# Next-generation sampling: Pairing genomics with large-scale herbarium sampling

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Plants are a ubiquitous and essential part of our lives. Estimates suggest there are hundreds of thousands of plant species known to science. How many species are there, really? How are they related? How many are threatened with extinction? Answering these questions in such an enormous clade of life is an important but daunting task for scientists.

Modern molecular techniques and, in particular, next-generation sequencing provide a powerful tool set to begin uncovering these answers. DNA regions can quickly be obtained and compared across species to infer relationships and distinguish between taxa with low levels of morphological differences. Obtaining sufficient sampling, however, becomes prohibitive when working with species-rich groups. Going to the field and collecting fresh plant material for hundreds of species is often not feasible. Enter herbarium specimens.

Dr. James Beck of Wichita State University and Dr. John Semple, at the University of Waterloo, have collaborated on a new study highlighting the role of herbarium sampling coupled with cutting-edge next-generation sequencing technologies to better understand plant diversity.

"What if we could bypass traditional sampling issues and really speed up the rate at which we discover and document plant biodiversity and reconstruct the plant tree of life?" asks Dr. James Beck, a researcher at Wichita State and the Botanical Research Institute of Texas and lead author of a recently published study in the June issue of *Applications in Plant Sciences*.

Botanists have been collecting, identifying, and storing plant specimens in herbaria for centuries. These collections now have the potential to drastically alter the way scientists collect data.

When groups of plants show very little genetic differences, a large genomic data set for large numbers of samples is necessary to understand the evolutionary processes within these groups and to accurately assess species diversity. To really get at the important and exciting question in biology, it is often necessary to have not only "big data" but also "big sampling." With recent, rapid advances in next-generation sequencing technologies, large genomic data sets are becoming increasingly obtainable. The bottleneck of many studies has now shifted to the number of species and individuals of each species that can be included in the study.

"All studies are limited by time and funding. Sampling from herbarium collections is one way to avoid the trade-off between projects that are feasible and those that are exciting," explains Beck. "We're really jumping up and down and waving our arms here—trying to convince the botanical community that large sets of herbarium DNAs could be the key to an array of novel, ambitious studies of plant diversity."

Beck and Semple tested this assertion on the goldenrods (genus *Solidago*), a notoriously difficult group of plants in the sunflower family. DNA was extracted from almost 100 herbarium specimens collected between 1970 and 2010. They then used a next-generation genotyping approach to identify groups of genetically similar individuals and compared these groups to those defined with traditional means. This "next-generation sampling" approach of pairing genomics with large-scale herbarium sampling showed considerable promise as sufficient data were obtained for 98% of samples, data which identified genetic groups that frequently matched morphologically defined species.

Beck urges that this is, by no means, a call to de-emphasize field work, though. On the contrary, expanding herbarium collections is more important than ever. Beck and Semple both curate collections at their institutions. As Beck explains, "We

understand the monumental effort by countless botanists that led to existing collections. Utilizing their specimens in order to better understand plant biodiversity and evolution is a clear way to honor and build upon this legacy."

**More information:** *Applications in Plant Sciences*, www.bioone.org/doi/pdf/10.3732/apps.1500014

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