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Editorial

Plant DNA Barcodes, Community Ecology, and Species Interactions

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1. Introduction

The community of biologists has been eager to realize the promise of DNA barcodes since the concept of a rapid method for genetic identification of species was first proposed in 2003. As we approach twenty years of DNA barcoding, the application of these short, but highly variable sequences continue to increase and methods continue to be developed that utilize this ever-expanding resource for multiple fields of biology. The nearly ten million DNA barcodes for life on Earth available today provide a database that is especially useful for ecology and evolutionary biology. In particular, DNA barcodes provide a rapid resource to identify taxa; to quantify and understand species richness; and to determine community interactions in primary and secondary habitats. Many ecologists, who are concerned with the assembly and maintenance of species richness at local and regional scales, have driven empirical and conceptual advances in the field of community ecology. At the same time evolutionary biologists have focused on the description and classification of species diversity, factors controlling the origin and ancestry of biodiversity, and the network of interactions that connect evolutionary units through time and space.

Today, thanks to the ever-expanding and well-curated DNA barcoding resources now available, fundamental biological questions can be more rigorously addressed regarding community evolution, assembly, productivity, and species interactions across and among diverse habitats and organisms, including plants, animals, fungi, and microorganisms. DNA barcodes are now routinely used to discover new species, to determine phylogenetic patterns of community diversity, and to uncover the complexities of interactions in almost all domains of life to understand diets, symbioses, pollinator networks, and historically challenging biomes, such as below-ground soil and deep-water marine communities. This Special Issue of *Diversity* addresses the wide variety of applications of DNA barcodes, especially in plants. The eleven papers included in this Special Issue illustrate how the DNA barcode library continues to be expanded, the range of ecological and evolutionary questions that can be answered with DNA barcodes, and how plant-human interactions are better understood using DNA barcodes as a research tool.

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2. Building the Plant DNA Barcode Library

The diversity of gene regions that serve as DNA barcodes continues to expand from the original cytochrome oxidase 1 mitochondrial sequences applied to many groups of animals. To date, no single gene region fits all lineages of life as a universal DNA barcode. For that reason, researchers continue to experiment and search for the most effective DNA barcode for specific clades on the Tree of Life and particular type or condition of tissues within organisms. In this Special Issue Dal Forno et al. [1] explored the application of DNA barcodes in both fresh and historical collections of lichen-forming basidiomycetes. Their results demonstrate that barcode sequences can effectively be generated from both fresh and historical collections more than 100 years old and that fungal ITS barcode sequences provide powerful resources for species delimitation in an integrative taxonomic framework., Omelchenko and colleagues [2] continued the quest to identify the most efficient regions for metabarcoding members of the grass family and suggest additional spacer regions from nuclear ribosomal DNA (e.g., ITS1 and ETS in addition to the more common ITS2 barcode) provide enhanced discriminatory power for species identification in mixed pollen samples of grass species. In a third paper Kenfack, Abiem and Chapman [3] tested the effectiveness and efficiency of applying the standard plastid plant barcode regions (rbcLa, matK and trnH-psbA) to over one hundred species of trees in a montane forest in Nigeria and concluded that the combination of rbcLa and matK is sufficient for species discrimination. As part of the Global Genome Initiative for Gardens, Gostel et al. [4] release in the Special Issue 2722 DNA barcode sequences from 174 families and 702 genera of land plants that represent taxa without previous barcode sequences in GenBank. Each of these papers represents a significant contribution to building the DNA barcode library for plants.

3. Using Plant DNA Barcodes to Understand Ecological Patterns and Evolutionary Processes

With the advancement of DNA barcodes as a reliable source for genetic species identification, biologists increasingly use this tool to track species interactions. Such studies are now being conducted across the globe in both temperate and tropical environments. The review by Gostel and Kress [5] in this Special Issue outlines the recent progress that has been made in these investigations as a result of novel computational and sequencing capacities, high-throughput barcoding methodologies, and the expansion of the global DNA barcode database.

Three additional papers in the Issue highlight how DNA barcodes help to uncover previously obscure interactions, e.g., mate location in highly complex tropical forests; the abundance and diversity of large mammalian herbivores and their woody plant food sources; and in plant-insect pollinator communities. In an attempt to uncover how Orthopterans (crickets, katydids, and grasshoppers) use acoustic cues to find mates, Palmer and colleagues [6] turned to plant DNA barcodes to test the specificity of food plants that could facilitate mate location in katydids on Barro Colorado Island in Panama. Their results showed that most katydids are generalist herbivores and food choice would most likely not facilitate mate location. In a semi-arid African savanna Freeman et al. [7] demonstrated the important role of megaherbivores in shaping vegetation across landscapes. Using data from plant DNA barcodes, they were able to ascertain that some habitats, which deter large mammalian herbivores, serve as refuges for plant species that otherwise are quite palatable to these animals. Finally, a comparison between plant metabarcoding and non-molecular methods of tracking plant-pollinator interactions demonstrated the advantages of a DNA barcode approach in determining the complexity of these communities [8].

4. Plant DNA Barcodes and Human Interactions

It should not be forgotten that one of the most important plant-animal interactions on the planet is between plants and humans. Three final papers in the Special Issue address the application of DNA barcodes to tracking medicinal plants, invasive species, and habitat conservation. Jamdade et al. [9] demonstrate that as the DNA barcode library is built for the flora of the United Arab Emirates the current plant DNA barcode regions provide sufficient markers for the safe usage, prevention of adulteration, and the regulation of medicinal plant trading. DNA barcode sequence data were employed by Yessoufou and Ambini [10] to build a molecular phylogeny of the 210 known naturalized alien woody plants in South Africa. Based on this phylogeny they demonstrated that the benefits humans obtain from an alien species had significant evolutionary signal, but that non-invasive species exhibited more benefits to humans than their introduced, invasive counterparts. Such phylogenetic metrics can also contribute to plant conservation. Pearl et al. [11] generated DNA barcodes for 366 species of plants in the heathland ecosystems in Queensland, Australia. The resulting measures of phylogenetic diversity found in these communities combined with other patterns of diversity suggested contrasting conservation and management implications for these historical "refugial environments".

This Special Issue of *Diversity* on "Plant DNA Barcodes, Community Ecology, and Species Interactions" provides a taste of the current variety of investigations and publications that are a result of the expansion of DNA barcodes in the biological sciences. It is hoped that the papers contained herein will inspire and encourage future applications of DNA barcoding to the exploration of ecological and evolutionary systems across the globe.

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