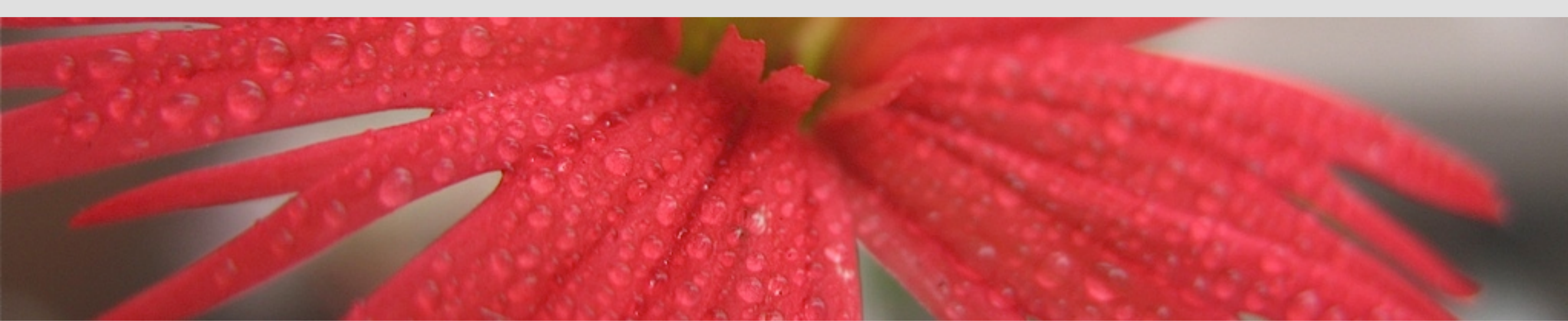


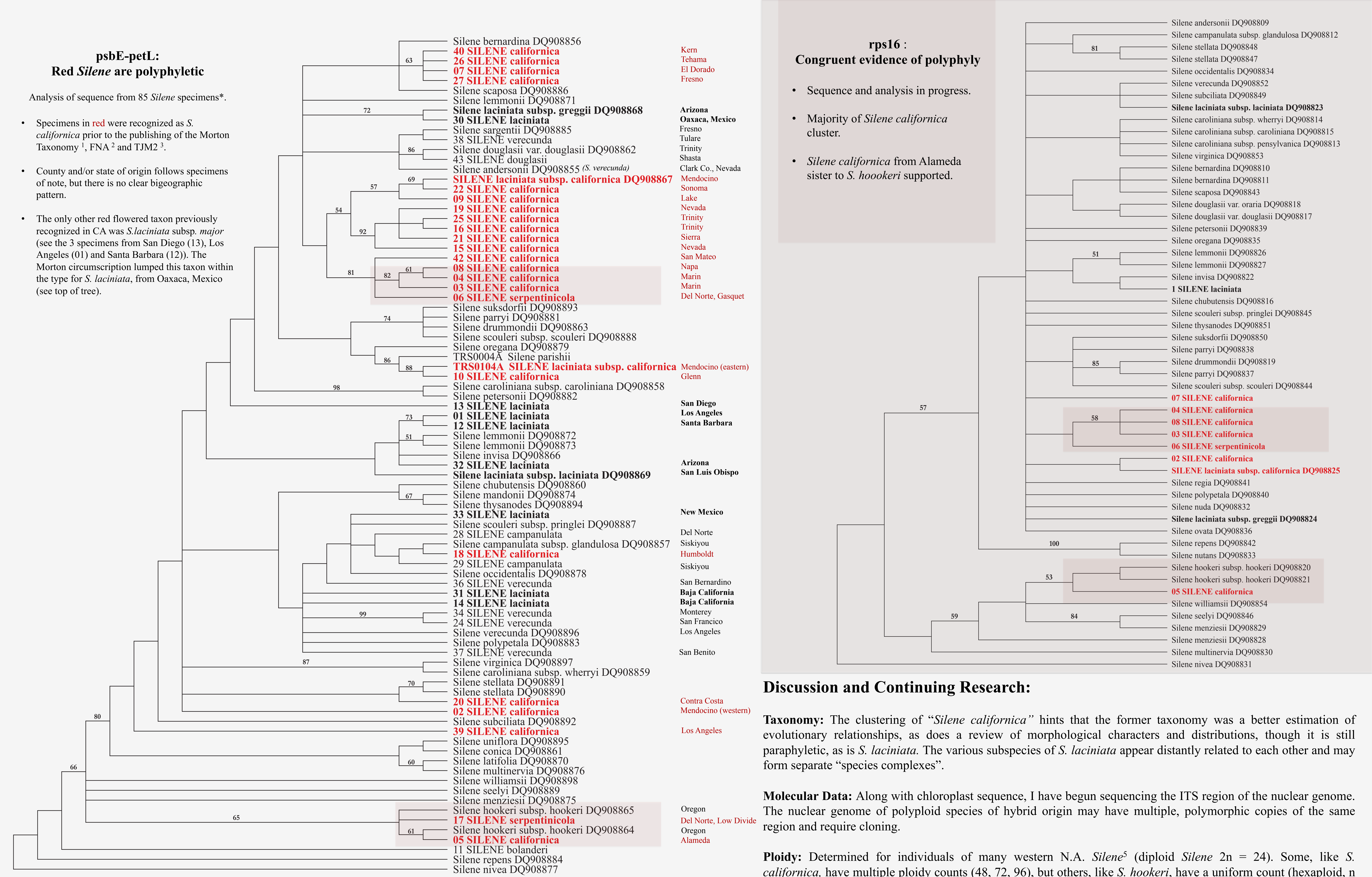


The Confusing Identity of Red Flowered *Silene* (Caryophyllaceae) in California

Two Chloroplast Genes Reveal Multiple Lineages

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Current taxonomy for *Silene* in North America lumps the former red flowered California endemic, *S. californica* Durand, into *S. laciniata* Cavanilles, with a center of diversity in central Mexico ^{1, 2, 3}. Based on morphology, this circumscription of *S. laciniata*, and specifically *S. laciniata* subsp. *californica* (Durand) J.K. Morton, along with the western Del Norte County endemic, *S. serpentinicola* Nelson, leaves many California populations of red flowered *Silene* outside of currently recognized taxa. Previous molecular research has not supported a close relationship between infraspecific groups now recognized in *S. laciniata* in California. Only one specimen previously identified as *S. californica* was included and so no conclusions could be drawn about species identity ⁴. Most California *Silene* are allopolyploids that likely formed from separate hybridization events, different populations, and even different members of a population, may represent distinct lineages ⁴. My analysis of populations of red flowered *Silene* throughout California explores whether these populations form a monophyletic group or represent distinct lineages.



Discussion and Continuing Research:

Taxonomy: The clustering of “*Silene californica*” hints that the former taxonomy was a better estimation of evolutionary relationships, as does a review of morphological characters and distributions, though it is still paraphyletic, as is *S. laciniata*. The various subspecies of *S. laciniata* appear distantly related to each other and may form separate “species complexes”.

Molecular Data: Along with chloroplast sequence, I have begun sequencing the ITS region of the nuclear genome. The nuclear genome of polyploid species of hybrid origin may have multiple, polymorphic copies of the same region and require cloning.

Ploidy: Determined for individuals of many western N.A. *Silene*⁵ (diploid *Silene* 2n = 24). Some, like *S. californica*, have multiple ploidy counts (48, 72, 96), but others, like *S. hookeri*, have a uniform count (hexaploid, n = 72). Flow cytometry may allow inference of chromosome number for sister terminal taxa and determine if there is a pattern that matches phylogenetic groupings.

*Majority rule consensus of maximum parsimony trees with bootstrap support. Sequence was obtained from GenBank, field collected specimens and herbarium sheets (40 from Scott Simono: ### SILENE...; 43 from GenBank: Silene...DQ#####; 2 from Tommy Stoughton: TRS####A), was assembled in Sequencher, aligned in ClustalX and McClade, and analyzed in PAUP.