DNA: the barcode of life?

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by Henry Nicholls

Efforts to describe all the species on earth will fail unless biologists begin to use DNA sequences as biological "barcodes", says Paul Hebert, professor of zoology at the University of Guelph in Canada. With the right funding and support from the taxonomic community, Hebert predicts that using DNA to identify and help categorize new species would make a complete inventory of life a feasible goal in as little as 20 years.

Traditionally, species have been identified and categorized on the basis of morphological differences, but parts of the academic community are becoming increasingly concerned that "morphological taxonomy", pioneered by Linnaeus in the 1750s, is no longer equipped to account for the extent of earth's biodiversity, frequently estimated at between 10- and 15-million species.

"Let's face it, the morphological approach has had 250 years to advance the task, and we're only 10% of the way towards the goalposts," said Hebert in a <u>report</u> out today on *BioMedNet News*. His solution, to which many taxonomists are strongly opposed, is to distinguish between species on the basis of similarities and differences in their DNA. If taxonomists fail to embrace molecular technology, Hebert is clear about the consequences: "There is no more likely death of a discipline than the failure to innovate."

A DNA-based taxonomy would vastly accelerate the final inventory of life, says Hebert. Each novel organism would be described rapidly and simply by a barcode - a number that corresponds to a sequence of its DNA. Hebert envisages this "gene species" as a first, mandatory step towards describing a real species. At a later stage, traditional taxonomists could make the formal morphological description of the specimen, which would then become associated with its DNA barcode, he suggests.

Although most taxonomists support a role for DNA in taxonomic research, some have expressed strong concerns about any move that would make DNA sequencing a mandatory step in the description of a new species.

Many think that describing a species using DNA is just expensive and unnecessary, and there is concern that such a move would exclude those in the developing world, who have limited access to sequencing technology.

"It would disenfranchise a large fraction of the taxonomic community," warned Charles Godfray, professor of evolutionary biology at Imperial College in London and director of the Natural Environment Research Council's Centre for Population Biology. Godfray propelled the idea of a "taxonomic crisis" into the public arena in a commentary published last year in the journal <u>Nature</u>.

Godfray and others are uneasy about using a single feature to identify species. "The molecular biology [of a species] is just a particularly valuable set of character states ... perhaps the most important set of character states, but it's not all there is," said Godfray.

Neverthless, Hebert remains unmoved. "I'm not surprised to find that people are getting shirty about it," he said. "To some extent, this is shaking the foundations of a tradition that's probably the oldest and noblest tradition in biology."