



# A Nuclear and Chloroplast Phylogeny of Maple Trees (*Acer* L.) and their close relatives (*Hippocastanoideae*, *Sapindaceae*)



Emma Frawley<sup>1,2</sup>, AJ Harris<sup>2</sup>, Jun Wen<sup>2</sup>  
1 Department of Environmental Studies, Bucknell University  
2 Department of Botany, National Museum of Natural History

## INTRODUCTION:

The primary goal of this study is to reconstruct a molecular phylogeny of the woody trees and shrubs in *Acer* (L.), *Dipteronia* (Oliv.), the two members of the *Acereae* tribe, and *Aesculus* (L.), *Billia* (Peyr.), and *Handelioidendron* (Rehder) of the *Hippocastanoideae* tribe. These five taxa make up the subfamily Hippocastanoideae in the family Sapindaceae. *Acereae* is especially interesting as it is a large, well-known, and horticulturally important tribe that differs from its close relatives morphologically (Fig. 1) and in species richness. No phylogeny using low-copy nuclear genes in *Acereae* has been previously published. Our study is the first to explore low-copy nuclear genes to test the monophyly of polytypic taxonomic sections of *Acereae*. This work is complementary to published phylogenies of *Acereae* using the nuclear ribosomal Internal Transcribed Spacer (ITS) and several chloroplast genes (Grimm, 2006, Renner, 2008). These prior studies show that some traditionally recognized sections of *Acereae* are monophyletic while others are not, and there are multiple geographically disjunct sections.

## OBJECTIVES:

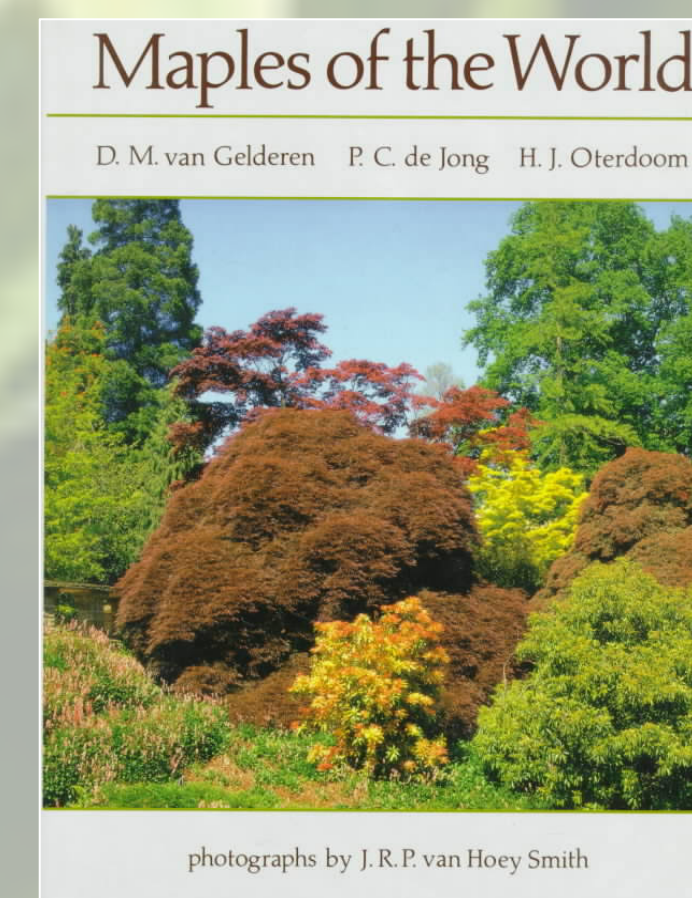
- To test the monophyly of the taxonomic sections of *Acer*.
- To assess geographic disjunctions and endemism within clades of *Acer*.

## METHODS:

Sampled to represent geographic, morphological, and taxonomic diversity of *Acer*.

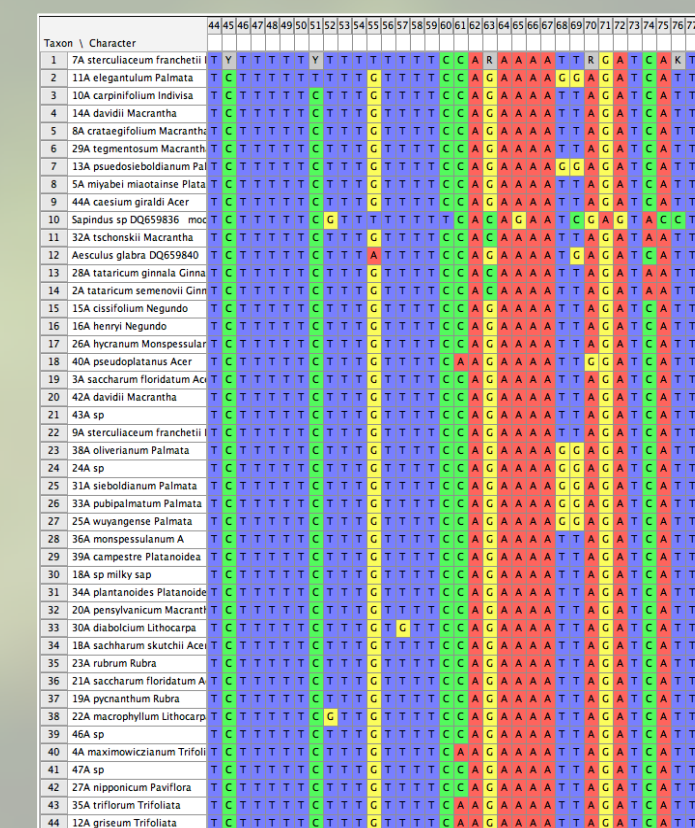


Emma collecting.

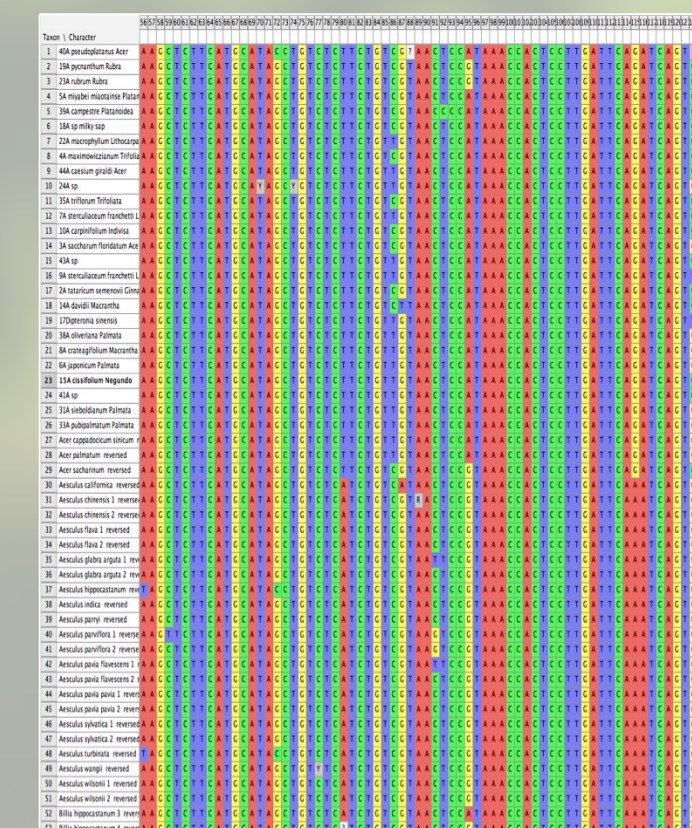


Reference text.

Obtained DNA sequences of nuclear DNA (*SQD1*, *AT103*) and chloroplast DNA (*psbM*) using standard PCR and Sanger sequencing methods.

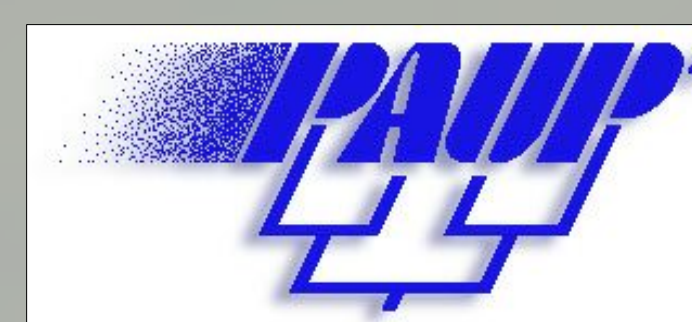
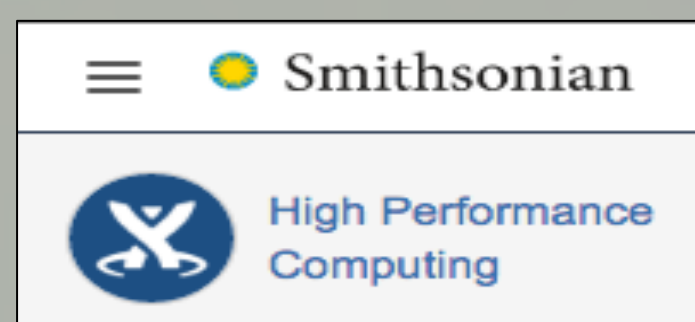


psbM alignment.



SQD1 alignment.

Performed phylogenetic reconstruction.



Programs used for phylogenetic work.

## ACKNOWLEDGEMENTS:

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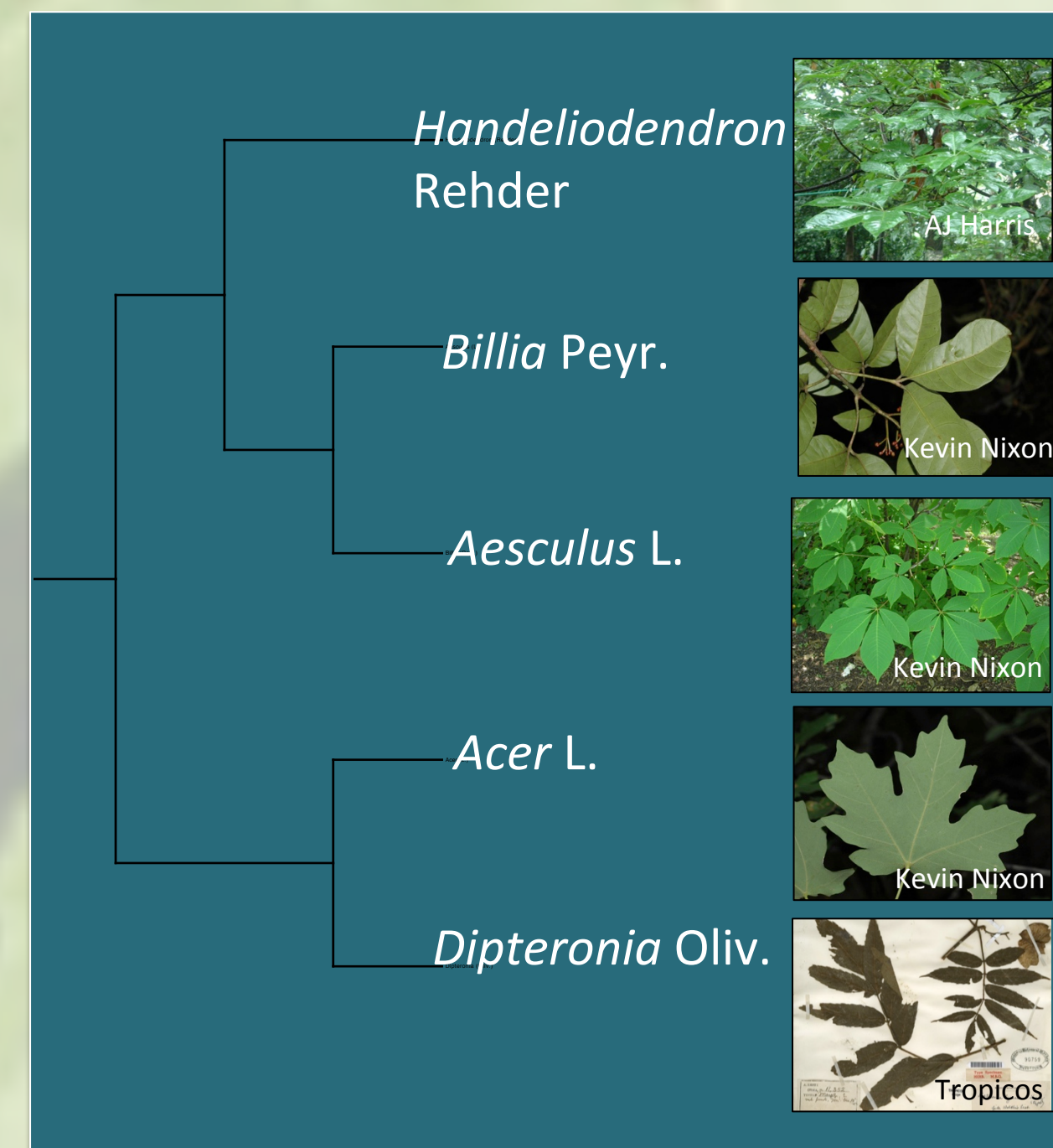


Figure 1. Phylogeny of Hippocastanoideae taxa showing morphological differences.

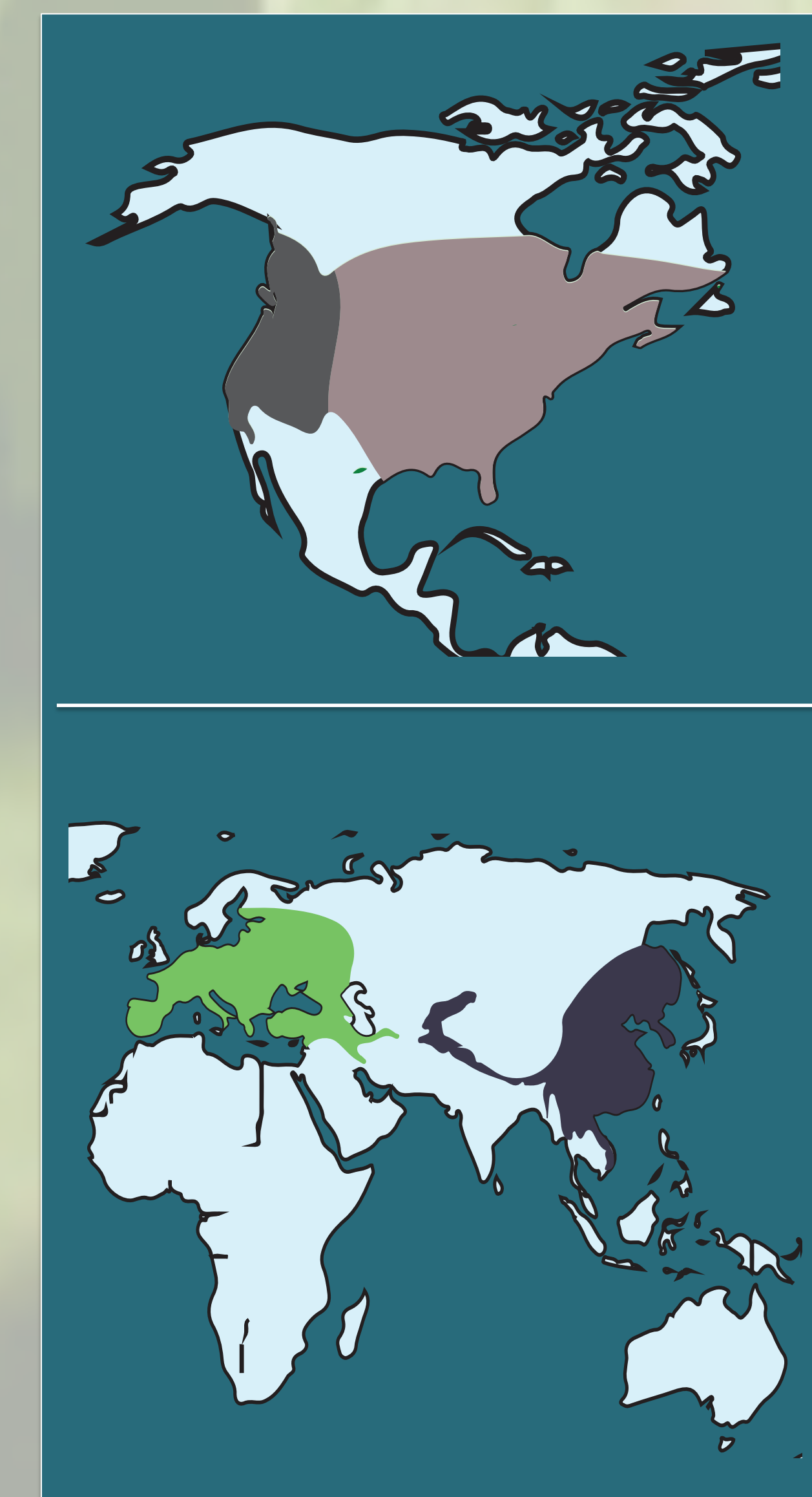


Figure 3. The map shows the continental areas of endemism of species of *Acereae*. Colors of areas of endemism correspond to colored circles in Figure 2.

## REFERENCES:

Grimm, Guido W., Susanne S. Renner, and Alexandros Stamatakis. *Evolutionary Bioinformatics Online* 2 (2006): 7-22. Web. June 2016. Renner, SS, GW Grimm, GM Schneeweiss, TF Stuessy, and RE Ricklefs. *Systematic Biology* 57.5 (2008): 795-808. PubMed. Web. June 2016.  
Photo Credits. Fig 1: Kevin Nixon at PlantSystematics.org, Tropicos.org, Fig. 4: Jieyao Feng, Darien Florez, and background image from ItsNature.org.

## RESULTS AND DISCUSSION:

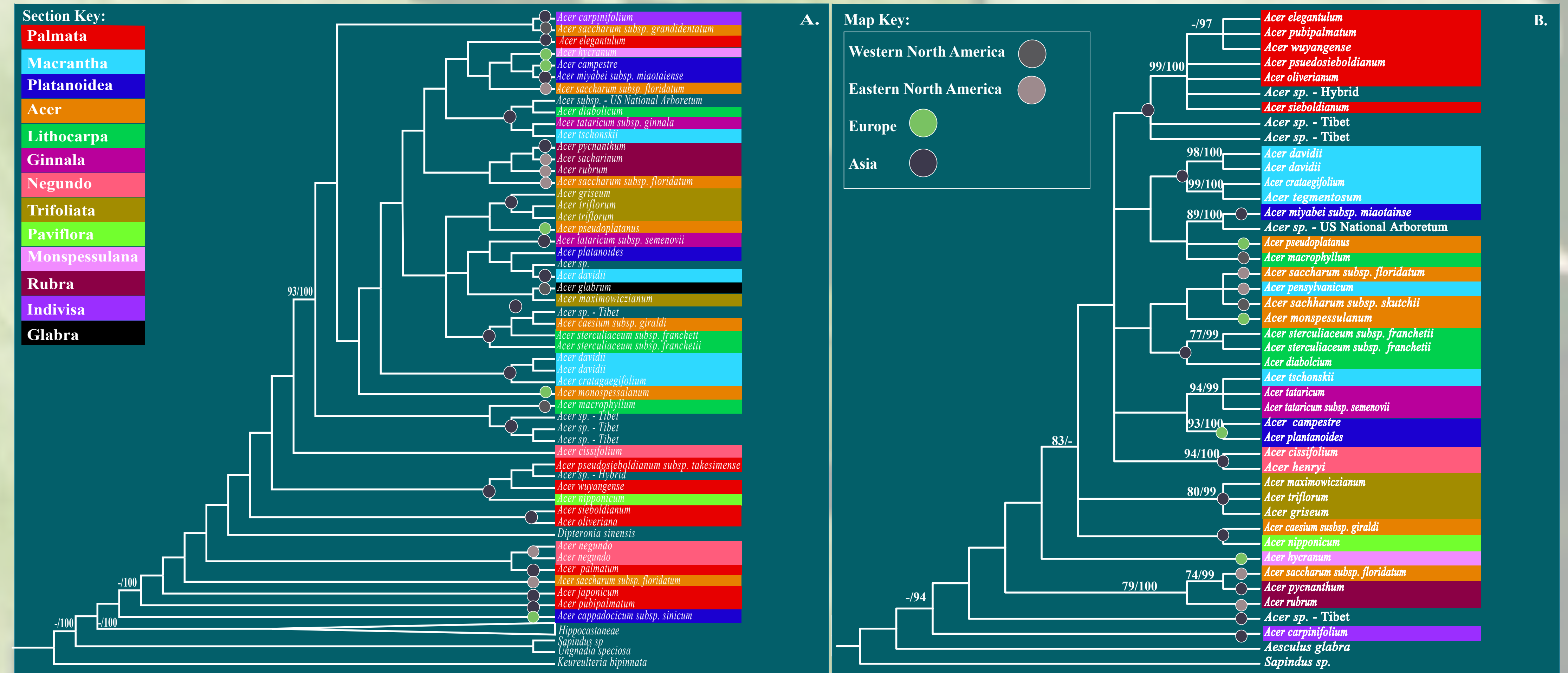


Figure 2. Phylogenetic trees. Numbers are support from Parsimony and Bayesian analysis in the form of Bootstrap/Posterior Probability values. (A) Nuclear phylogeny using *AT103* and *SQD1* data. (B) Chloroplast phylogeny using *psbM* data. Colored-circles correspond to colored areas of endemism in Figure 3.

## Monophyly of *Acereae* sections compared among previous and current studies. Monophyly represented via \*.

Sections	Chloroplast DNA		Nuclear DNA	
	Renner (2008)	Our study	Grimm (2006)	Our study
Palm.	*12	*6	*13	*8
Macr.	*7	6	12	5
Plat.	*6	3	*12	4
Acer	8	6	16	7
Lith.	*2	*4	1	4
Ginn.	*2	*2	2	2
Neg.	3	*2	2	3
Trif.	*7	*3	*6	*4
Parv.	N/A	1	N/A	1
Mons.	N/A	1	N/A	1
Rubr.	*4	*2	*3	*3
Indiv.	N/A	1	1	1
Glab.	N/A	1	N/A	1

Table 1. The number in each cell refers to the number of species sampled for that section.. Starred (\*) cells were monophyletic in that study. Unstarred cells were not found to be monophyletic.

## Monophyly of sections of *Acer*:

- Sections *Palmata*, *Trifoliata*, and *Rubra* were monophyletic.
- Sections *Macrantha*, *Lithocarpa*, *Ginnala*, and *Negundo* formed clades in our chloroplast phylogeny and in previous studies (Table 1).
- Section *Platanoidea* was not monophyletic in either data set, contrary to previous studies.
- Section *Acer* was paraphyletic, and this result is consistent with prior studies.

## Geographic disjunctions and endemism:

- Our chloroplast data was more geographically centered and had fewer disjunct clades than our nuclear data.
- Both data sets showed large, endemic Asian clades (Fig. 2).

## FUTURE WORK:

Ultimately we will utilize this phylogenetic framework of Hippocastanoideae to:

- Evaluate the evolution of functional traits, such as specific leaf area and seed weight, in the subfamily (Fig. 4).
- Better understand the disparity in species richness among genera in the subfamily through analysis of evolutionary rates across the tree.
- Evaluate biogeography in the subfamily, specifically concentrating on continental disjunctions (historical biogeography) and colonization success (ecology).



Figure 4. *Acer* samaras being measured for specific leaf area.