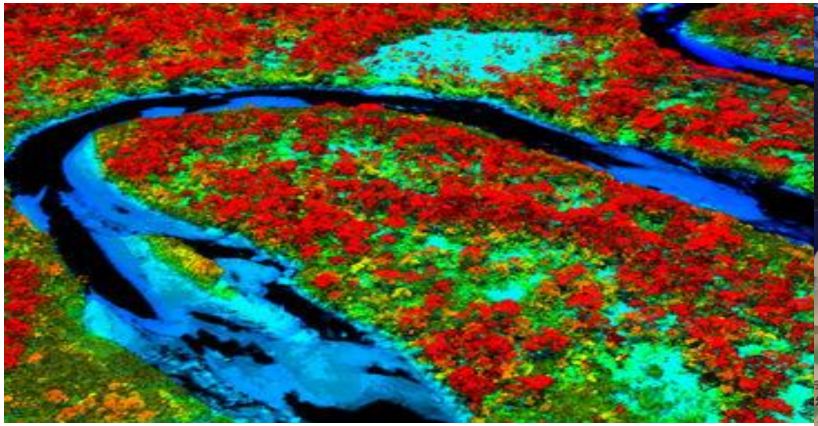
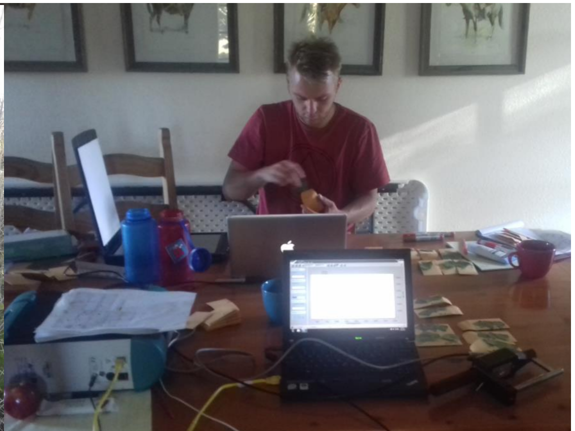
High throughput phenotyping at the cottonwood common gardens



Chris Doughty and Eleanor Thomson

NAU
NORTHERN
ARIZONA
UNIVERSITY
School of Informatics,
Computing, and
Cyber Systems



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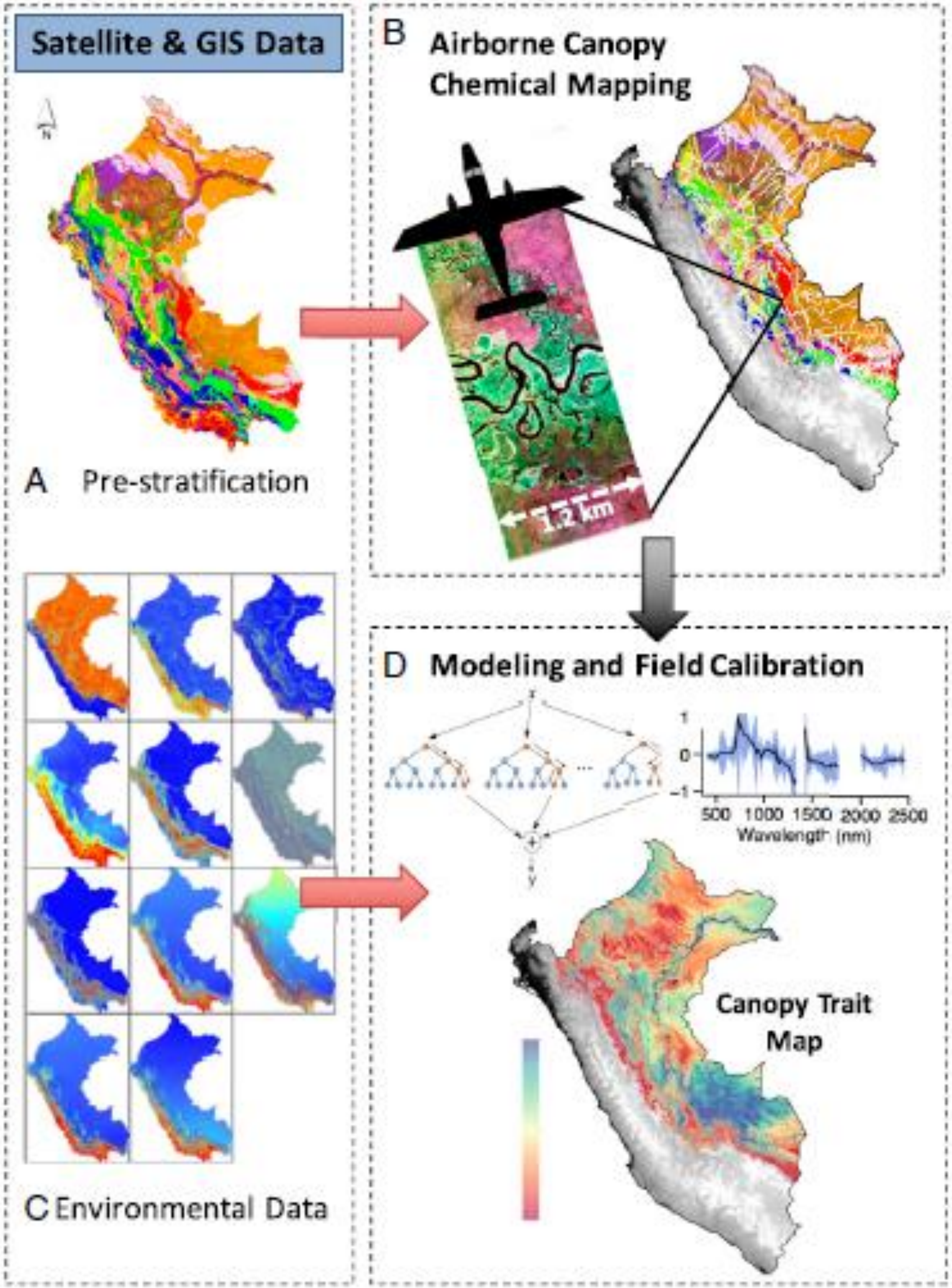
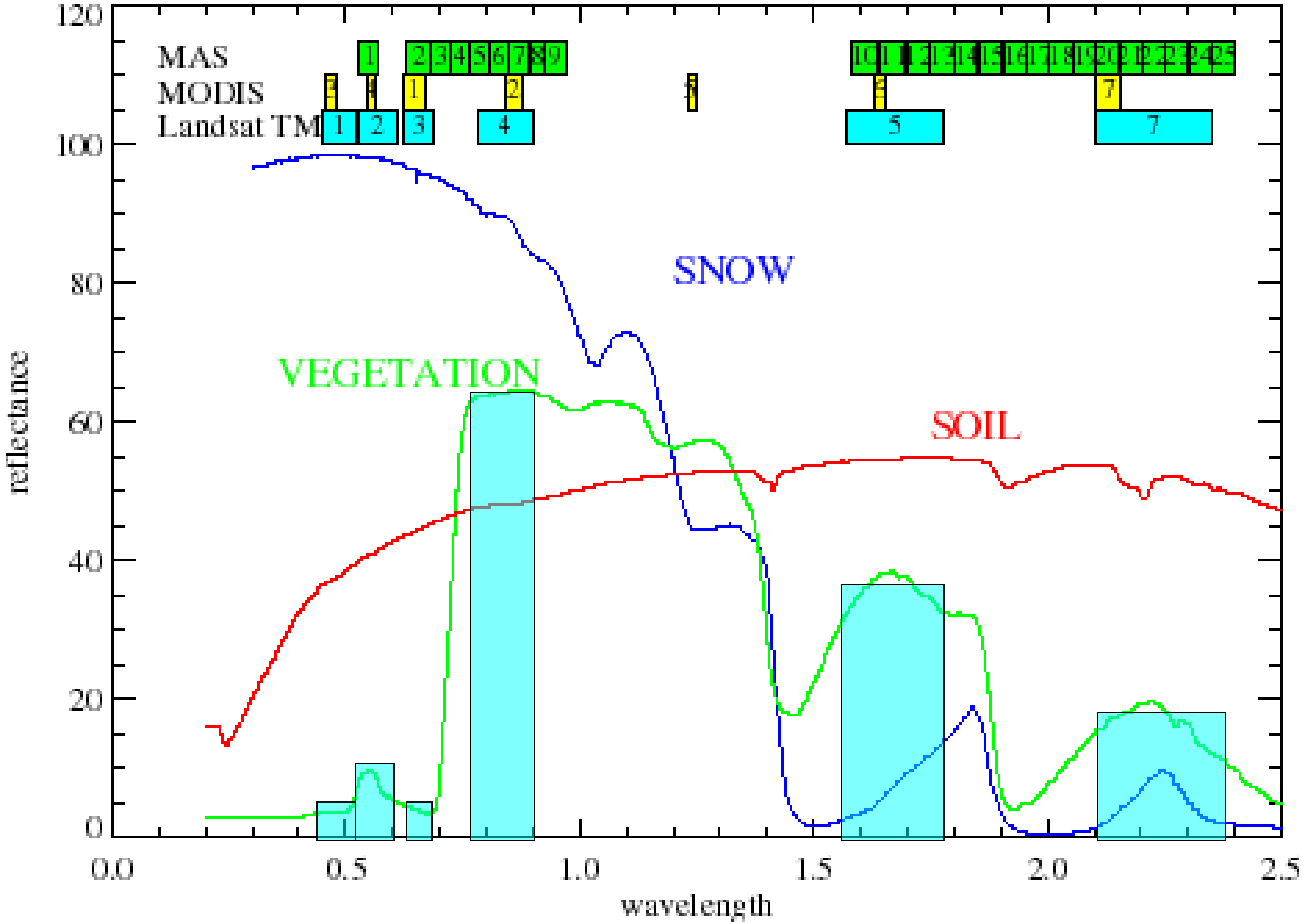


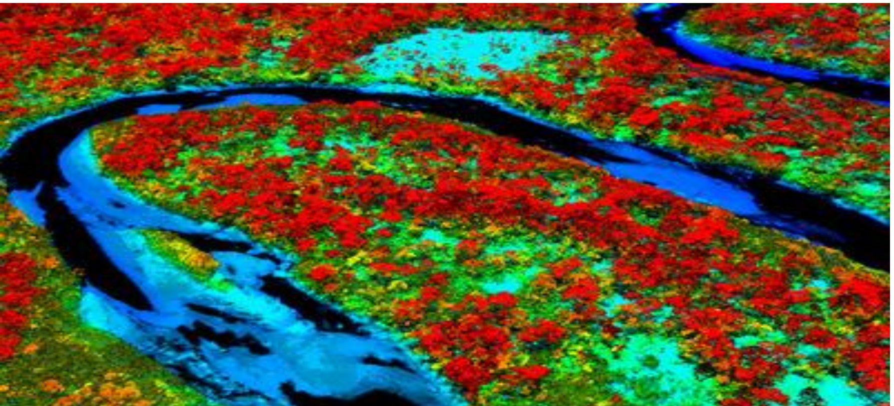
Asner et al 2016

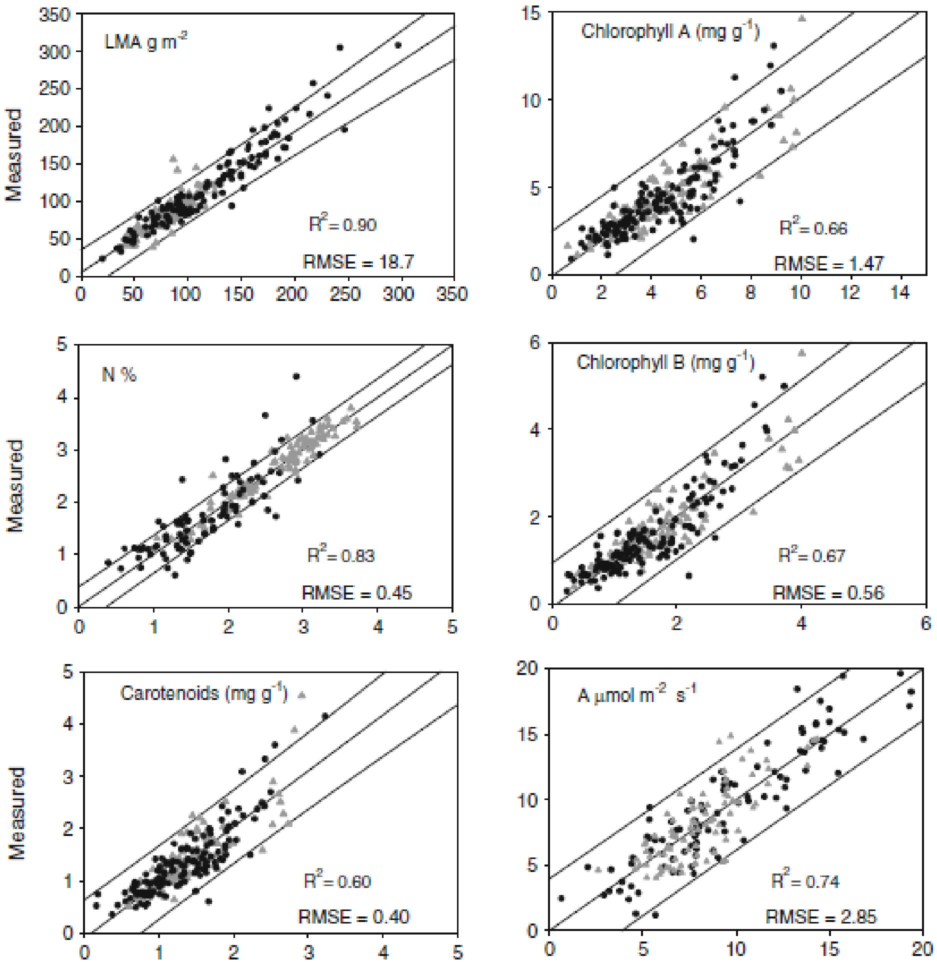
REFLECTANCE SIGNATURES



Using leaf spectroscopy to predict leaf traits

- Many leaf traits, including photosynthesis (Amax), can be predicted via leaf spectral properties.

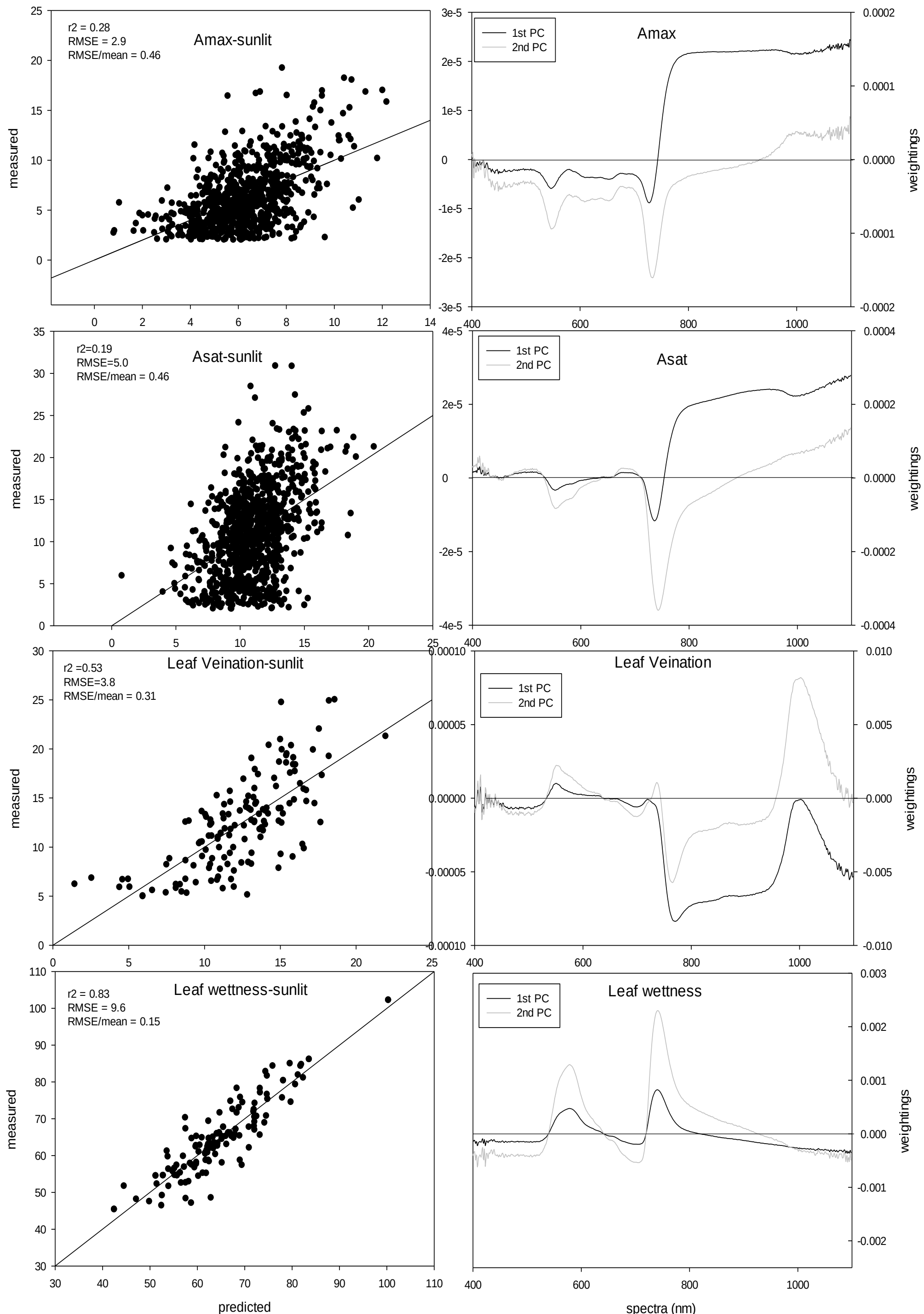




Doughty et al 2011

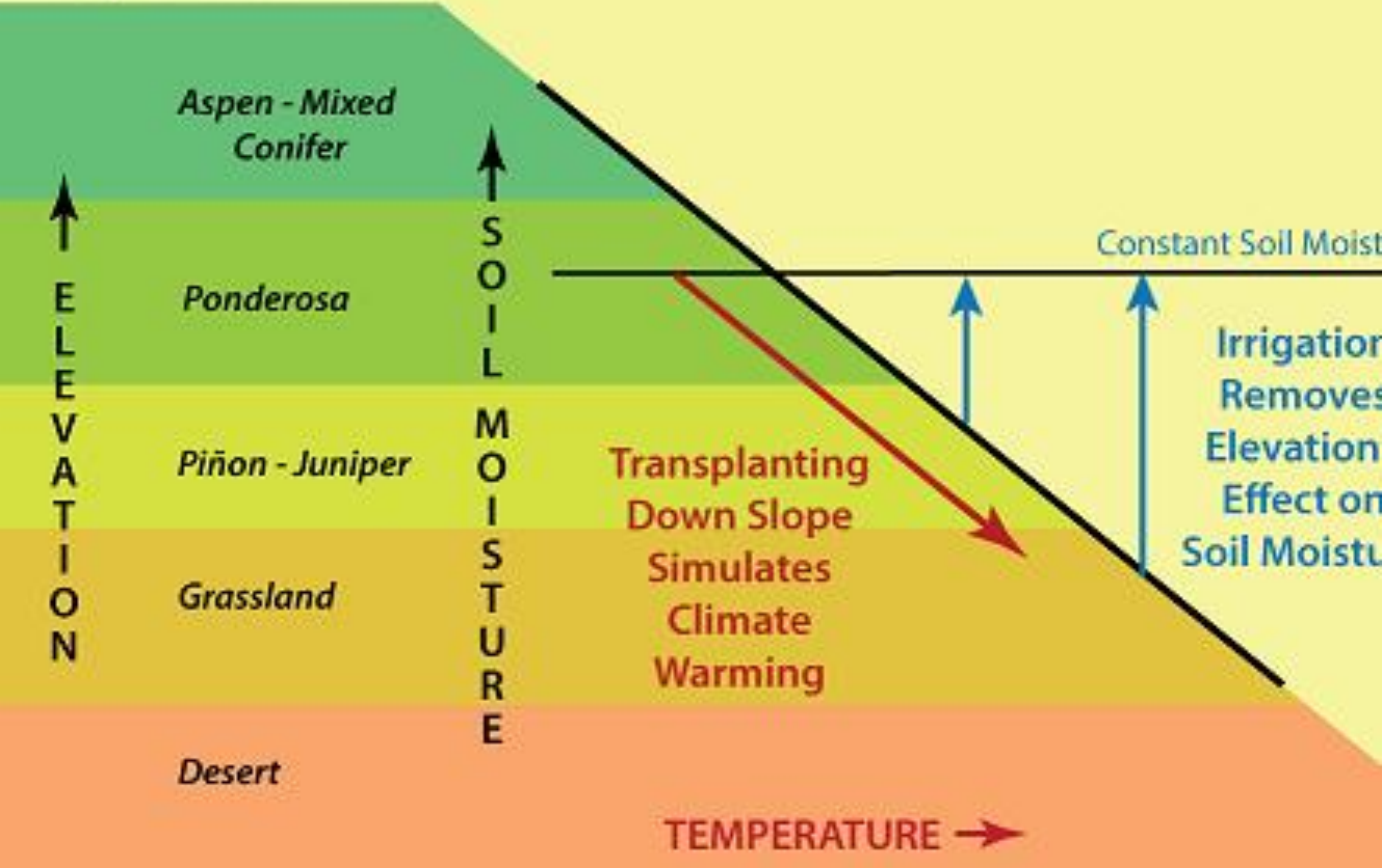
Can we predict other non-leaf traits?

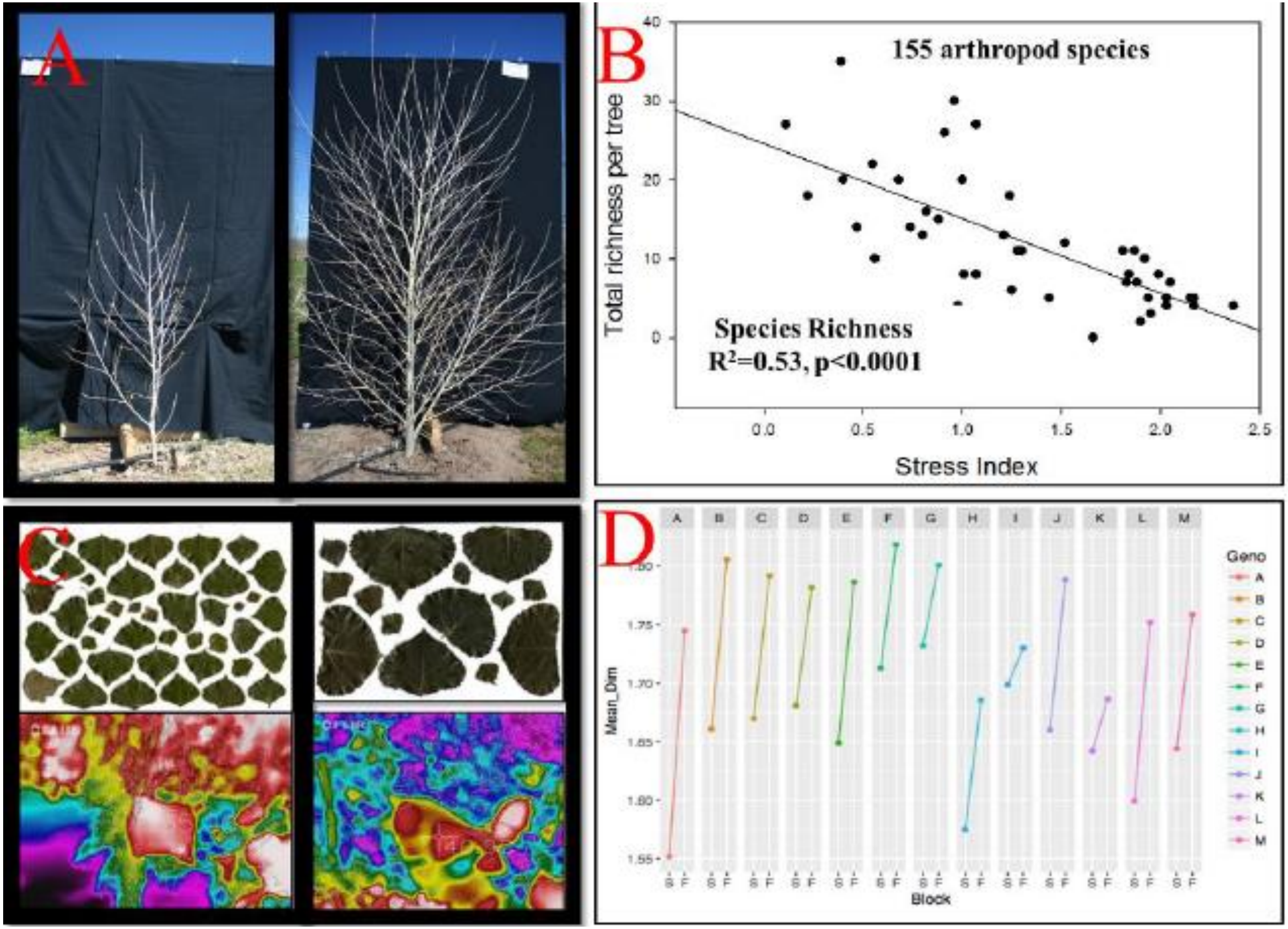
- We can predict traits like photosynthesis, wood density, veination and leaf wetness with spectroscopy

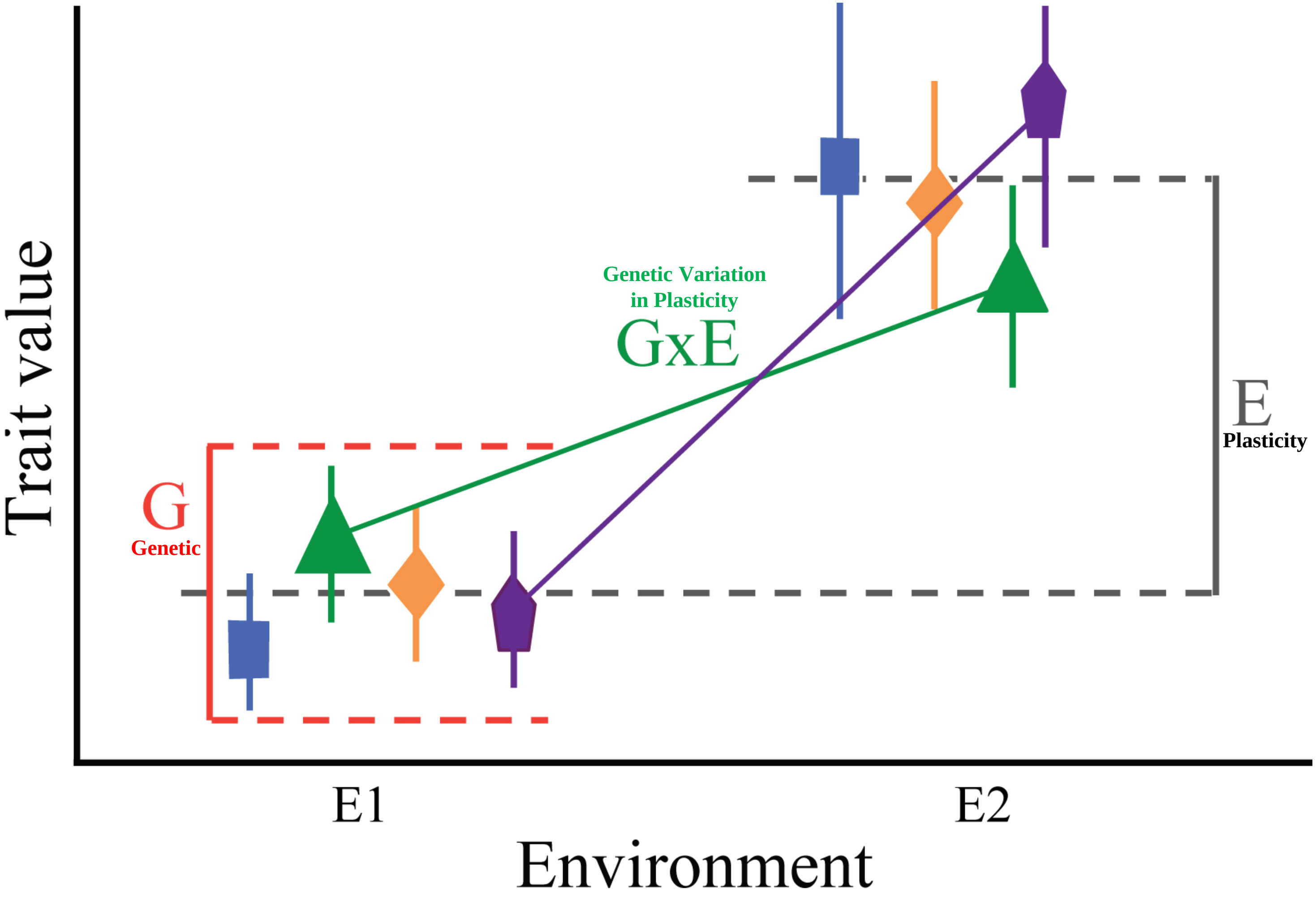


Doughty et al 2017

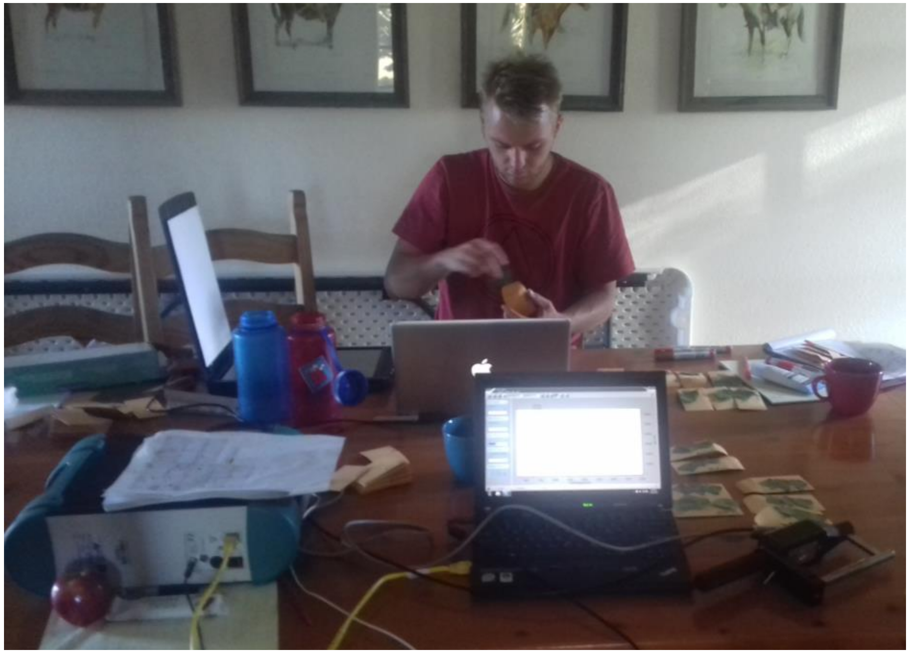
SEGA
Vegetation Zones




A
B
155 arthropod species
Total richness per tree
40
30
20
10
0
0.0
0.5
1.0
1.5
2.0
2.5
Stress Index
Species Richness
R²=0.53, p<0.0001
C
D
A B C D E F G H I J K L M
Mean_Dim
1.80
1.75
1.70
1.65
1.60
1.55
S F
Block
Geno
A
B
C
D
E
F
G
H
I
J
K
L
M

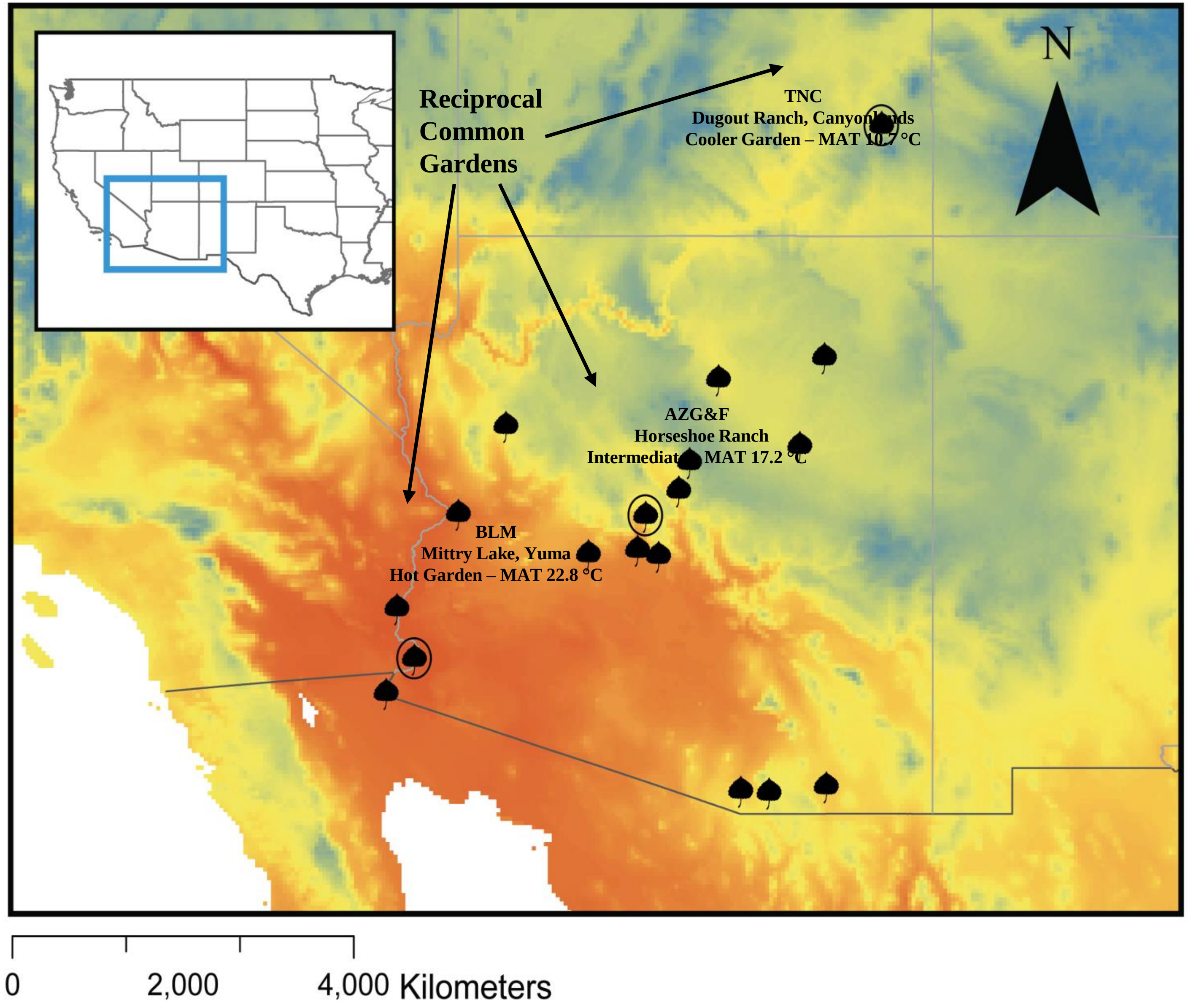


A two-environment reaction norm showing the components of phenotypic variation of four genotypes: G = trait variation due to population genetics within a single environment, E = trait variation due to change in environment (plasticity), GxE = the variation in plasticity among genotypes. Phenotypic variation (V_P) = V_G + V_E + V_{GxE}. From Cooper et al. 2018 Global Change Biology.

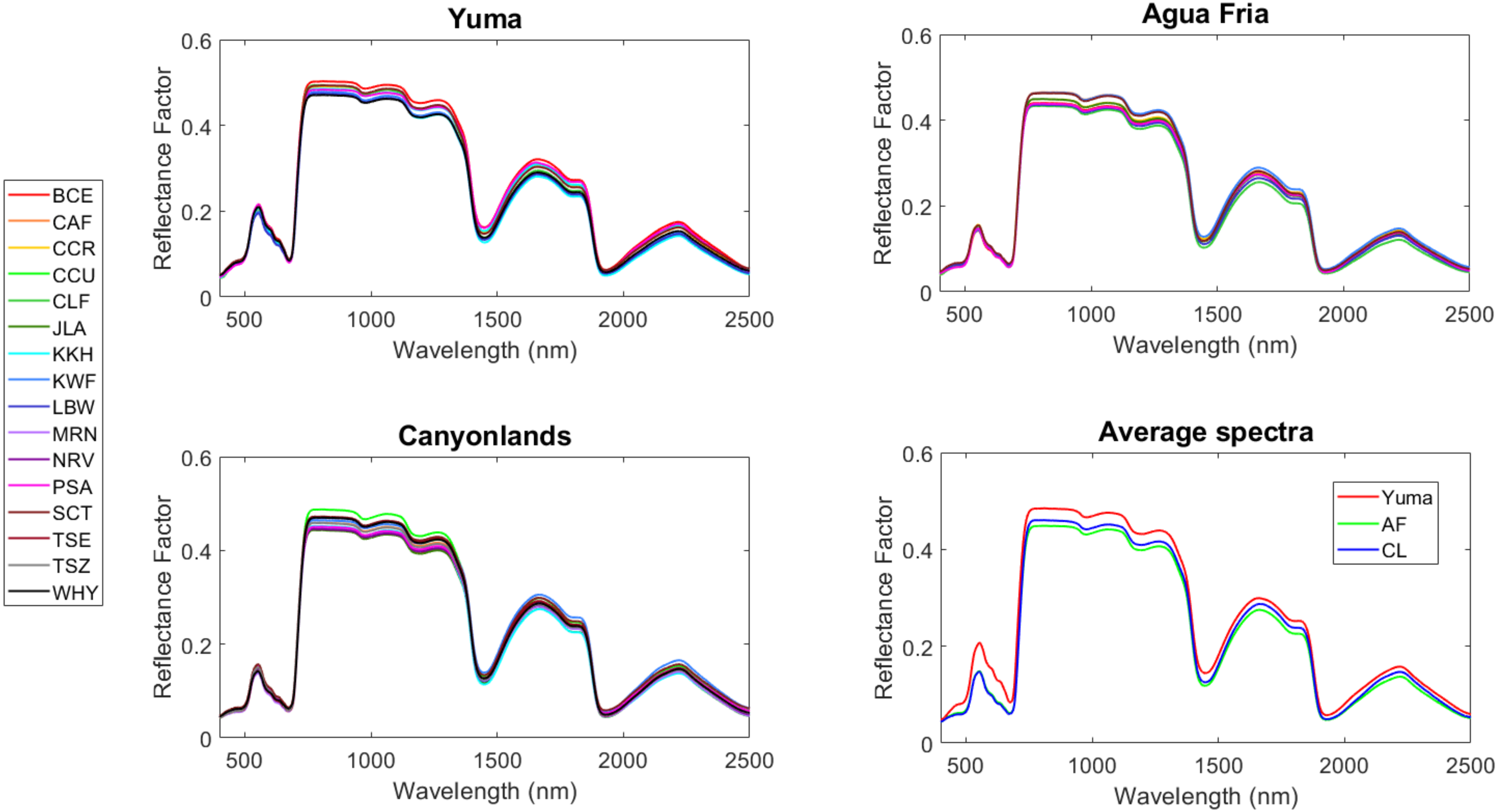


37 PSA
37 PSA
110-16
37 PSA
97-
37-PSA

Reciprocal common gardens show finer scale local adaptation within the Sonoran desert ecotype

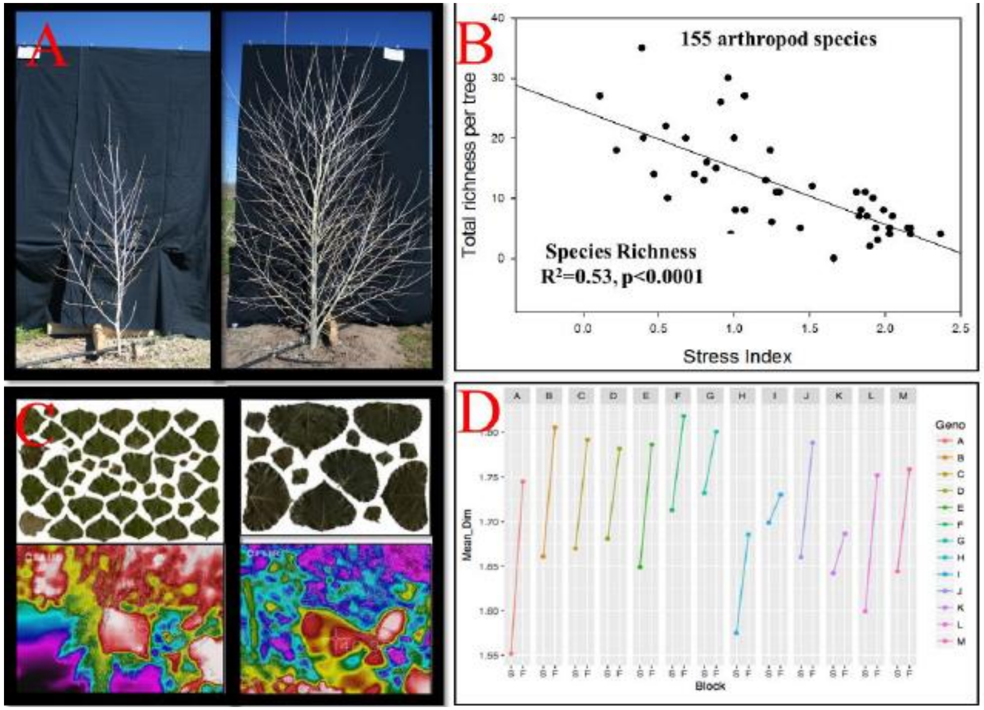


(Cooper et al. 2018 Global Change Biology)

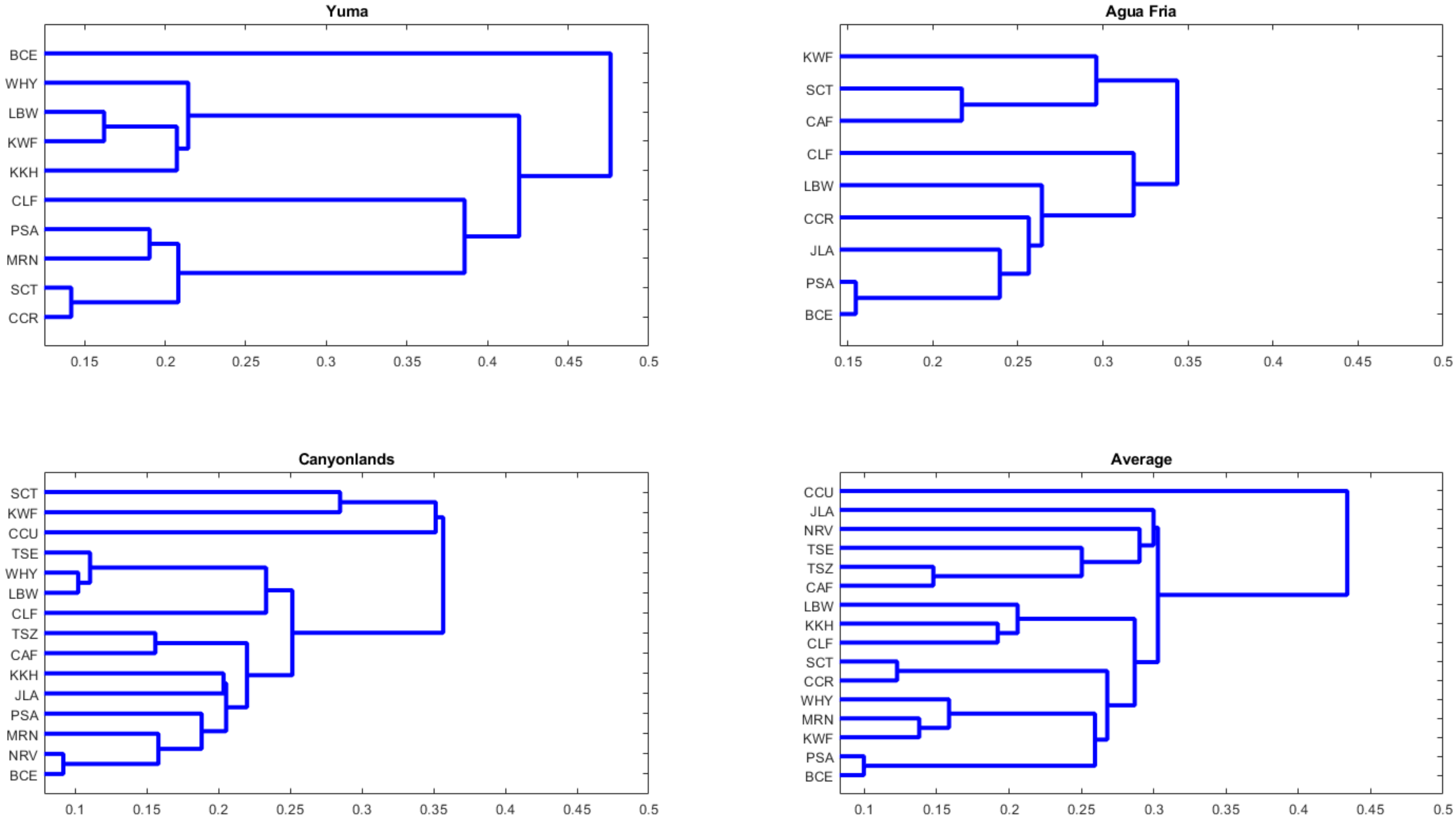

Yuma
Agua Fria
Canyonlands
Average spectra
Reflectance Factor
Wavelength (nm)
0
0.2
0.4
0.6
500
1000
1500
2000
2500
BCE
CAF
CCR
CCU
CLF
JLA
KKH
KWF
LBW
MRN
NRV
PSA
SCT
TSE
TSZ
WHY
Yuma
AF
CL

Preliminary Methods

- Hierarchical cluster analysis
- Partial least squares regression
- Need more traits for comparison!



Hierarchical cluster analysis applied to the average spectra of each population sampled in each garden.



Yuma

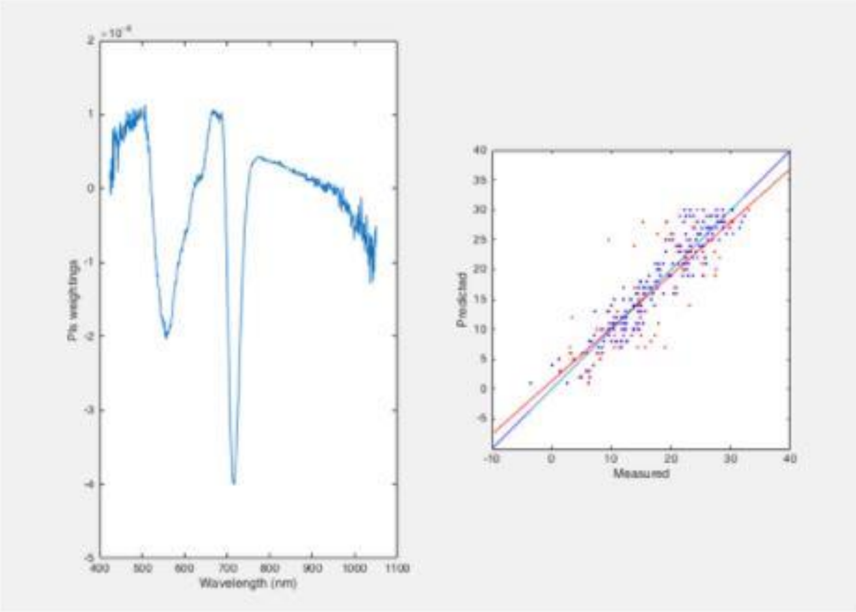
Agua Fria

Canyonlands

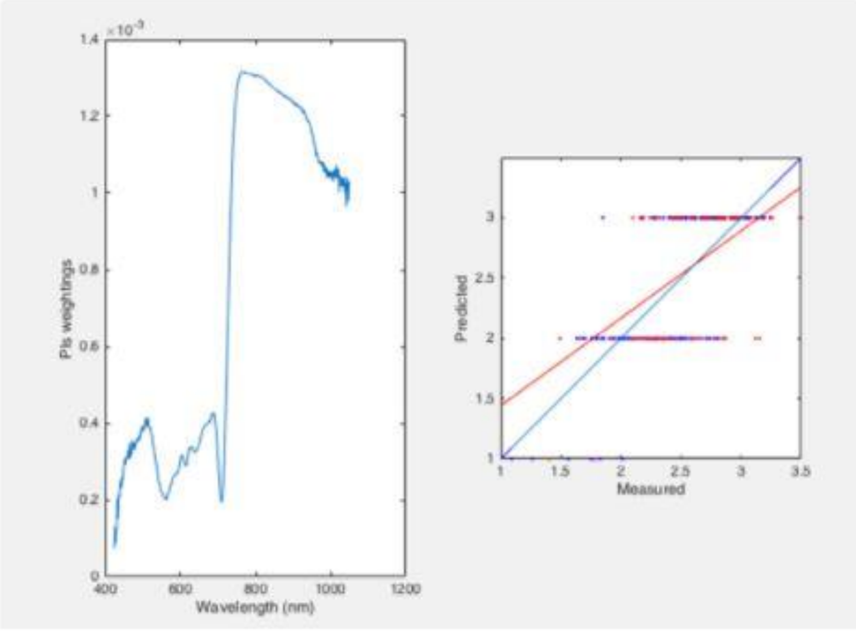
Average

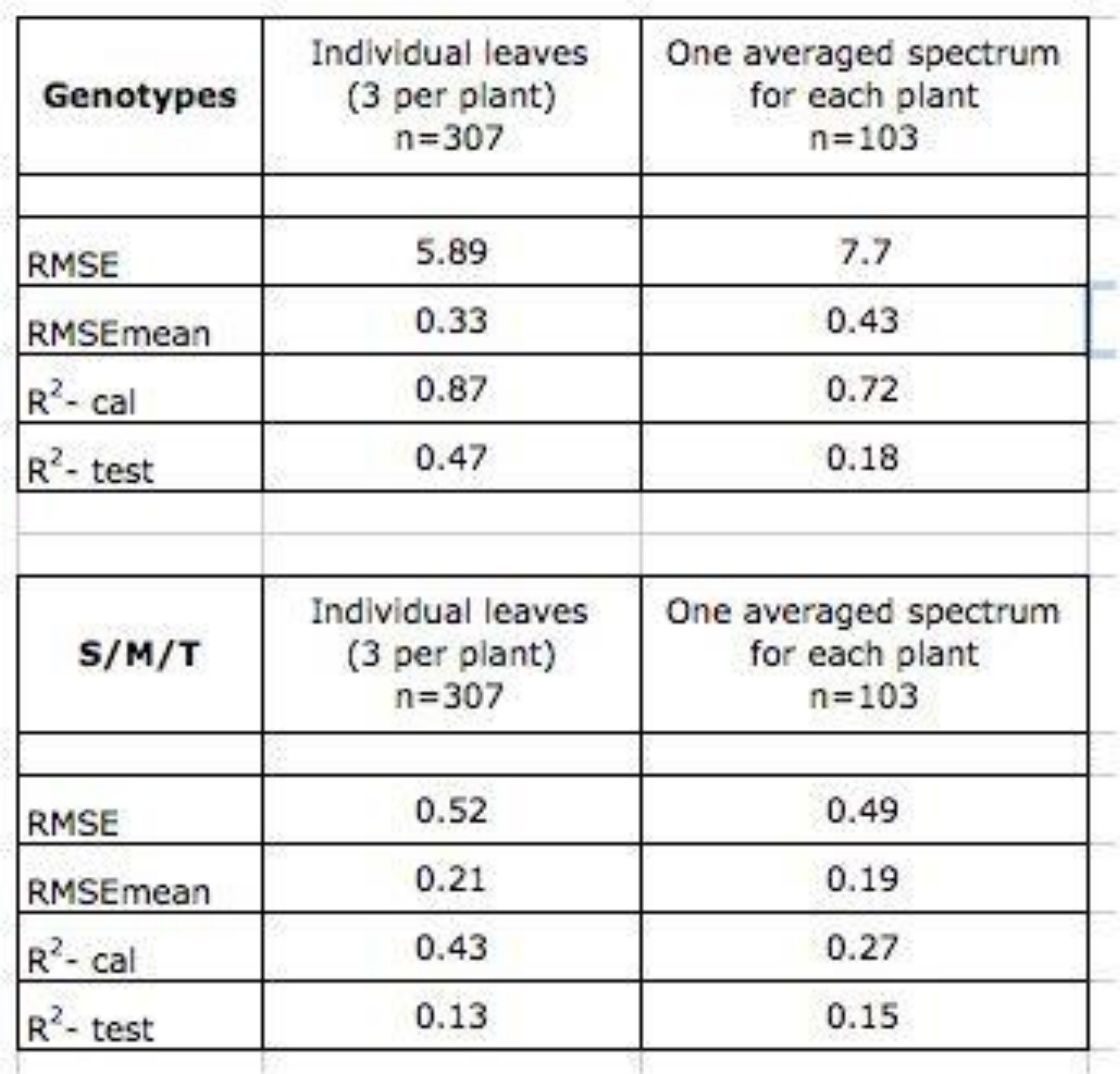
Strong predictions of both genotypes and plant height

Genotypes



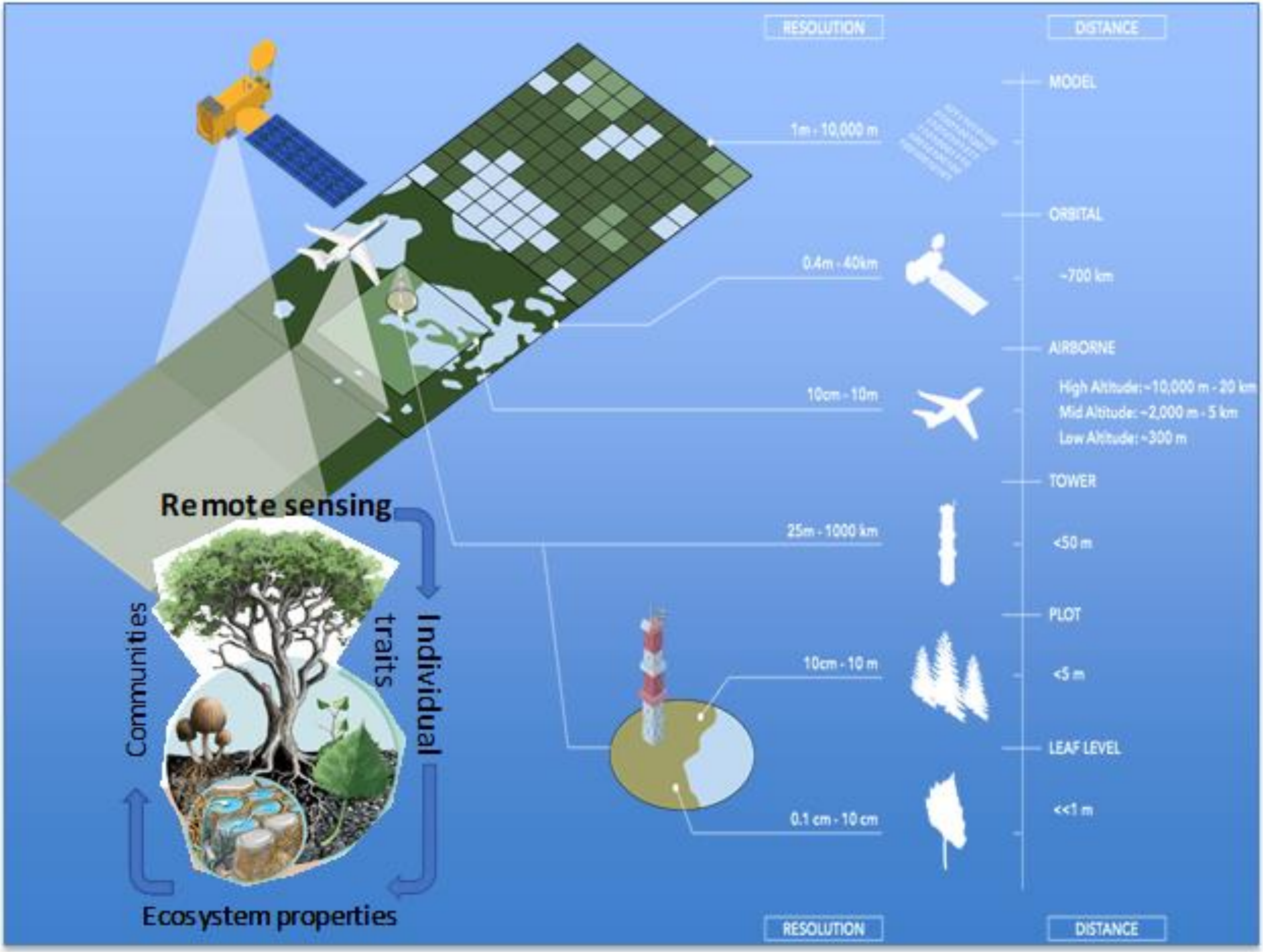
Height





Genotypes	Individual leaves (3 per plant) n=307	One averaged spectrum for each plant n=103
RMSE	5.89	7.7
RMSEmean	0.33	0.43
R^2- cal	0.87	0.72
R^2- test	0.47	0.18

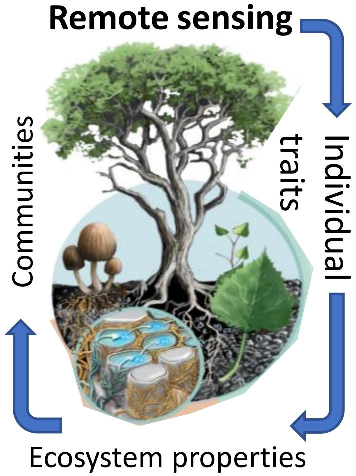
S/M/T	Individual leaves (3 per plant) n=307	One averaged spectrum for each plant n=103
RMSE	0.52	0.49
RMSEmean	0.21	0.19
R^2- cal	0.43	0.27
R^2- test	0.13	0.15


RESOLUTION
DISTANCE
MODEL
1m - 10,000 m
ORBITAL
0.4m - 40km
~700 km
AIRBORNE
10cm - 10m
High Altitude: ~10,000 m - 20 km
Mid Altitude: ~2,000 m - 5 km
Low Altitude: ~300 m
TOWER
25m - 1000 km
<50 m
PLOT
10cm - 10 m
<5 m
LEAF LEVEL
0.1 cm - 10 cm
<<1 m
RESOLUTION
DISTANCE
Remote sensing
Individual traits
Ecosystem properties
Communities

Genes-to-Ecosystems: Scaling from Critical Plant Species to Global Ecosystems for Precision Conservation & Security of Natural Resources

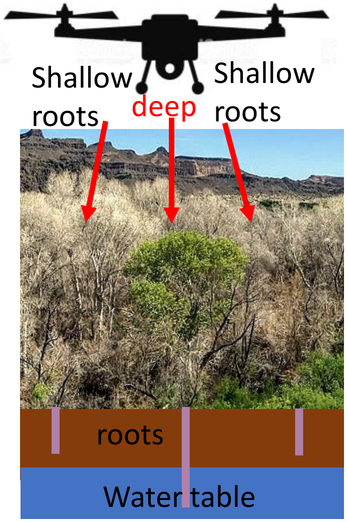
MISSION

- Climate change and invasive species are altering ecosystems at an unprecedented rate, leading to massive mortality of plants that provide key ecosystem services including food, fiber, fuel, and clean water.
- By combining high performing plant genotypes with microbes that promote stress tolerance, we will restore ecosystem services to degraded lands, promoting global health and security.



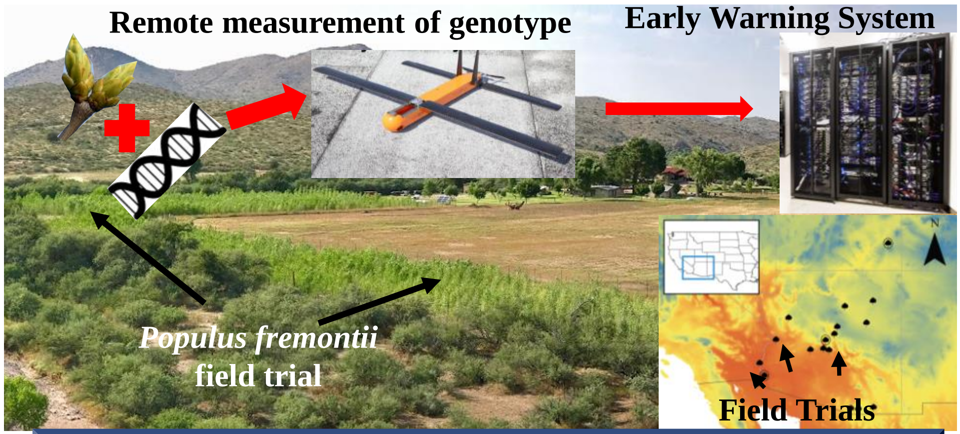
WIN STRATEGY/KEY TECHNOLOGIES

- We can integrate genetics and environment to develop predictive models of landscape scale shifts as a function of the environment.
- Hyperspectral remote sensing and lidar predicts tree genetics and phenotype, enabling prediction of future plant traits that promote drought tolerance needed in a warmer world.



NEEDS DESCRIPTION

- We have demonstrated that individual leaf spectroscopy predicts key plant traits.
- A suite of technologies is needed to scale trait detection to landscape and global levels.
- We can succeed by combining Raytheon's expertise and capacities in hyperspectral remote sensing with NAU's infrastructure and expertise in genetics, ecology and remote sensing.



END USER/CUSTOMER

- Predict vulnerable environmental regions before an environmental catastrophe leads to famine, instability and migration.
- *Customers: DoD, DHS, FEMA*
- Infer gene by environment interactions to predict vulnerability to climate change.
- *Customers: USFS, NPS, USDA, BLM, BOR*

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