Severe cottonwood mortality due to drought at Bill Williams River National Wildlife Refuge, AZ – © Photos by Tom Whitham, March 28, 2017

Conserving Riparian Habitat and Biodiversity in a Changing Environment: A Genetics Approach

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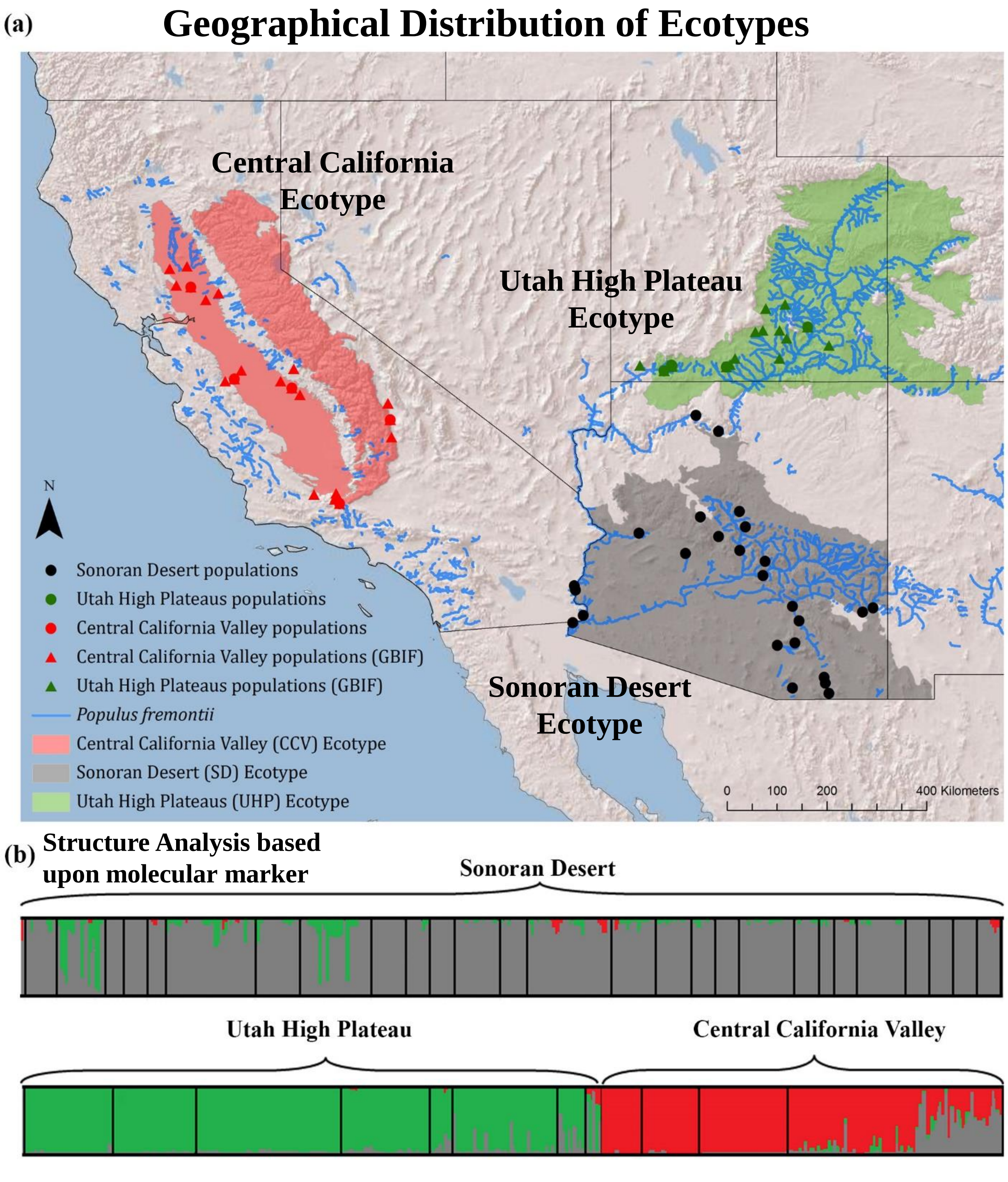
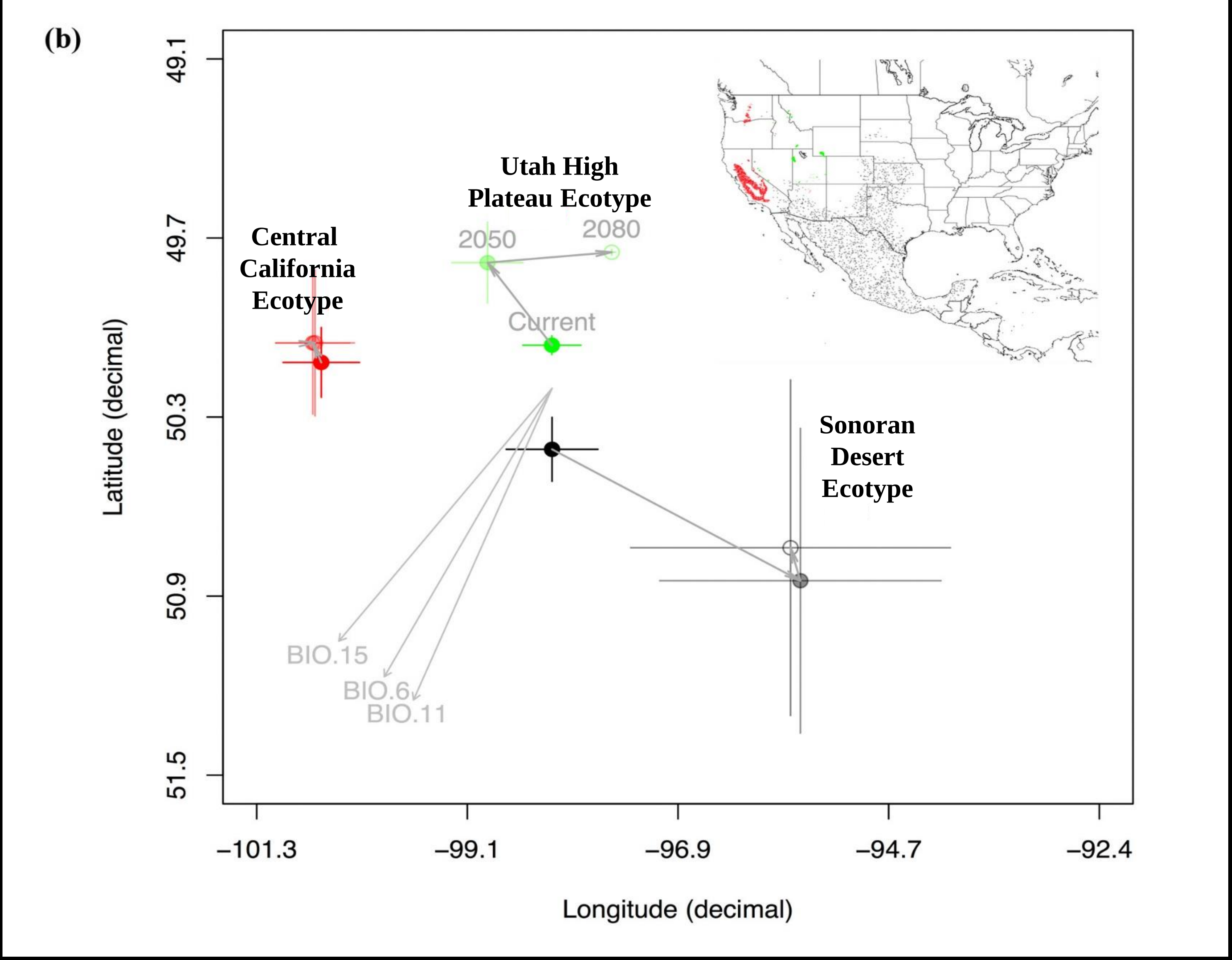
Record droughts and lack of stream flows have resulted in high mortality and rivers at risk in the American Southwest. Since local stock is not adapted to this altered environment, what populations and genotypes should be planted?

SEGA site at The Arboretum at Flagstaff – A network of sites to develop solutions to global change challenges



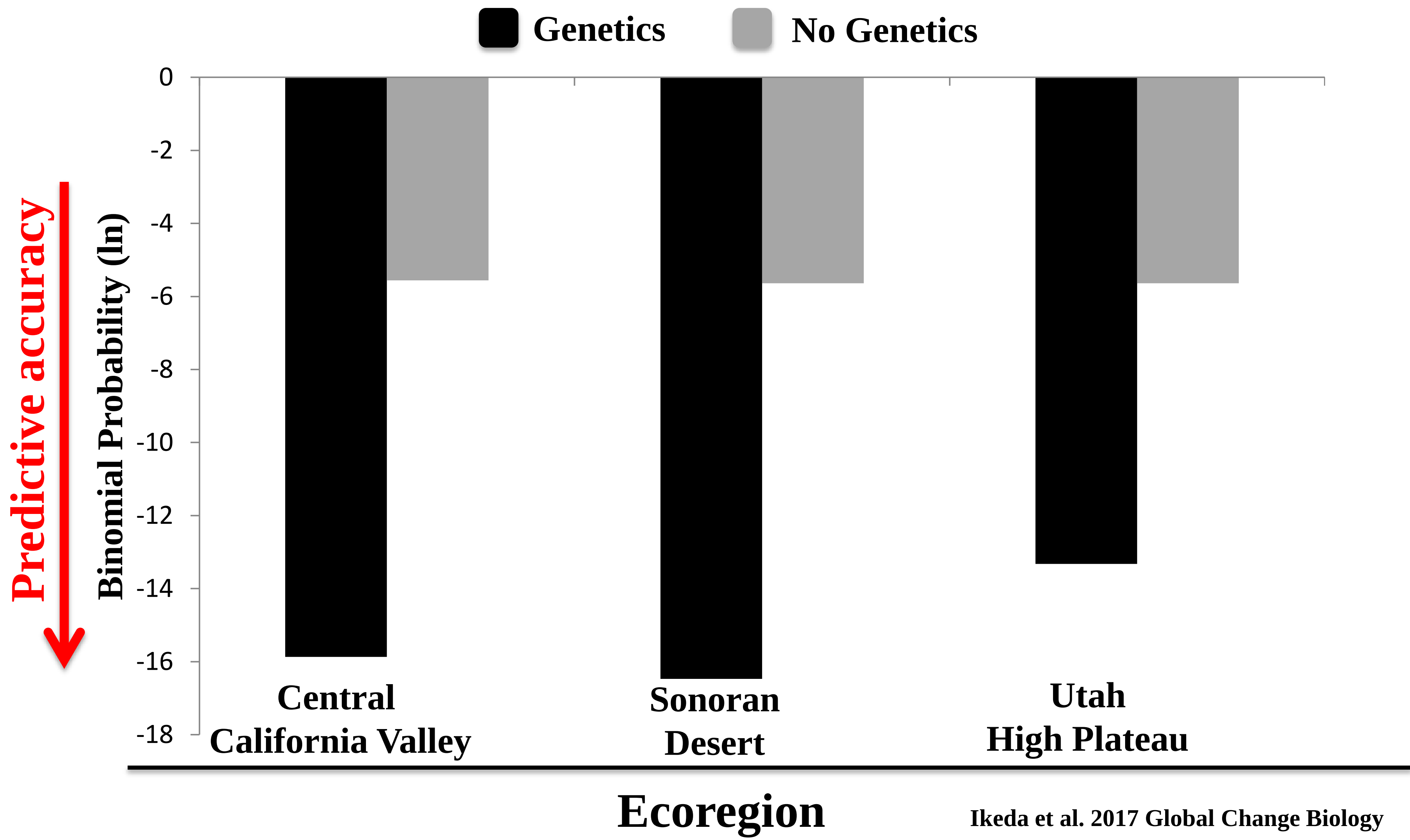
Locally adapted ecotypes have evolved in response to environmental differences across the range of *P. fremontii*.

Ikeda et al. 2017 Global Change Biology



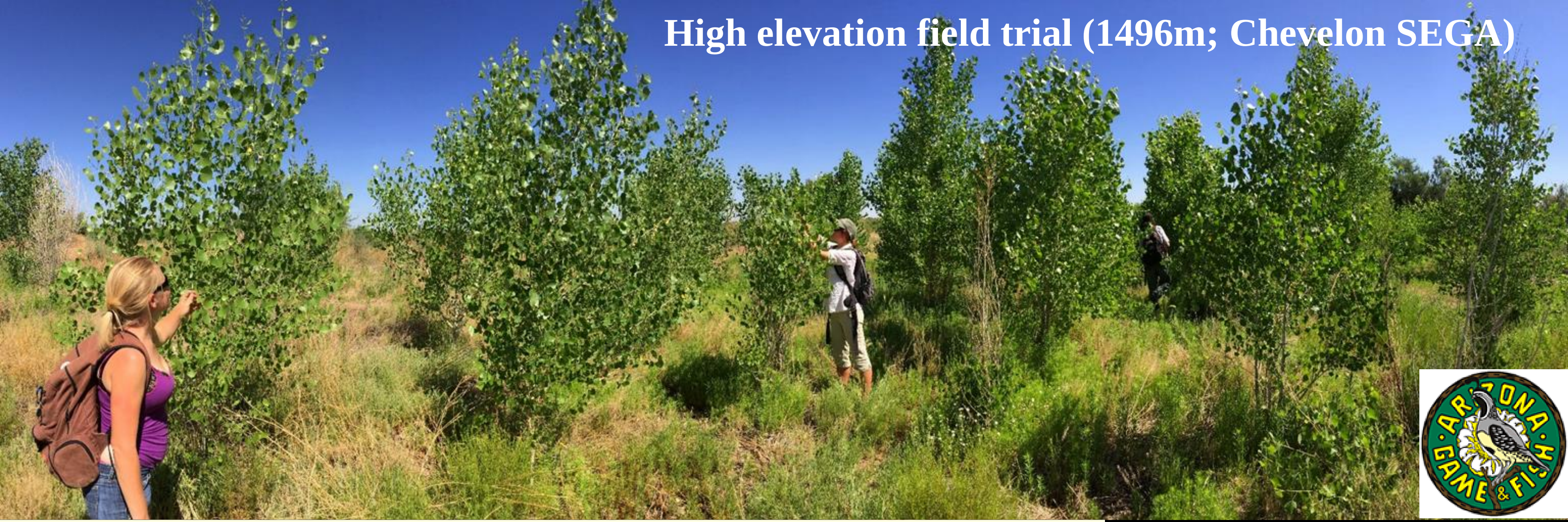
Using genetically informed ecological niche modeling (gENM) with Maxent, we found that the regions occupied by different ecotypes will shift with projected climate change and will diverge spatially even more than their current distributions (Ikeda et al. 2017 Global Change Biology).

Genetics-based models are up to 12x better at predicting ecoregion test points



Ikeda et al. 2017 Global Change Biology

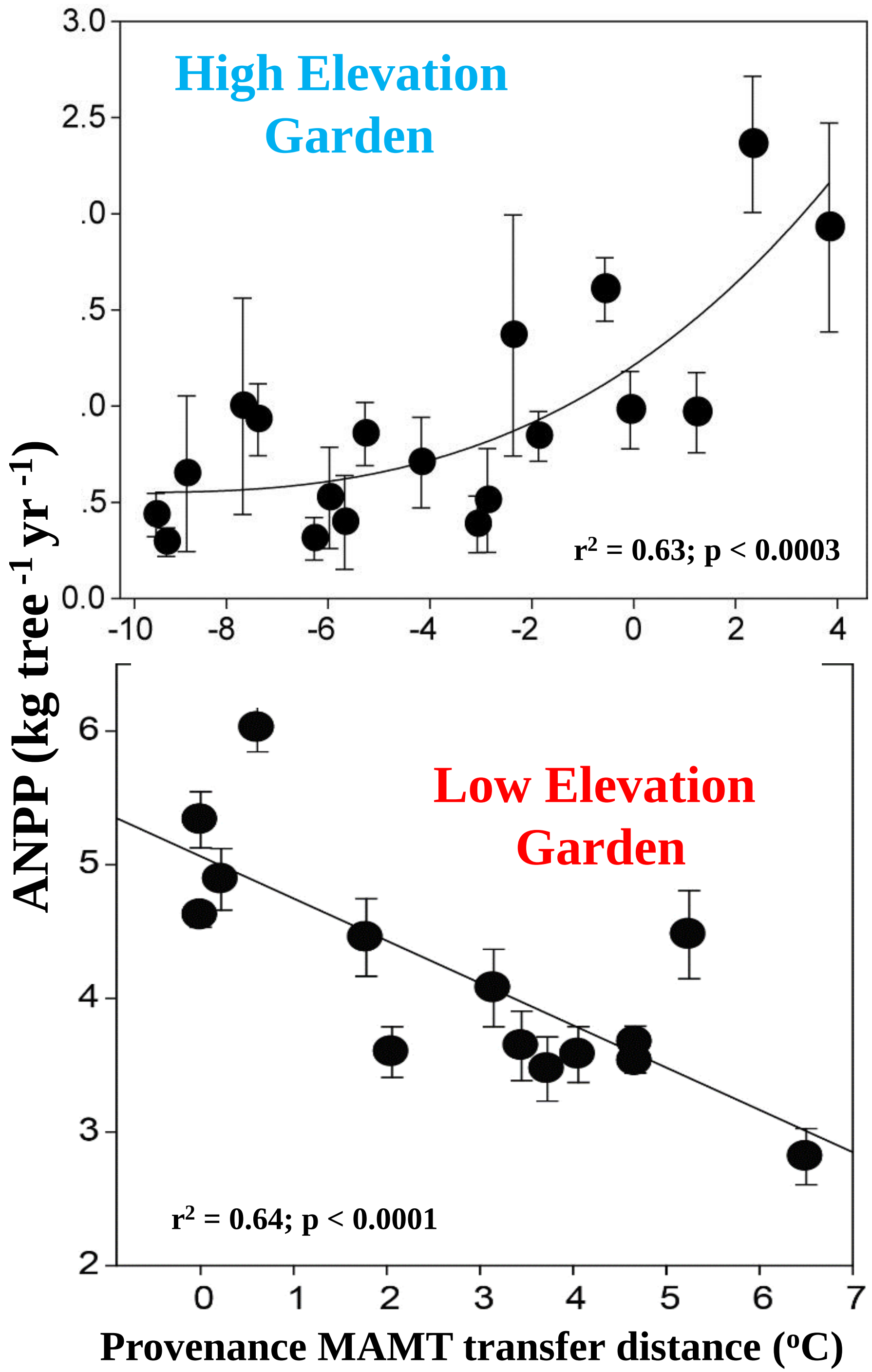
High elevation field trial (1496m; Chevelon SEGA)



Low elevation field trial (87m; Cibola National Wildlife Refuge)

18 months after planting

Reciprocal Fremont cottonwood gardens
© Photos by Tom Whitham



Reciprocal field trials at low and high elevations of Fremont cottonwood.

1. Plants that are locally adapted today will become locally maladapted for tomorrow's predicted climate.

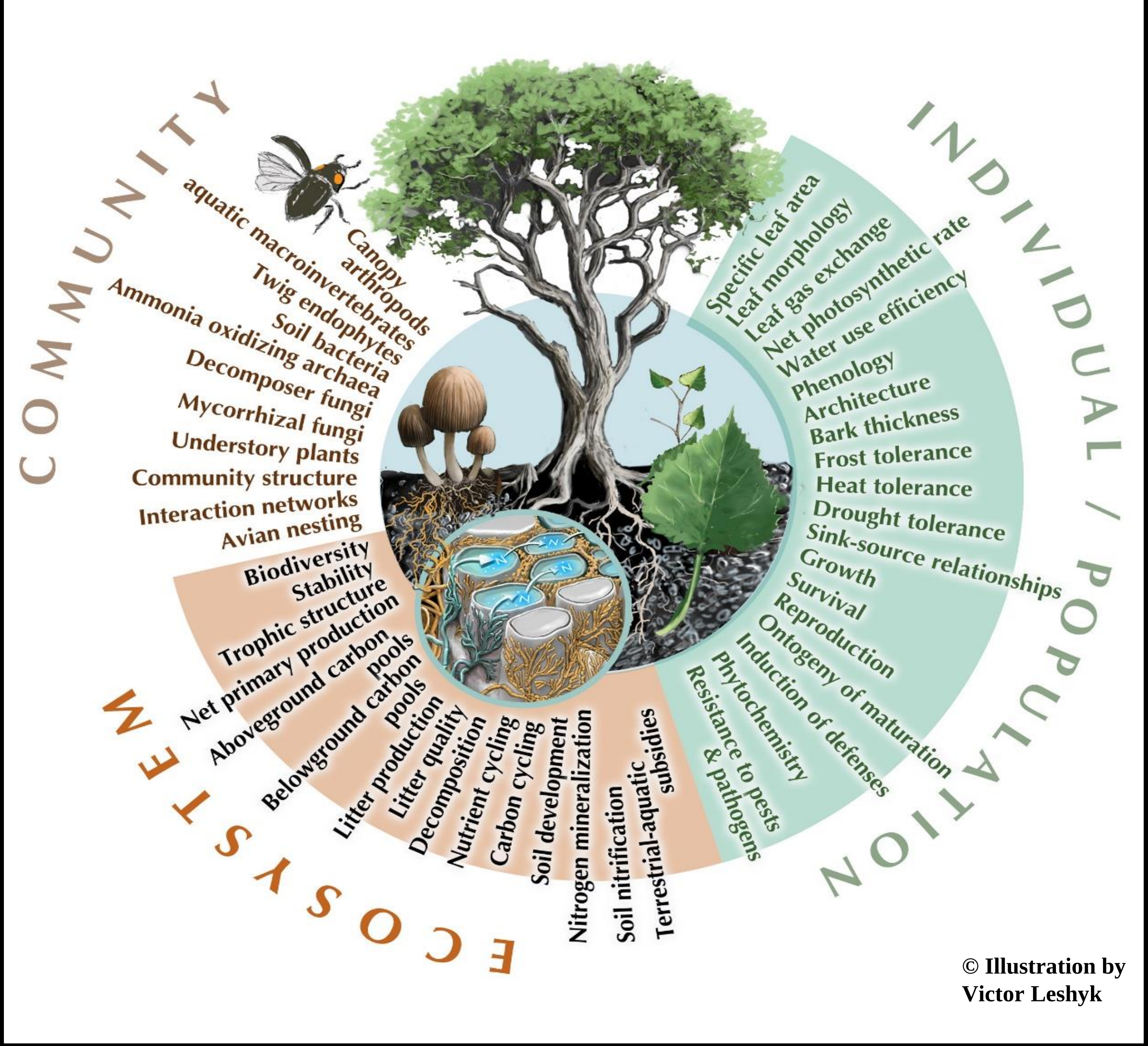
2. Planting with local stock today won't be tomorrow's best practice.

3. A lot restoration money is at stake, so we better get it right (e.g., $626 million riparian BOR restoration project on the Lower Colorado River).

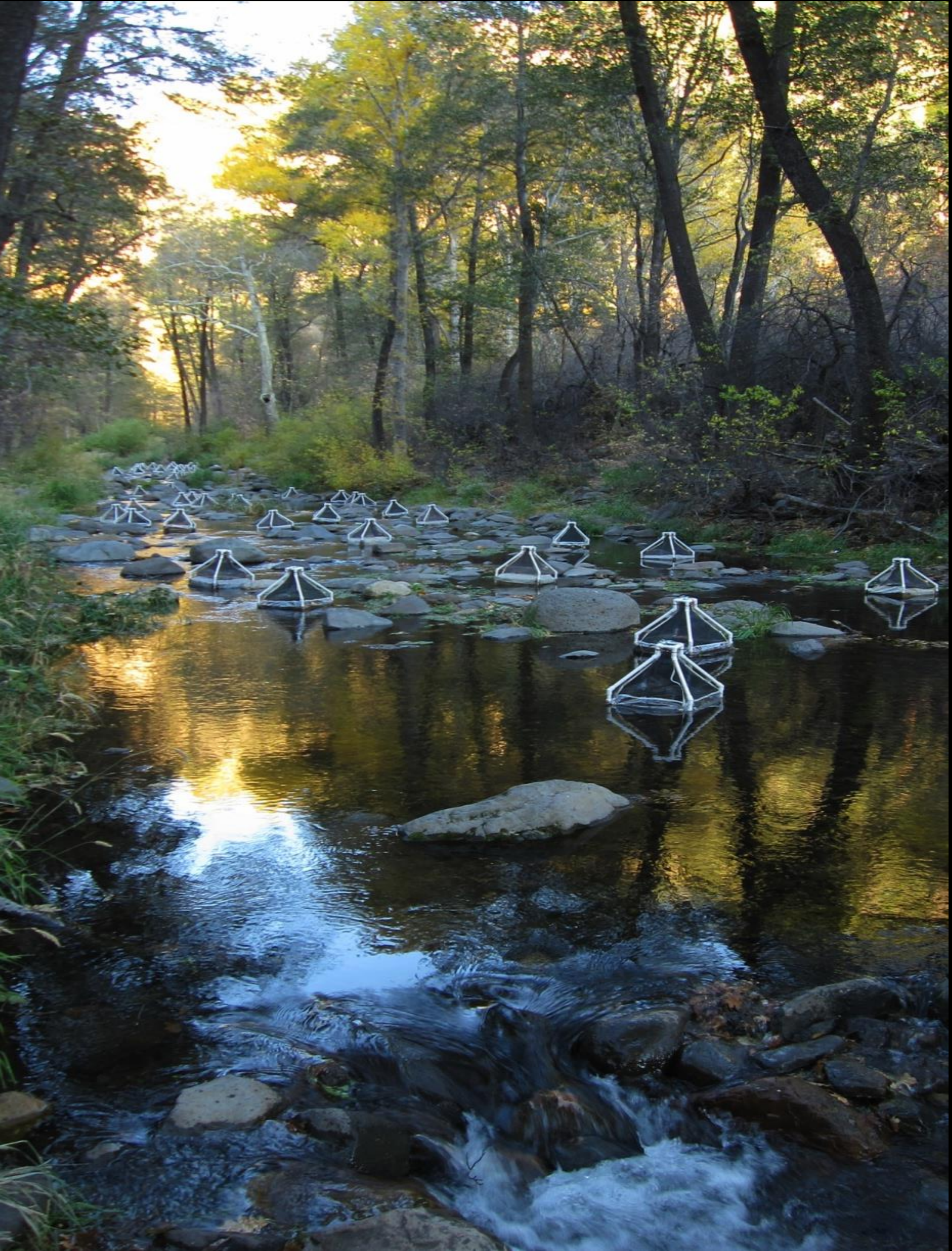
Grady et al. 2011 Global Change Biology, 2013 Functional Ecology, 2015 Restoration Ecology

Genotypes from desert populations root deeper and faster than genotypes from high elevation populations.

Jackie Parker's rooting expt., unpub. data



Documented functional traits of individuals and populations result in extended heritable community and ecosystem phenotypes.

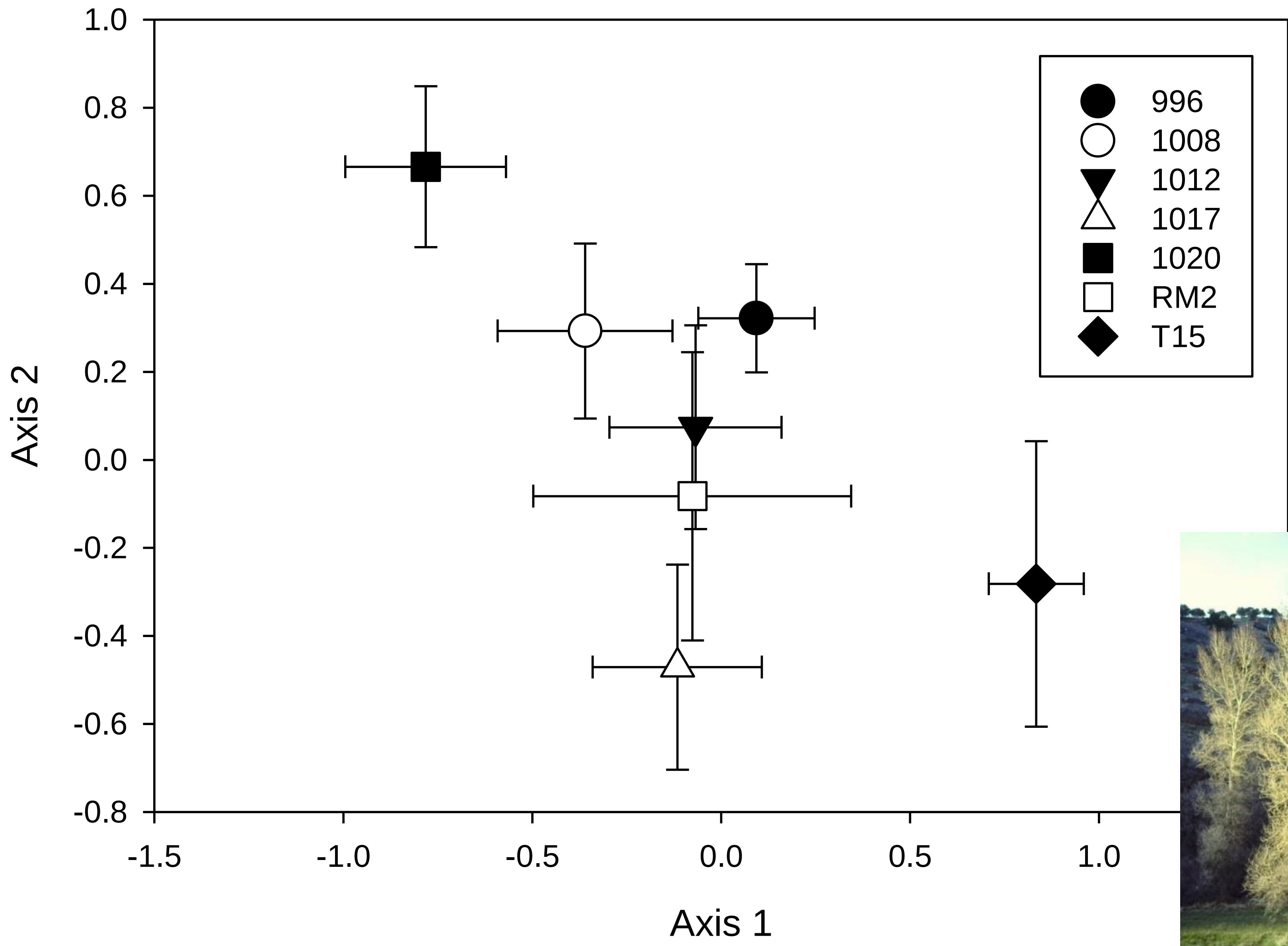


Genetic "footprints" of trees can be large: The genetic links between terrestrial and aquatic ecosystems.

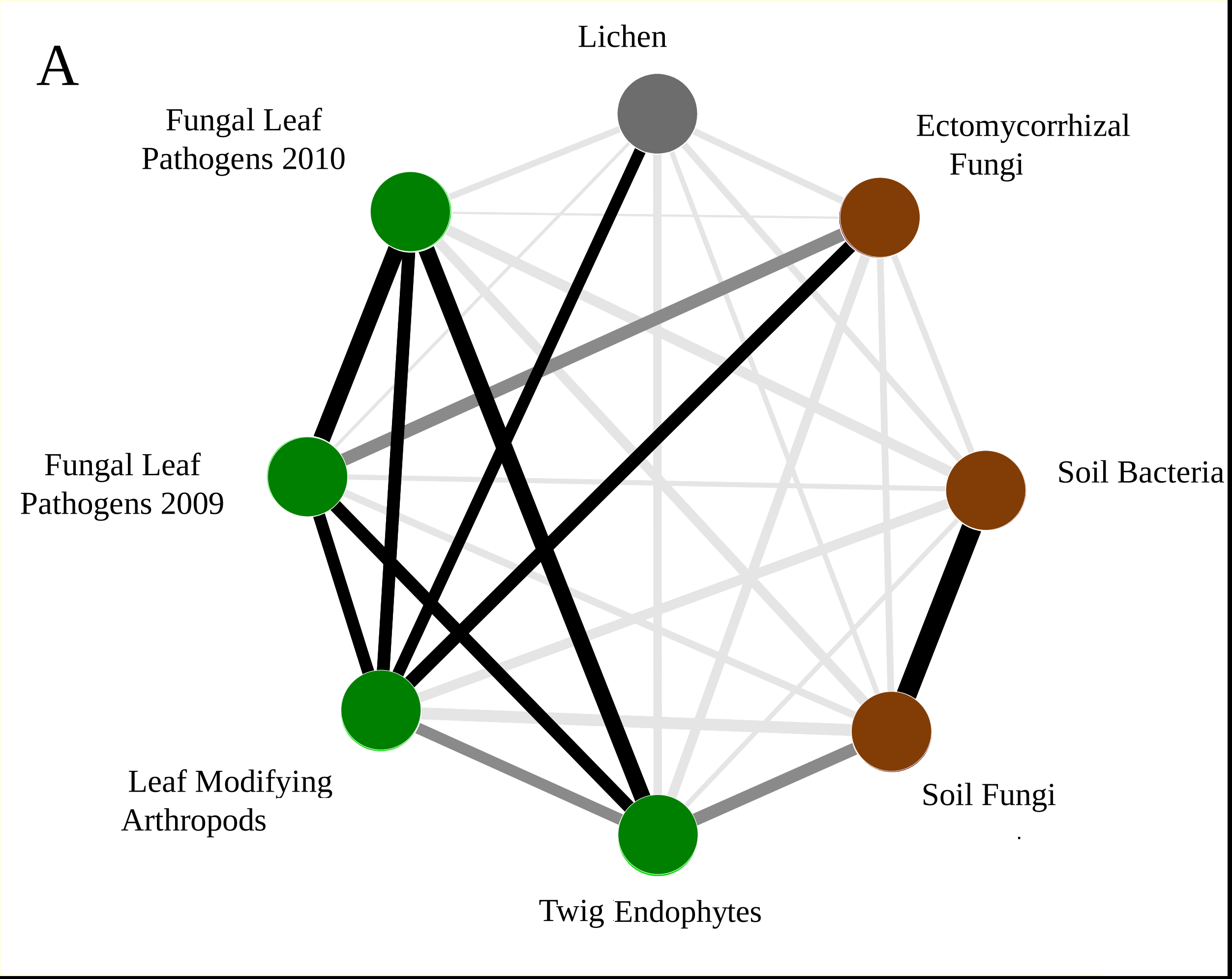
Intraspecific differences in cottonwoods affect stream macro-arthropod communities.

Populus angustifolia

Emergence trap photo by Zacchaeus Compson



Different genotypes of *P. angustifolia* support different stream macro-invertebrates. **Compson 2016 Ecosphere**

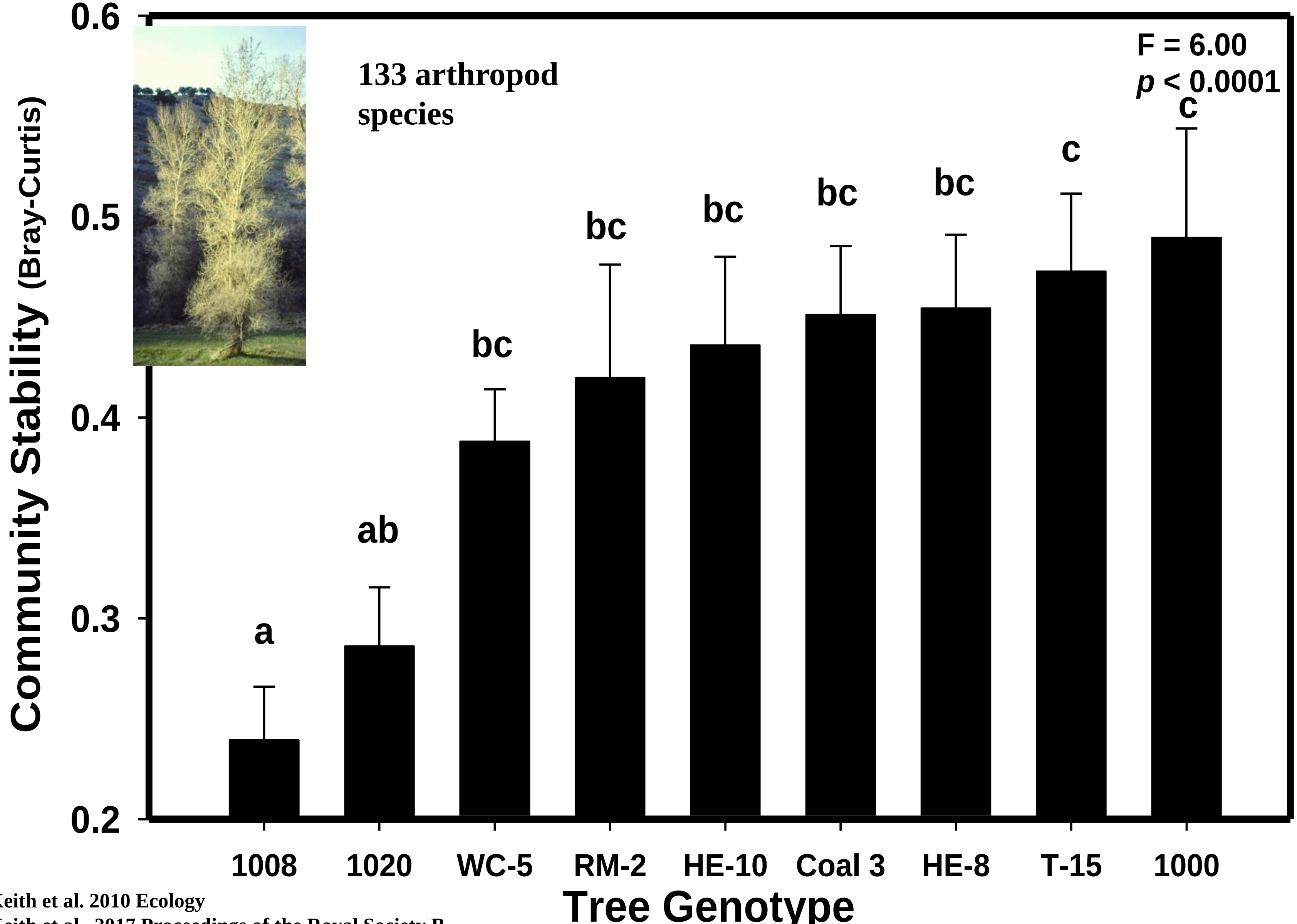


Lamit et al. 2015
Journal of Ecology

Populus angustifolia

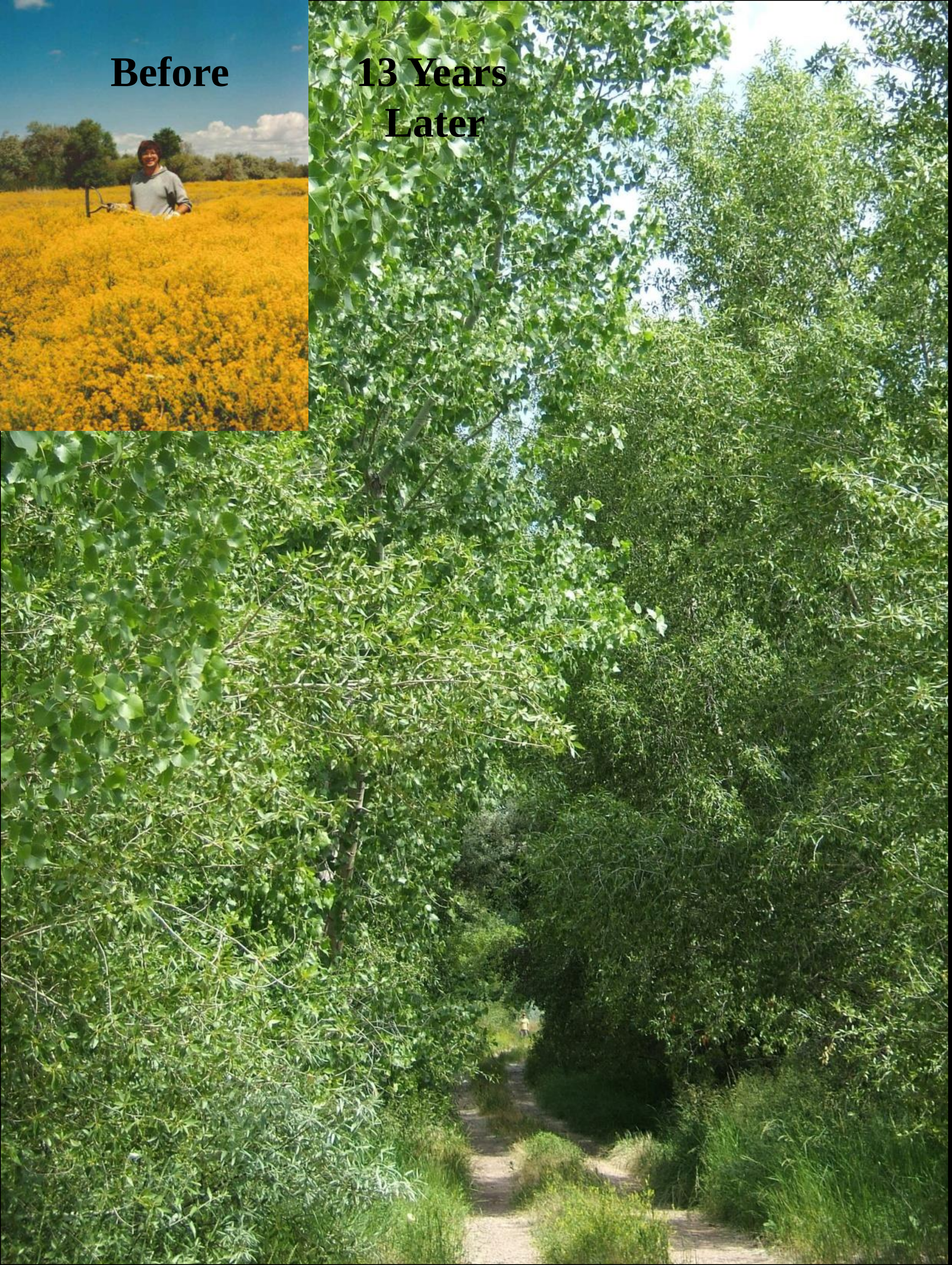
The network of correlated communities is defined by individual tree genotypes – the importance of maintaining network structure in restoration.

Community-genetic correlations **- changes in the composition of one community among plant genotypes that are mirrored by changes in the composition of another community.**



Keith et al. 2010 Ecology
Keith et al. 2017 Proceedings of the Royal Society B

Community stability, richness & abundance in *P. angustifolia* are heritable plant traits. Over 3 years, species turnover rates were genotype dependent ($H^2_C = 0.32$), richness ($H^2_C = 0.30$) & abundance ($H^2_C = 0.35$).

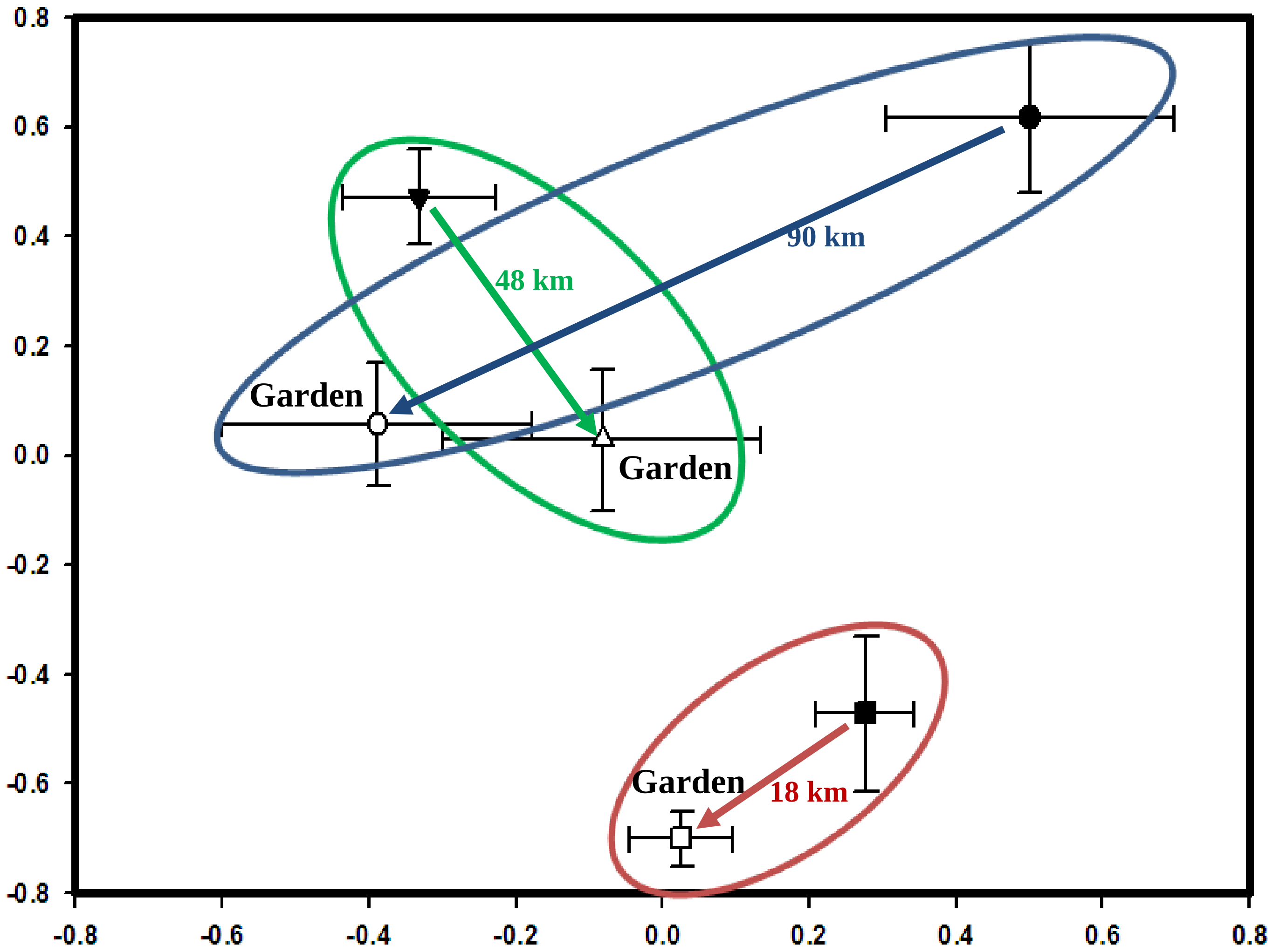


A fundamental issue in assisted migration is if you move plants to mitigate the impacts of climate change, will plants acquire the communities of their home sites? In other words,

if you build it will they come?

Odgen Nature Center restoration site
© Photo by Tom Whitham

Up to a point, if you built it they will come.



With transfers of 18 and 48 km, garden and wild trees support similar communities, but at 90 km they are quite different (© Keith et al. unpublished data).

Key factors that affect Fremont cottonwood performance in restoration.

1. Use genetically appropriate stock for future climates that will be 1-3 degrees hotter as local stock will not likely survive future conditions (e.g., Grady et al. 2015 Restoration Ecology).
2. Use genetically appropriate stock for each ecoregion (e.g., Ikeda et al. 2017 Global Change Biology, Bothwell et al. 2017 Molecular Ecology).
3. Use genetic stock that has survived in tamarisk altered soils as those from tamarisk-free sites are not as well adapted to this invasive species (e.g., Grady et al. 2015 unpub. data).
4. Inoculate with drought tolerant mycorrhizal mutualists (e.g., Gehring et al. 2017 PNAS).
5. Plant adjacent to willows that act as nurse plants (e.g., Parker et al. unpub. data).
6. Use intact communities that are coevolved (cottonwoods and willows that have come from the same site; don't mix and match from different sites; Grady et al. 2017 Oikos).
7. Select for root architecture to reach a deeper water table (e.g., with declining water tables deep rooting genotypes do best; Fischer et al. 2006 Oecologia, Parker et al. unpub. data).
8. Use genotypes that support high biodiversity (some genotypes support few species while others support a lot (e.g., Keith et al. 2010 Ecology, Keith et al. 2017 Proc. Royal Soc. B).

Collaborators in Community Genetics and Genetics-Based Restoration

Rachel Adams – plant ecology
Joe Bailey – community ecology
Helen Bothwell – phylogeography
Aimée Classen – soil ecology
Sam Cushman – landscape genetics
Rachel Durben – community ecology
Dylan Fischer – ecophysiology
Jeff Garnas – entomology
Steve Hart – ecosystem/soil ecology
Lisa Holeski – genetics & chemistry
Julia Hull – endophytes
Art Keith – insect community ecology
Andrew Krohn - molecular ecology
Carri LeRoy – aquatic ecology
Lisa Markovchick – micoribal ecology
Nashelly Meneses – ecological genetics
Jackie Parker – plant ecology
David Smith – landscape ecology
Amy Whipple – ecological genetics
Todd Wojtowicz – litter arthropods
Adam Wymore – aquatic ecology

Gery Allan – molecular ecology
Randy Bangert – biogeography
Posy Busby – ecological plant pathology
Zacchaeus Compson – aquatic ecology
Steve DiFazio – molecular ecology
Luke Evans – population ecology
Paul Flikkema – systems engineering
Catherine Gehring – microbial ecology
Erika Hersch – ecological genetics
Kevin Hultine – invasive species
Nathalie Isabel – molecular ecology
George Koch – ecophysiology
Jamie Lamit – microbial ecology
Rick Lindroth – chemical ecology
Tamara Max – molecular ecology
George Newcombe – plant pathology
Brad Potts – quantitative genetics
Steve Shuster – theoretical genetics
Tom Whitham – community ecology
Troy Wood – ecology
Matt Zinkgraf – molecular genetics

Petter Axelsson – transgenic trees
Rebecca Best – ecology & evolution
Abraham Cadmus – ecophysiology
Hillary Cooper – phylogenetics
Rodolfo Dirzo – community ecology
Sharon Ferrier – conservation ecology
Kevin Floate – insect ecology
Kevin Grady – restoration
Joakim Hjältén – ecology
Dana Ikeda – climate modeling
Karl Jarvis – phylogeny
Tom Kolb – plant physiology
Matthew Lau – network modeling
Jane Marks – aquatic ecology
Richard Michalet - facilitation & ecology
Emily Palmquist – hydrology
Jen Schweitzer – ecosystems
Chris Sthultz – plant ecology
Gina Wimp – community ecology
Scott Woolbright - molecular genetics

GO & NGO collaborators: Mikael Ingraldi – Arizona Game & Fish Dept., Charles Schelz – National Park Service Mary McKinley – Ogden Nature Center, Gregg Garnett – Bureau of Reclamation, Kris Haskins – The Arboretum at Flagstaff, Paul Burnett – Utah Dept. of Natural Resources, Billy Cordasco – Babbitt Ranches

Outreach – Dan Boone, Ryan Belnap, Lara Schmit, Victor Leshyk - NAU

MacroSystems, MRI, FIBR

Removing invasive tamarisk and camelthorn on the Little Colorado River and restoring using new guidelines with the support of Babbitt Ranches & the Nina Mason Pulliam Charitable Trust.

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