A System for Creating, Storing, and Identifying Plant Voucher Specimens from a Large Sampling Area

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A procedure for processing and storing plant voucher specimens was developed during an extensive ecological survey conducted as part of ongoing long-term monitoring of the CAP LTER regional ecosystem...

Collection

Ca. 5000 plant specimens were collected in 10 cm X 10.5 cm envelopes.

Advantages of collecting voucher specimens:

1)Identifications can be verified, made, and changed at a later date

2) Plant material can be subjected to DNA sequence analysis for additional identification support

Uses

Potential uses for this data:

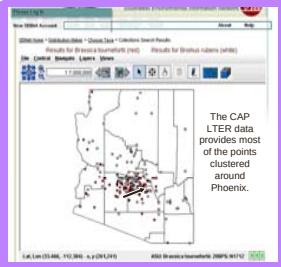
1)Making distribution maps with Seinet

2)Comparing diversity across different landscapes

3)Analyzing genetic differences within a species across the CAP LTER study region

4)Using as baseline data for comparing to future survey results

5)Utilizing DNA barcoding for identifying unknowns



Distribution map of *Bromus rubens* and *Brassica tournefortii made from herbarium and CAP LTER data*

http://seinet.asu.edu/distributionMaker/mapApplet.jsp?file=taxon4&file1=taxon5

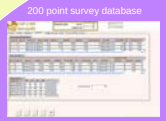
Storage

Data Storage

Locality, date, associated species, and plot descriptions are stored in two different databases and are available at:
http://seinet.asu.edu/collections/selection2.jsp

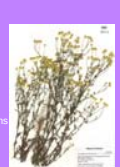
Specimen Storage

The ca. 5000 specimens fill 29 boxes and use just over ½ a herbarium cabinet, whereas 5000 regular-sized herbarium specimens would fill FIVE herbarium cabinets!




5 herbarium cabinets

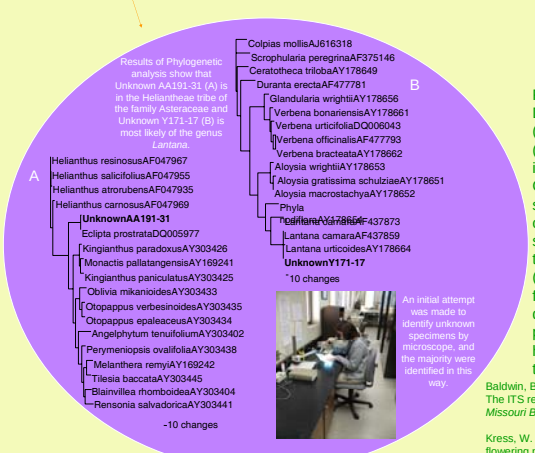

Storage boxes hold 150-200 plant specimens


Regular-sized herbarium specimens are 43 cm X 30.5 cm


Plant vouchers are stored in 10 cm X 10.5 cm envelopes

Collection housed in the Arizona State University herbarium

Identification



An initial attempt was made to identify unknown specimens by microscope, and the majority were identified in this way.

Phylogenetic trees made using GenBank Accessions

Identification by DNA

Fifteen unknown plant specimens were selected for identification by DNA sequencing of the nuclear rDNA internal transcribed spacers (nrDNA ITS), a region commonly used for plant phylogenetic studies (Baldwin etal. 1995) and recently proposed for applying DNA "barcoding" identification approaches to flowering plants (Kress et al. 2005). Genomic DNAs were extracted from leaf tissue of each unknown, and samples were amplified for the ITS1-5.8S-ITS2 region by polymerase chain reaction methods using the primers ITS18ML and ITS26ML and sequenced at ASU's DNA Laboratory. Edited sequences from four of the unknowns were subjected to BLAST similarity searches (http://www.ncbi.nlm.nih.gov/BLAST/) to identify nrDNA ITS sequences from potentially related taxa in Genbank, which were then aligned into a data matrix using ClustalX. Phylogenetic analyses (maximum parsimony) were conducted using PAUP* (Swofford, 2002), using heuristic search options that included SIMPLE addition sequence and tree-bisection-reconnection (TBR) branch swapping.

Baldwin, B. G., M. J. Sanderson, J. M. Porter, M. F. Wojciechowski, C. S. Campbell, and M. J. Donoghue. 1995. The ITS region of nuclear ribosomal DNA: a valuable source of evidence on angiosperm phylogeny. *Annals of the Missouri Botanical Garden* 82: 247–277.

Kress, W. J., K. J. Wurdack, E. A. Zimmer, L. E. Weigt, and D. H. Janzen. 2005. Use of DNA barcodes to identify flowering plants. *Proceedings of the National Academy of Sciences USA* 102: 8369-8374.

Swofford, D. L. 2002. *PAUP**. Phylogenetic Analysis Using Parsimony (*and other Methods). Version 4. Sinauer Associates, Sunderland, Massachusettes.