Improving our understanding of metacommunity structure using DNA barcoding

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Background: A long-standing area of debate in community ecology has centered on niche theory versus neutral theory. While the debate has resulted in observations supporting each theory, theoretical frameworks have largely neglected the role of evolution. By incorporating genetic diversity data into community analyses it may be possible to determine under what conditions niches and neutral processes play a greater role in shaping a community and whether the genetic structure of a community impacts this. Barcode data will improve species-level identifications and allow researchers to incorporate evolutionary history into analyses. To test whether grouping species by using coarse taxonomic resolution masks the relationship between taxonomic composition and environmental variables, we characterized 21 stream invertebrate communities focusing on the five most abundant aquatic insect orders:Coleoptera, Diptera, Ephemeroptera, Plecoptera, and Trichoptera, plus the often-neglected class Oligochaeta.

Results: We found that the proportion of community composition variability explained by the environment decreased or did not change with increasing taxonomic resolution (family, genus, and DNA barcode cluster levels). This suggests ecological inter-changeability of closely related taxa in this system, given the environmental variables we measured. Significance: These findings suggest that ecological filtering may play a greater role at a family level than a species level. We will explore how estimates of variation in genetic diversity can improve our understanding of the role of niche and neutral processes. Determining the effect genetic diversity and species diversity have on spatial dynamics will greatly improve our understanding of community dynamics. In the face of great environmental change, due to climate change and other anthropogenic factors, understanding why species live in certain areas will help provide information about the chance of local species extinctions, changes to species viability and recovery, and predictions of how the communities will shift. Such information will also help focus conservation efforts.

Highlight and new discoveries in the Mexican cladocera

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1Centro de Investigación en Biodiversidad (CIB) as well as the Genome Sequencing Laboratory at the National Institute of Genomic Medicine (MexBol), which is supported by the National Council of Science and Technology (CONACYT). The creation of the laboratory was to support the participation of researchers across Mexico in the International Barcode of Life (iBOL) project. Results: From 2009 to date, staff within the BL-Chetumal Node performed about 27,000 DNA extractions and PCR amplifications in a wide range of taxa. For the DNA sequencing, 20,615 PCR products were sent to the Canadian Centre for DNA Barcoding (CCDB) as well as the Genome Sequencing Laboratory of Biodiversity and Health, Institute of Biology in the Universidad Nacional Autónoma de Mexico (UNAM). With results from this laboratory, it was possible to describe a new species of cladoceran (Leberis chihuahuensis) and a fish (Hypholoptra conur) as well. Many cryptic species have been highlighted, for example in the Lepidoptera (Aedephila, Aeterocampa, Bibbii, and Hammond) coenos (Mastigiasaurrus almayruphenus), and rotifers. For the first time in Mexico, we identified the eggs and larvae of fishes to the species level. This helped assess the ecological impact of some exotic species, such as the identification of prey of the lionfish (Pterois volitans) in the Caribbean and confirmation of the presence of an invasive frog, Iliorhraphysa platynotus, in the Yucatan Peninsula. We also developed new primers for difficult groups, such as freshwater microcrustaceans. Significance: We consider that barcodes are a powerful tool to understand this megadiverse region of the world, but continued and enhanced efforts are required for the construction of the reference database, because most of Mexico's biodiversity still remains unknown.

Background: The Barcode of Life-Chetumal Node (BL-Chetumal Node) belongs to the laboratory network of the Mexican Bar-