On hotspots and the use of indicators for reserve selection

In a wide-ranging and stimulating TREE review, Reid recently concluded that focusing on a handful of readily surveyed indicator groups could be of limited use in identifying priorities for conserving biodiversity as a whole. His reasoning was straightforward: a suite of taxa5,8 had now shown that, at the relatively fine scales relevant to reserve planning, there is little congruence in the richest sites for different groups (see also Reid 6, 7). Hotspots – defined variously as the richest sites for all species, or for endemic, rare or threatened species – seldom coincide across taxa. More importantly, and (not explicitly discussed by Reid), other studies show that sets of priority sites identified by considering between-taxa complementarity, as well as species richness (which represent diversity far more efficiently than do hotspots9,10), also show poor cross-taxon overlap. However, although high congruence in the most important sites for conserving different kinds of organisms would be extremely useful for conservation planning (and fascinating from an evolutionary perspective), its absence is not sufficient justification for rejecting the use of indicators for reserve selection. This is because whether the priority sites for one group embrace priority areas for other taxa is fundamentally less important than the extent to which they capture species from those taxa. What really matters in testing the use of indicators for reserve selection is the representation of diversity as a whole in the key sites for just one focal group. Towards the end of his review, Reid mentions unpublished results from Oregon (referred to in Ref. 10) showing that cross-taxon capture of species by the complementarity sites for single taxa is actually rather high. Another recent review cites similar evidence from other studies11. An extensive new analysis across 50 forest reserves in Uganda confirms these findings and provides an explanation for them, which in turn suggests that, in some areas, the use of indicators for reserve selection holds more promise than Reid seems to imply12.

Working on a dataset covering 2452 species of woody plants, large moths, butterflies, birds and small mammals that took nearly 100 man-years of survey effort to compile, Howard and colleagues13 first showed that in Uganda, as elsewhere, patterns of species richness (controlling for forest area) show poor congruence across groups. Nevertheless, complementarity-based sets of priority sites identified using data on single taxa capture species richness across all groups with roughly the same efficiency as sets built up using information on all taxa; data on birds and butterflies perform particularly well. The reason is that Uganda’s environmental heterogeneity, and each taxon exhibits similar biogeographical patterns across the country. Consequently, pairs of forests that complement each other well for one taxon do so for other groups too, and a priority set for one taxon embraces all the main habitat types for other groups. In this case, lack of cross-taxon congruence in species richness is not enough to invalidate the use of indicators because of high congruence in complementarity.

How general are these results likely to be? Other studies have shown that complementary areas for focal taxa sometimes capture diversity in other groups rather less well than in Uganda, but these deal with ‘temperate situations where the focal taxa themselves are relatively speciose4,14, or contain far fewer species than there are candidate sites for their conservation9,10. Further work is now needed to assess whether the Uganda results hold for less heterogeneous parts of the tropics, where high species richness coupled with very limited funds for biodiversity surveys suggest that the payoffs of using indicators for reserve selection would be greatest.

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Biodiversity hotspots in the developing world

Reid’s TREE ‘review’ of biodiversity hotspots considers the potential value of having surrogate measures of species richness or endemism. It is evident that higher-taxon richness patterns can be combined to create even better surrogates for overall species diversity. A clearly stated unstated assumption is that ‘if only a partial survey of a region has been undertaken, the cumulative list of higher-taxon encountered will converge on the total number of taxa more rapidly than will the cumulative list of species’. This might apply to well surveyed developed countries, although it does not necessarily hold for poorly surveyed developing countries. At a global or continental scale, Africa is in desperate need of setting conservation priorities. On a finer scale it suffers from heavy biased survey. The geographical bias of studies in, for example, the disciplines of behavior and conservation biology, is towards three countries: South Africa, Kenya and Tanzania have been well represented by biological research activities in the last two decades. In the other African countries, where good estimates of total species richness might not be available for some taxa, we cannot simply accept that the cumulative lists of higher taxa encountered converge on the total number of taxa more rapidly than will the cumulative list of species. Local scientists from two neighbouring countries, South Africa and Namibia15, have recently demonstrated the major problems of recognizing biodiversity hotspots within and between their own regions. Regions in South Africa experienced biased survey due to the positioning of roads, urban areas and nature reserves16, while Namibia suffered because it is the most and country in sub-Saharan Africa. The selection of higher taxa that render the greater proportional overlap between neighbouring countries may alleviate the problem. Subtract the negative effects of partial surveying and developing countries could start to grow with biodiversity hotspots and sequoet conservation priority.

The unbiased survey of species richness in developing countries may turn up hotspots if the cumulative lists of higher taxa encountered converge on the total number of taxa more rapidly than the cumulative list of species.

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