

Biodiversity hotspots and beyond: the need for preserving environmental transitions

A great deal of effort and many resources are directed at identifying and conserving regions of high species diversity^{1,2}. Although defining 'biodiversity hotspots' helps prioritize areas for conservation, overemphasis on such sites ignores the need for preserving adaptive variation across environments. A more comprehensive approach would be to include regions important to the generation and maintenance of biodiversity, regardless of whether they are 'species rich'. With climate change threatening large-scale shifts in species distributions and the habitats on which they depend, the hotspots of today are unlikely to be the hotspots of tomorrow. Only by maximizing adaptive variation can one hope to preserve the evolutionary response to changing climate and environmental conditions.

The 'hotspot' approach to species preservation is risky, particularly when applied at a local scale. Preserving populations in only one pure habitat type, such as central tropical rainforests, is analogous to building an investment portfolio made up of a single stock. Diversifying risk by conserving populations from across diverse habitats will ensure that adaptive variation is maximized. Species are assemblages of populations that are often distributed across a landscape of habitat types and those populations have specific adaptations to regional environmental conditions. Populations are being lost at a much higher rate than are species³ and, consequently, the loss of populations in unique habitats could result in the loss of novel adaptations that are necessary to meet future environmental challenges⁴. A strategy is urgently needed that preserves the adaptive diversity represented by the range of populations within a species, thus assuring the maximum potential of that species to respond to future environmental conditions.

We believe that one strategy for conserving the maximum amount of adaptive variation is to preserve populations that occur along environmental gradients, thus preserving the full range of populations across habitats, as well as the unique traits of those populations. Adaptive diversity within species is often well represented along environmental gradients or ecotones that represent the transition from one habitat type (e.g. tropical rainforest) to another (e.g. grassland or savanna)⁵. Recent research on a wide range of taxa suggests that environmental gradients are important in diversification and speciation⁶⁻⁹.

There is little current emphasis on the conservation of ecological gradients. Recent attempts to prioritize conservation areas ignore these regions entirely^{1,10}. We maintain that a more sound conservation strategy would focus on both hotspots of biodiversity and on associated transitional zones. Given future uncertainty, preserving such areas will maximize the probability of a viable response at the species level to changing climatic conditions. In the absence of extensive data on population variation, we suggest that this diversity is likely to be summarized along environmental gradients. Saving the biota of the Earth will require greater efforts to preserve not only the pattern of biodiversity but also the processes that generate and maintain it. Integrating information on both pattern and process will ensure that the capacity for populations to change with changing environments is preserved.

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Wolbachia, mitochondria and sterility

Wolbachia and mitochondria are both α -proteobacteria that have evolved an intracellular lifestyle^{1,2}. They both inhabit host cytoplasm, and are maternally transmitted. The results recently reported by Gemmell and Allendorf³ in *TREE* suggest that this resemblance could well be extended to their effects on host reproduction.

As noted by Frank and Hurst⁴, maternally inherited symbionts are subject to sex-biased selective pressures: their effect on male fitness does not affect their own fitness. Therefore, symbionts that reduce male fitness can, in theory, reach high frequencies. As reported by Gemmell and Allendorf³, the results of Ruiz-Pesini *et al.*⁵ support this view: mitochondrial mutations inducing male sterility are frequent in some human populations.