Major recommendations for introduction/reintroduction of *M. congdonii* in the northern portion of its range

1) At least six Conservation Units for *M. congdonii* are warranted based on microsatellite and chloroplast DNA evidence (Figures 1 and 2). These units are recommended as the first level of subdivision to consider recovery activities and boundaries for moving germplasm. The cpDNA data suggest there are distinctive lineages and/or sets of lineages in each of these units. Variation across these units accounts for approximately 25% of the genetic diversity in the taxon. Two of these units are in the northern portion of its range.

2) Given the genetic distinctiveness, small population sizes, and location at the edge of the species range, the Monocline and Panoche populations are a very high priority for conservation of populations and genetic diversity and, by some definitions, could be considered to represent a cryptic phylogenetic species. These northernmost populations are the only known representatives of a unique, derived cpDNA haplotype, cpMcB, and may represent divergence and adaption that is critical for the species to survive climate change. Genetic distinctiveness of these populations is also supported by the microsatellite data; even when the inferred number of populations is two, these two populations are genetically distinct from the remaining populations (Figure 3). Additional resources required for careful population management without any potential for contaminating or swamping small populations are warranted. This may require seed bulking at a completely different site than the others and with methods that involve more investment per seed.

   In addition, considerations for maintaining the cpDNA haplotype structure between these two populations is also warranted as Monocline is the only population where only the cpMcB haplotype was found (Figure 4) and leaving it that way will help ensure that lineage is maintained. Both populations are dominated by a single microsatellite allele per locus, but rare alleles are also present so it is important to collect seed from as many individuals as possible to ensure some genetic diversity in the collection. Surveys for additional populations in these areas that may represent this lineage and additional genetic diversity are recommended (although this has probably already happened).

   We recommend that any seed introduction in Panoche Creek and Silver Creek watersheds should come from the Panoche populations and any introduced populations in the Ciervo Hills should come from the Monocline population.

3) Comparison of genetic uniqueness and richness among populations indicates that most of the smaller populations (in terms of numbers of individuals and patch size: Panoche/ Monocline, Jacilitos1/2, BLM8300, BLM9100, and BLM8500) are genetically distinct but low in allelic richness and the larger populations are less distinct, but richer in allelic diversity (Figures 5 and 6). Even small populations in close proximity can be relatively distinct from each other (e.g., Figure 7 - BLM8300 and BLM8500). A pattern of high diversity between populations and low genetic diversity within populations is expected for a strongly selfing taxon. Thus, different populations and both small and large populations

should be considered for establishing new populations. In addition, small populations, even though low in genetic diversity, are valuable for conserving rare alleles and haplotype diversity.

4) Given that small and geographically discrete populations are important for genetic diversity on the landscape level, even when in close proximity to other populations (<0.2 mile), all introductions/reintroductions should be very careful to not displace existing populations even if small. Surveys for existing populations or considerations about possibly dormant populations are warranted even if germplasm is coming from a nearby population.

5) Introductions to Skunk Hollow and Anticline Ridge should probably come from seed collected at PVER given its proximity and large size. Introductions to Warathan Creek and Kreyhagen Hills should probably come from Jacilitos Creek populations. The two Jacilitos Creek populations are similar but not identical and should probably be amplified separately so that the existing differences can be used to either ensure maximum diversity for a given introduction population or to allow for keeping that diversity separate in introduced subpopulations.

   For introductions on North Kettleman Dome, it makes most sense to use material in closest proximity to any introduction site, but use extreme caution that there is not an existing population nearby that represents another small but genetically divergent population. The proposed introductions between BLM 6800 and BLM 9100 are not recommended. Population BLM 8500 is not near any of the proposed introduction sites but it should be specially noted as the only population where the rare haplotype cpMcS was found, and therefore should be kept distinct.

Fig. 1 Distribution and frequency of chloroplast haplotypes found in *Monolopia congdonii* (A-E and S) in the six proposed *M. congdonii* conservation units. A represents the ancestral haplotype (cpMcA). The other populations mapped are from Rarefind (California Natural Diversity Database 2015).

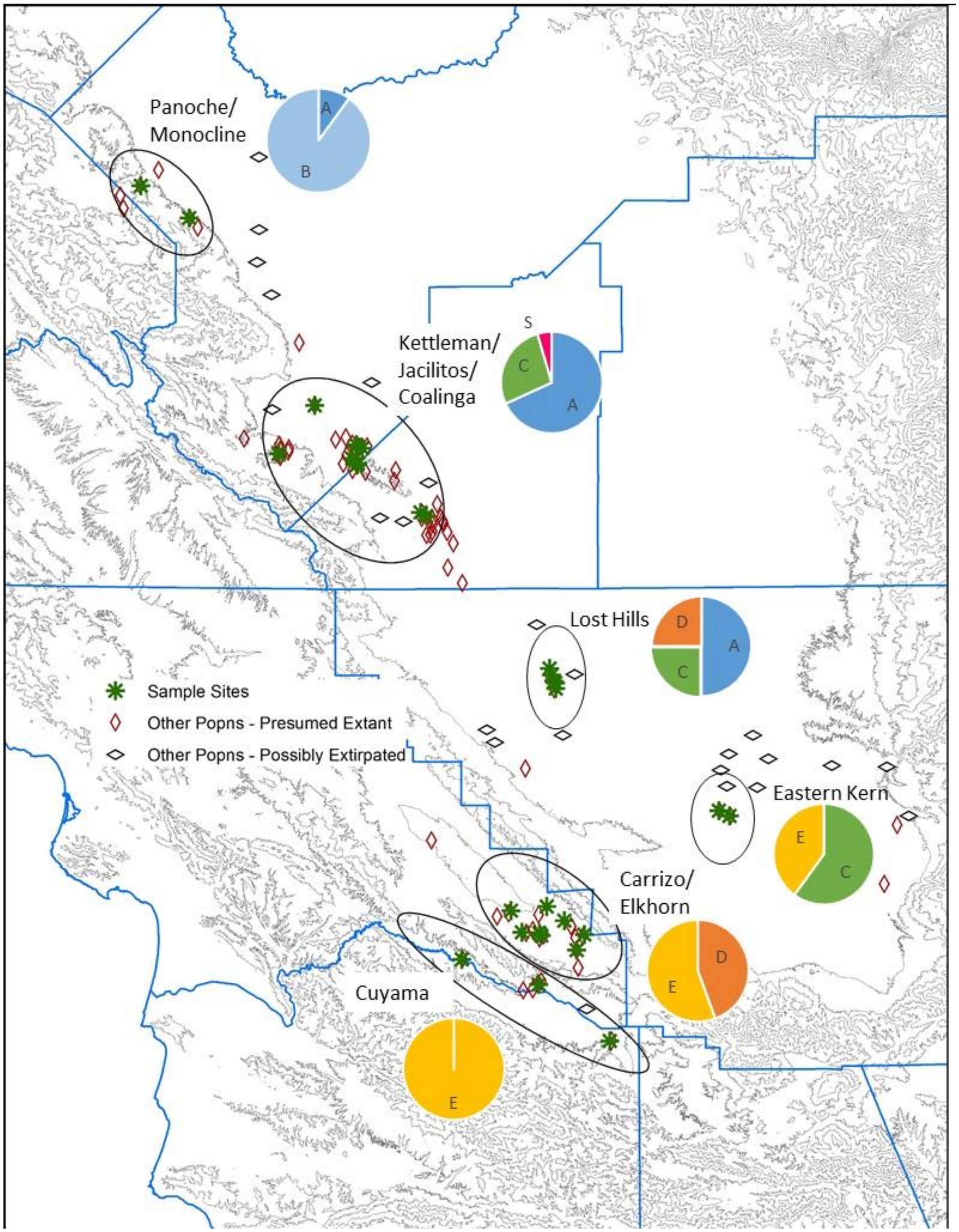

Figure 2. Principal Coordinates (PCoA) of *Monolopia congdonii* microsatellite data showing Conservation Units and concordance with cpDNA data (circles).

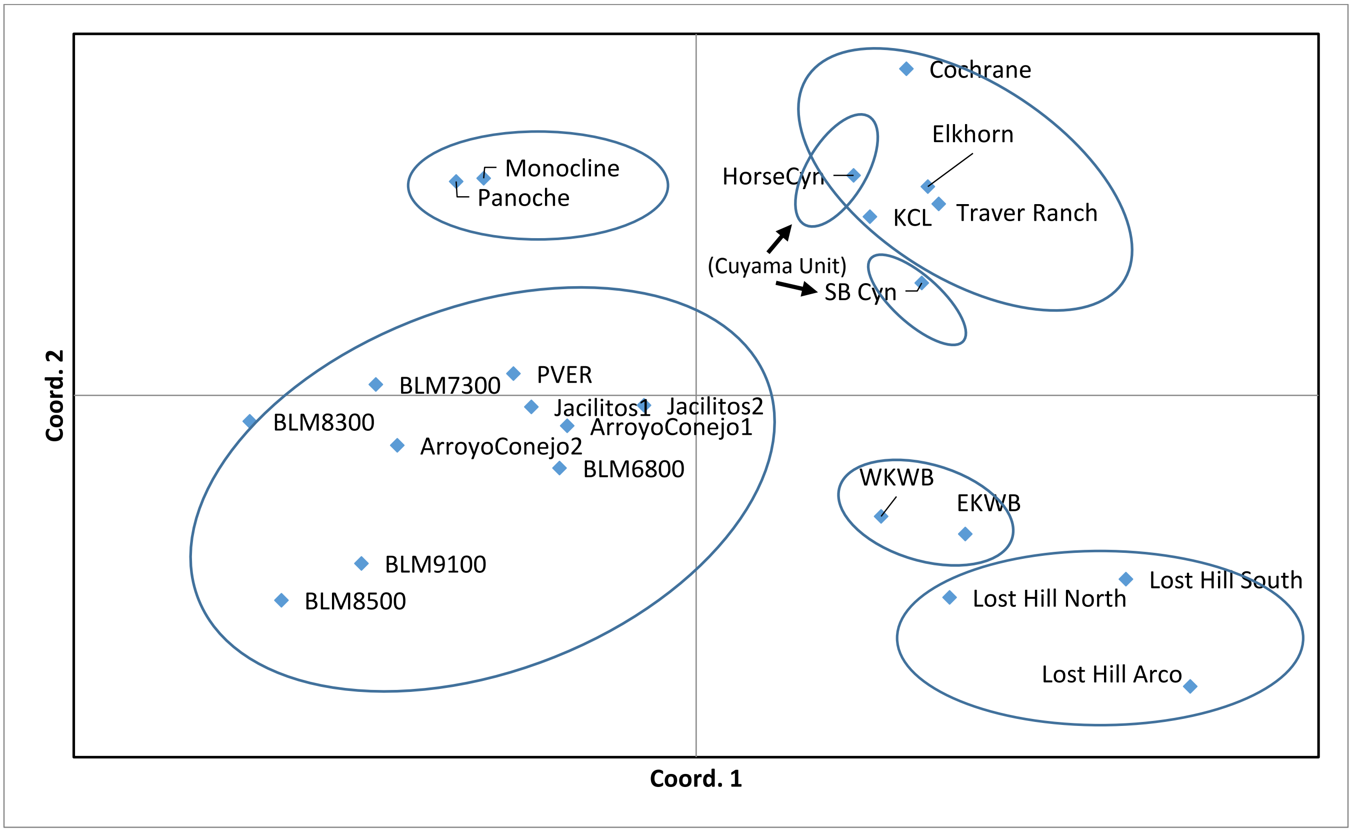

Figure 3. Diagram showing assignment of samples to populations based on microsatellite data using an inferred population size of 2. Vertical axis indicates probability of assignment of each sample to each inferred population and the numbers on the horizontal axis refers to the sampled populations. Sample populations 1 and 2 are Panoche and Monocline Ridge. The remaining sampled populations (3-12) are from PVER, Jacilitos Canyon, Kettleman Hills (North and Middle Domes).

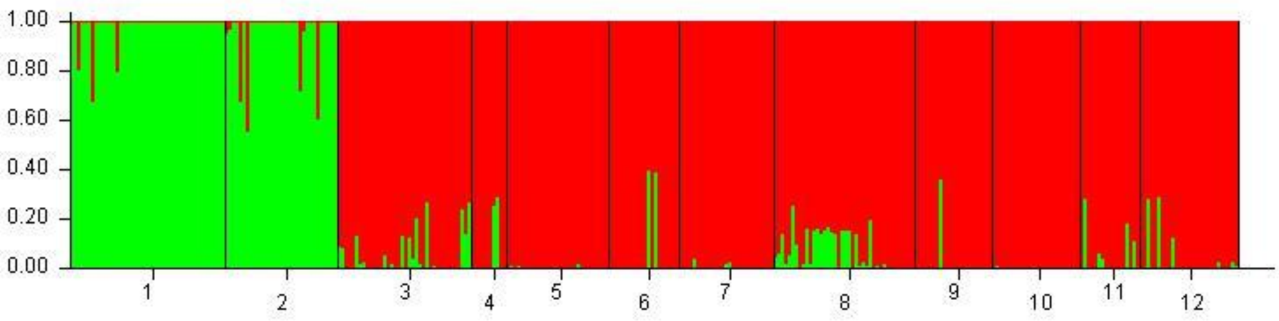

Fig. 4 Distribution and frequency of chloroplast haplotypes (A-C, S) within the two northern proposed *Monolopia congdonii* conservation units. S represent a haplotype similar to the single haplotype found in *M. stricta* from other parts of its range. The other populations mapped are from Rarefind (California Natural Diversity Database 2015).

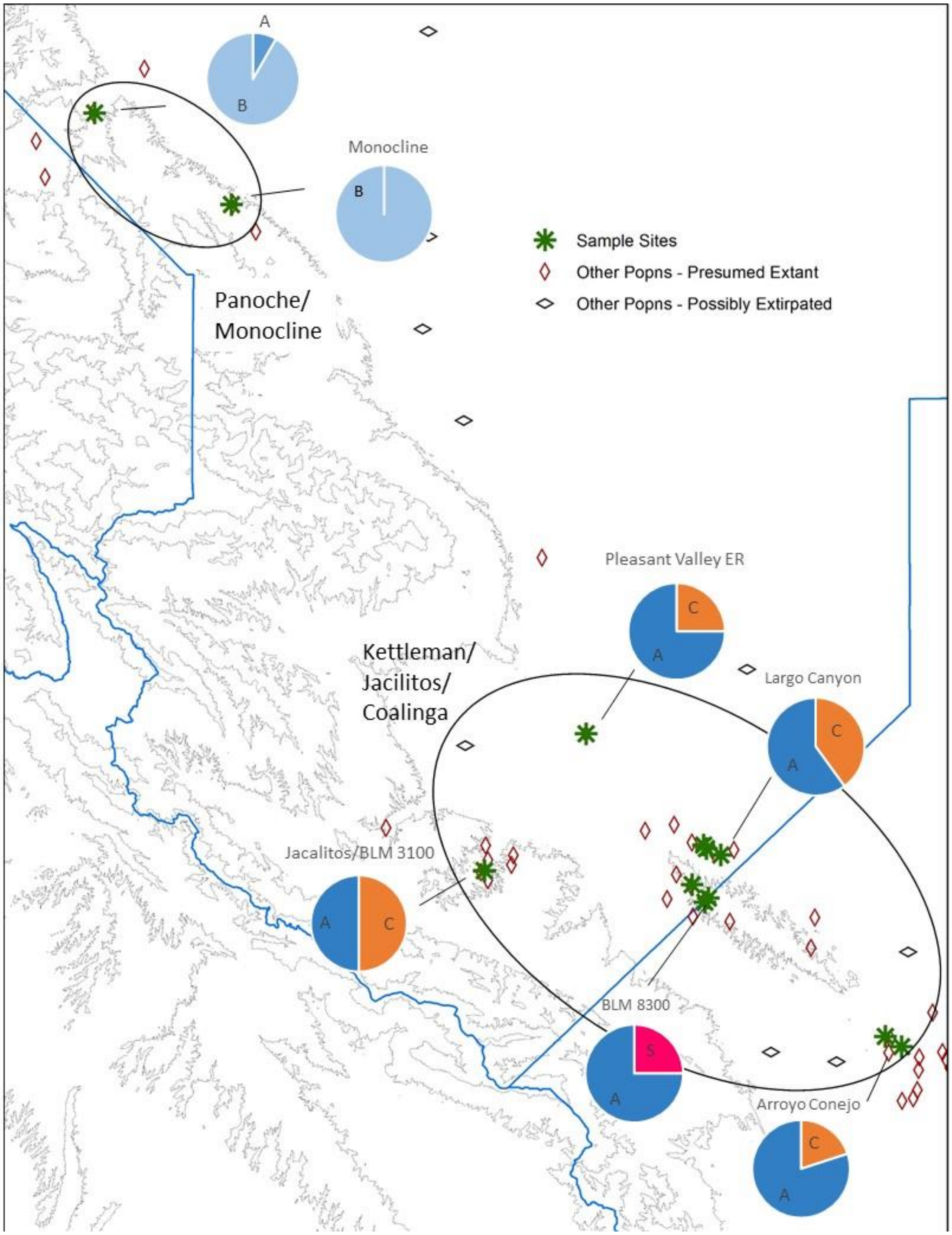

Figure 5. Principal Coordinates of the Northern Populations of *Monolopia congdonii* showing similarity among larger populations and uniqueness of smaller populations.

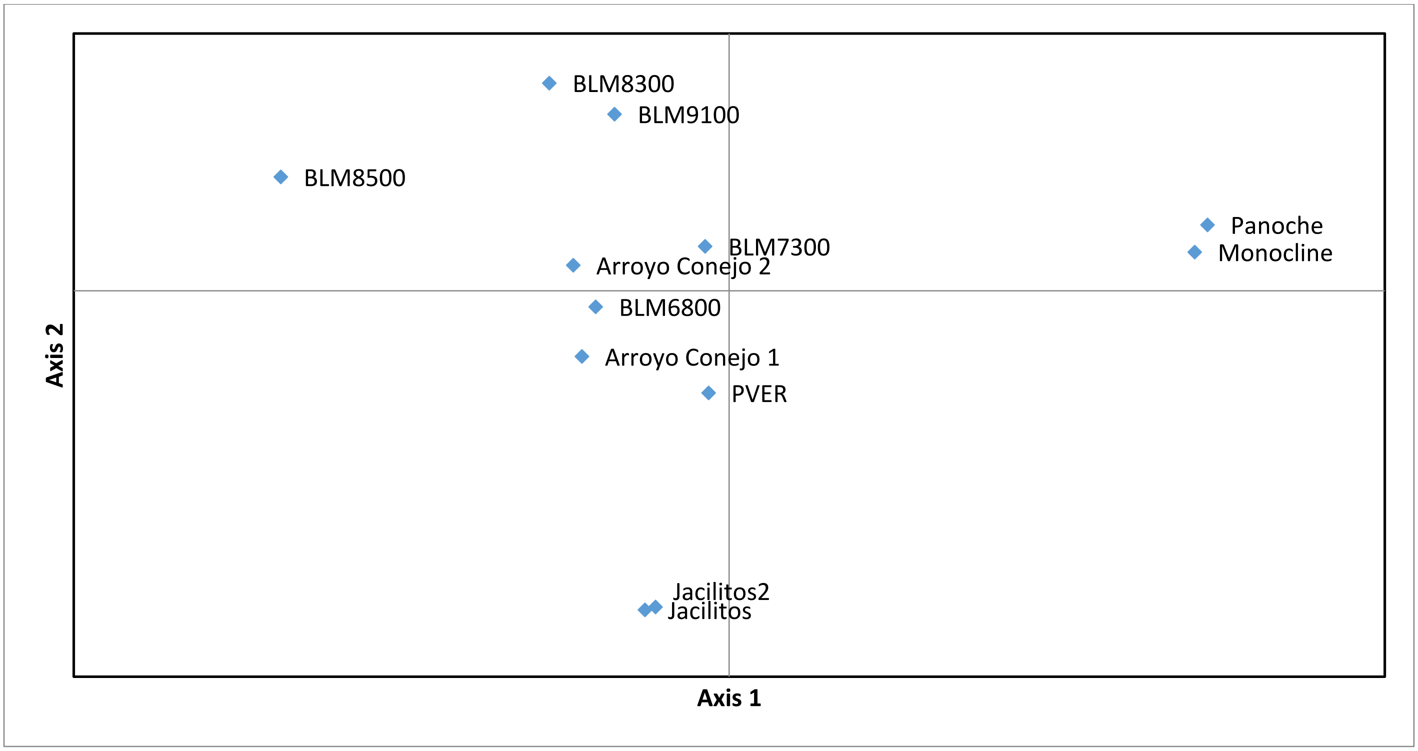

Figure 6. Relationship between allelic richness and genetic distinctiveness for the 12 northern populations sampled for microsatellite data. The relationship is identical for richness versus mean pairwise Fst and He.

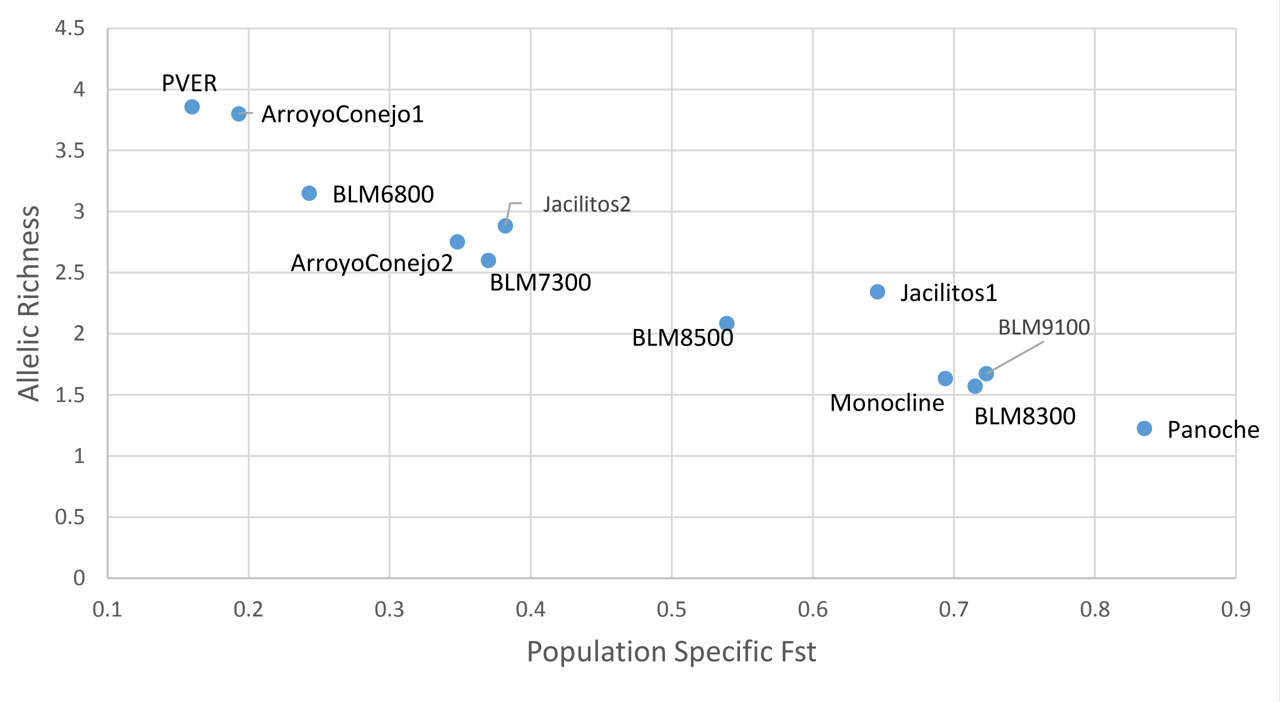

Figure 7. Genetic similarity between populations sampled in the North Kettleman Hills. The width of lines connecting populations is proportional to the genetic distance between the populations. Note the comparison between the two largest populations (BLM6800 and BLM7300) has the smallest Fst value despite the distance between the two populations relative to others. Also, the largest Fst values are generally between the smallest populations.