

Genetic Diversity of North American Wild Kidney Bean (*Phaseolus polystachios*) in the Eastern United States

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ABSTRACT

North American wild kidney bean or thicket bean (*Phaseolus polystachios* (L.) Britton, Sterns, & Poggenb.) is a perennial vine found in the eastern United States from Texas to Connecticut. Habitat destruction and urbanization are limiting its distribution: e.g., it was once prevalent in the Detroit River International Wildlife Refuge, but has not been seen there since the late 1800's. Crop wild relatives are a critical source of genetic diversity, often holding untapped genes for breeding of domesticated plants in agriculture for disease resistance, yield, quality, and adaptation to climate change, as well as ecologically important members of natural habitat. The closest cultivated relative of *P. polystachios* is *P. lunatus*, the lima bean. Through coevolution in its natural habitat, *P. polystachios* may have acquired true resistance to the ubiquitous pathogen white mold (*Sclerotinia sclerotiorum*) and provide a source for interspecific transfer. The Western Regional Plant Introduction Station of the National Plant Germplasm System holds over 17,000 accessions of *Phaseolus* from 47 species groups, but has only 10 accessions of the wild *Phaseolus polystachios*, 5 of which were only recently collected in Florida. Planning is underway for a collection trip throughout the Midwest to increase the diversity of *P. polystachios* within the collection. Understanding genetic diversity is critical for identifying areas to target for recovering maximum genetic representation. Molecular markers are an important tool for analyzing the extent and distribution of genetic diversity within and among wild populations and are important for identifying geographic gaps for collecting underrepresented genotypes. We analyzed nine accessions from the USDA collection along with sixteen herbarium samples provided by the Smithsonian Institution using 231 AFLP molecular markers from six primer combinations. While the DNA from the herbarium samples was somewhat degraded, markers at and below 200 bp were readily discernible and showed four distinct clusters. One herbarium sample from Florida was distinct from the others and, because of the lobed leaves, is likely *P. smilacifolius*. The USDA accession from Texas was very unique and has been reclassified as *P. texensis*. The level of distinction among the samples studied here reinforces the need for continued collection of this diverse species.

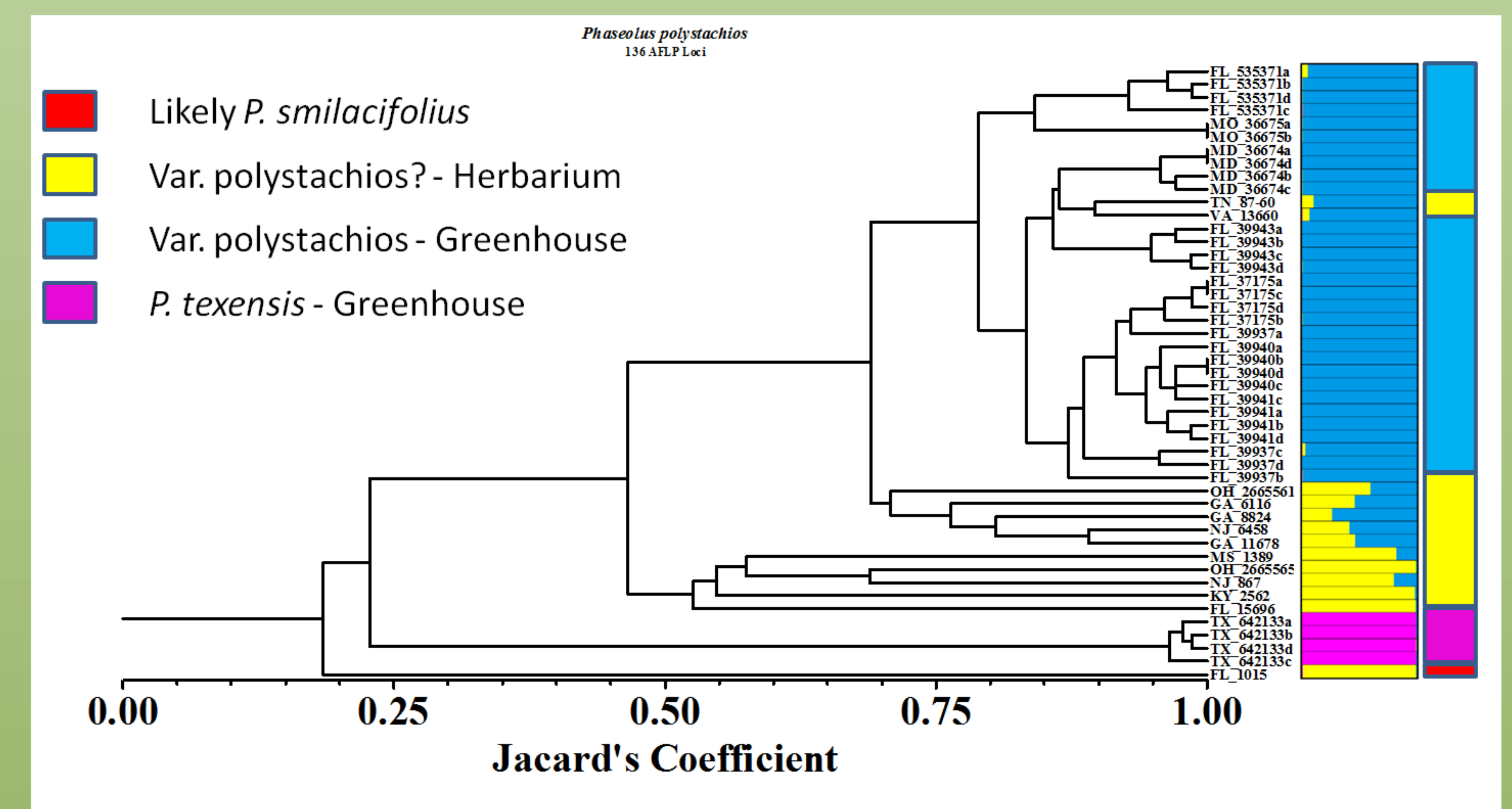


Fig. 2 Relationships among the analyzed accessions from softwares NTSys-pc and STRUCTURE.

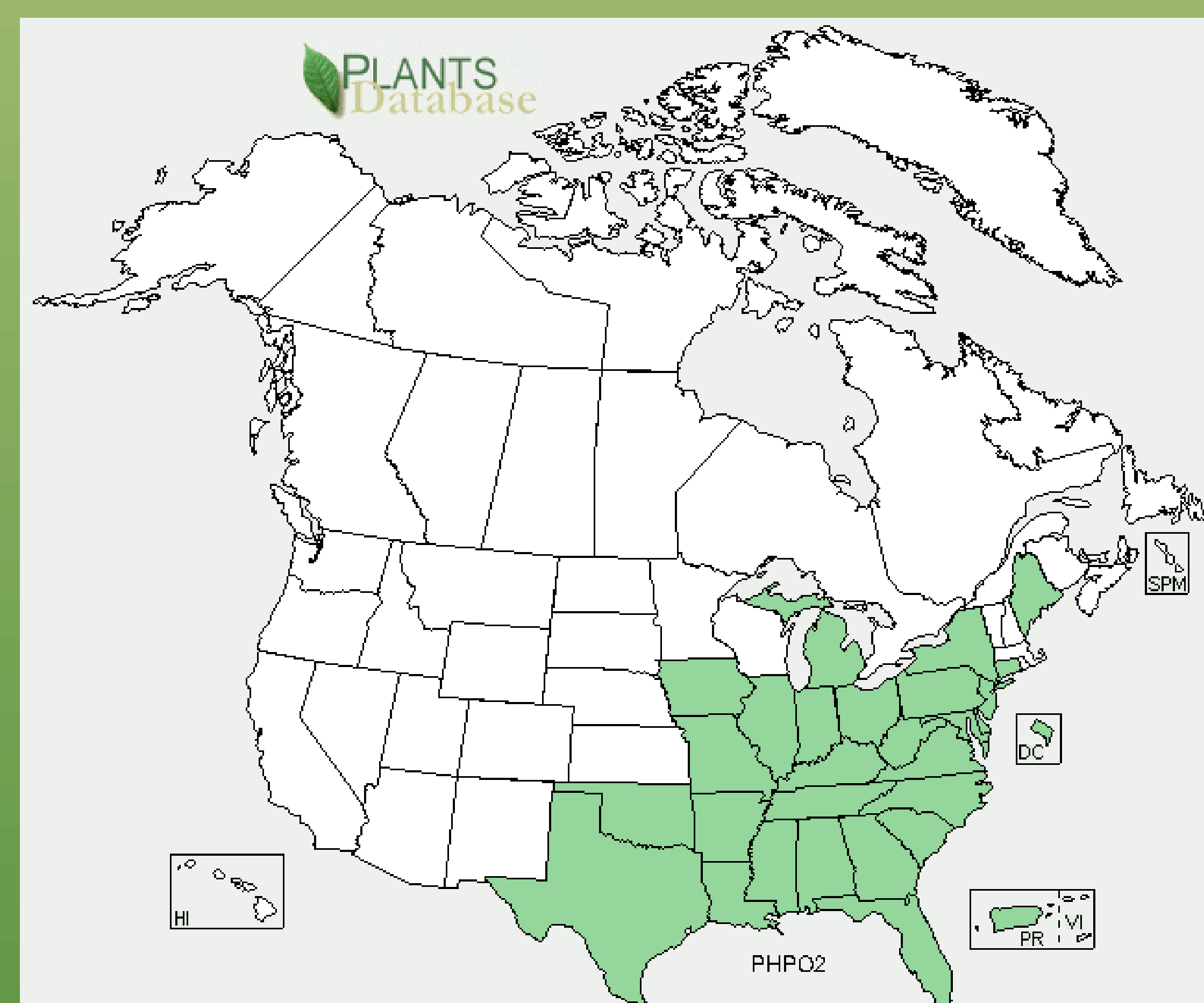


Fig 1. Habitat of *P. polystachios* USDA Plants (Database <http://plants.usda.gov/core/profile?symbol=PHPO2>)



Results

Cluster analysis found 4 major groupings (Fig 2.). The Texas accession TX_642133 has been reclassified to *P. texensis*, and the lobed leaves of the Florida accession FL_1015 indicate that it is likely *P. smilacifolius*. Plants within accessions were closely related, as were most of the Florida accessions. Herbarium samples, more geographically and temporally divergent, were more distinct. This study indicates that a considerable amount of genetic diversity for this species is available for exploitation and interspecific transfer.

Literature cited

- Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software *STRUCTURE*: a simulation study. *Mol. Ecol.* 14:2611-2620.
- Falush, D., M. Stephens, and J.K. Pritchard. 2003. Inference of population structure using multilocus genotype data: Linked loci and correlated allele frequencies. *Genetics* 164:1567-1587.
- Falush, D., M. Stephens, and J.K. Pritchard. 2007. Inference of population structure using multilocus genotype data: Dominant markers and null alleles. *Mol. Ecol. Notes* 7:574-578.
- Rosenberg, N.A. 2004. *DISTRUCT*: a program for the graphical display of population structure. *Mol. Ecol. Notes* 4:137-138.
- Vos, P., R. Hogers, M. Bleeker, M. Reijans, T. van der Lee, van der; M. Hornes, A. Frijters, J. Pot, J. Peleman, M. Kuiper, and M. Zabeau. 1995. AFLP: a new technique for DNA fingerprinting. *Nucleic Acids Research* 23(21): 4407-4414.

Materials and Methods

Plant Material. Available accessions were grown in the greenhouse, sampled, freeze-dried, and pulverized in a Genogrinder 2000. Accessions donated by the Smithsonian Institution were pulverized in the same manner.

Molecular Markers. Amplified Fragment length Polymorphic (AFLP) markers were generated using the restriction enzymes PstI And MseI.

Population Differentiation. Relationships among accessions were depicted in a tree generated using NTSys-pc. Accessions to be compared were grouped by individual plants, without *a priori* classification, into *K* clusters using the software *STRUCTURE*, which identifies genetically similar populations based on genotypes in Hardy-Weinberg equilibrium (Falush et al., 2003, 2007; Pritchard et al., 2000; Pritchard and Rosenberg, 1999).