



DNA Barcoding – What to Expect

Remember in *Star Trek* when Bones McCoy would arrive on a planet with his tricorder and instantly get a reading on its life forms? Now, imagine a similar device in your hands that could tell you the name of any species you encountered in your backyard, along your ecological transect, or among a quarantined shipment of oranges. Through a satellite, this device would automatically link the user to all available data on the web concerning that species: are those eggs from an invasive bug species? Is that mushroom poisonous? What butterfly will that caterpillar grow up to be? Is that plant a weed species? And, imagine the price of the device being affordable enough to be sold through a company such as the Sharper Image as a fancy identification guidebook that could be given to budding naturalists or backyard enthusiasts as a birthday or Christmas present, at the cost of pennies per use; a “Bio-pod”, with its little LCD screen and access to the encyclopedia of life. No longer is a forest just a bunch of trees, but instead lots of species, all with different names, characteristics, histories, etc. That’s not just an ant, but a certain kind of ant, with its own little quirks and attributes. Could this spur an increase in bio-literacy and a greater concern for the present pace of degradation impacting the planet? This world is not so far off.

This vision is the one proposed by an international network of museums, institutions and researchers called the Barcoding of Life Consortium. “DNA barcoding” is the term used for developing a set of global standards and protocols to generate a comparative genetic database for every species on the planet. In addition to species identification, DNA barcoding has been proposed as a tool to assist in discovering new species, an important task because the current pace of description has been woefully inadequate. It is estimated that over 80% of the earth’s species are as yet undescribed. Thus, proponents argue that harnessing this new technology can speed up the discovery process, a critical need as diverse habitats are being lost before we even know what life they harbor.

However, as with most major movements, DNA barcoding has attracted significant controversy within the scientific community. Many researchers who work on taxonomy – the science of describing new species – are concerned that a single gene region, such as the one proposed for DNA barcoding, is not sufficient for discovery and the adoption of this method could lead to significant error, both because of over-lumping and over-splitting of real species. Up until now, there have been no good comprehensive data to test barcoding performance across a diverse group, to understand how well the method can be expected to perform.

Two researchers from FLMNH now have addressed this issue in their new paper appearing in this month’s journal of the *PLoS Biology*. Chris Meyer and Gustav Paulay use an extensive genetic database of the well-known and fervently collected marine snail group commonly known as cowries. They use the database to address error rates for DNA barcoding in both the species identification and discovery phases. While they find that identification of known entities is highly successful (~96% correct), they caution against the use of barcoding in the discovery phase. Barcoders have proposed using a threshold value of genetic difference to assess whether a sample matches an existing species or is sufficiently different to warrant its recognition as new. Meyer and Paulay’s data suggest a minimum error rate of approximately 20% for species discovery. A small threshold will oversplit actual species, whereas a large threshold will lump distinct entities. There is no magic threshold that can eliminate one type of error, without increasing the other.

These results can be interpreted however one sees fit. Many would be happy with an 80% success rate for poorly known groups. Others may find 20% lumping unacceptable. Both Meyer and Paulay see DNA barcoding as an incredible tool for identification, but stress that in order to approach high levels of success among most major kinds of organisms, the hard work remains. “There are no shortcuts to good taxonomy,” states Meyer, as most groups show a range of attributes that make simple generalizations impossible. Yet, there is hope that DNA barcoding can capture the imagination and enthusiasm of the general public and provide a new groundswell of financial support and infrastructure. “The barcoding consortium has provided the banner we can all rally around. It has the potential to present a unified voice across diverse ecosystems and organisms stating our critical needs to address biodiversity in a concerted effort. It’s a very exciting time.”