

Points of view

Neutralist evolution and strict monophyly adversely affect biodiversity study

by

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Abstract

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Several news services recently cited articles by Clare & al. (2007) and Kerr & al. (2007) that reported the discovery of 15 new bird species for North America, and six new bat species from Guyana, based on barcoding of the mitochondrial DNA locus COI. These are largely cryptic species, with little to distinguish them morphologically from closest relatives.

The use of molecular information alone to distinguish new species is total nonsense. Matrilineally inherited evolutionarily neutral base changes of DNA track pedigrees or genealogy of individuals, not populations. Even recombinantly exchanged nuclear genes only track ancestry of individual, largely genetically isolated populations. Species, however, are not simply lines of descent, but are perceived units showing descent with modification. Species may be maintained by stabilizing selection even though populations are at any particular time genetically isolated. Surviving ancestors continue to accumulate neutral DNA base changes yet may retain an essential identity (phenotype and niche) after genetic isolation. Insisting on paraphyly when viewing species represented by exemplars terminal on a molecular tree forces the splitting of species into populations (nuclear genes) or even individuals (mitochondrial and chloroplast genes), all of which may then be termed “cryptic species” and named as new species (or genera or families). This is

Resumen

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what comes of abandoning the “modification” in “descent with modification” and basing classification on phylogeny alone.

If a phylogenetically complex (isolated populations) species were to split off a new species (different phenotype and niche) from somewhere central, the sister group to the new species would have to be named a separate species, and many of the branches lower in the tree must also. The patristic distance, measured as numbers of neutral base changes in DNA between two end members among the populations of the species, could (and probably would) be greater than the patristic distance between the new species and the nearest population of the ancestral species. When doing biodiversity triage, would one choose to protect the two end members of the original species (same phenotype and niche) because they are “phylogenetically distant” (through neutral mutations) and let the new species die off? Or, better, recognize the adaptation and fitness of the phenome in a particular environment as more important for evaluating biodiversity than the neutrally evolving genome?

Biodiversity investigated with molecular analysis alone is rendered a mere game by excessive atomization due to focus on neutral evolution and forced monophyly. Eventually, with enough exemplars and exploration of fan-shaped pedigree charts (matriline-

eally inherited traits), all individuals could be named, or perhaps we can just stop with the panmictic deme in those cases when lack of resolution from mitochondria and chloroplasts requires studying recombining traits from nuclear genes.

I foresee a paradigm shift back to biosystematics and the Modern Synthesis. Molecular analysis does not protect biodiversity. Taxonomic recognition of a unique phenotype interacting with a particular range of environmental variables with a characteristic reproductive system, in combination, does.

References

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- Kerr, K.C.R., Stoeckle, M.Y., Dove, C.J., Weigt, L.A., Francis, C.M. & Hebert, P.D.N. 2007. Comprehensive DNA barcode coverage of North American birds. *Molecular Ecology Notes* (Online Early Articles). <http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2006.01657.x>