

Beyond species counts: Using evolutionary history to inform conservation

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Earth's species are disappearing at an astonishing—and troubling—rate. As human activity continues to put pressure on ecosystems around the world, the rate of loss continues to climb. How we slow this devastating loss and protect the enormous number of species on Earth is of considerable importance, and debate.

Unfortunately, it is not feasible to simply protect everything. Limited funds require conservation planners and policy makers to prioritize the preservation of specific regions and ecosystems. An often-used strategy is to identify areas of high [species richness](#) and high endemism—a region containing a high proportion of species that are found nowhere else in the world—in order to set conservation priorities.

This, and other long-used approaches, have a major shortcoming, though: they ignore evolutionary history.

"By not considering diversity resulting from evolutionary history, current biodiversity assessments may be overlooking unique and important regions for conservation," explains Dr. Roxanne Kellar, lead author of a recent study aimed at testing different assessment tools and biodiversity metrics. The study—a collaboration between scientists at the University of Nebraska and the University of Missouri—is freely available in a recent issue of *Applications in Plant Sciences*.

Despite strong arguments to incorporate [evolutionary history](#) into [conservation strategies](#), phylogenetic diversity metrics have not been

widely adopted by conservation planners. "The goal of our research is to provide empirical tests of the many tools available to ecologists and [conservation](#) planners and to provide potential users the means to decide which metrics are most useful in their particular situation," says Kellar.

Kellar and colleagues tested a dozen commonly used phylogenetic diversity metrics, focusing on two large flowering plant families found in prairie ecosystems: the sunflower and pea families. Their results highlight the differences between biodiversity metrics and the difficulties of obtaining sufficient data to accurately calculate these metrics.

The most challenging aspect of calculating [phylogenetic diversity](#) metrics is the acquisition of a phylogeny, or evolutionary tree, for the area of interest. Researchers must sample a large percentage of the species present in the area under investigation and obtain the same set of genes for each of these species.

"There is a misconception about the availability of data in online sequence repositories such as GenBank," says Kellar. "Although this is an enormous, and important, resource for genetic data, it is often insufficient for accurately calculating biodiversity metrics, leaving researchers to generate this data themselves."

However, once a phylogeny is obtained, it is fairly simple to calculate all of the metrics. Kellar and colleagues are optimistic, "As more sequence data are generated from high-throughput sequencing and more phylogenies are published across the tree of life, calculating multiple, reliable biodiversity metrics will become increasingly routine."

More information: P. Roxanne (Steele) Kellar, Dakota L. Ahrendsen, Shelly K. Aust, Amanda R. Jones, and J. Chris Pires. 2015. Biodiversity comparison among phylogenetic diversity metrics and between three

North American prairies. *Applications in Plant Sciences* 3(7): 1400108.
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