Journal of Biogeography

EDITOR'S CHOICE

March 2010

This edition of 'Editor's Choice' includes 3 articles recently published in *Journal of Biogeography*.

Giant pandas in fragmented forest landscapes: where do they live?

The giant panda is among the world's most threatened animals. Due to an expanding human population in China, coupled with intensifying agricultural and industrial activities, giant pandas are now confined to forest patches in the mountainous areas of south-western China. Their forest habitat is being increasingly fragmented and habitat loss continues to occur outside of protected areas. However, little is known about the distribution pattern of giant pandas at a landscape level, and no quantitative studies have attempted to address giant panda distribution in relation to forest fragmentation. Effective conservation requires an understanding, and monitoring, of the response of giant pandas to forest fragmentation.

In a recent study, Tiejun Wang, Xinping Ye, Andrew K. Skidmore and Albertus G. Toxopeus presented a new approach to integrate remote sensing and landscape ecology. Their aim was to model the spatial distribution of giant pandas by quantifying the effects of forest fragmentation on the distribution of the giant panda population at the landscape scale. The result reveals that the size and shape patterns of forest patches are important factors in determining the distribution of giant pandas – panda density is highest in large and contiguous forest patches that are clustered together. Among current panda distribution areas, the Qinling Mountains were observed to have least forest fragmentation and the highest density of individuals, while the Xiangling and Liangshan regions have most fragmentation and the lowest panda density.

The authors further examined the performance of the model using field occurrence data, finding that landscape pattern can explain panda distribution adequately when other environmental factors, such as elevation and slope, are included.

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Source paper: Wang, T.J., Ye, X.P., Skidmore, A.K. & Toxopeus, A.G. (2010) Characterizing the spatial distribution of giant pandas (*Ailuropoda melanoleuca*) in fragmented forest landscapes. *Journal of Biogeography*, doi:10.1111/j.1365-2699.2009.02259.x.

Image: A wild giant panda wandering in fragmented forests in the Qinling Mountains. Photograph by Naxun Zhao.

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Using invasive megaherbivores to rethink the Australian megafaunal extinctions

Australia is renowned for its biological peculiarities, many of which are attributed to its unusual evolutionary history – associated with being an isolated continent. One difference to other continents is the absence of large herbivores – the biggest kangaroos weigh just 65 kg. However, there were numerous species of giant marsupials, some exceeding one tonne, up until around the time of human colonization, 50 thousand years ago. The cause of these late Pleistocene megafaunal extinctions in Australia remains hotly contested.

In a recent paper in *Journal of Biogeography*, David Bowman, Brett Murphy and Clive McMahon have shed new light on these extinctions by comparing the diets of two bovines introduced to northern Australia by the British in the early 19th century. They show that the diet of the banteng, an endangered Southeast Asian domesticated bovine that never spread far from its point of introduction in coastal western Arnhem Land, consists mainly of browse (woody plants). In contrast, the Southeast Asian water buffalo, which has rapidly colonized the Arnhem Land region, has a more generalized diet, switching from grass in the wet season to browse in the dry season.

Analysing published data on feeding ecology, the authors show that the extinctions of marsupials in the late Pleistocene were characterized by a disproportionate loss of browsers. Indeed, northern Australia's largest surviving native browsers, just 1% of the size of banteng, are restricted to isolated rocky habitats, while the largest marsupial grazers, 4% of the size of buffalo, are widespread. These observations lend support to the theory that widespread landscape burning by humans, and the associated expansion of grass-dominated vegetation, may have played an important role in the megafaunal extinctions. This is also consistent with the limited invasion success of the browsing banteng – it remains confined to an isolated area with abundant rain forest patches. Rain forests are limited by frequent and widespread burning. In contrast, the mixed-feeding buffalo has been able to aggressively invade vast tracts of grassy savanna that are frequently burnt.

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Source paper: Bowman, D. M. J. S., Murphy, B. P. & McMahon, C. R. (2010) Using carbon isotope analysis of the diet of two introduced Australian megaherbivores to understand Pleistocene megafaunal extinctions. *Journal of Biogeography*, doi: 10.1111/j.1365.2699.2009.02206.x.

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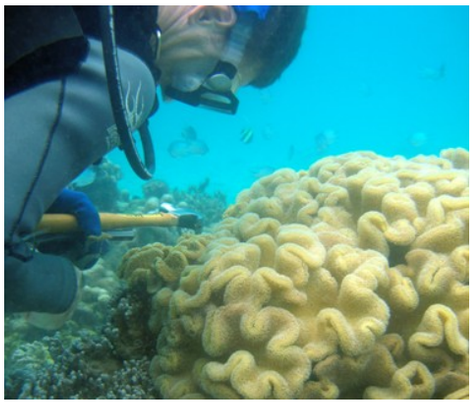
Coral reef communities in 'hot water'

Global warming is harming many of the world's ecosystems, particularly coral reefs, which depend on symbioses between reef-building corals and micro-algae (dinoflagellates in the genus *Symbiodinium*). These symbioses are especially sensitive to thermal stress. Periods of high sea surface temperatures disrupt these partnerships and corals begin to appear white, or bleached, as damaged symbiont cells are lost from their tissues. The continued warming of oceans and increasing frequency of 'coral bleaching' and mortality threatens the integrity of coral reef ecosystems. Yet, many species-rich coral communities develop and grow in regions where water temperatures are high and water quality is often turbid. By comparing and contrasting coral–algal symbioses from isolated regions with different environments, researchers may be able to determine the extent to which corals can respond to significant changes in climate by associating with physiologically different symbiont species.



A paper published recently by LaJeunesse *et al.* in the *Journal of Biogeography* examined the extent to which temperature and water clarity influences the ecological and evolutionary processes that are potentially important in the response of coral–algal symbioses to global warming. The researchers used molecular genetic methods to characterize the diversity of symbionts that occur within corals and other symbiotic cnidarians living in the 'warm' Andaman Sea (Thailand) and in the 'cooler' western Indian Ocean (Zanzibar, Tanzania). Unlike the western Indian Ocean and the similarly cool central Great Barrier Reef in Australia, 'stress-tolerant' algal symbionts (primarily members of *Symbiodinium* Clade D) were found to occur frequently among corals from the Andaman Sea, especially at inshore locations, where water temperatures and turbidity are highest.

The significant regional (and local) differences in coral–algal combinations suggest that these symbioses can become adapted to various environmental conditions when provided with enough time. However, phylogenetic, ecological, and population genetic data indicate that regionally adapted partnerships have evolved over many centuries and millennia. This time-scale has important implications for the capacity

of coral–algal symbioses to adjust to climate change by forming new and stable associations with 'stress-tolerant' symbionts. The current rate of warming may therefore be too rapid for most symbioses to respond successfully in the near term.

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Source paper: LaJeunesse, T.C., Pettay, D.T, Sampayo, E.M., Phongsuwan, N., Brown B., Obura, D.O., Hoegh-Guldberg, O. & Fitt, W.K. (2010) Long-standing environmental conditions, geographic isolation and host–symbiont specificity influence the relative ecological dominance and genetic diversification of coral endosymbionts in the genus *Symbiodinium*. *Journal of Biogeography*, doi:10.1111/j.1365-2699.2010.02273.x.

Images: Collecting tissues from the soft coral *Sinularia* in Zanzibar, Tanzania. Courtesy of T.C. LaJeunesse

Intertidal coral communities from Phuket, Thailand. Warm and turbid conditions appear to have significantly influenced the regional dominance of a "stress-resistant" host-generalist species of symbiotic dinoflagellate, *Symbiodinium trenchi* in Clade D, and the evolution of numerous closely related host-specialized species. Courtesy of T.C. LaJeunesse.

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