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**VETERINARY & LIFE
SCIENCES**



The skink used in the study is the widely distributed Bar-shouldered skink, *Ctenotus inornatus*. (Photo: B. Maryan)

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Island hopping: insights from Kimberley island skinks inform conservation of island systems

Conservation of island systems — either true islands surrounded by water, or ‘islands’ of habitat surrounded by human activities — requires an understanding of the special characteristics of islands and their impacts on the biodiversity found on them.

Both the limited size and the relative isolation of islands constrains the amount of biodiversity they can support – be it the number of species living on an island or the genetic diversity within an island population of a given species. Thus, the study of these systems is of great interest to the conservation of biological diversity and its persistence in the face of continued habitat loss and fragmentation.

There are more than 2,600 islands in the Western Australian Kimberley region. These islands are a significant conservation resource as mainland Kimberley region faces increased impacts from invasive species, habitat fragmentation, grazing, mining and altered fire regimes.

We explored the conservation potential of Kimberley islands to understand the ecology and genetics of island populations and to inform the management of island systems. We investigated patterns of genetic diversity and relatedness among island populations of the bar-shouldered skink (*Ctenotus inornatus*). Bar-shouldered skinks are habitat generalists that are abundant throughout the Kimberley and its islands.

This species has not experienced population decline, and therefore is an ideal model system to represent the influence of landscape factors on genetic structure without the confounding elements of rarity or endangerment.

Methods and results

We examined 41 islands and seven mainland populations in the vast Kimberley environment (Figure 1), a much greater scope and sampling effort than is typical of island studies, contributing to the value and the reliability of the insights generated.

Results and discussion

Genetic relatedness of skink populations between islands (Figure 2) was not related to the geographic distances between islands, but was well-explained by landscape connectivity models that accounted for the large difference in resistance to dispersal between land and ocean. To determine the degree of isolation of an island, it is necessary to incorporate a nuanced understanding of the difficulty organisms experience to traverse a landscape and the routes they follow, which are often not the shortest, straight-line paths. Reliable estimates of island isolation can be used in management planning. For example, those islands that are least isolated for skinks may also be least isolated for aggressive invasive species such as the cane toad. Because of their increased invasion risk, these islands should be closely monitored.

Islands and the organisms that inhabit them provide valuable information to conservation biologists. Islands are real world analogues of isolated patches of natural habitat that remain in human-modified landscapes. In addition, islands are valuable conservation resources in their own right: Islands are often acknowledged as a refuge for species with declining mainland distributions, and the populations inhabiting islands may be unique from mainland populations of the same species due to genetic consequences of long-term isolation.

(Photos: Ric How)



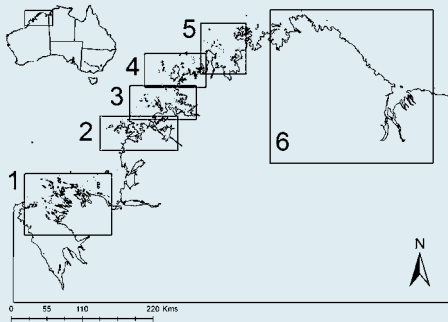


FIGURE 1 Location of the five island groups and the two ungrouped islands in the Kimberley. 1, Yampi Group. 2, Augustus Group. 3, Prince Regent Reserve Group. 4, Mainland Channel Group. 5, Mitchell Plateau Group. 6, Sir Graham Moore Island and Adolphus Island sites

Island populations of these skinks retained varying degrees of genetic diversity, which was greatest for islands that were closer to the mainland (Figure 3), supporting the ‘island-hopping’ model of island connectivity.

There was a stark reduction in genetic diversity on Irvine Island following fire.

Conclusions and recommendations

Island populations are an interesting dichotomy in conservation biology. On the one hand, they can be a refuge for species where mainland populations have been decimated by loss of habitat and predation by exotic predators. On the other hand, island populations usually have reduced genetic diversity and are more susceptible to extinction through genetic

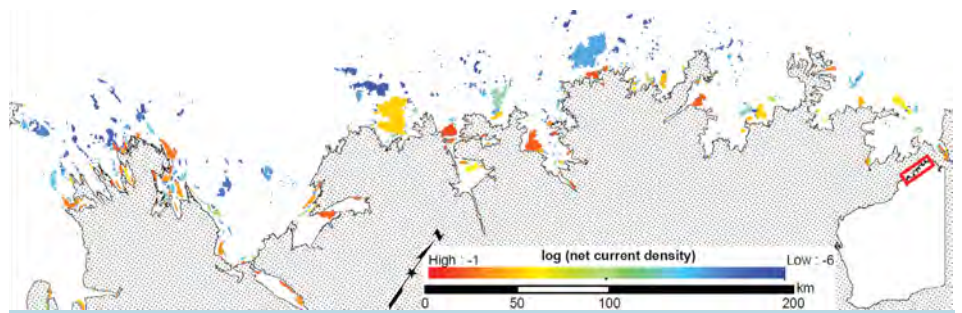


FIGURE 3 Expected movement rates (as proxied by the variable ‘net current density’) from the mainland to all possible islands in the Kimberley, as estimated by a landscape connectivity model that assigns much greater difficulty of moving over ocean than over land. Islands predicted to have lower rates of individuals traversing them are more isolated

and demographic processes. This study has been able to measure and quantify the levels of genetic diversity within a large number of islands in the Kimberley region. Using this genetic information, and information based on connectivity between island populations determined that ‘island-hopping’ routes allow organisms to minimise difficult ocean passages.

Less isolated islands may therefore hold the most potential for conserving biodiversity.

Large-scale disturbances can have substantial impacts on populations. The many vertebrate species that are less abundant than *C. inornatus*, or have intrinsic characteristics that are associated with endangerment, may be even more susceptible to the effects of environmental change. As a result, the increased intensity or frequency of disturbance events poses a considerable threat to island populations. ■

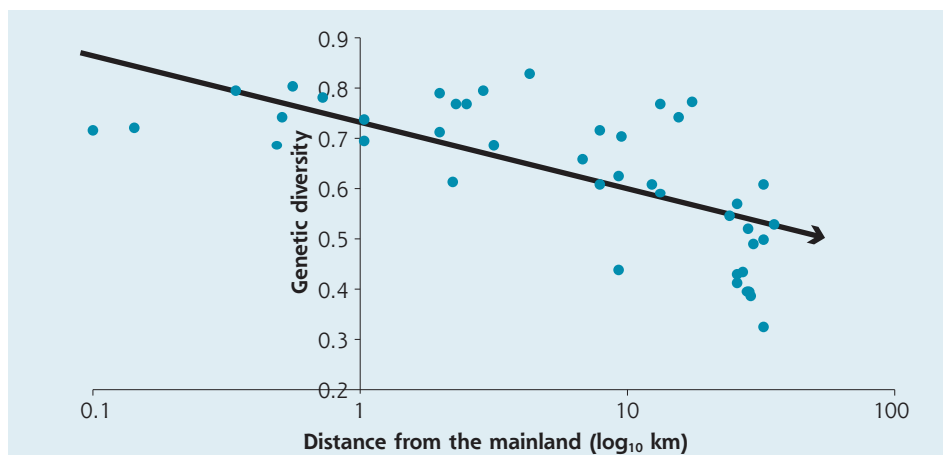


FIGURE 2 Islands further away from the mainland lose genetic diversity at 1% per km

More information

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