

Survey of *Diorhabda* spp. along Rio Grande

A unique opportunity to monitor
population expansion and hybridization

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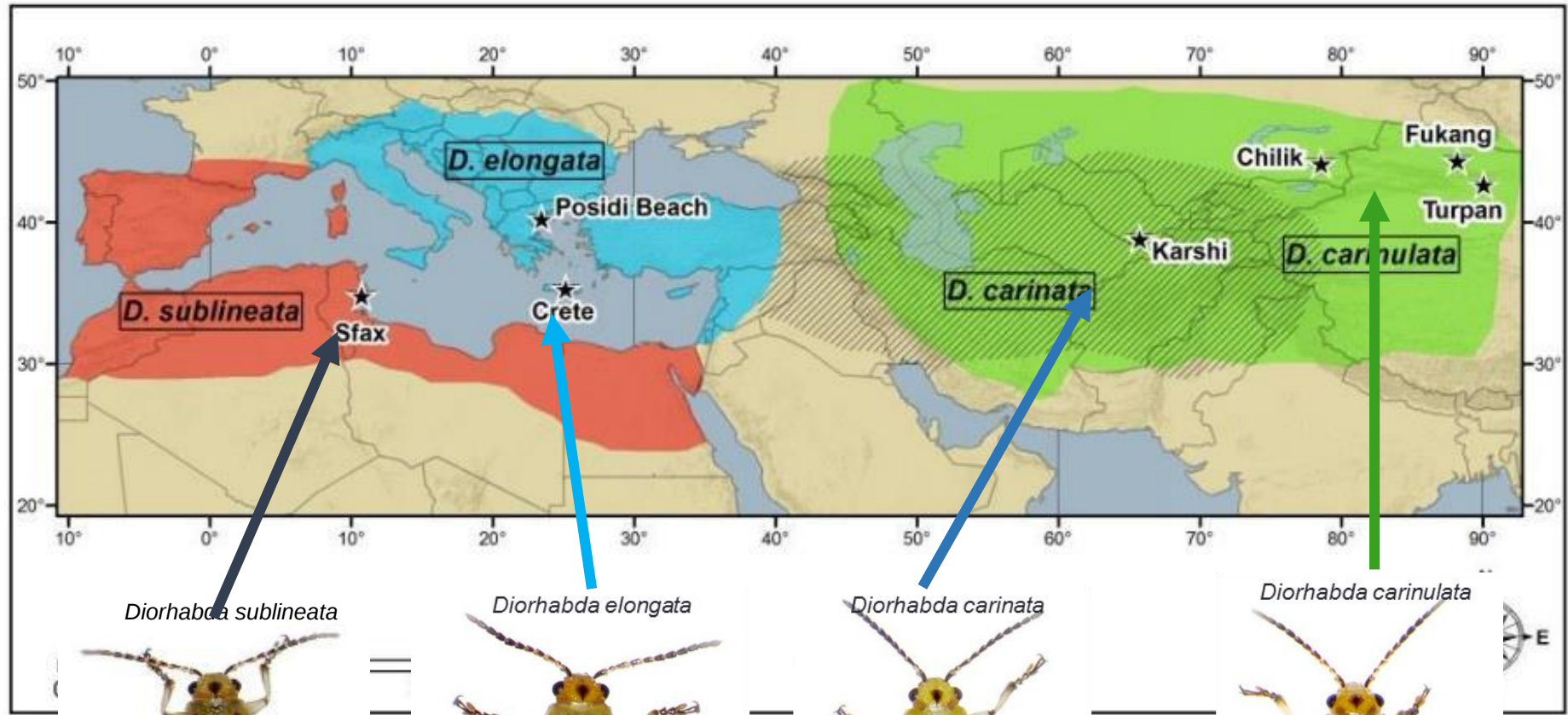
History of *Diorhabda* spp. in Western U.S.

- Original populations collected in Fukang, China and in Chilik, Kazakhstan
 - Lovell – WY
 - Lovelock and Schurz – NV
 - Pueblo – CO
 - Owens Valley – CA
 - Temple - TX
 - Delta – UT
- Upon failure of establishment of beetles in locations south of 37° N latitude other populations were collected in
 - Sfax, Tunisia
 - Crete, Greece
 - Karshi, Uzbekistan
 - Turpan, China



Diorhabda elongata

Diorhabda spp.



Tunisia



Crete

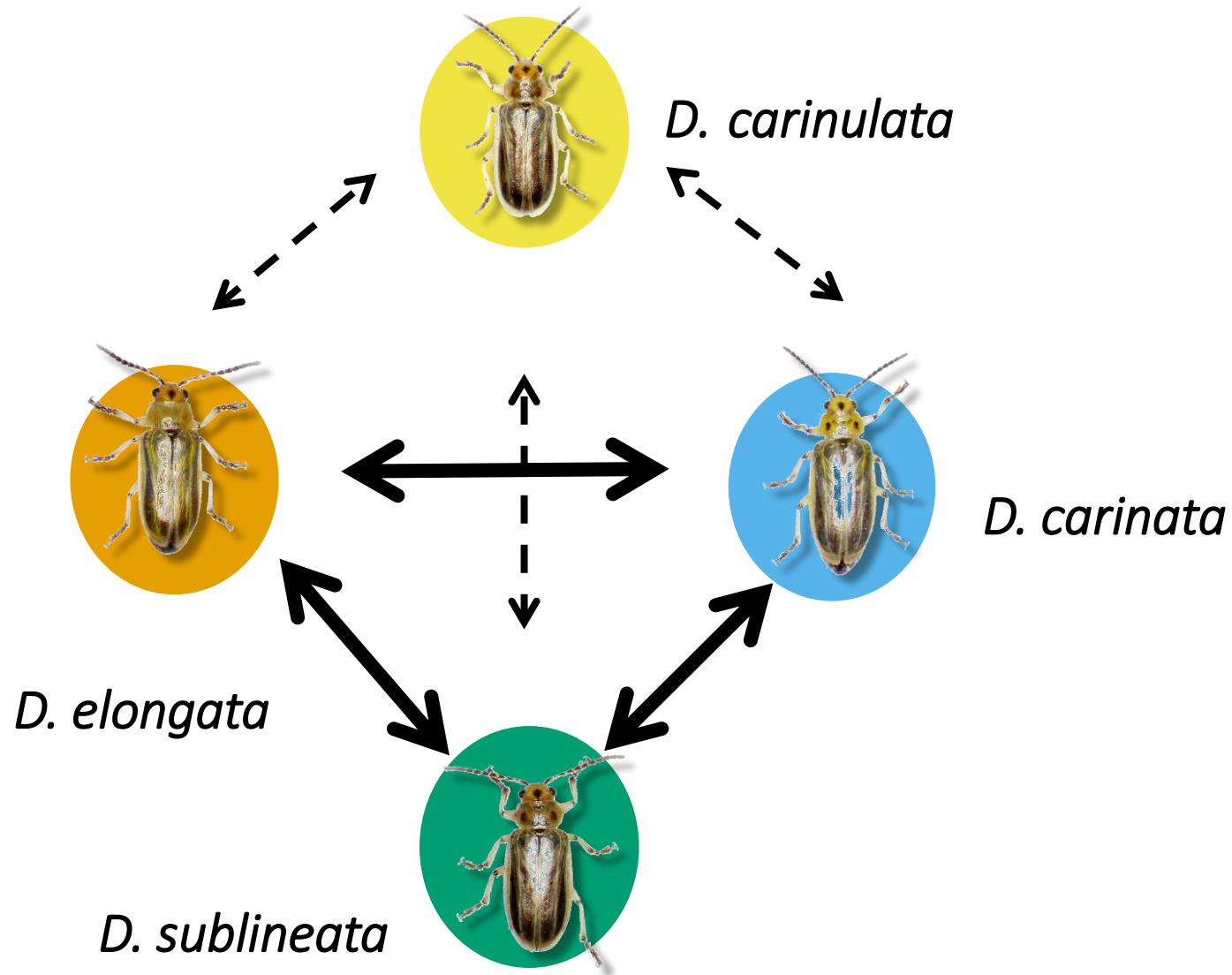


Uzbekistan

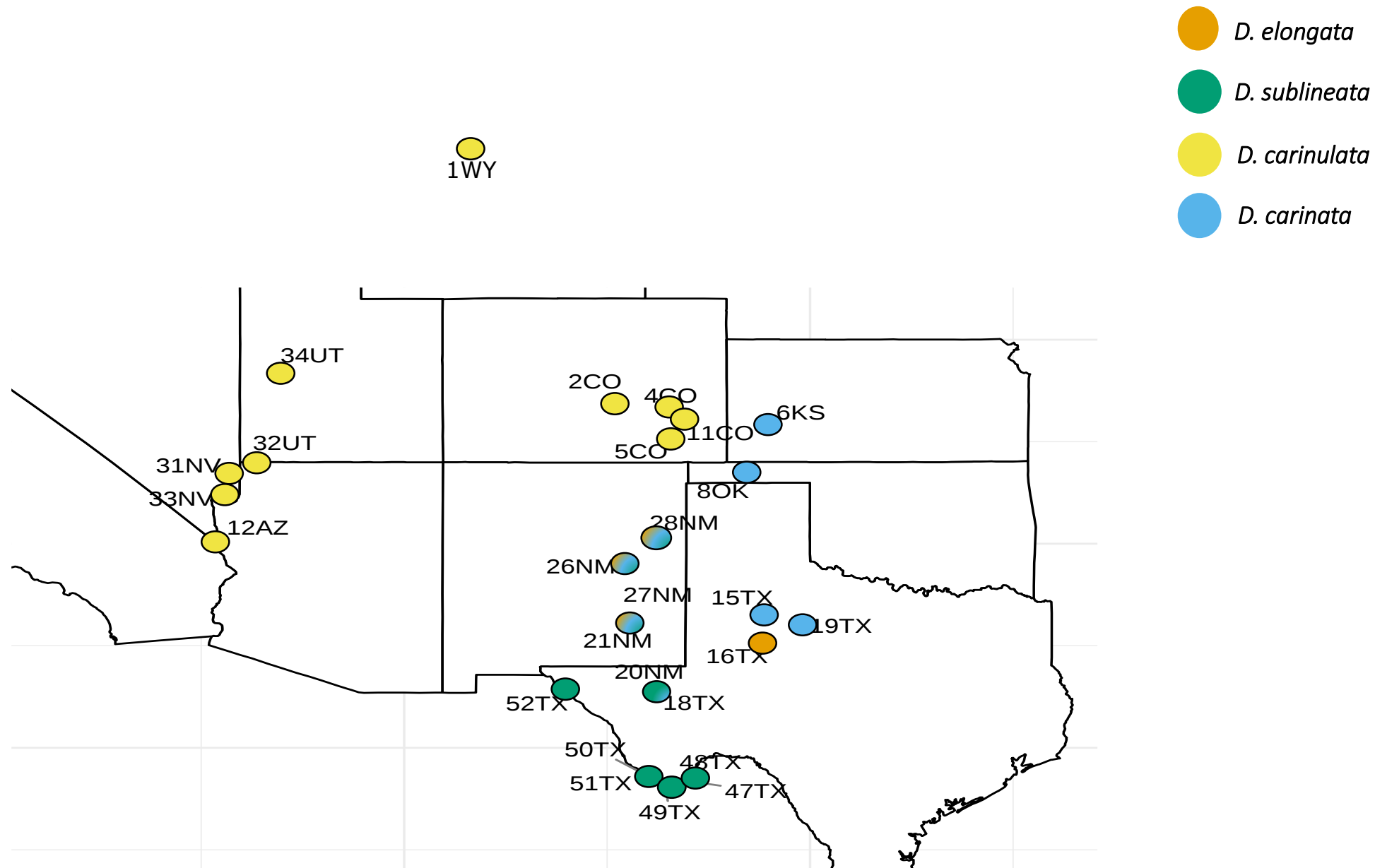


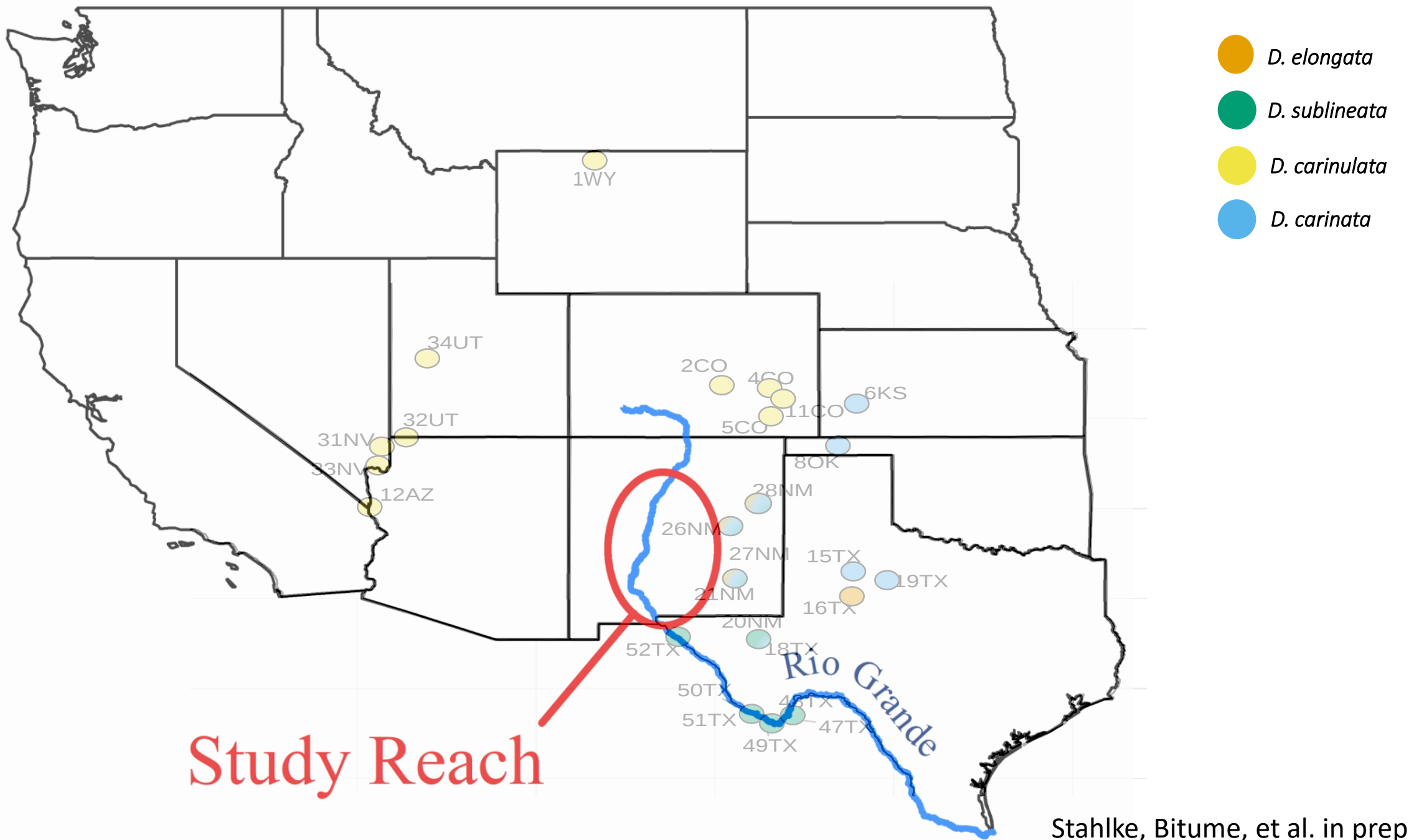
Chilik, Fukang

Hybridization and admixture in biocontrol



- **Relief from inbreeding** load due to culturing
- **Novel combinations** may allow adaptation to novel environment
 - Increase in efficacy or risk
- **Incompatibilities** may decrease fitness





Identification methods

Mitochondrial CO1 - Sanger Sequencing

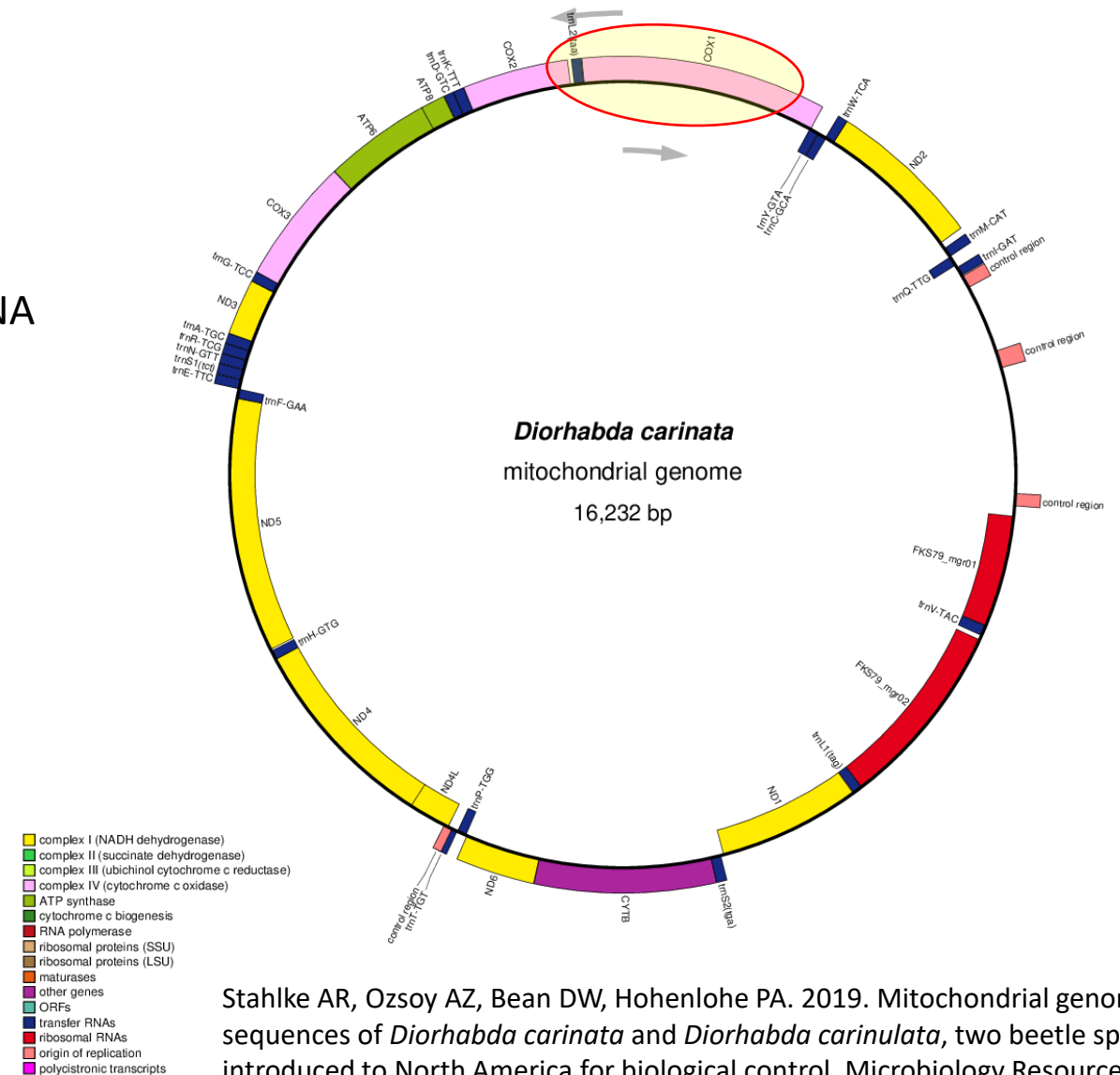
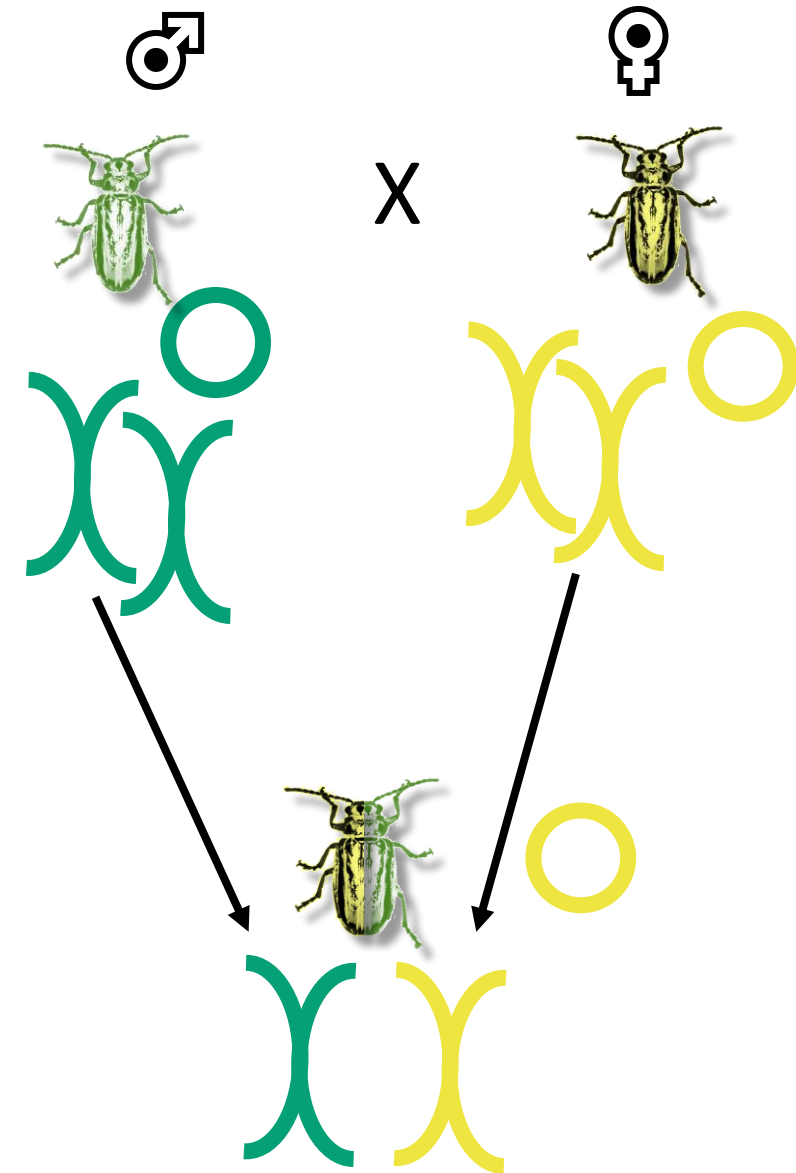
- Focuses only on one gene
- Gives information of the maternal heritage
- Does NOT reveal hybridization status
- ~\$17/ sample

RADseq - Whole genome – reduced representation

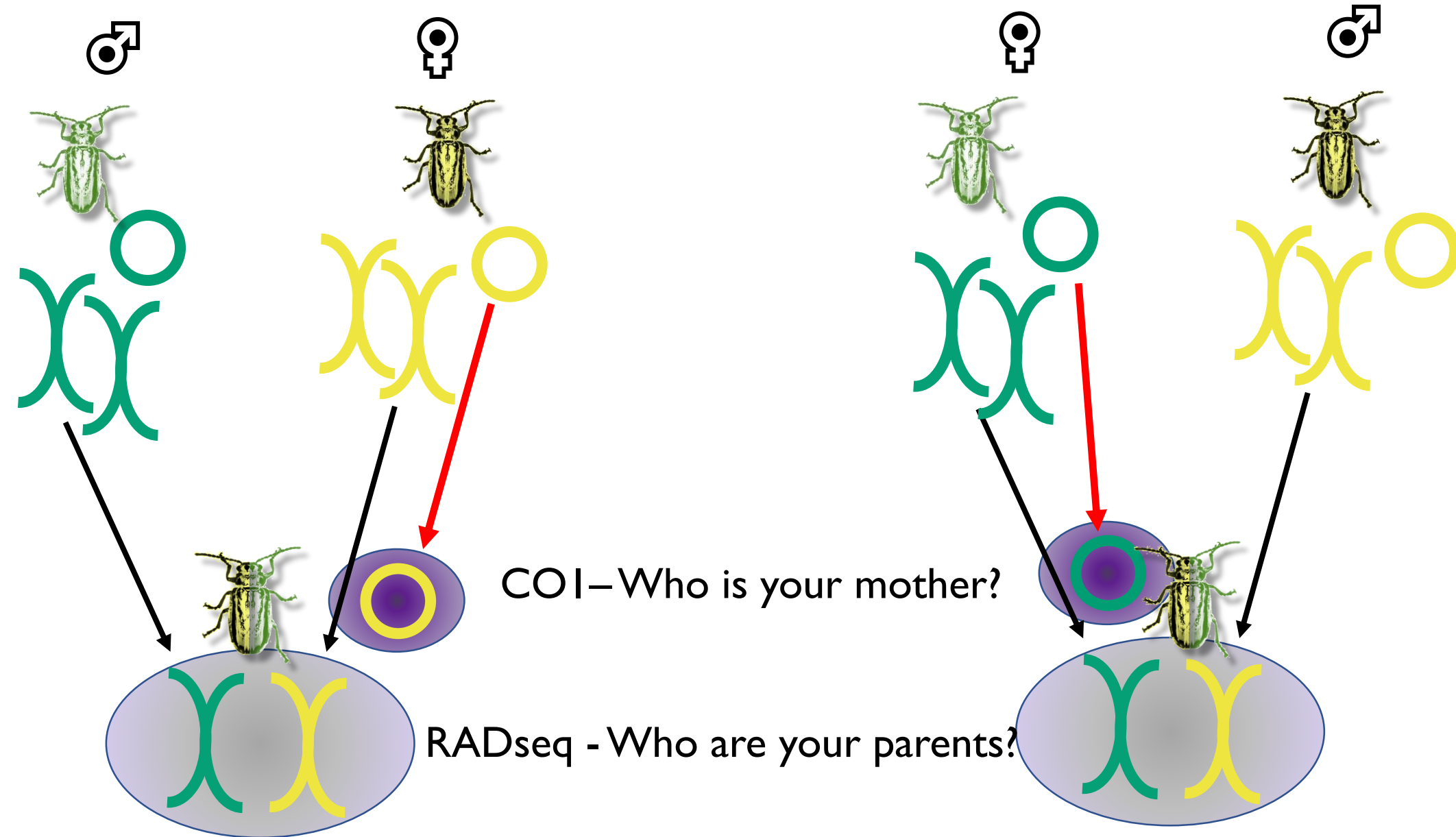
- 1,000s of loci in the whole genome
- Reveals hybridization status
- Can provide both neutral and adaptive markers
- ~\$8 → ? / sample

Nuclear DNA - from both parents

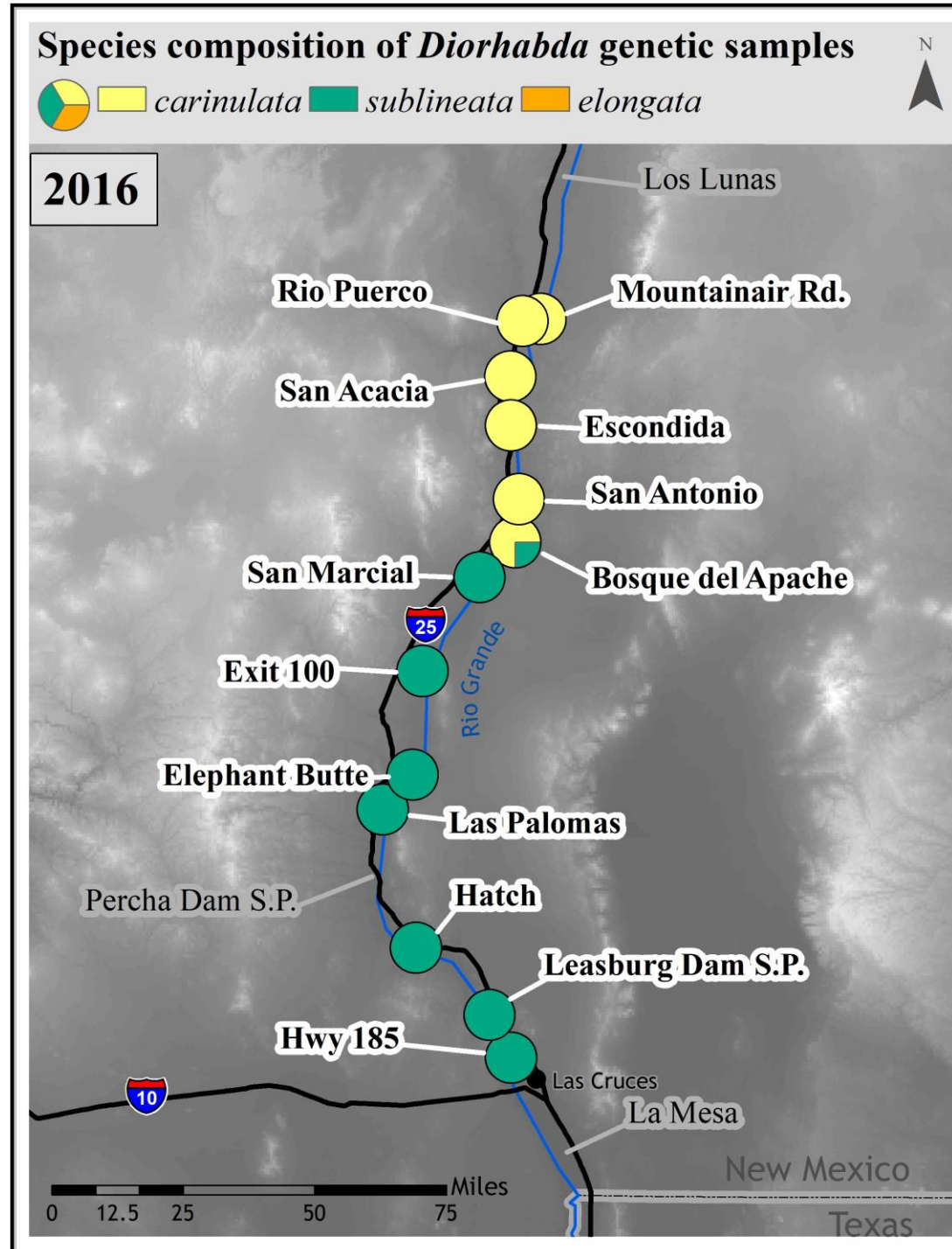
Mitochondrial DNA - from the mother



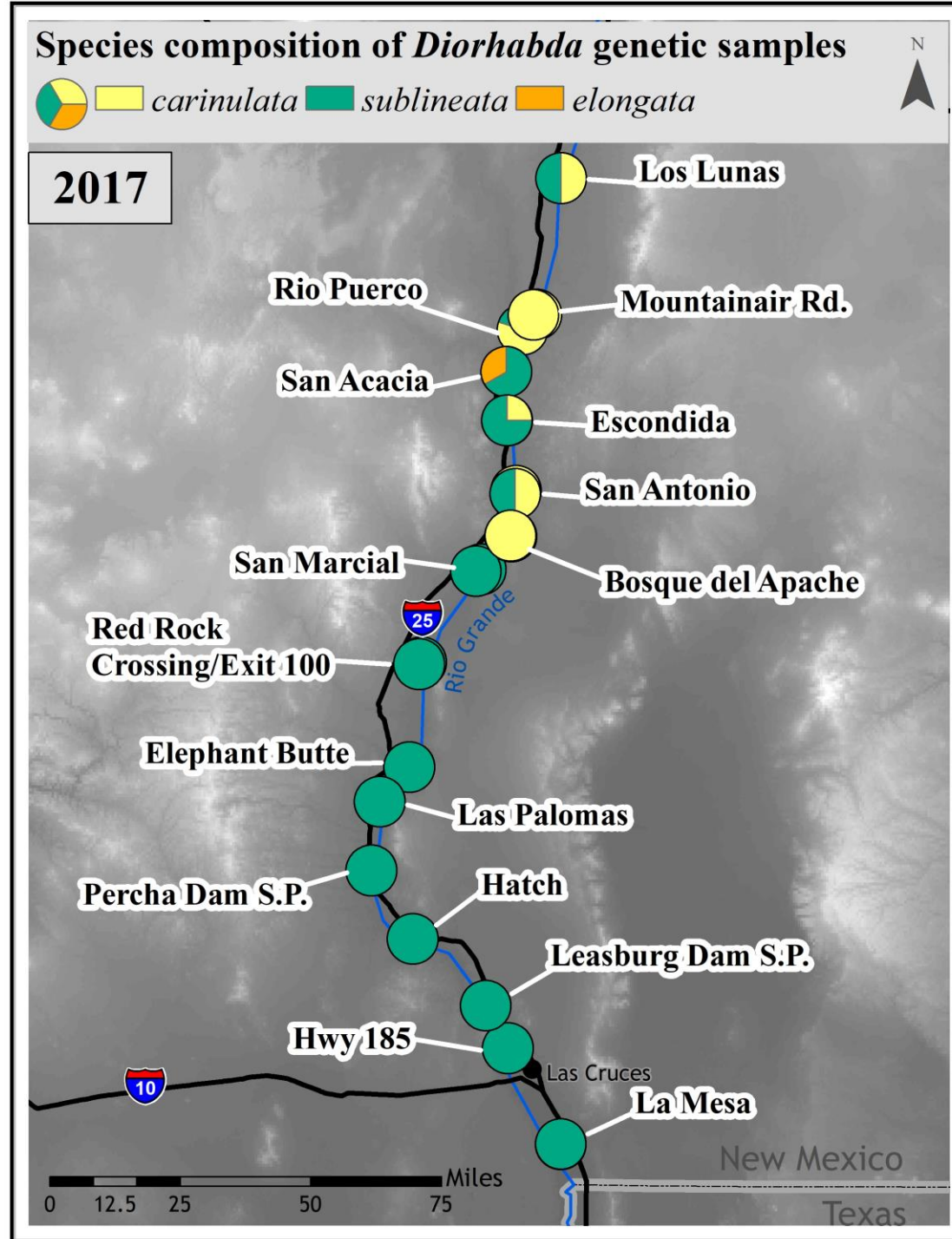
Stahlke AR, Ozsoy AZ, Bean DW, Hohenlohe PA. 2019. Mitochondrial genome sequences of *Diorhabda carinata* and *Diorhabda carinulata*, two beetle species introduced to North America for biological control. Microbiology Resource Announcements 8:e00690-19.



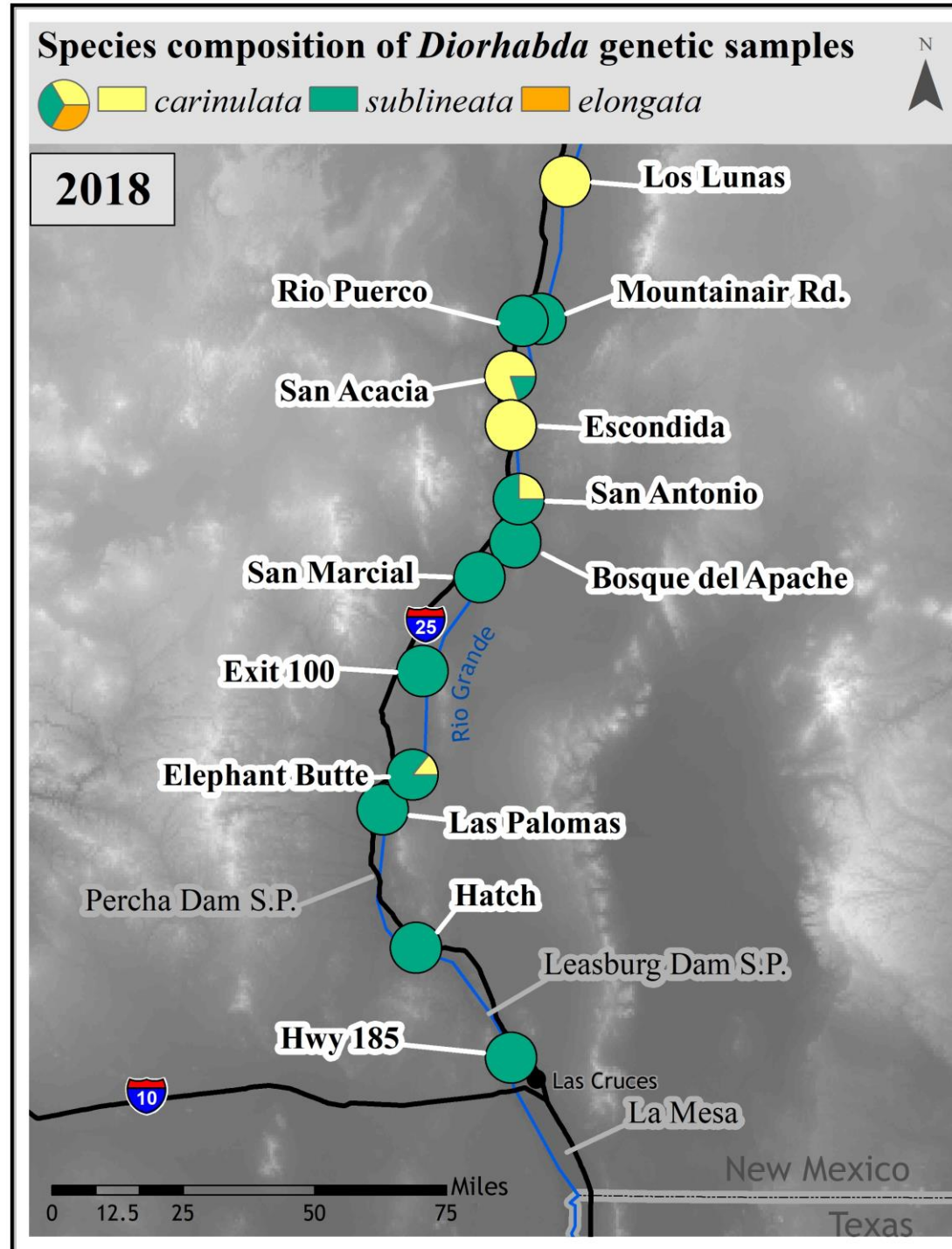
CO1



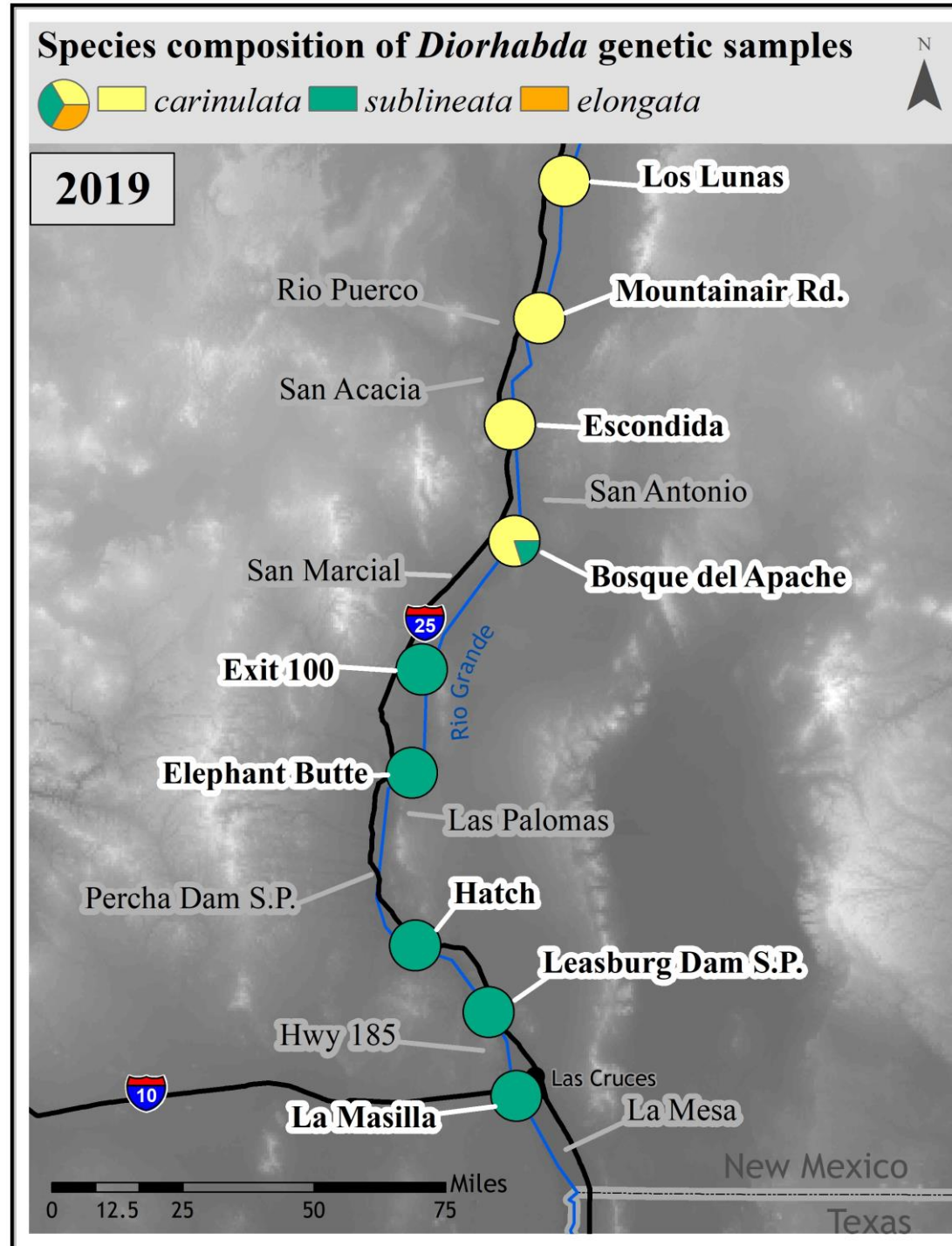
CO1



CO1



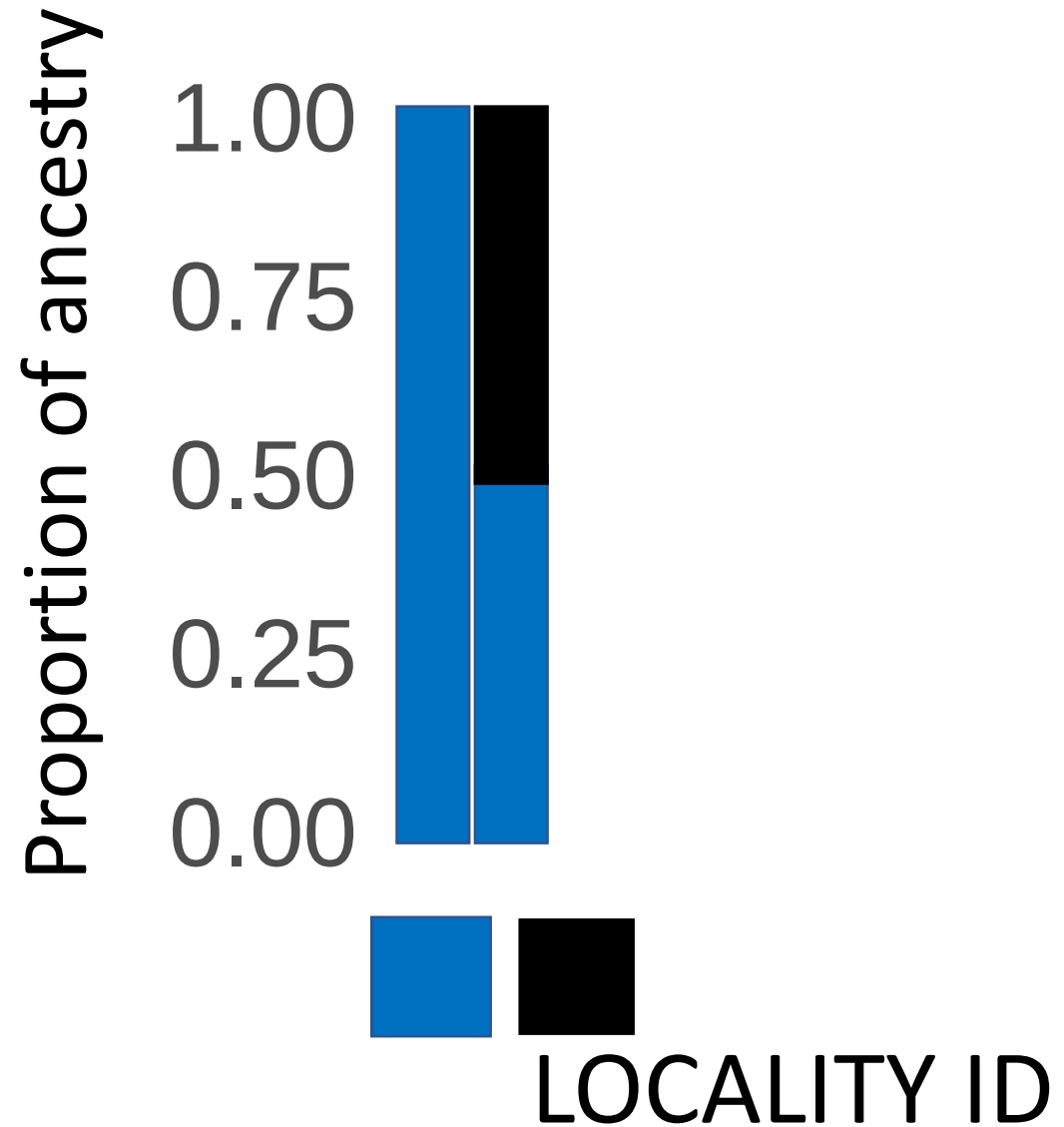
CO1



Who is where?

STRUCTURE, a Bayesian clustering algorithm that calculates the posterior probability of genetic data fitting K clusters given a model of allele frequency distributions

Probability($X | K$)



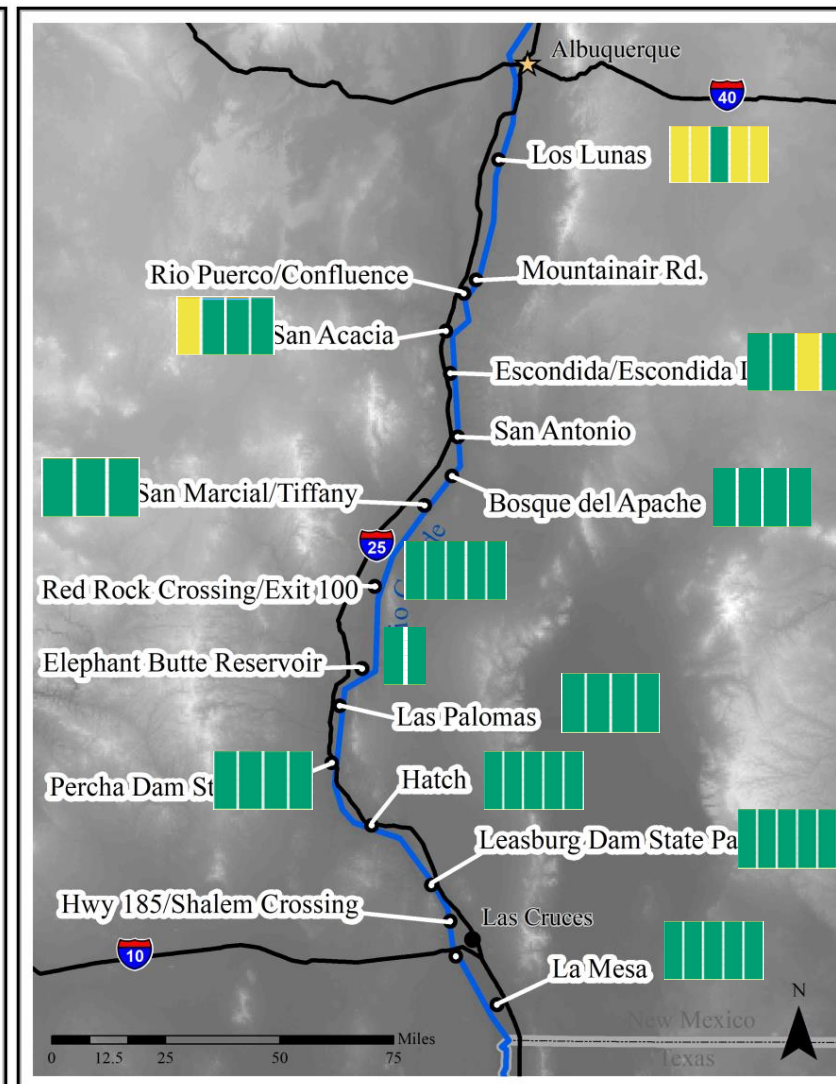
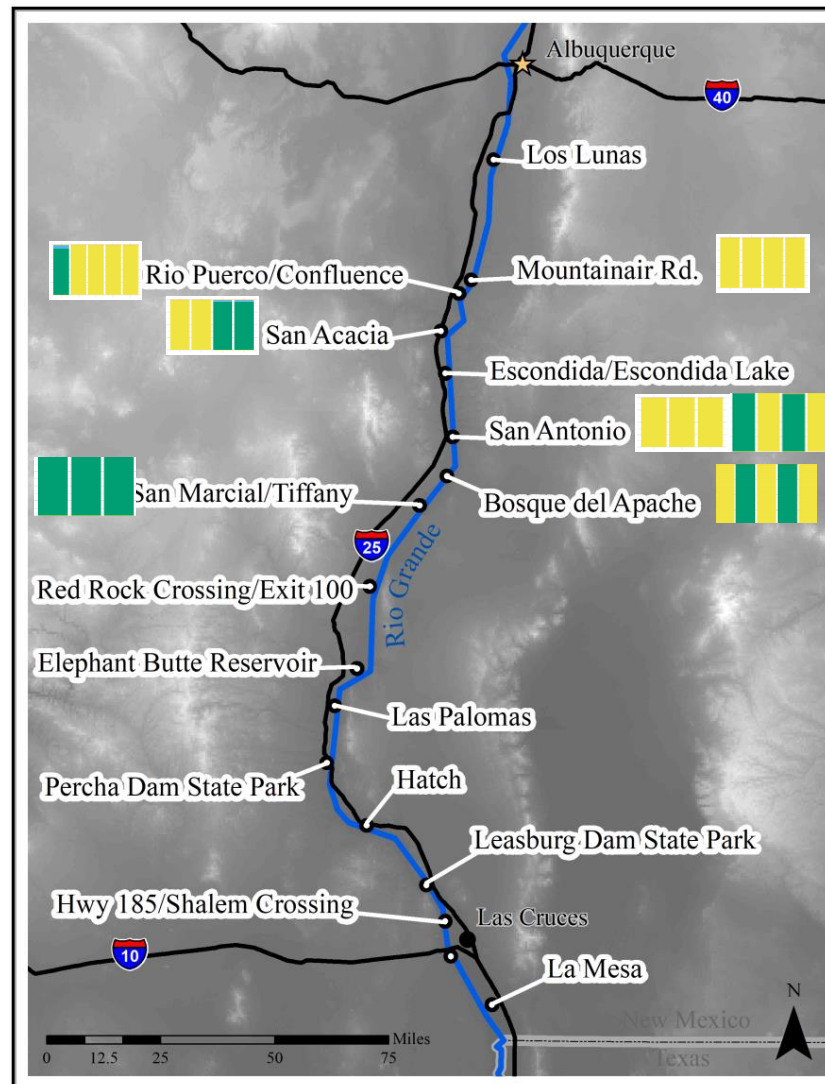
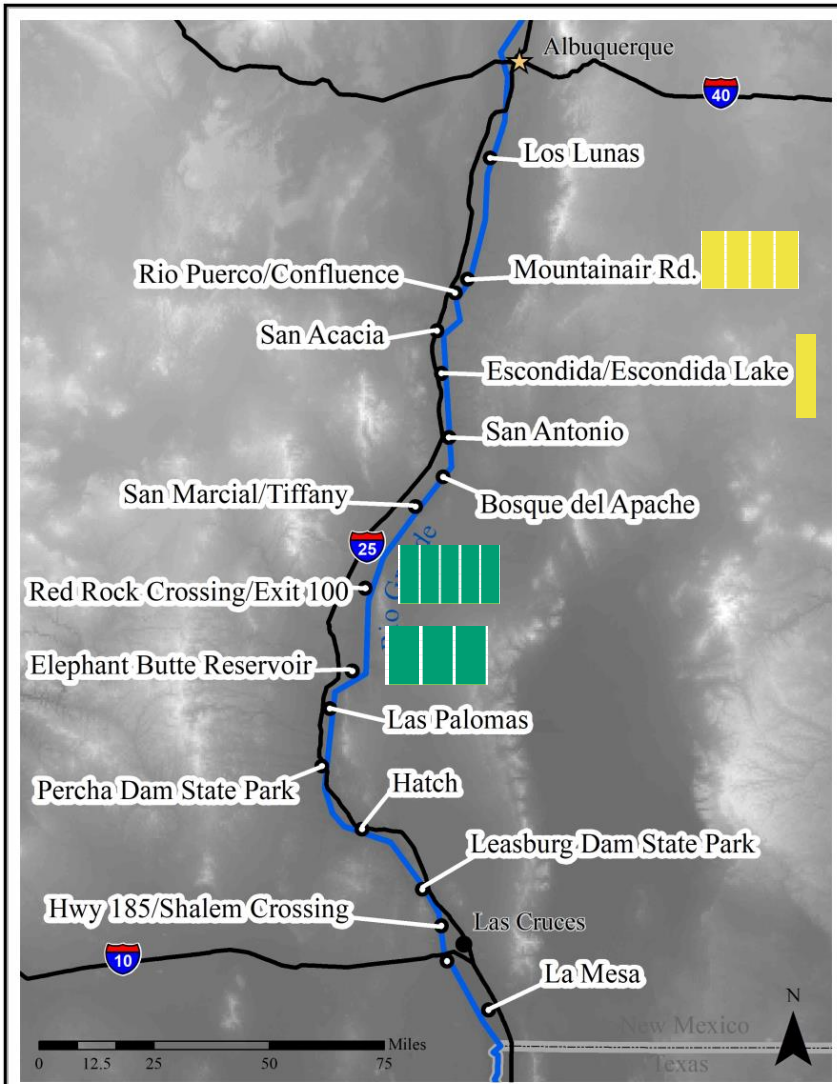
2017

May

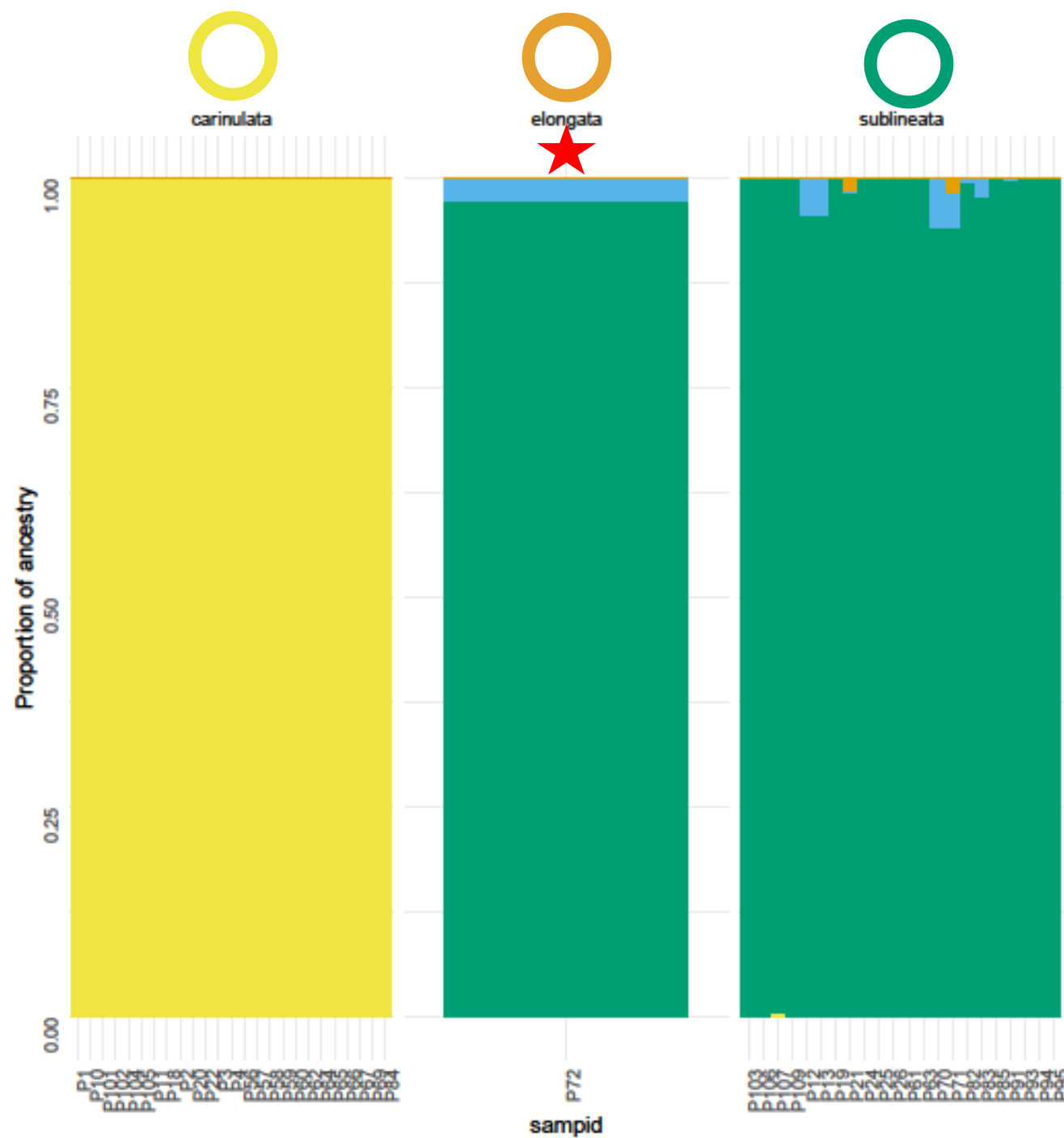
July

September

-  *D. elongata*
-  *D. sublineata*
-  *D. carinulata*
-  *D. carinata*



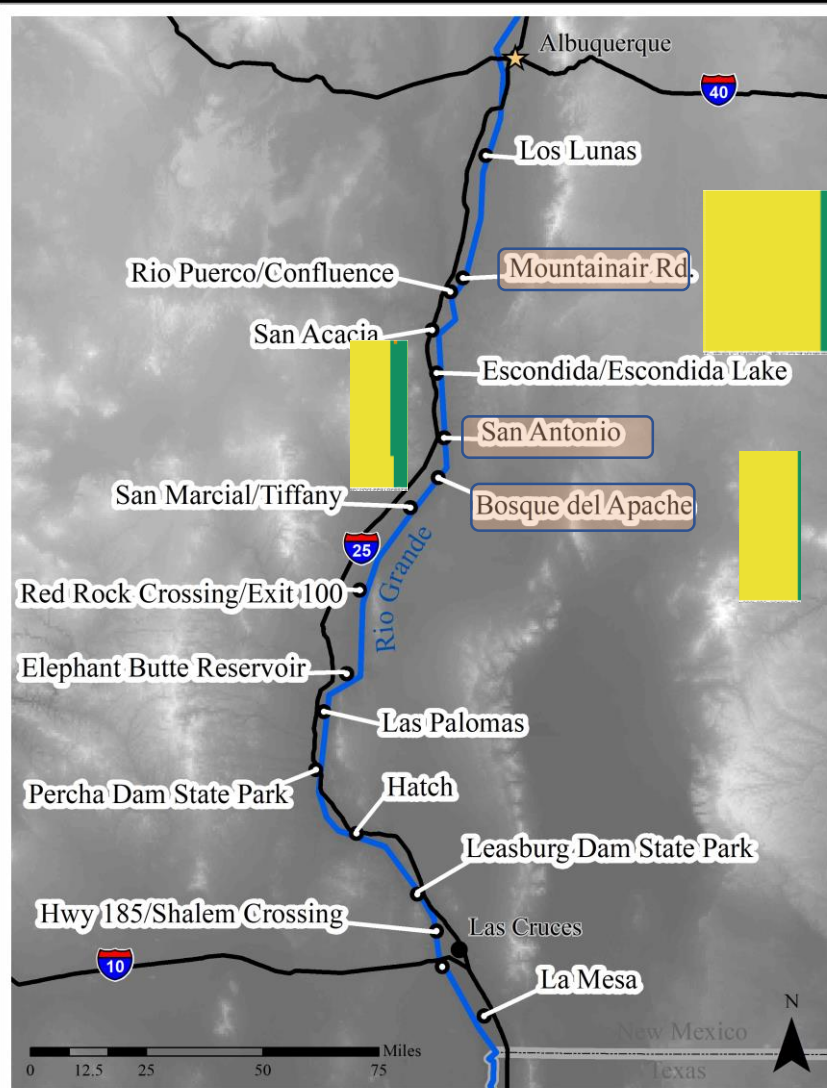
2017 COI ~ RADseq



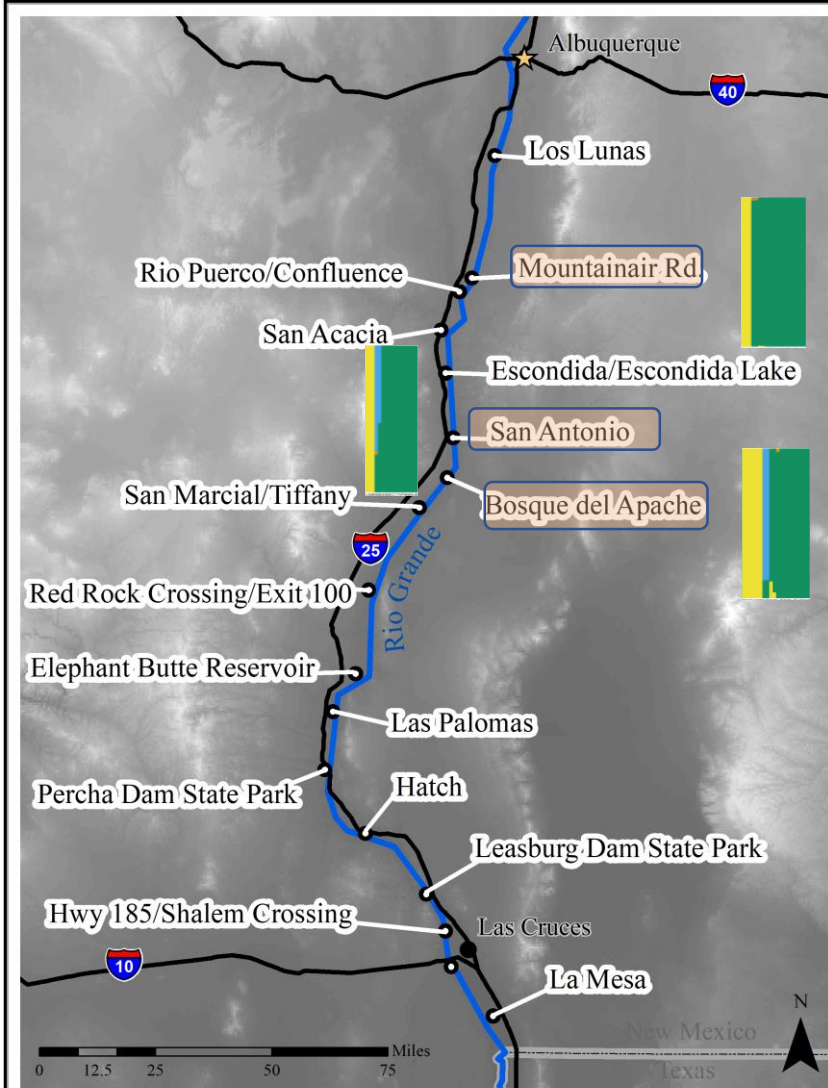
2018

-  *D. elongata*
-  *D. sublineata*
-  *D. carinulata*
-  *D. carinata*

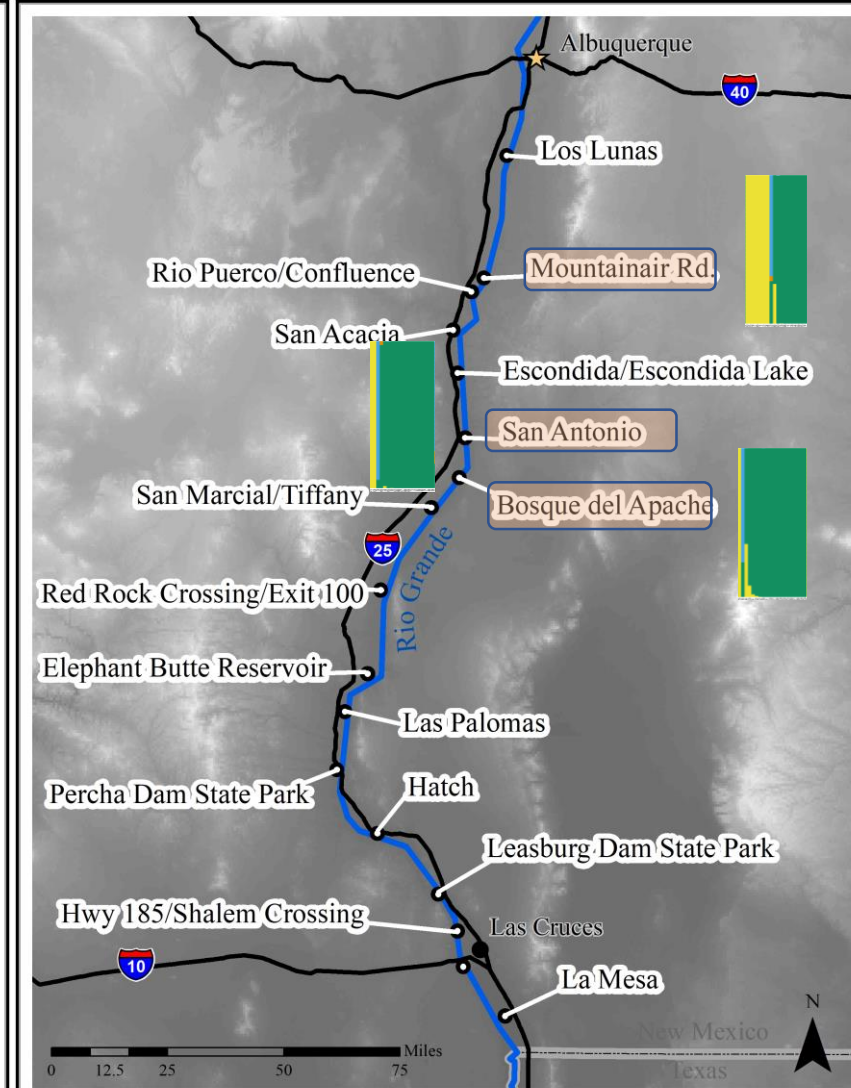
May



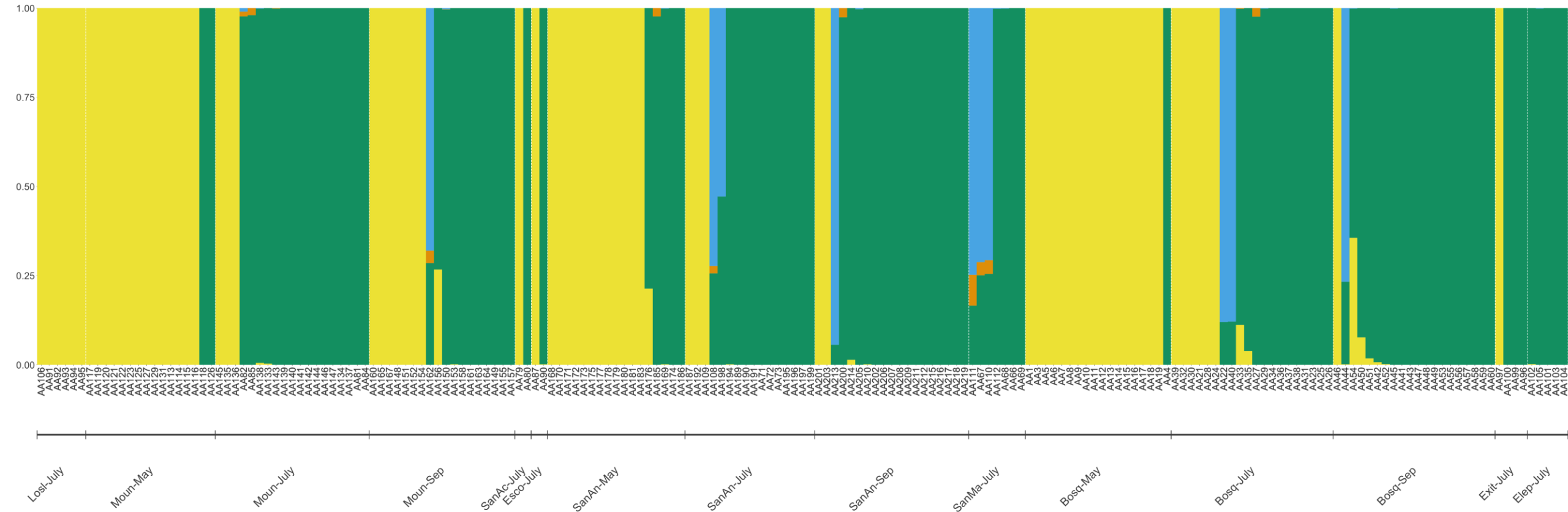
July



September



Over time-2018

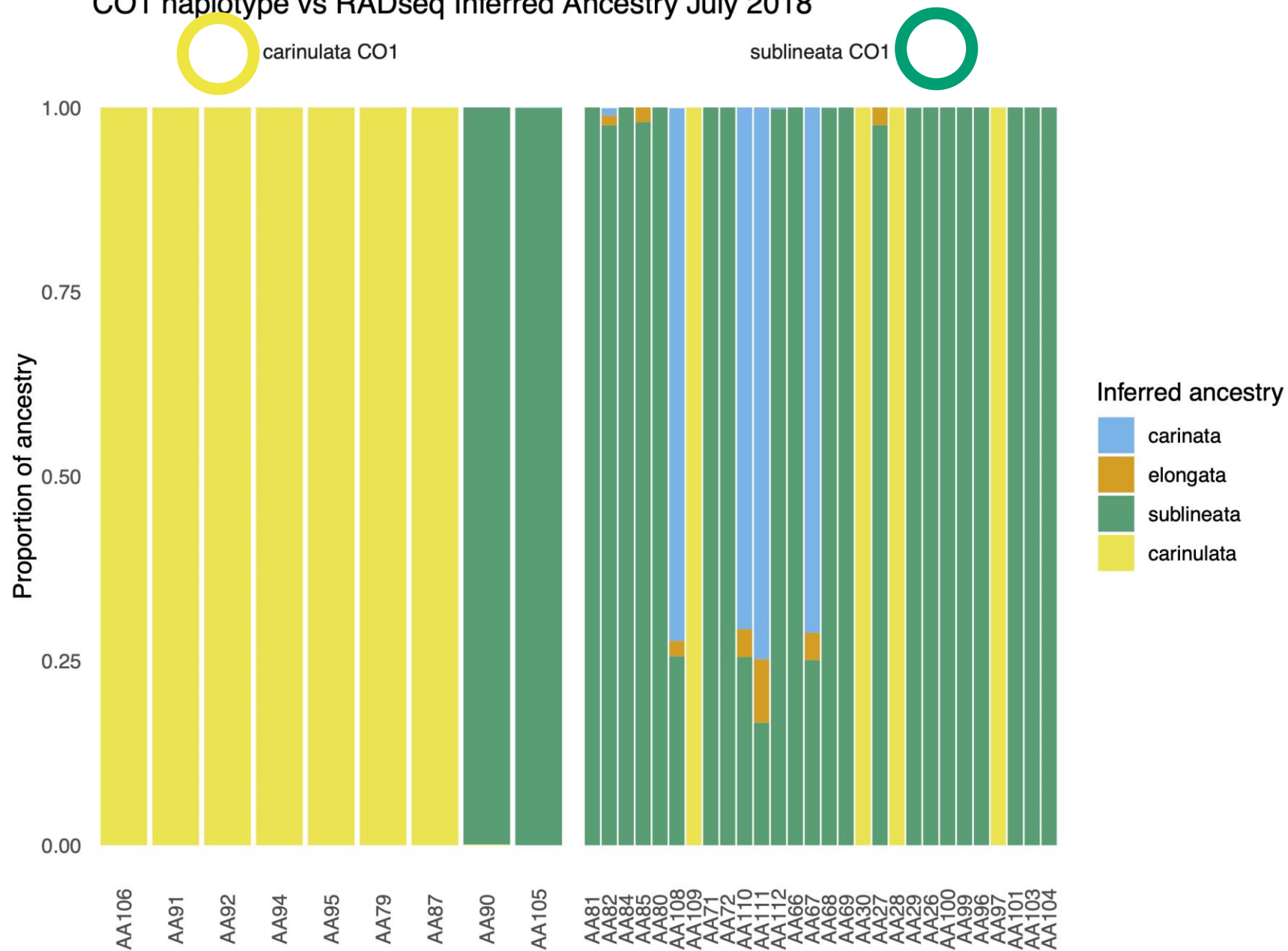


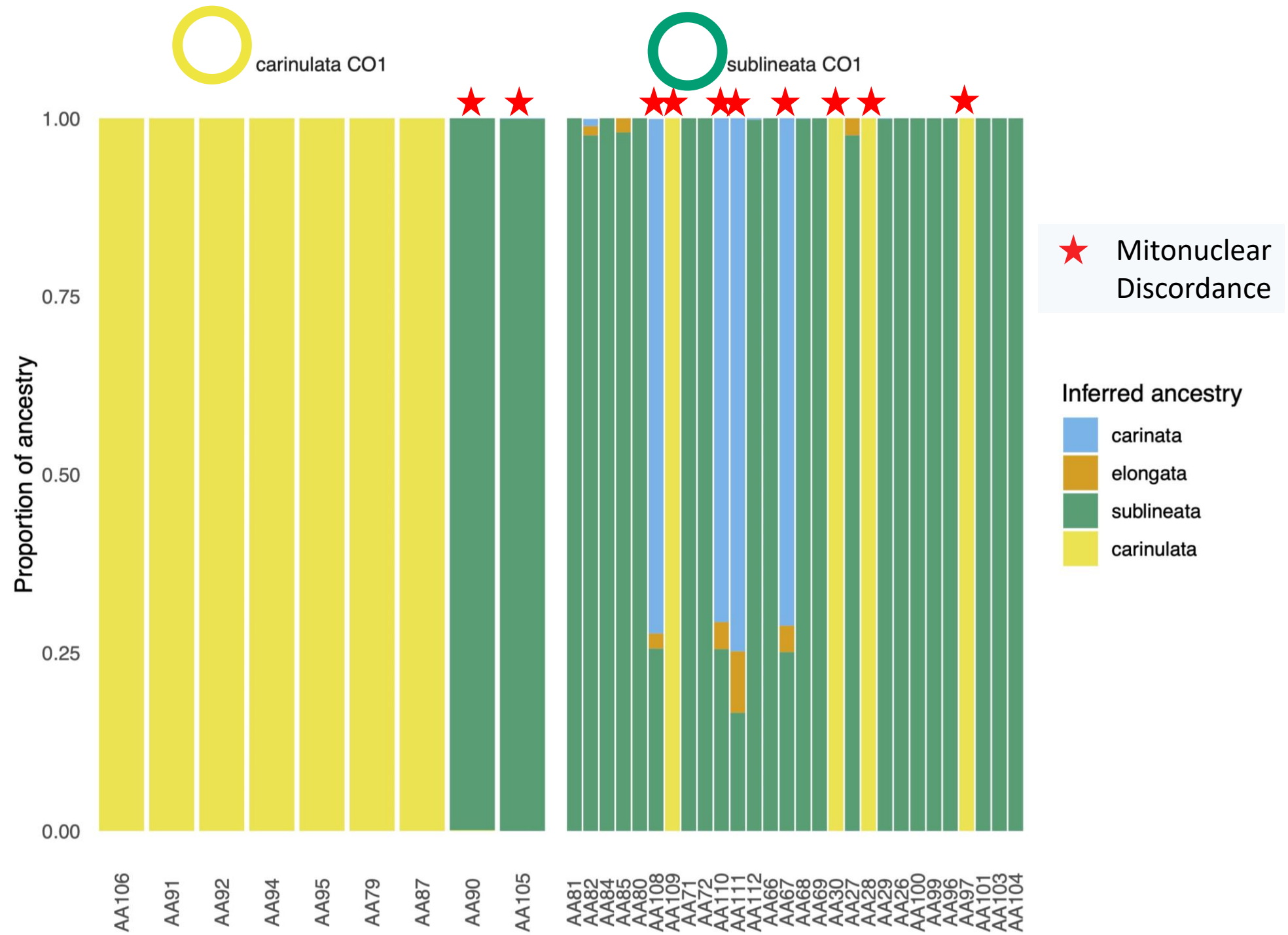
Inferred ancestry



2018 COI $\neq$ RADseq

COI haplotype vs RADseq Inferred Ancestry July 2018





Take away

- *D. carinulata* seem to have stalled around Bosque del Apache
- *D. sublineata* have expanded their range to the north
- *D. carinulata* present early in the season then *D. sublineata* take over
- They are hybridizing!
 - Evidence of *D. sublineata* x *D. carinata* (x *elongata*)
 - But also *D. sublineata* x *D. carinulata*
- Discordance

Acknowledgements

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