaluation of the General Dynamic Model of Oceanic Island Biogeography, recently proposed by Robert J. Whittaker and colleagues, which merges the geological evolution of islands with the biological evolution happening on them. Borges and Hortal used the framework provided by this new model to study the relationship between the number of species that are single island endemics (i.e.,



exclusive of each island) and the age, area and isolation of each island.

Within the Azores, cave species appear to have evolved quite quickly, producing a number of species during the initial stages of development of the islands, when cave systems formed by lava tubes and volcanic pits were abundant and pristine due to the high volcanic activity. When the islands settle, cave systems start to collapse, diminishing the area available for cavernicolous species, which eventually end up either facing extinction or surviving in the small crevices of the soil under the forest. This rapid pace of diversification and early decline is exclusive to cave arthropods and does not appear to be evident for the other arthropod groups studied. In most islands some lineages are still evolving into new species, so older islands show more exclusive species than younger ones, except for the older island, Santa Maria, where some groups show some decrease in the pace of diversification. Such differences between groups are caused by the opposing roles of the two components of diversification. When speciation is predominant,

diversification is positive and the number of endemic species on an island increases. This pace slows down as extinction takes the lead, and diversification gets slower and eventually negative when the islands age and erode and they start to lose species numbers. While for most arthropods the Azores is a land full of opportunities, those inhabiting caves already feel the pressure of living in aging islands.

Other factors, such as dispersal capacity, also affect the pace of diversification within the Azores, suggesting that the diversity of evolutionary responses in different kinds of organisms is so wide that no general model, like the one proposed by Whittaker and colleagues is able to predict the pattern and process of diversification of all living groups. What this model does, however, is to allow integration of deviations from the general pattern into a common theoretical framework. By relating these deviations with the particular characteristics of each group, we might be able to ascertain how and why evolutionary processes happen on the isolated archipelagos that constitute some of the few long-term experiments provided by nature.

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Source paper: Borges, P. A. V. & Hortal, J. (2008) Time, area and isolation: factors driving the diversification of Azorean arthropods. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.01980.x.

Image: Caldeira Corvo. Courtesy of J. Hortal



Comparing present and past expansion processes in a desert bird

The trumpeter finch (*Bucanetes githagineus*) is a small bird from arid lands whose breeding range is currently expanding northwards, probably as a consequence of global warming. This expansion has been well documented in the north-western area of its distribution (Northwest Africa and the Iberian Peninsula), where its range has increased about 250 km in the last 25 years. The long occurrence of the species in the Canary Islands allows the study of its current and past expansion processes, its colonization patterns and the genetic mechanism involved.

A study by Barrientos and colleagues published in *Journal of Biogeography* specifically compares the genetic features of breeding trumpeter finch populations from the Canary Islands, the recently established population in the Iberian Peninsula and the presumed source population in Northwest

Africa. It also tests the prediction that rapid range expansion of a species commonly results in a homogeneous genetic structure and reduced genetic diversity in the peripheral population as a result of consecutive bottlenecks.

The study found that, at present, birds from the Canary Islands are genetically differentiated from those in North Africa and the Iberian Peninsula. Although it was not possible to confirm unequivocally that the Canary Island and the Iberian populations come from Northwest Africa, the genetic results, supported by historical data, suggest that this is probably the case. In contrast to expectations, the expanding population in the Iberian Peninsula has a relatively high genetic diversity, similar to that found in North Africa. The results suggest that there must have been, and

probably remains, a strong gene flow from Africa towards the Iberian localities that prevents bottlenecks.

Insights were also gained into the mechanism of range expansion, showing that birds from the main breeding nucleus in the Iberian Peninsula strongly contribute to other breeding and non-breeding areas in the south-eastern Iberian Peninsula.

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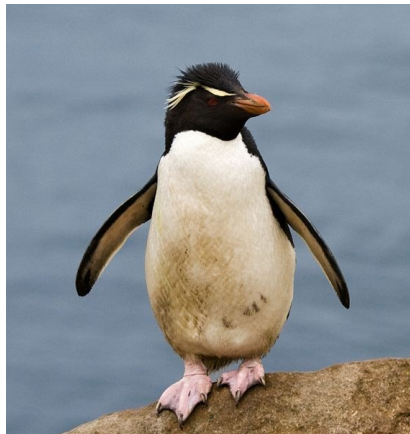
Source paper: Barrientos, R., Kvist, L., Barbosa, A., Valera, F., López-Iborra, G.M. & Moreno, E. (2008) Colonization patterns and genetic structure of peripheral populations of the trumpeter finch (*Bucanetes githagineus*) from Northwest Africa, the Canary Islands and the Iberian Peninsula. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.01995.x

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Past climate transition explains penguin genetic diversity

Penguins are a family of marine birds occupying a wide variety of environments throughout the Southern Hemisphere, from the tropical Galapagos to Antarctica. Recent studies have shown that the genetics of penguin populations are much more complex than previously thought because of the existence of several genetically different lineages within the same morphological species. These sibling species are unique models for understanding the evolutionary origins of species. The case of rockhopper penguins is particularly interesting because the three sibling species are located on either side of the subtropical convergence (STC), a major oceanographic boundary between subtropical and sub-Antarctic watermasses: while the northern rockhopper penguin breeds on subtropical islands north of the STC, the southern and eastern rockhoppers breed on sub-Antarctic islands south of the STC.

In a recent study in the *Journal of Biogeography*, Marc de Dinechin, from the French Centre National de la Recherche



Scientifique (CNRS), and colleagues investigated the role of past geographical movements of the subtropical convergence in the split between rockhopper penguin lineages. They used isotopic datings of the emergence of Amsterdam Island, in the southern Indian Ocean, to calibrate a molecular clock and date the divergence between rockhopper penguin lineages from both sides of the subtropical convergence. The split between sub-Antarctic and subtropical rockhopper penguin lineages was estimated at c. 0.9 million years, which

corresponds to the mid-Pleistocene transition, a major change in climate cyclicity. Palaeoceanographic data show that this transition was associated with a southward relocation of the subtropical convergence. This shift may have isolated the northernmost populations of the Atlantic Ocean, thus initiating the split between rockhopper penguin lineages.

This study highlights the role of watermasses and their temperature boundaries in the distribution of the Southern Ocean fauna. It also highlights the role of climate-driven ecological isolation in speciation processes as a generator of biodiversity.

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Source paper: de Dinechin, M., Ottvall, R., Quillfeldt, P. & Jouventin, P. (2008) Speciation chronology of rockhopper penguins inferred from molecular, geological and palaeoceanographic data. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.02014.x

Image: Adult *Eudyptes chrysocome chrysocome* in the Falklands Islands rookery. Photo © Samuel Blanc

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Do migratory pathways affect regional abundance of wintering birds? A test in northern Spain

The distribution of organisms at regional scales is commonly interpreted as the result of spatial variation in habitat suitability. However, the possibility that geography itself may affect distribution patterns has received less attention. For example, the abundance of wintering bird populations might be influenced by the cost of reaching areas located far away from the main migratory pathways. To explore this idea, a team from the Universidad Complutense of Madrid studied the abundance distribution of three common migratory passerines (meadow pipits, common chaffinches and European robins) wintering in farmlands located in the 600-km long Cantabrian coastal sector of northern Spain. This is an area roughly perpendicular to the west-Pyrenean migratory pathway, which drives European migrant birds into the Iberian Peninsula.

Despite the effects of climate, vegetation structure and local abundance of breeding conspecifics, the winter abundance of all three species decreased with the distance from their main

migratory route in the western Pyrenees. This result supports the view that the sectors located near the migratory pathway seem to be more easily occupied by migrants, in turn supporting the idea that proximity to passage areas may explain the fine-grain regional patterning of species abundance in wintering grounds.

The existence of purely geographic effects on habitat occupation by wintering birds has important conservation implications. Other things being equal (e.g. habitat suitability), sites located inside or near migratory pathways should be treated as cornerstone sites for the conservation of migratory birds because they are used during both migration and wintering periods.

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Source paper: Tellería, J.L., Ramírez, Á., Galarza, A., Carbonell, R., Pérez-Tris, J. & Santos, T. (2008) Do migratory pathways affect regional abundance of wintering birds? A test in northern Spain. *Journal of Biogeography*, 10.1111/j.1365-2699.2008.01983.x.

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Venomous snakes illuminate ancient speciation patterns in Middle American highlands

The extreme topography, the interdigitation of diverse habitats, and the dynamic tectonic and climatic history of Middle America – Central America and Mexico – have synergistically led to the tremendous biodiversity and endemism of the region. This complexity has, however, drastically complicated the identification of specific historical processes that have globally shaped the region's biodiversity. To open new windows of insight into this problem, an international team of investigators from multiple institutions have leveraged comparative phylogeographical analyses across multiple lineages of highland venomous snakes to identify major underlying tectonic events that appear to have shaped the region's highland biodiversity. Their results provide the first modern explicit spatial and temporal model for major events that underlie patterns of speciation in the region, and provide a broad predictive hypothesis for other codistributed organisms.

Earlier speciation models for highland taxa in the region that lacked explicit estimates

of divergence times and phylogeny had identified Pleistocene climatic cycling as a major force contributing to speciation and endemism in the region. In contrast, results from this study suggest that all recognized species of highland pitvipers diverged prior to the end of the Pliocene. These results imply that Miocene and Pliocene tectonics, rather than Pleistocene climate change, were responsible for generating the impressive recognized highland pitviper species diversity, and raise the broader question of how important were Pleistocene climatic changes in generating the region's biodiversity.



Middle American is perhaps the most important nexus of speciation and historical gene flow in the Western Hemisphere, yet much controversy regarding the tectonic and geological events that have shaped this region exist. The biogeographic approach applied in this study provides new encouragement and future motivation that continued comparative phylogeographic research may deliver tremendous insight for assembling a synthetic physical and biotic inference of the region's history and evolution.

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Source paper: Castoe, T.A., Daza, J.M. Smith, E.N., Sasa, M.M., Kuch, U., Campbell, J.A., Chippindale, P.T. & Parkinson, C.L. (2008) Comparative phylogeography of pitvipers suggests a consensus of ancient Middle American highland biogeography. *Journal of Biogeography*, doi: 10.1111/j.1365-2699.2008.01991.x

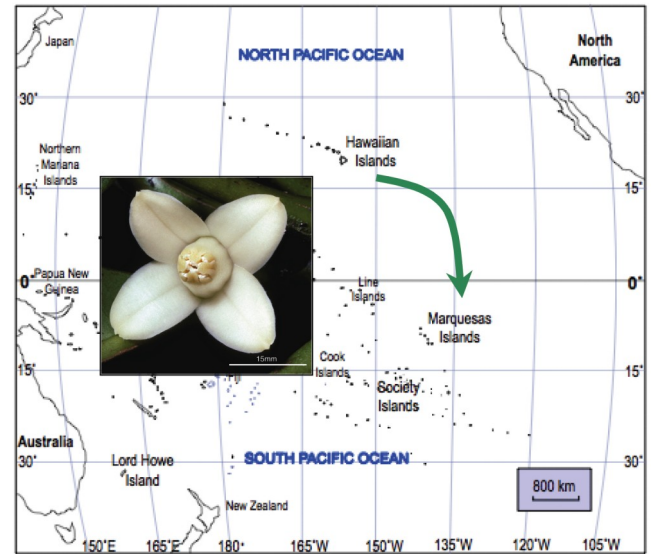
Image: *Bothriechis nigroviridis*. Photo courtesy of Al Coritz.

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The Hawaiian Archipelago is a stepping stone for dispersal in the Pacific

The Hawaiian Archipelago is one of the most isolated island chains on Earth, more than 2600 km from its nearest continent. A majority of its diversity has been presumed to have been derived from long-distance dispersal from source areas with high biodiversity in the western Pacific, through stepping-stone island chains. As the last island archipelago in the chain of stepping-stone islands in the Pacific, and given its extreme isolation from any continent, the Hawaiian Archipelago has been assumed to be a sink for dispersals, not a source. However, results from recent evolutionary studies using molecular data are revealing an emerging trend that the Hawaiian Islands can act as a stepping stone for the dispersal of plants and animals in the Pacific, and even as a source for continental colonization.

A recent study in *Journal of Biogeography* by Danica Harbaugh and colleagues represents one of the strongest examples to date of plant dispersal out of the Hawaiian Islands to other areas of the Pacific. Using abundant molecular data, the biogeographic patterns of the plant genus *Melicope* (and the related genus *Platydesma*) (Rutaceae) were elucidated. The results revealed at least one long-distance dispersal event to the Marquesas Islands, located in the South Pacific, probably by a migrating bird. These results join mounting evidence suggesting that the Hawaiian Islands are not the last-stop in dispersal across the Pacific. This paper suggests a number of other plant groups that should be examined, or re-examined, in order to determine if they also follow this biogeographic pattern.



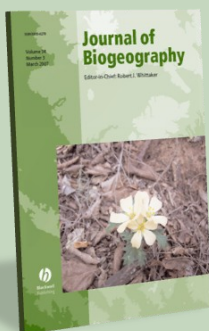
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Source paper: Harbaugh, D.T., Wagner, W.L., Allan, G.J. & Zimmer, E.A. (2008) The Hawaiian Archipelago is a stepping stone for dispersal in the Pacific: an example from the plant genus *Melicope* (Rutaceae). *Journal of Biogeography*, doi:10.1111/j.1365-2699.2008.02008.x

Image: Map of the Pacific region showing the long-distance dispersal of *Melicope* (+ *Platydesma*) from the Hawaiian Islands to the Marquesas Islands. The photograph shows a flower of *P. spathulata*. Courtesy of G. D. Carr

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