

Molecular view reassesses species

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Helena Baird anticipated that delving into the molecular details of amphipod species in the Antarctic would yield novel insights, but the PhD student from the University of Tasmania in Australia did not anticipate that her findings would so convincingly bolster growing calls for a thorough revision of Antarctic biodiversity and species' distributions.

Using genetic data for two sibling amphipod species – *Eusirus perdentatus* and *Eusirus giganteus* – collected throughout the Antarctic, Baird and her colleagues found strong evidence lurking in the DNA sequences for five additional, distinct, reproductively isolated species. Her study was published online in July in *Molecular Ecology* (2011; doi:10.1111/j.1365-294X.2011.05173.x). “Reports of cryptic species are exponentially increasing, reinvigorating an ongoing debate over ‘what is a species’, given the many important implications for biodiversity estimates and conservation”, says Baird.

Indeed, there are currently over 20 different species concepts, all based on different criteria. For example, the “phylogenetic species” concept separates species that have been evolutionarily independent for a long enough period of time that distinctive diagnostic traits begin to emerge, whereas the “ecological species” concept designates species based on their ecological niche.

But genomics adds a new wrinkle to the debate. Comparing DNA sequences increases the resolution at which scientists can calibrate species and often increases the number of new candidate species identified. For example, scientists using a reference library of DNA “barcodes” of 752 North American freshwater fish species – published in the June 28



The Antarctic amphipod *Eusirus perdentatus* is now considered a complex of three cryptic species.

issue of the *Proceedings of the National Academy of Sciences (PNAS)* – reported that 138 of those named species may represent as many as 347 candidate species, possibly a 28% increase in diversity (2011; doi: 10.1073/pnas.1016437108).

Louis Bernatchez, a coauthor of the *PNAS* study and an aquatic biologist at the University of Laval (Quebec City, Canada), says taxonomists have traditionally been responsible for assigning names to species by relying almost wholly on morphological descriptions. But, he says, such an approach requires a great deal of time and effort, which is simply not feasible given the drastic rates of biodiversity loss: “We need to accept that genetics can speed things up and reveal these cases of cryptic variation, which are relevant if our goal is to conserve biodiversity”.

On June 21, Peter Teske, an ecologist at Rhodes University (Grahamstown, South Africa) and colleagues reported in *BMC Evolutionary Biology* (2011; doi:10.1186/1471-2148-11-176) that DNA sequence data from *Pyura stolonifera* – a type of sea squirt – samples from Africa, Australasia, and South America revealed at least five distinct species, and those five could be easily subdivided into biogeographically relevant lineages depending on the genetic markers used. As a result, the researchers found that multiple genetic lineages can be native to a

specific geographic region, greatly complicating the detection of invasive species.

“It may sound cynical, but I don’t believe in ‘species’ anymore”, says coauthor Nigel Barker, a molecular ecologist at Rhodes University. “The ‘species’ is a convenient starting point for many exercises and investigations, but when molecular- or population-level tools and techniques are applied, the concept tends to disintegrate.”

Ed Louis, a molecular geneticist at the Henry Doorly Zoo (Omaha, NE), has described 21 species of lemurs in Madagascar, using a combination of molecular genetics and diagnostic morphological characteristics. His efforts have contributed to the stunning increase in lemur species identified over the last three decades, from 36 in 1982 to 101 in 2011. At issue is whether the genetic methods often used to designate species uncovered cryptic diversity worthy of species status or artificially inflated the species count.

And that is the crux of an oftentimes contentious debate: to what extent can – or should – genetic information be used to determine species? If taxonomists are considered lumpers or splitters, based on whether they prefer few or many species’ designations, the number and type of DNA sequences available will only make the lumper/splitter dilemma even more complex.

Louis says only more data – sure to become available once DNA sequencing costs become affordable enough to compare large chunks of (or entire) species’ genomes – will refute his assertions.

Most ecologists expect that, in the future, some combination of morphological and genetic analyses will be used to define species. But biodiversity metrics may move beyond species. “At the end of the day, these unique gene pools have been carved out over millions of years and should be recognized for conservation, if not strictly for taxonomy”, says Bernatchez. ■