Introduction:

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- The milkweed genus Asclepias (Apocynaceae) has been a model system in studies of plant reproduction, plant defense, plant-animal interactions, and increasingly plant genomics (Fishbein et al. 2018).
- Asclepias species are the sole host plant for the larvae of monarch butterflies, a species of high conservation concern.
- There are over 130 species of Asclepias in the Americas; there are 75 in the United States and Canada, 75 in Mexico and Central America, and 8 in South America.
- The phylogeny (evolutionary relationships) of Asclepias has been used as a basis to study the evolution of adaptations to insect herbivory and drying climates (Agrawal et al. 2009, Fishbein et al. 2018).
- The Sonoran Desert Clade consists of nine species in the southwestern United States and northern Mexico and is the earliest diverging group of Asclepias species (Fig 1., Table 1).
- The unusual traits of the Sonoran Desert Clade make it an important group for studying adaptations to aridity; the phylogenetic relationships of this group are still not well understood.
- Whole chloroplast DNA sequences (plastomes) are a useful source of data for determining phylogenies.



Sonoran Desert Clade

Fig 1. These are pictures of the 9 species of the Sonoran Desert Clade

Species	Location
A. albicans	Sonoran Desert in Arizona, California, Baja California, Baja California
A. coulteri	Sierre Madre Oriental in Guanajuato, Hidalgo, Querétaro, San Luis Po
A. cutleri	Colorado Plateau in Arizona, Utah
A. leptopus	Sierra Madre Occidental in Chihuahua, Sinaloa, Sonora
A. macrotis	Mountain slopes in desert and grassland in Arizona, Colorado, New Texas, Chihuahua, Coahuila, Sonora
A. masonii	Sonoran Desert on Isla Magdalena in Baja California Sur
A. sperryi	Mountain slopes in desert in Texas, Coahuila
A. subulata	Sonoran Desert in Arizona, California, Nevada, Baja California, Baja C
A. sudapnylla	Coastal dunes in Sinaloa, Sonora

Table 1. Habitat and distribution of the Sonoran Desert Clade species.

Phylogeny of Sonoran Desert Milkweeds Resolved with Plastid Genome Sequences Shelby Gentry and Mark Fishbein **Oklahoma State University**

Methods:

- 1-9 samples of each Sonoran Desert Clade species were obtained and sequenced through "genome skimming" by Fishbein and Straub lab members (Straub et al. 2011; Weitemeir et al. 2014). 17 new plastomes were assembled for this part of the project following the steps of Fishbein et al. (2018).
- Sequence reads were filtered and trimmed to remove low quality data in Geneious.
- Geneious or IOGA.
- In Geneious, portions of contigs matching a reference plastome (A.nivea_022431) were found using BLAST and then aligned to the reference to produce a draft plastome.
- To finish the assembly of the plastome sequence the trimmed reads were mapped to the draft to fill in gaps between contigs.
- Multiple sequence alignments were produced using the online implementation of MAFFT, with other representatives of American and African milkweeds used as outgroups.
- Character exclusion sets were produced using GBLOCKS executing in Mesquite to omit ambiguously aligned regions.
- IQTREE was used to find the best fit model of sequence evolution and to estimate the maximum likelihood (ML) phylogeny with clade support estimated by fast bootstrapping.



Sur, Sonora otosí, Tamaulipas

w Mexico, Oklahoma

California Sur, Sonora

• Reads were then assembled into contiguous sequences (contigs) using either

A. cutleri_1659 Utah * — A. cutleri_0917 Utah * A. cutleri_1606 Utah * A. cutleri_1645 Utah *

Fig 2. Maximum likelihood tree of the Sonoran Desert clade tree. Colors represent individuals of the same species. States are included from where the individual is collected. Branches in bold have 100% bootstrap support; numbers indicate support less than 100%. Asterisk's indicate newly assembled plastomes.

• 17 new plastomes were assembled:

- single lineage. (Fig 2.)
- only one individual of A. subaphylla.
- two different clades. (Fig 2.)
- subaphylla, A. masonii, and A. albicans) groups. (Fig 2.)

- indicating they had separate origins (Fig 2.)

Conclusion/Discussion:

- mostly between 90 and 100%.
- of eastern and western clades.

- among the species in the Sonoran Desert Clade.

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Results:

• Range of sequence reads assembled per sample: 39,914 to 411,110

• Range of depth of coverage of the assembled plastomes: 26.8 to 360.6

• Range length of assembled plastomes: 129,899 to 136,946

• The Sonoran Desert Clade doesn't have multiple clades; all nine species form a

• For five of the nine species all of the sampled individuals were each other's closest relatives: A. cutleri, A. macrotis, A. sperryi, A. leptopus, and A. masonii; there was

• For the remaining three species at least one sample was grouped with a different species. A. coulteri sample 1790 was as closely related to A. sperryi and A. macrotis as to the other A. coulteri samples. A. albicans and A. subulata were intermixed in

• The original divergence of the Sonoran Desert clade was into eastern (A. coutleri, A. sperryi, A. macrotis) and western (A. cutleri, A. leptopus, A. subulata, A.

• Individuals within a species that came from relatively close geographical locations seem to be more closely related on the phylogenetic tree. (Table 1, Fig 2.)

The hybrid individuals (A. albicans x subulata) are placed in two separate clades

The phylogeny from plastomes sequences is well resolved with bootstrap values

• The results demonstrate that the original step in diversification was the formation

• A. cutleri was found on a very long branch compared to other species. This has to deal with how the species experienced more evolutionary changes than the others. The reason for this is unknown and needs further study. (Fig 2.)

• An interesting relationship that was found was the relationship between A. masonii and A. subaphylla. These two species are very rare and grow in restricted geographical locations (A. masonii on a single island off the shore of Baja California Sur and A. subaphylla on the coast of Sonora and Sinaloa), however they are each other's closest relatives. (Table 1., Fig 2.)

For the species in which the individuals don't form clades it is possible that there is hybridization among species (Fig 2), because there are known hybrids between A. albicans and A. subulata. That makes their relationships difficult to determine.

These results are found useful in furthering the knowledge on the relationships

References:

Acknowledgements: