

Herbivory passing the limits

How many plant species will a tropical insect feed upon? This question has been at the centre of a heated debate that is trying to decide on the probable number of species on Earth. In 1982, Terry Erwin startled the biological community by guesstimating there to be ten times more species than was previously thought. To arrive at such numbers, he projected the temperate levels of insect-host specificity on the diverse flora of the tropics. However, such extrapolations have been challenged by other tropical entomologists, such as Yves Basset, who, in 1992, showed that host specificity was actually very low among free-living insects on the Australian rainforest tree *Argyrodendron actinophyllum*. But in commenting upon Basset's seminal paper, Kevin Gaston noted in *TREE* that it was clearly a first case study from a single tree species, and that before convincing conclusions could emerge 'sound information on host use has to be built up over long periods of time and...with great patience'.

After a further decade of work, Basset now joins Vojtech Novotny *et al.* [1] in

reporting the results on one of the most thorough host-selection study ever conducted in the tropics: 1010 free-living and leaf-chewing insect species were studied extensively on 59 species of woody plants in a lowland rainforest in New Guinea. This sampling effort was only made possible through the involvement of local parataxonomists—an approach that is proving increasingly important for successful work in the tropics. The pattern in the data set is clear: <4% of the species were actually specialized on a single host-plant species, whereas most of the species were more generalized, feeding on several plant species within a given plant genus. These figures suggest that host specialization in a tropical rainforest might indeed be much lower than in temperate forests, but that most leaf-chewing insects will still be specialists at the level of plant genera.

The results of Novotny *et al.* clearly come with some caveats. First, their methods will only apply to the more abundant members of a hyperdiverse tropical insect community. In the current material, this

excludes some four out of five species from the actual analysis. Second, free-living leaf-chewers are not all there is to bugs in the rainforest, and the degree of host specificity might or might not be higher among other insects. Third, gnawing away at leaves is not all that a leaf-chewer does in its life: among the species that are generalists as adults, an unknown proportion might still be specialists as larvae. Nevertheless, the current results strongly suggest that there are tens, rather than hundreds, of host-specific insects on any one tropical tree species. This estimate is an order of magnitude lower than the original values used by Erwin in 1982, which should put some much-needed realism into future estimates of global biodiversity [2].

1 Novotny, V. *et al.* (2002) Host specialization of leaf-chewing insects in a New Guinea rainforest. *J. Anim. Ecol.* 71, 400–412

2 Novotny, V. *et al.* (2002) Low host specificity of herbivorous insects in a tropical forest. *Nature* 416, 841–844

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Reconstructing rapid climate change from a snail's pace

Models are now commonly used to make inferences about the demographic past, but little attention has been given to the inference of complex, explicitly geographical population histories. Because the universe of potential histories can be infinitely large, external independent information, such as fossil or paleoclimatic data, can be instrumental for modeling complex histories. This approach can be enhanced further by using bioclimatic modeling, in which past distributions are reconstructed from an integration of paleoclimatic data with information from the contemporary ecological and physiological limits of a species.

Such an approach is key to Hugall *et al.*'s new study [1] on the effects of Pleistocene climate change on the fauna from the wet-tropical forests of North Queensland, Australia. By basing the bioclimatic model on the endemic snail *Gnarosophia bellendenkerensis*, the chances of recovering historical biogeographical details were increased because of the fine-scale

persistence and low vagility of the species, thereby revealing the location of potential refugia, as well as the magnitude of change of suitable habitat in the fragments.

Interestingly, not only did the snail's phylogeographic structure correspond to the predicted location of refugia, but a general agreement was also observed between quantitative estimates of population expansion from the sequence data and the models predicted changes in habitat size.

Hugall *et al.* also considered these phylogeographic patterns in a comparative context. They showed that patterns of genetic variation in the snail represented a composite of various phylogeographic patterns observed in several vertebrate taxa. The model identified both common phylogeographic patterns that were predicted by the shared biogeographical history of the rainforest taxa, as well as idiosyncratic differences among the species. Because the model represents an independent demarcation of historical population structure, Hugall *et al.* were able

to deduce that the departures from the predictions of the model arose from varied responses to the size and magnitude of change of suitable habitat, apparently reflecting different habitat requirements for species persistence.

Although the results from the study are based on a qualitative fit of the data to the bioclimatic model, the utility of this approach for understanding the responses of species to past climate change and locating historical refugia is clear. This suggests that a fusion of these spatially explicit paleodistributional models with coalescent simulations to yield a statistical framework will indeed be promising for evaluating evolutionary questions.

1 Hugall, A. *et al.* (2002) Reconciling paleodistribution models and comparative phylogeography in the Wet Tropics rainforest land snail *Gnarosophia bellendenkerensis*. *Proc. Natl. Acad. Sci. U. S. A.* 10.1073/pnas.092538699

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