



Fig. 1. Immature fruit of *Arctostaphylos glandulosa* subsp. *crassifolia* taken at Torrey Pines State Park, California. Photo by Dylan O. Burge.

Deciphering plant genomes can affect plant conservation policies

Conservation genetics of the endangered Del Mar manzanita (*Arctostaphylos glandulosa* subsp. *crassifolia*) based on RAD Sequencing data

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Significance statement

The advent of accessible DNA sequencing techniques has led to an unprecedented understanding of speciation and to question taxonomic relationships that had once been stable. Besides adding elements to question, yet again, what plant species are, these findings raise dilemmas regarding species conservation. The study of Burge and colleagues is relevant to the binational conservation debate concerning the US and Mexico. Their study also highlights the power of using genomic data along with morphological traits. As a researcher working on the taxonomy of *Washingtonia*, a group of palms found in the US and Mexico, I found Burge's team discussion on plant conservation very pertinent.

A team of botanists led by Dylan O. Burge has used genomic and morphological data to confirm plants know nothing about country boundaries.

Arctostaphylos glandulosa Eastw. subsp. *crassifolia* (Jeps.) P.V.Wells, commonly known as Del Mar manzanita, is a beautiful shrub that grows in the chaparral of San Diego County and northern Baja California. Despite being considered an endangered plant in San Diego, Del Mar manzanita has no special legal status in Baja California. To complicate things further, the group of researchers considered Del Mar Manzanita could exchange genetic material—hybridize—with a close relative, Eastwood manzanita (*A. glandulosa* Eastw. subsp. *glandulosa*; including *A. glandulosa* Eastw. subsp. *zacaensis* (Eastw.) P.V.Wells). Hybridization would result in plants having intermediate characteristics, thus making identification, and conservation, problematic. Burge’s research is another example of the growing dilemma in conservation biology resulting from the clarification of taxonomic relationships.

To find out whether Del Mar and Eastwood manzanitas were indeed two different subspecies, the team of California-based botanists turned to a powerful molecular technique: a type of DNA sequencing known as RAD sequencing. The team also used morphological data from stems and leaves, such as trichomes, to look for differences between both taxa and to see whether the genetic patterns matched those of the morphological data.

RAD sequencing is a useful method to study plants that lack a previously published reference genome. This is because during the analysis of RAD data, it is possible to construct a type of reference genome using the sequence data from the plant with the greatest number of RAD clusters. This genome can then be used to compare the rest of the individuals’ DNA and call differences at individual DNA bases. These differences are termed Single Nucleotide Polymorphisms (SNPs).

One of the caveats of the study was the low number of individual samples the researchers could collect. However, they could not differentiate subspecies using morphological traits since plants varied within the same location.

The researchers also found Del Mar and Eastwood manzanita belong to two distinguishable genetic groups and that hybridize. The fact that they hybridize would suggest del Mar Manzanita is a widespread taxon occurring in Mexico and the US. However, when looking only at the regional scale, del Mar Manzanita could be considered to only occur in San Diego County, where one of the easily recognizable genetic groups occurs. The authors consider necessary to have a larger sample to make a formal taxonomic decision on *A. glandulosa* which would impact the conservation of this species in both countries.