

Movement of insect-transmitted viruses & bacteria between ag crops & native plants

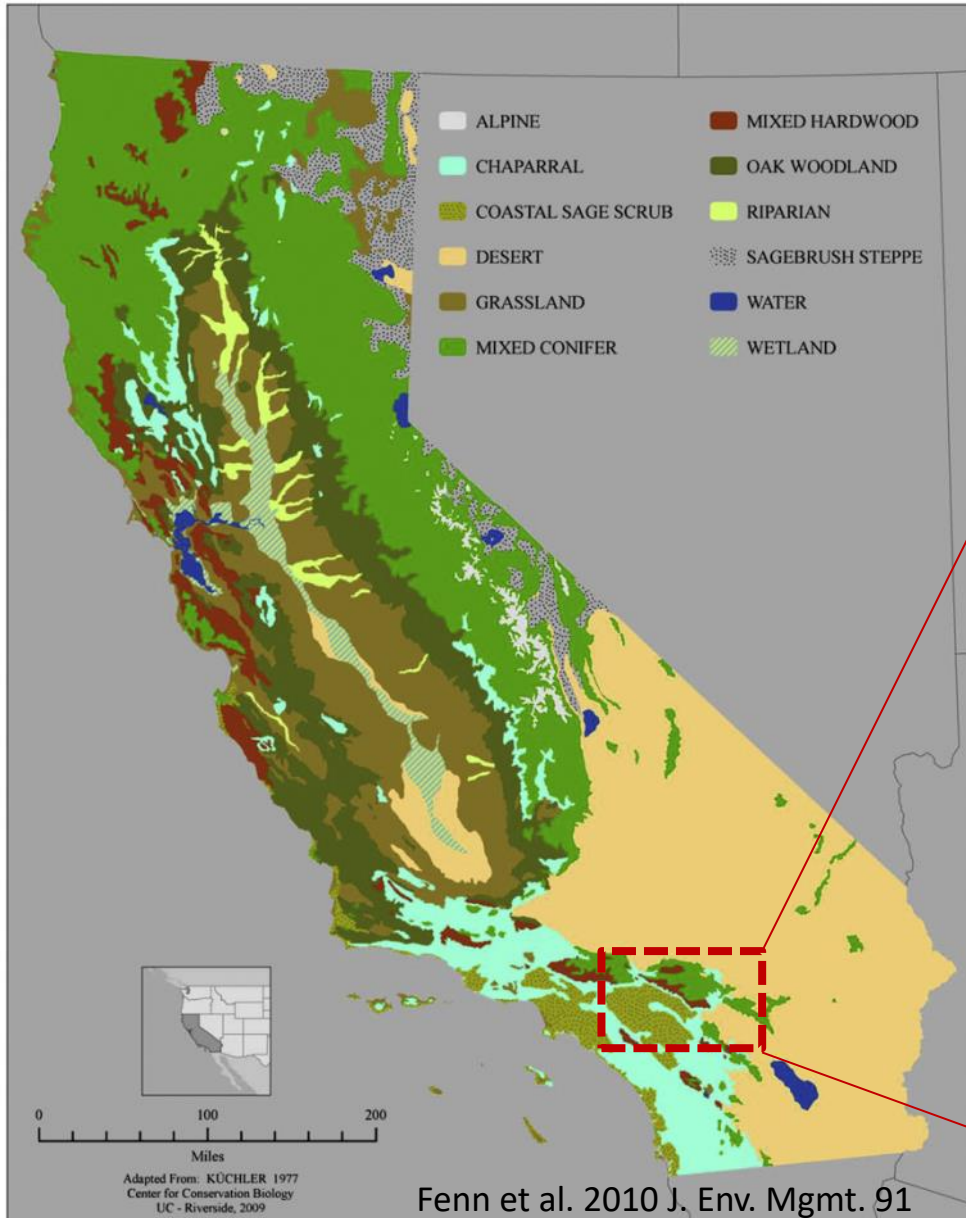
Jaimie Kenney

Tessa Shates, Marco Gebiola, **Kerry Mauck**
UC Riverside Department of Entomology

California Forest Pest Council
Annual Meeting 2024

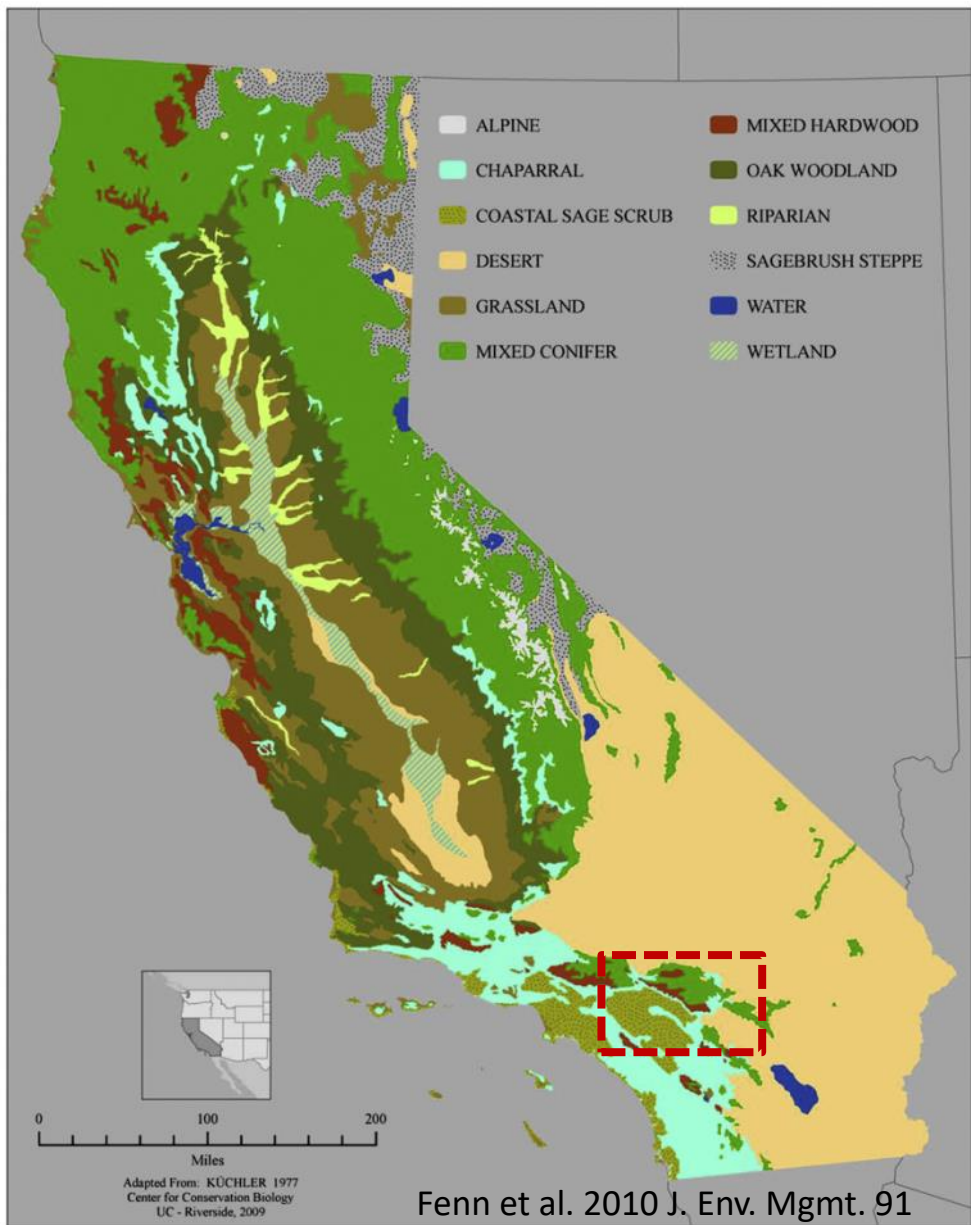


California has a rich diversity of habitats populated by heat and drought-adapted perennial plants

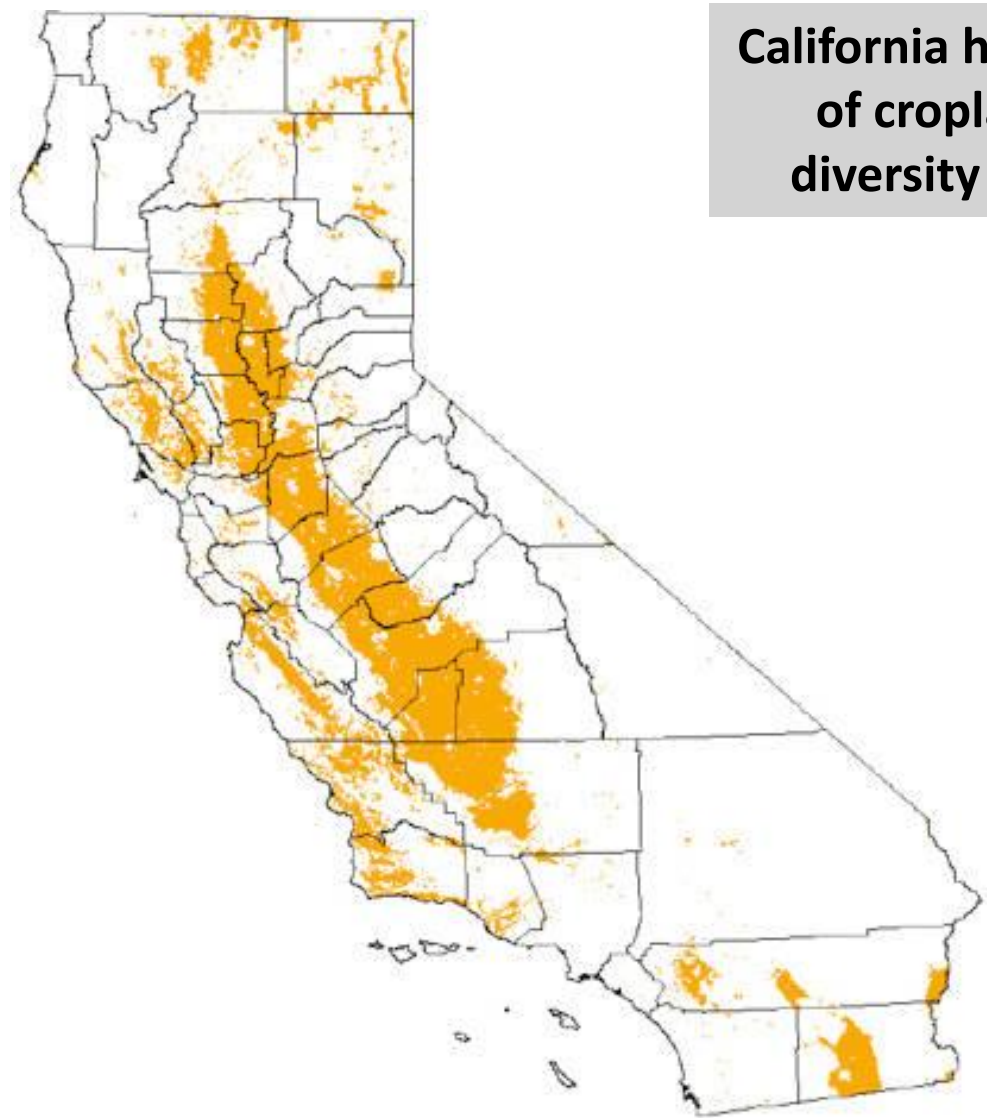


Fenn et al. 2010 J. Env. Mgmt. 91



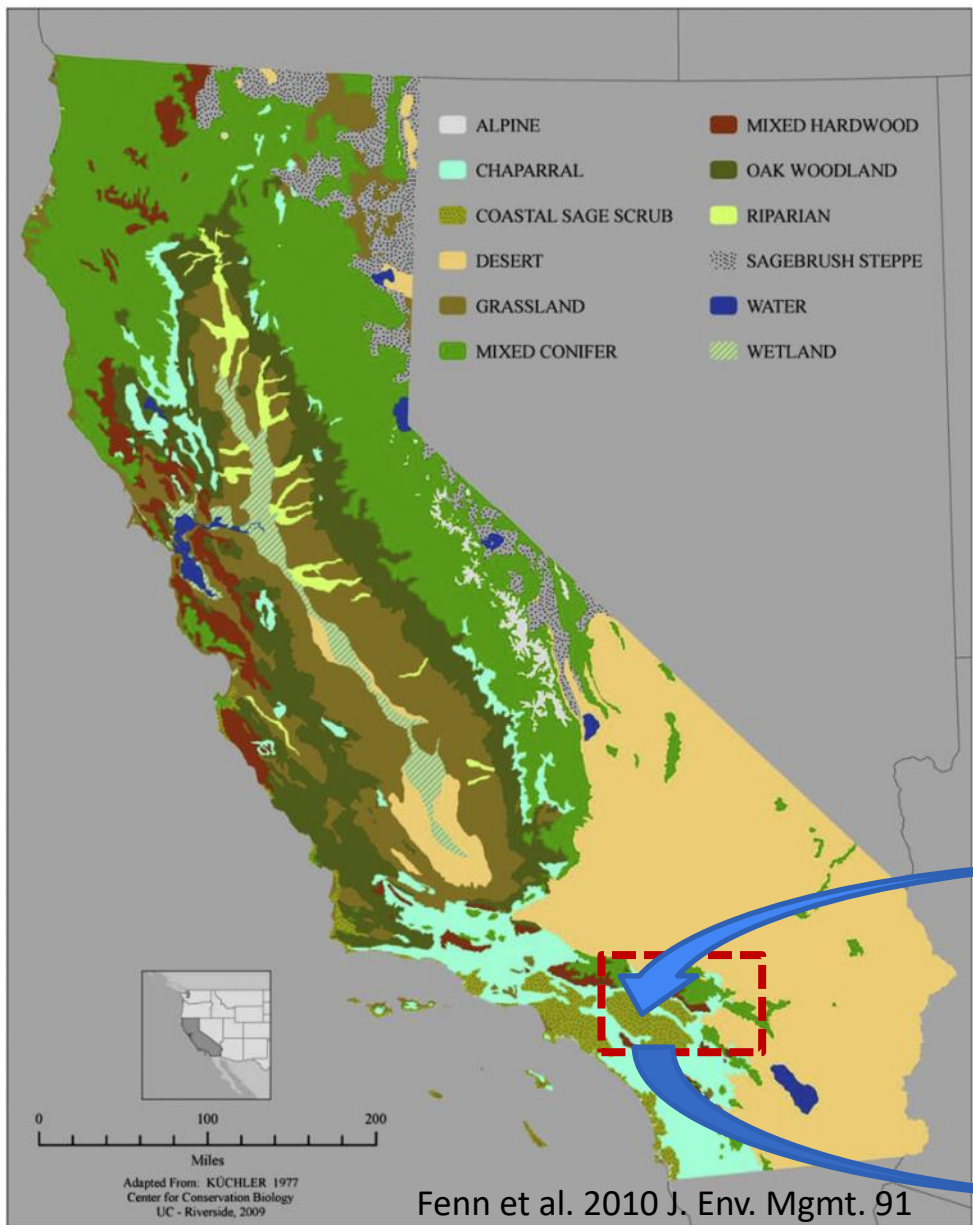


Cropland



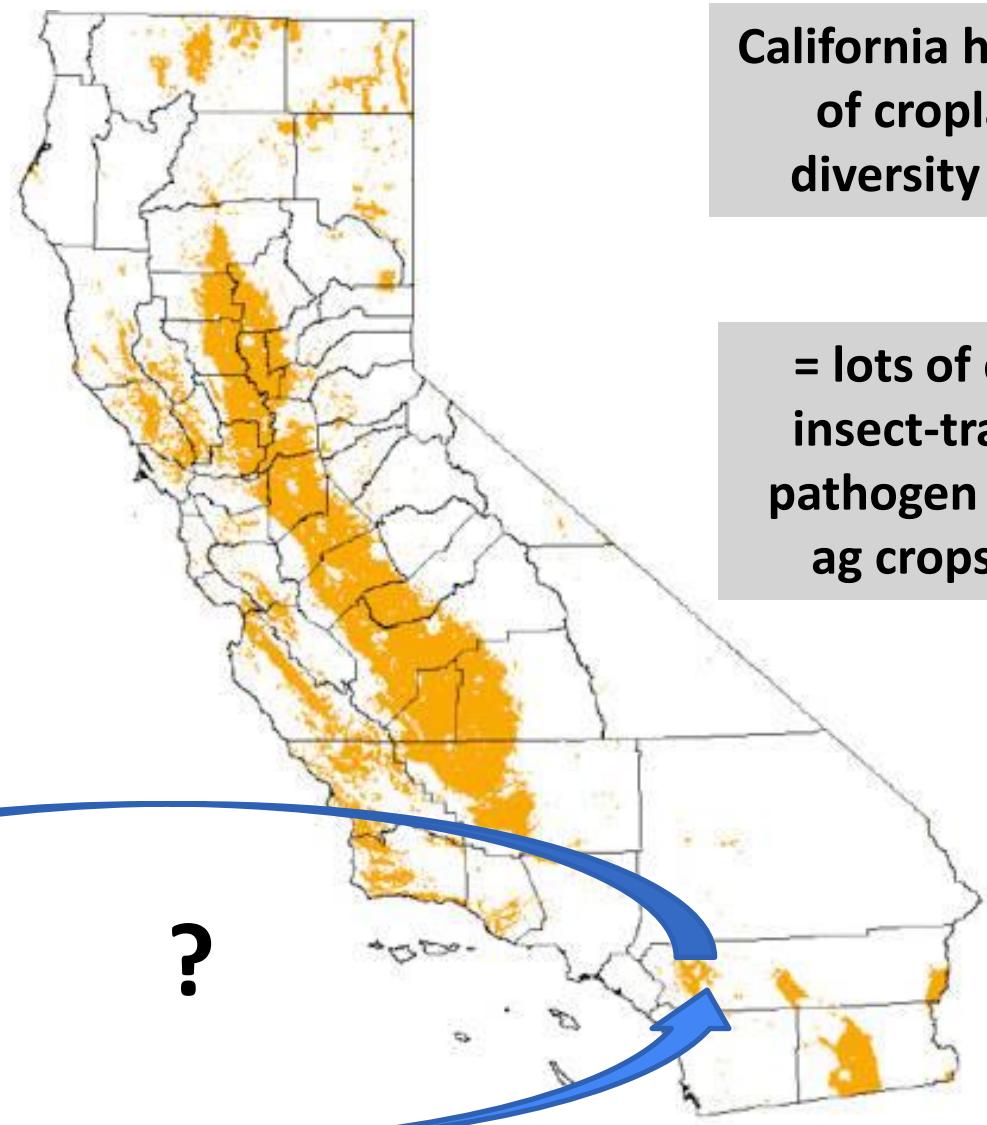
California has an abundance of cropland and huge diversity of crop plants.

Source: UCANR



Fenn et al. 2010 J. Env. Mgmt. 91

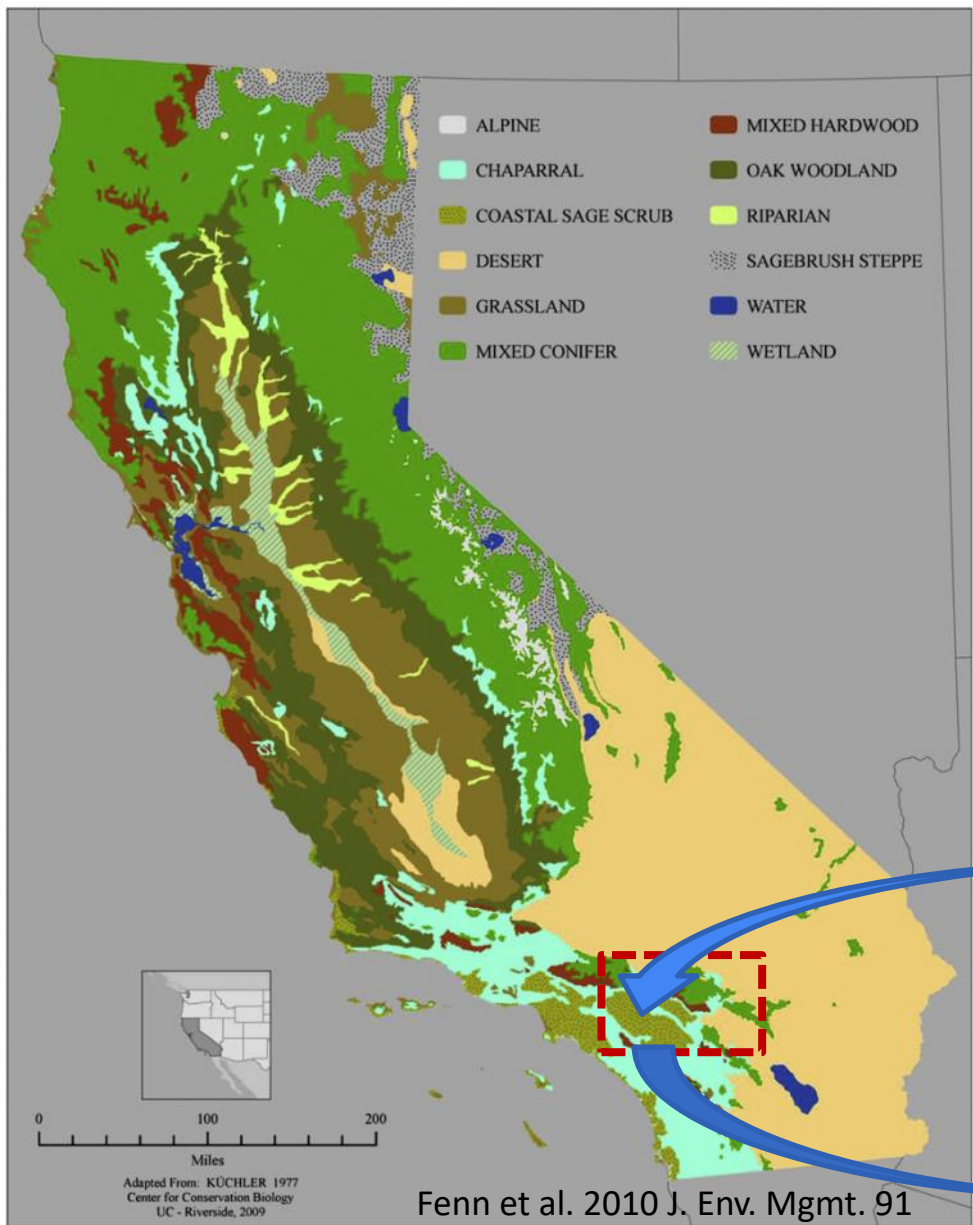
Cropland



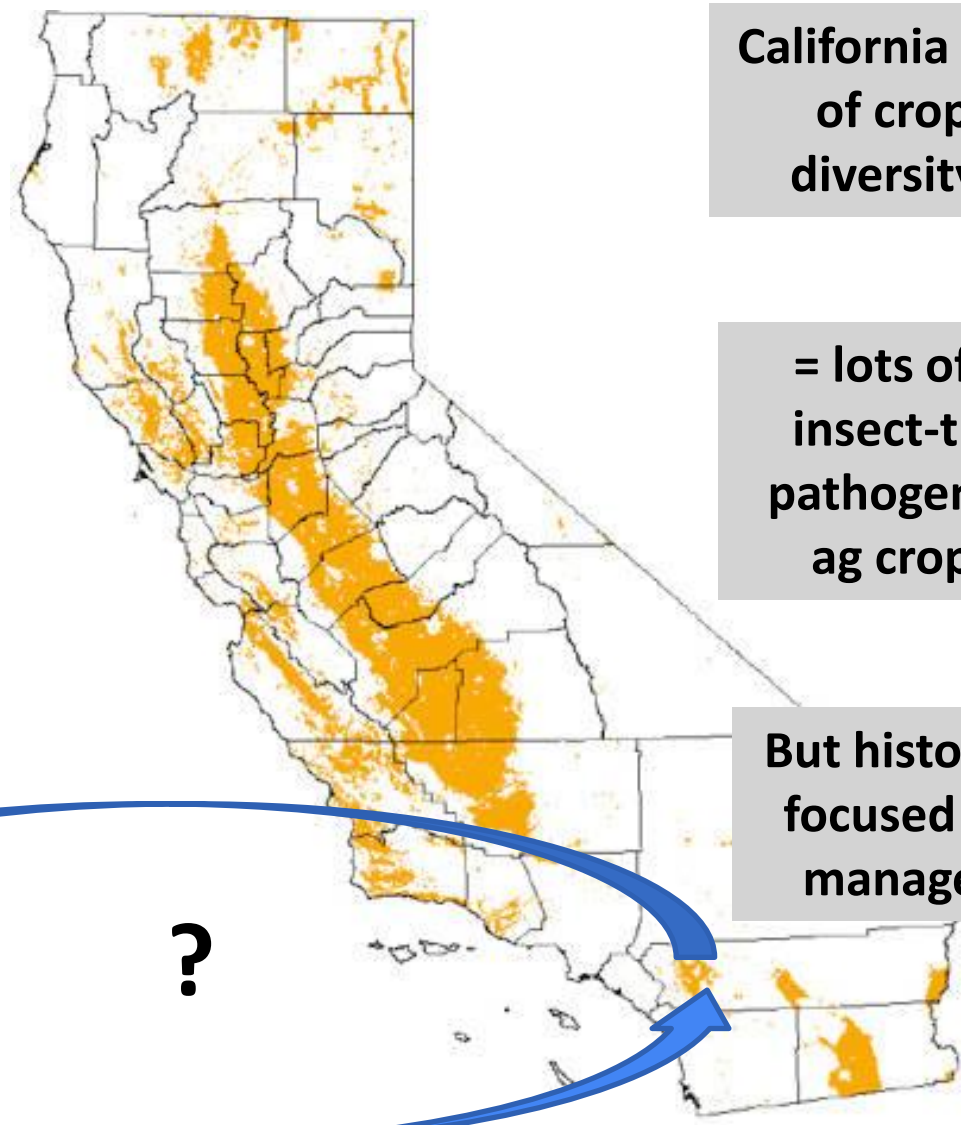
California has an abundance of cropland and huge diversity of crop plants.

= lots of opportunity for insect-transmitted plant pathogen movement from ag crops to wild plants

Source: UCANR



Cropland



California has an abundance of cropland and huge diversity of crop plants.

= lots of opportunity for insect-transmitted plant pathogen movement from ag crops to wild plants

But historically research has focused mostly on disease management in ag crops

?

Source: UCANR

Two study systems in the Mauck Lab:

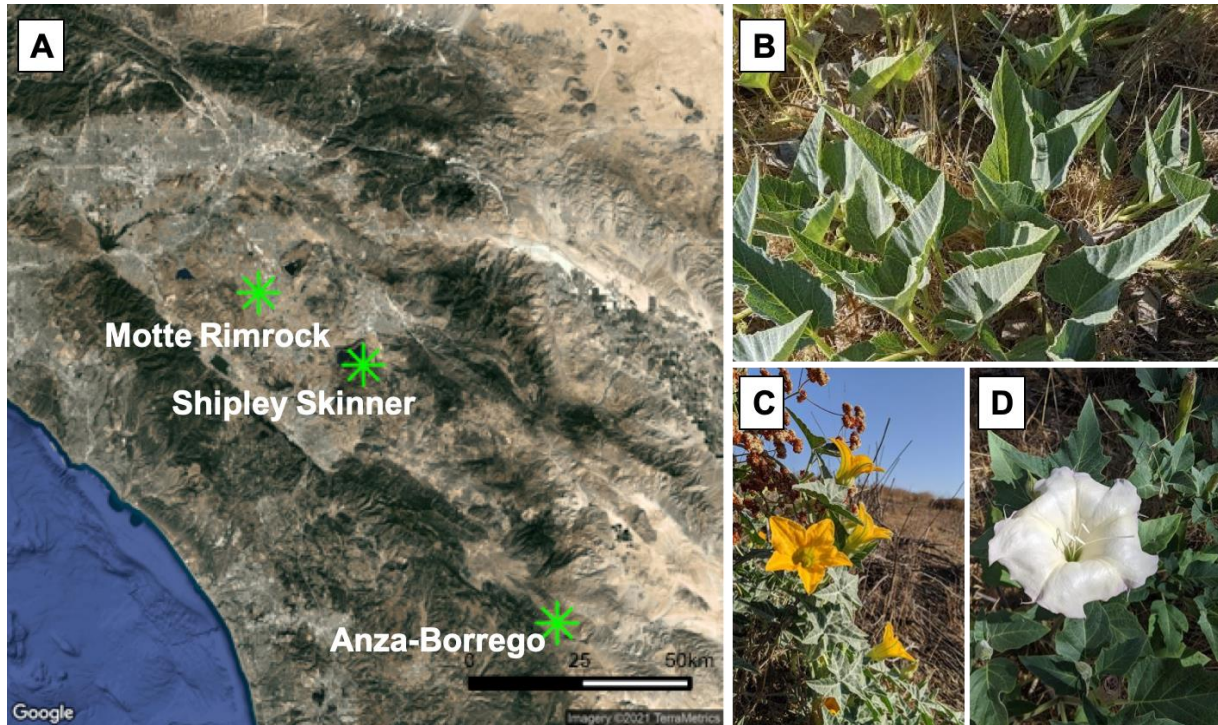


**Aphid- and whitefly-transmitted viruses
in summer drought tolerant native
perennials**



**Ca. *Liberibacter solanacearum* and
psyllids in native nightshades**

Characterizing the viromes of summer drought tolerant native perennials



[B] *Cucurbita foetidissima*

[C] *Cucurbita palmata*

[D] *Datura wrightii*



Characterizing the viromes of summer drought tolerant native perennials

Predictions:

1. Hosts are frequently infected with “crop” viruses
2. Co-infections are common
3. Crop viruses negatively affect wild host performance



Characterizing the viromes of summer drought tolerant native perennials

Virome sequencing

dsRNA extraction



Illumina sequencing



Host filtering & virus assembly
Virus identification by BLASTN
Database of plant viruses (about 11,500 whole genomes)

Targeted RT-PCR

Used to confirm host associations detected via untargeted sequencing

For dominant viruses. Used to determine prevalence
~25% of target host populations sampled



Dr. Tessa Shates

Manipulative experiments

Dominant viruses brought into culture

Seeds collected from target host populations



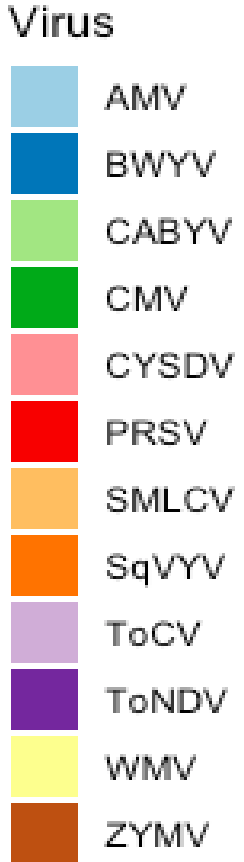
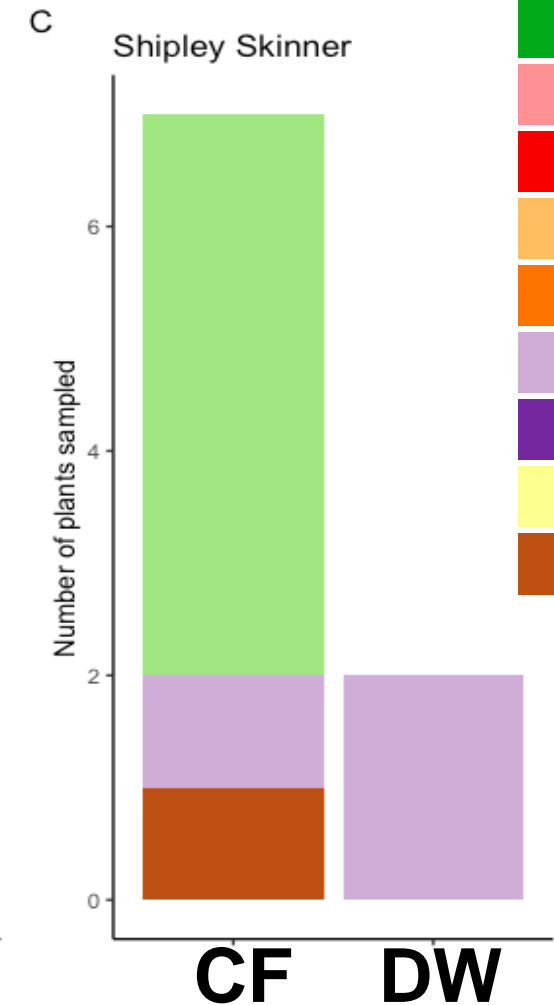
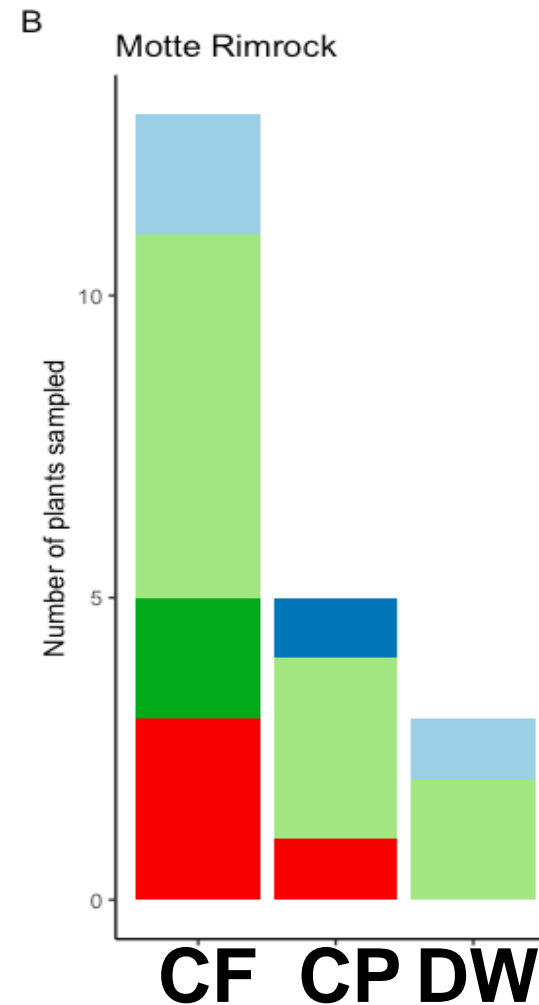
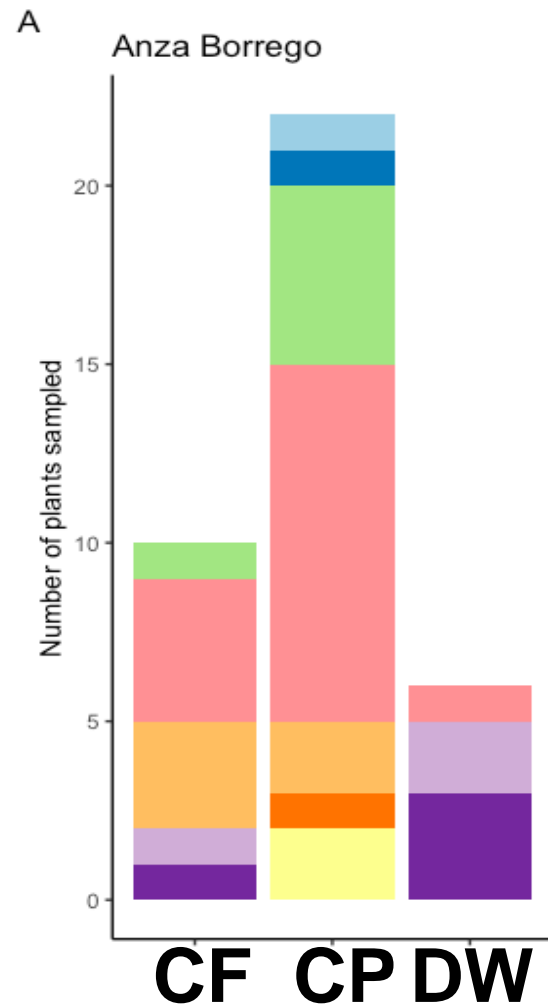
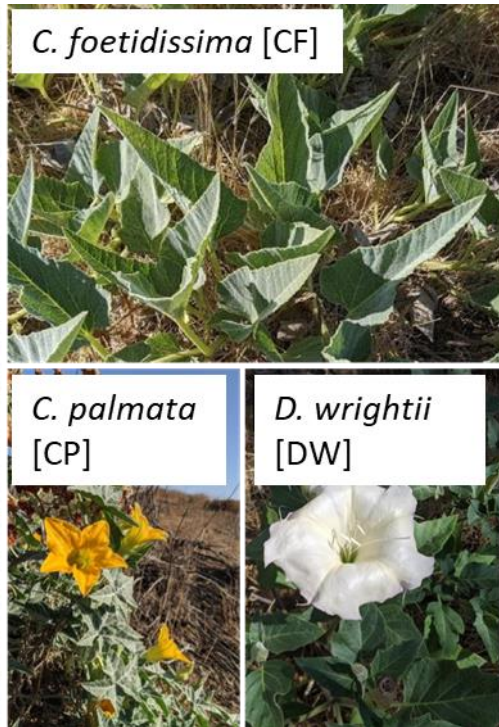
Controlled inoculations using vectors
Track metrics of plant health
Confirm infections

Prediction 1: Hosts are frequently infected with “crop” viruses

At least 12 confirmed crop-associated viruses

Also assembled four putatively novel viruses in the *Partitiviridae* family

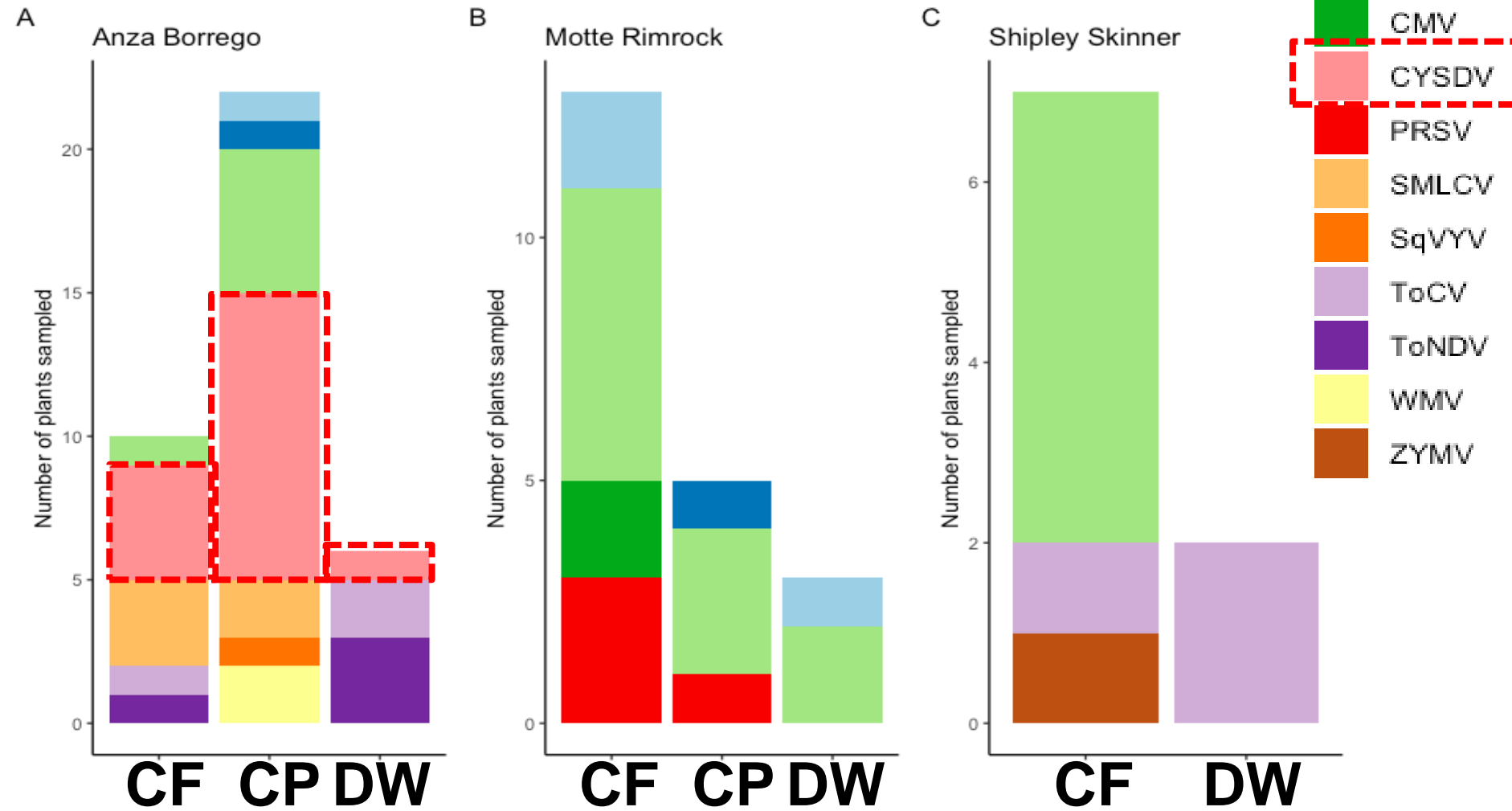
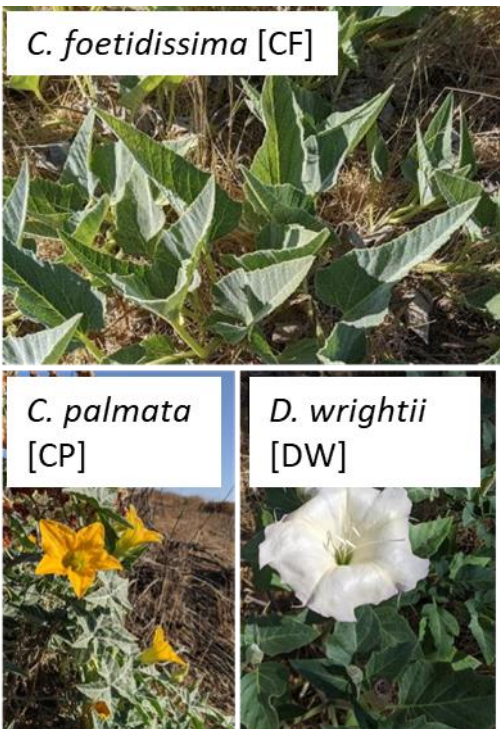
All plants infected with at least one virus



Prediction 1: Hosts are frequently infected with “crop” viruses

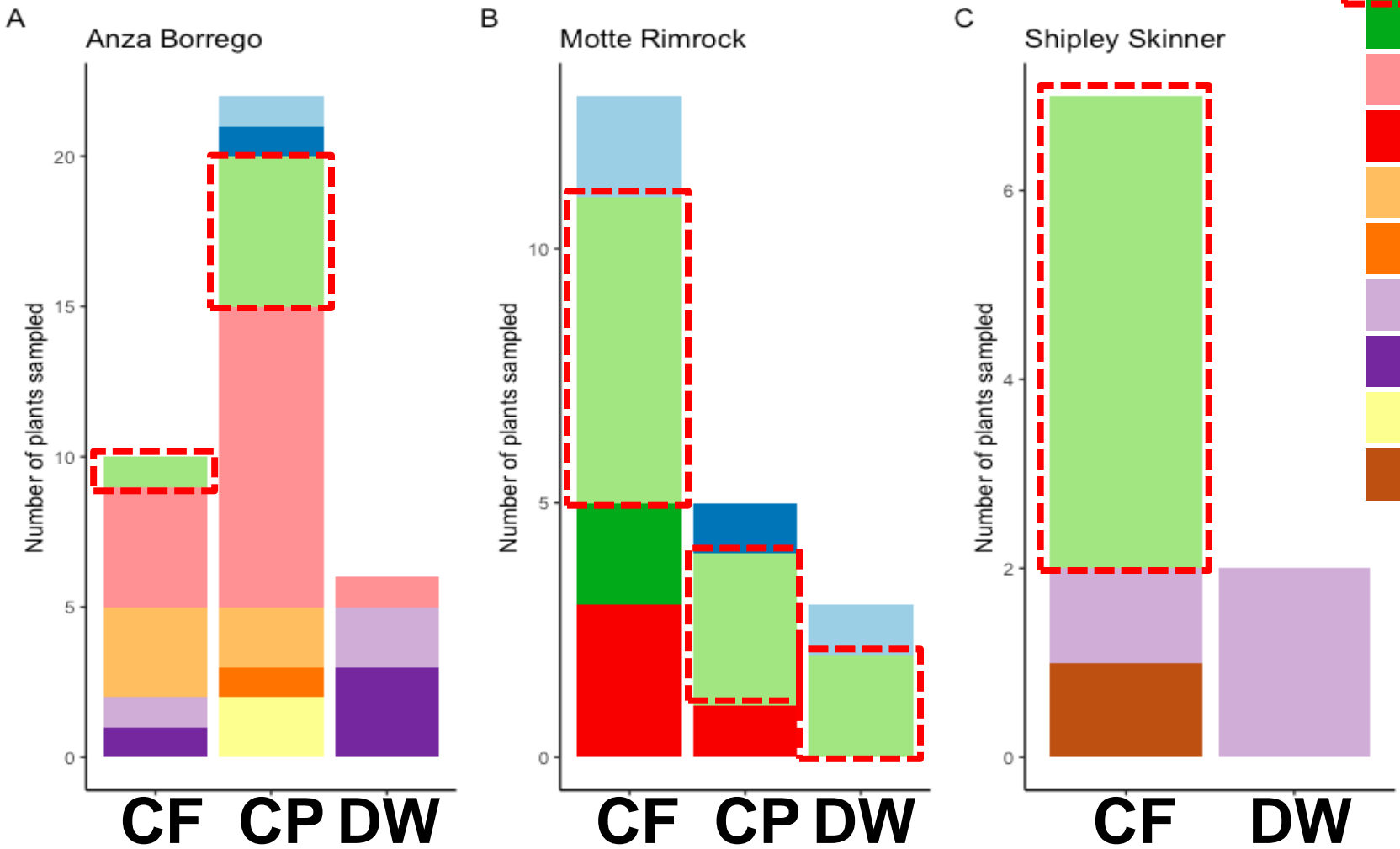
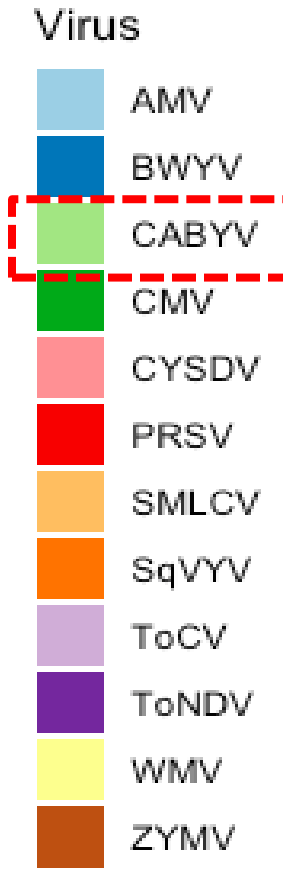
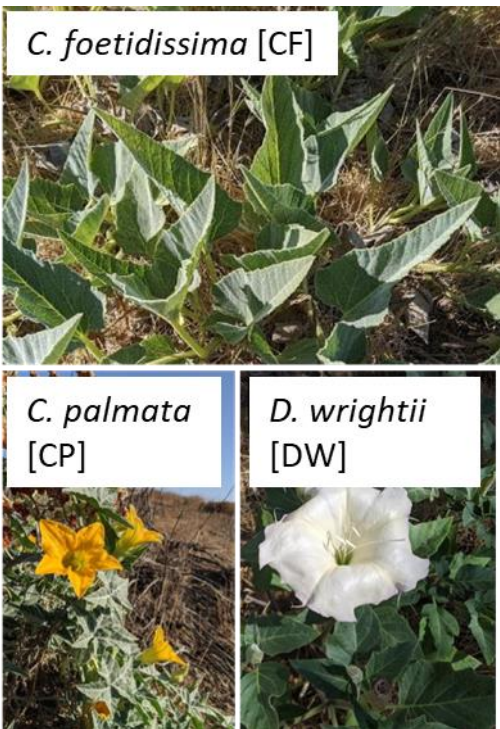
Cucurbit yellow stunting disorder virus (CYSDV)

Introduced to CA in 2007. Present in the site closest to the point of invasion in CA: the Southern Desert agricultural zone



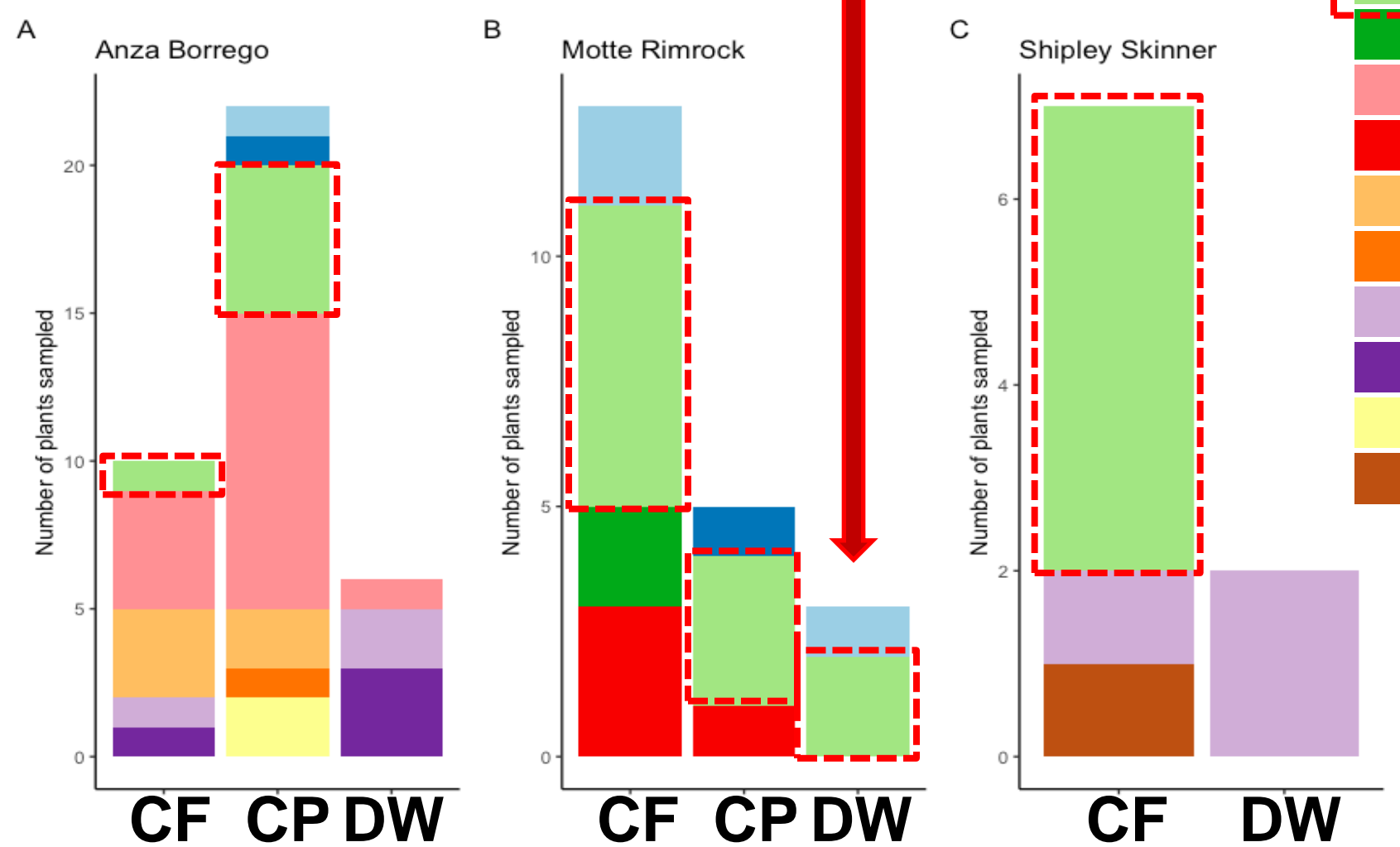
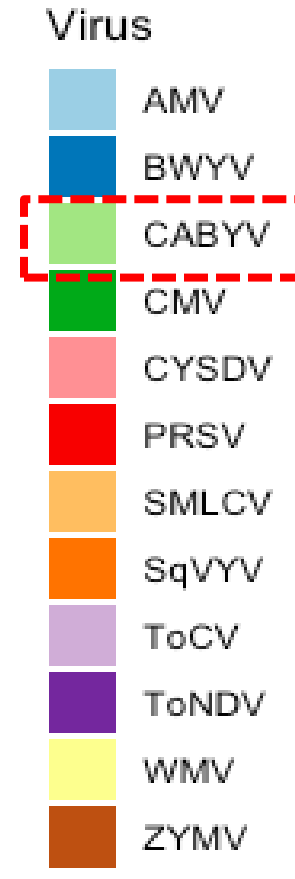
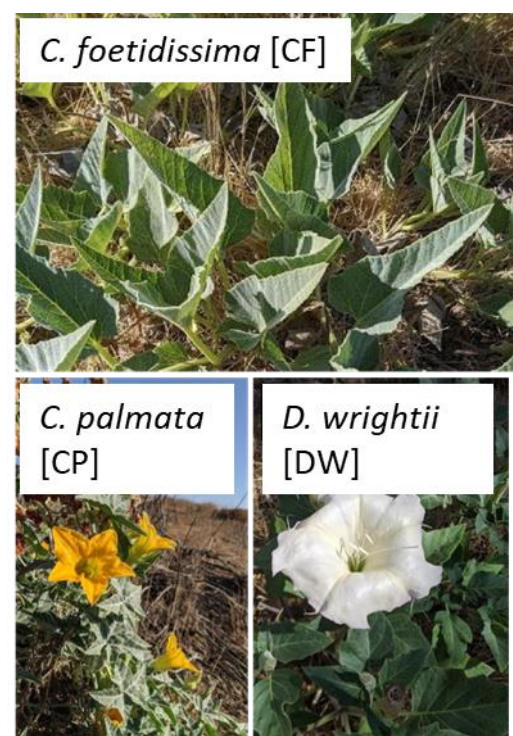
Chronic infections of perennial hosts may lead to novel virus-host associations

Cucurbit aphid-borne yellows virus (CABYV) is present across all three sites and is frequently detected. *CABYV* is an aphid-transmitted yellowing virus introduced to California in the 1990s



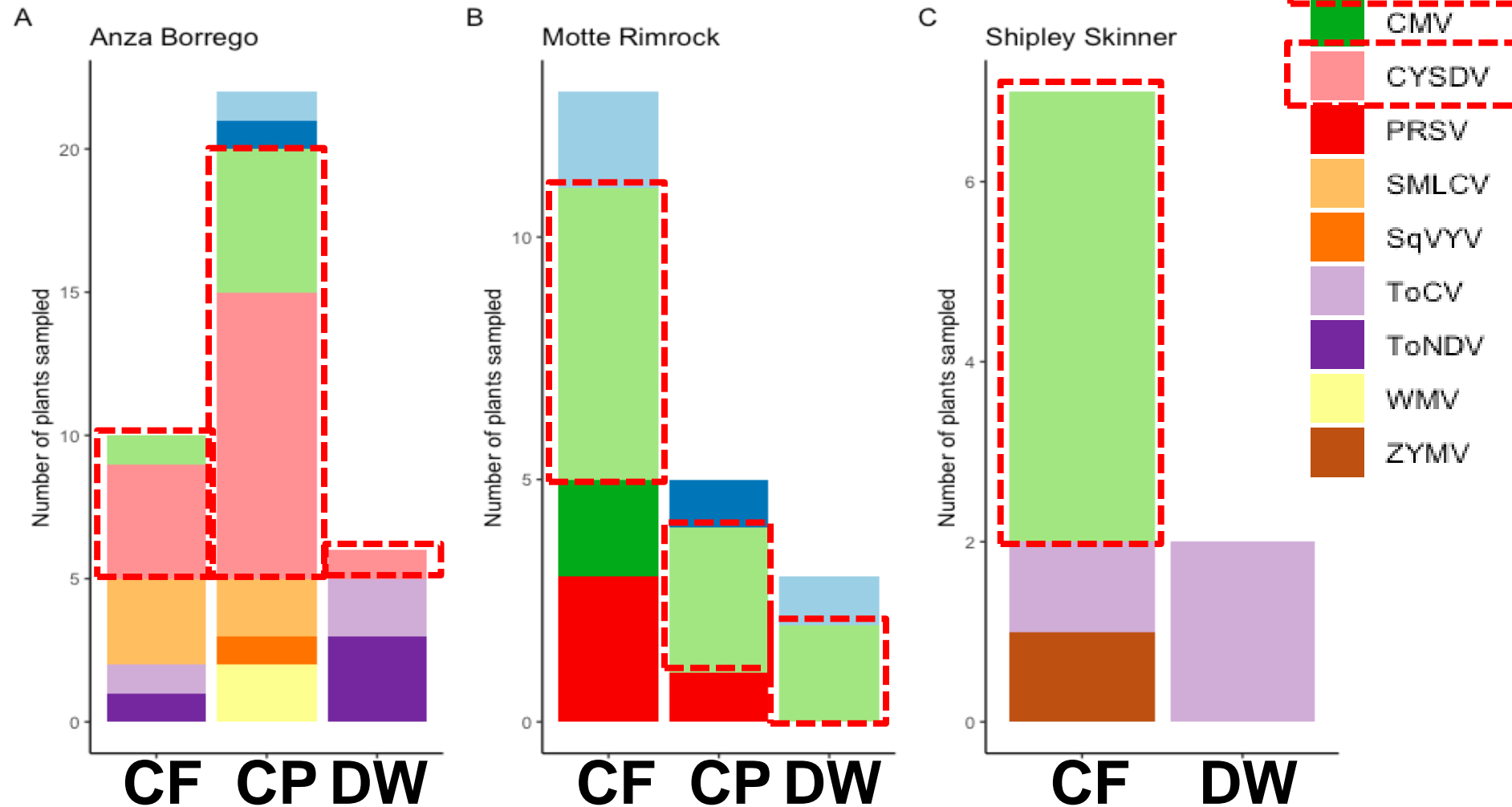
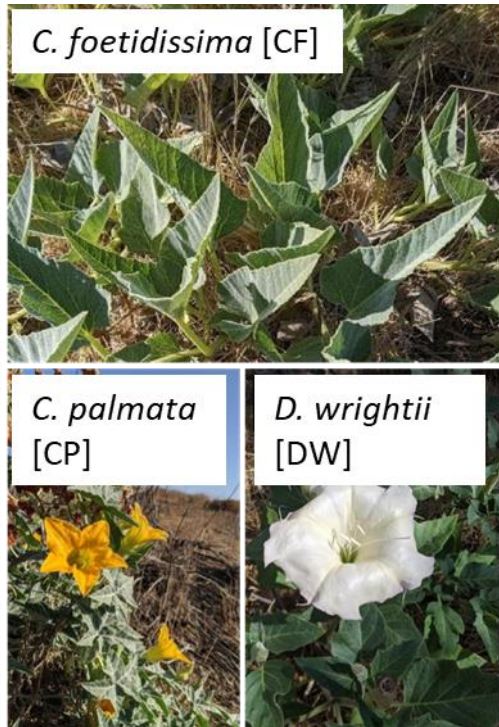
→ Chronic infections of perennial hosts may lead to novel virus-host associations

**CABYV is a virus that typically infects cucurbit crops...
...but we found infections in the non-cucurbit (*Datura wrightii*) host**

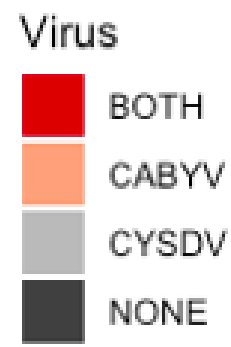
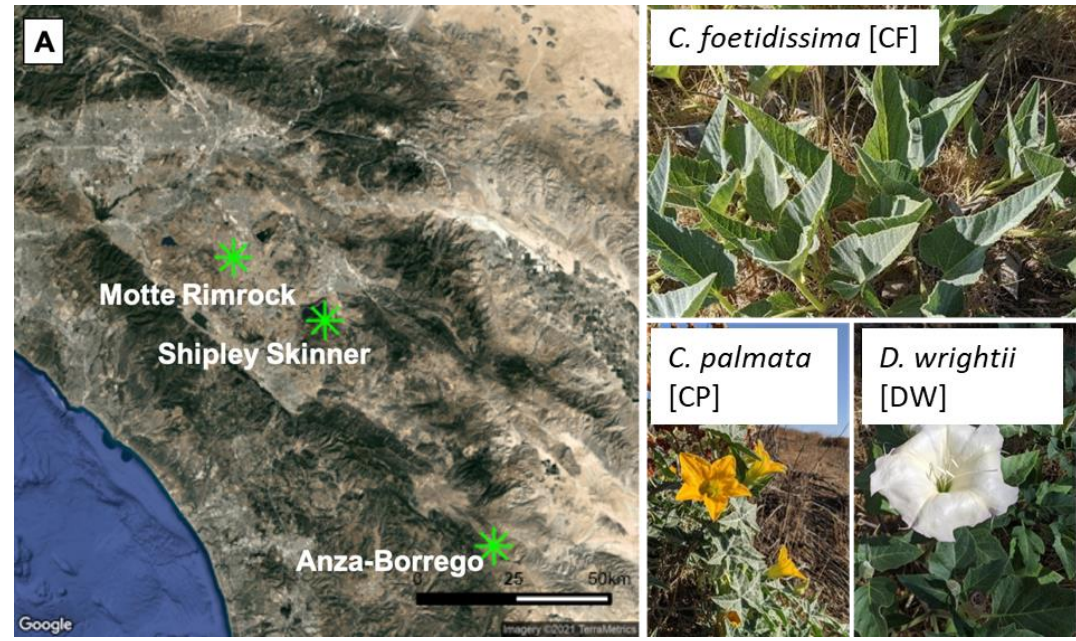
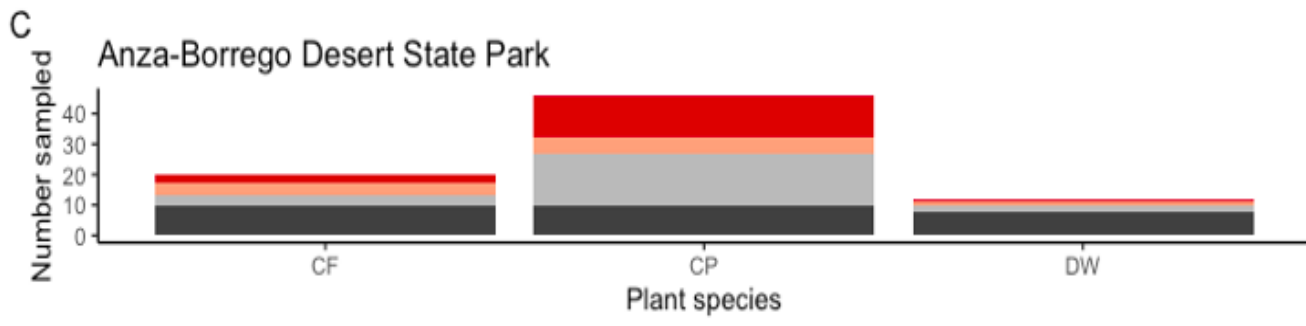


Prediction 2: Co-infections are common

Focused on CABYV and CYSDV: two introduced yellowing viruses transmitted by different vectors

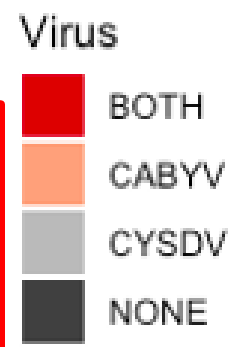
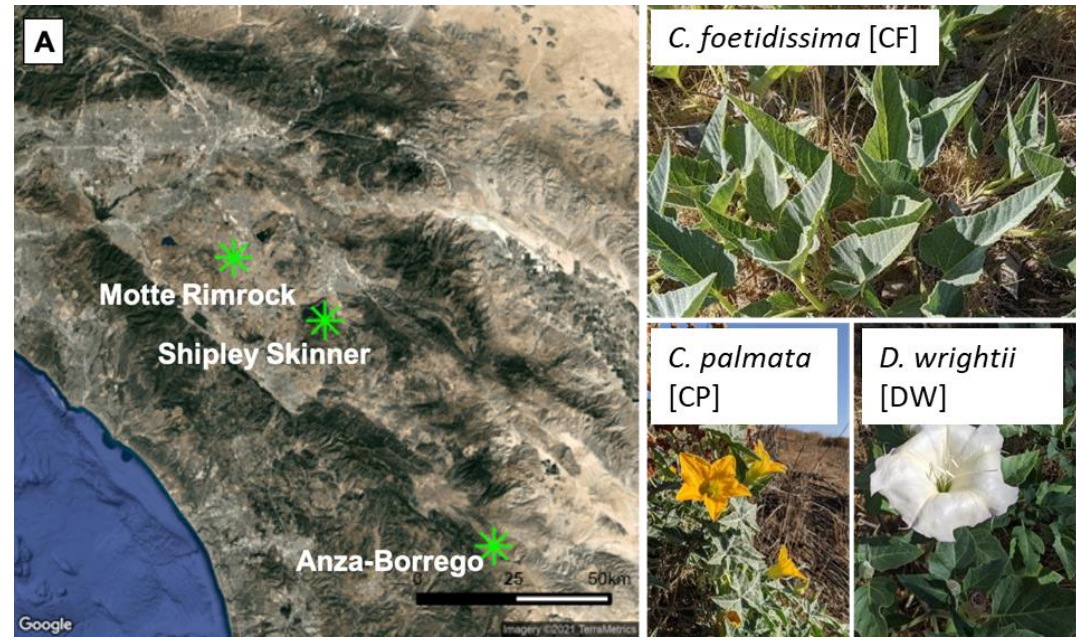
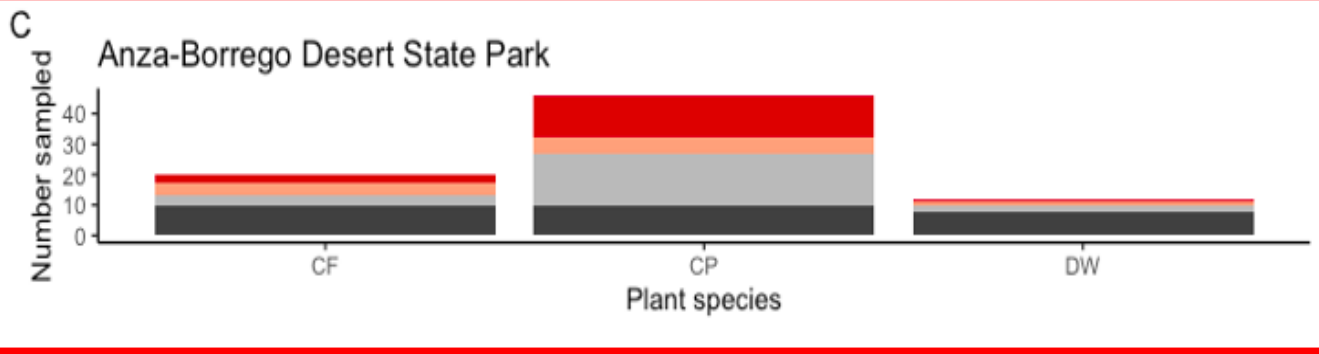
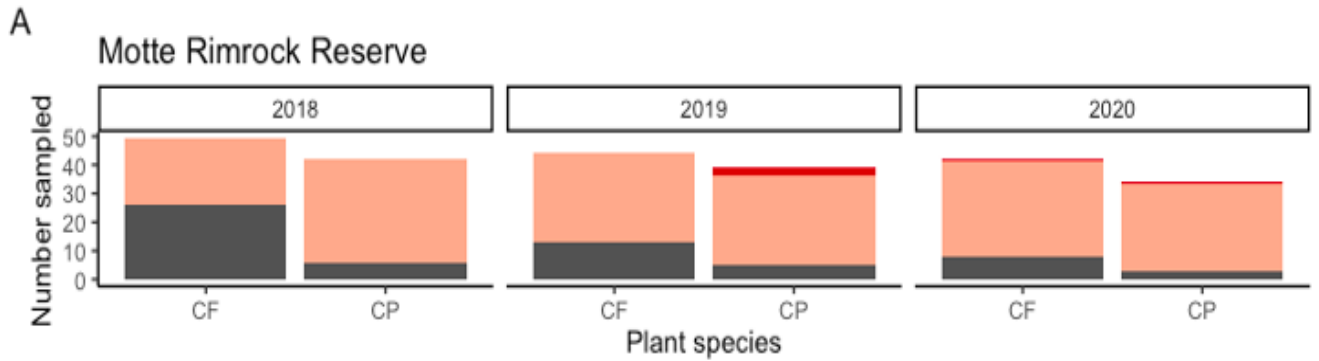


Targeted sampling and detection of CABYV and CYSDV by RT-PCR



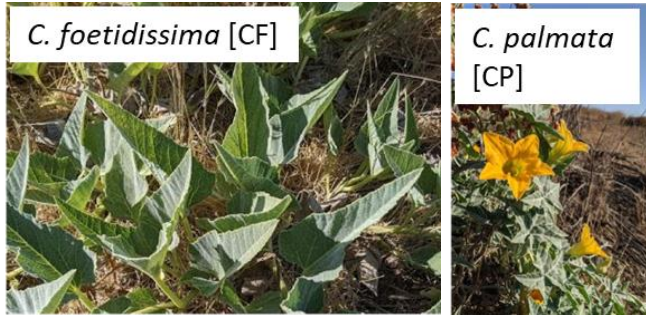
CABYV prevalence among sampled wild cucurbit hosts ranges from 10% to over 90%!

Targeted sampling and detection of CABYV and CYSDV by RT-PCR



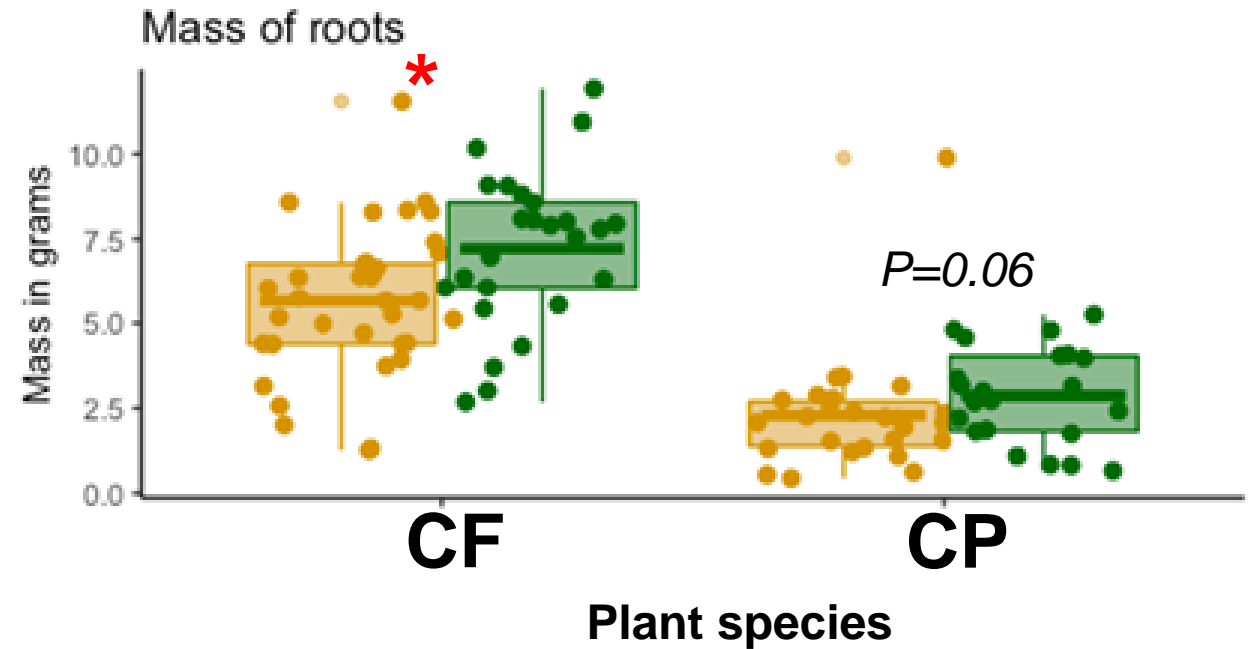
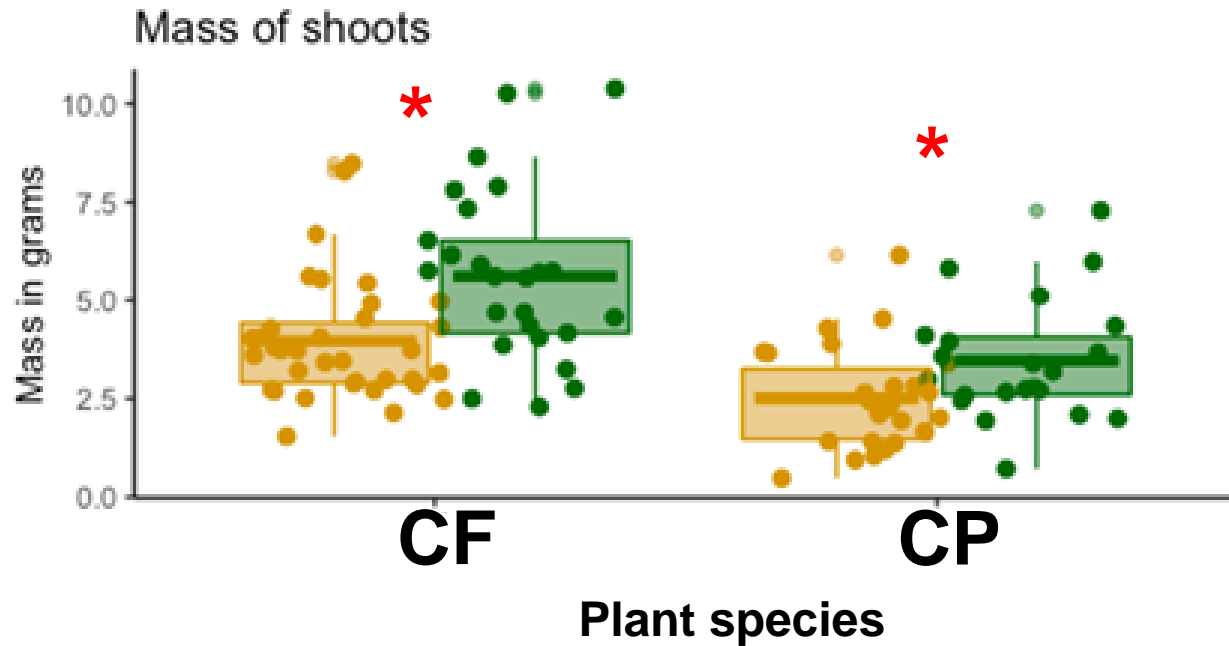
In Anza-Borrego, 42% of CABYV-infected CF and 73% of CABYV-infected CP were also infected with CYSDV!

Prediction 3. Crop viruses negatively affect wild host performance



In greenhouse experiments, CABYV infection reduced shoot and root mass

Yellow = CABYV, Green = Mock



Two study systems:

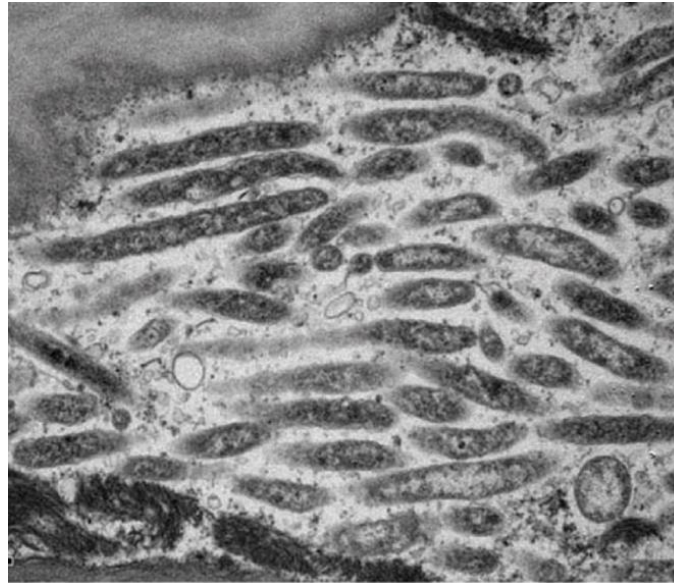
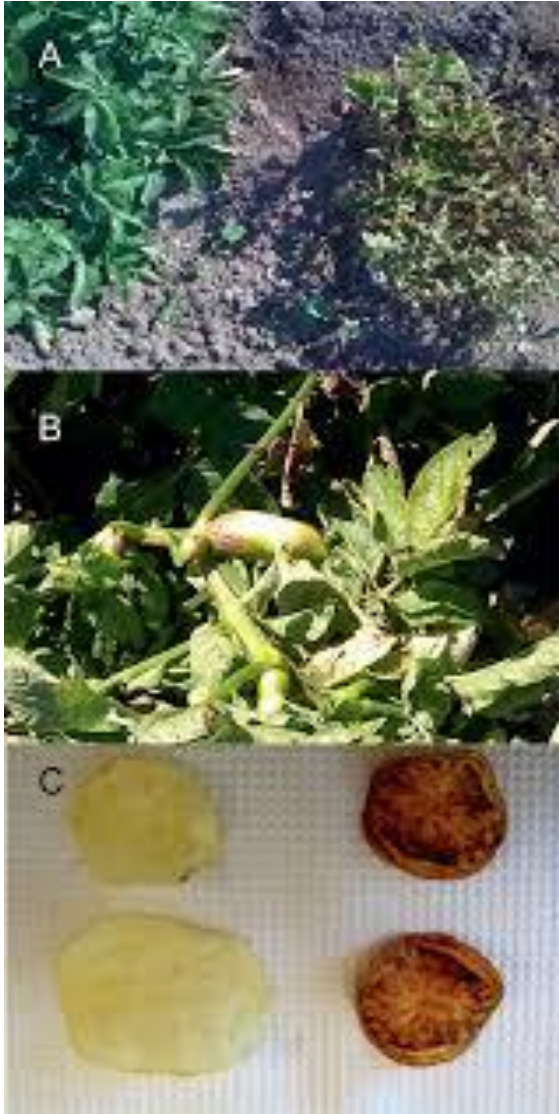


Invasive aphid- and whitefly-transmitted viruses in native squash



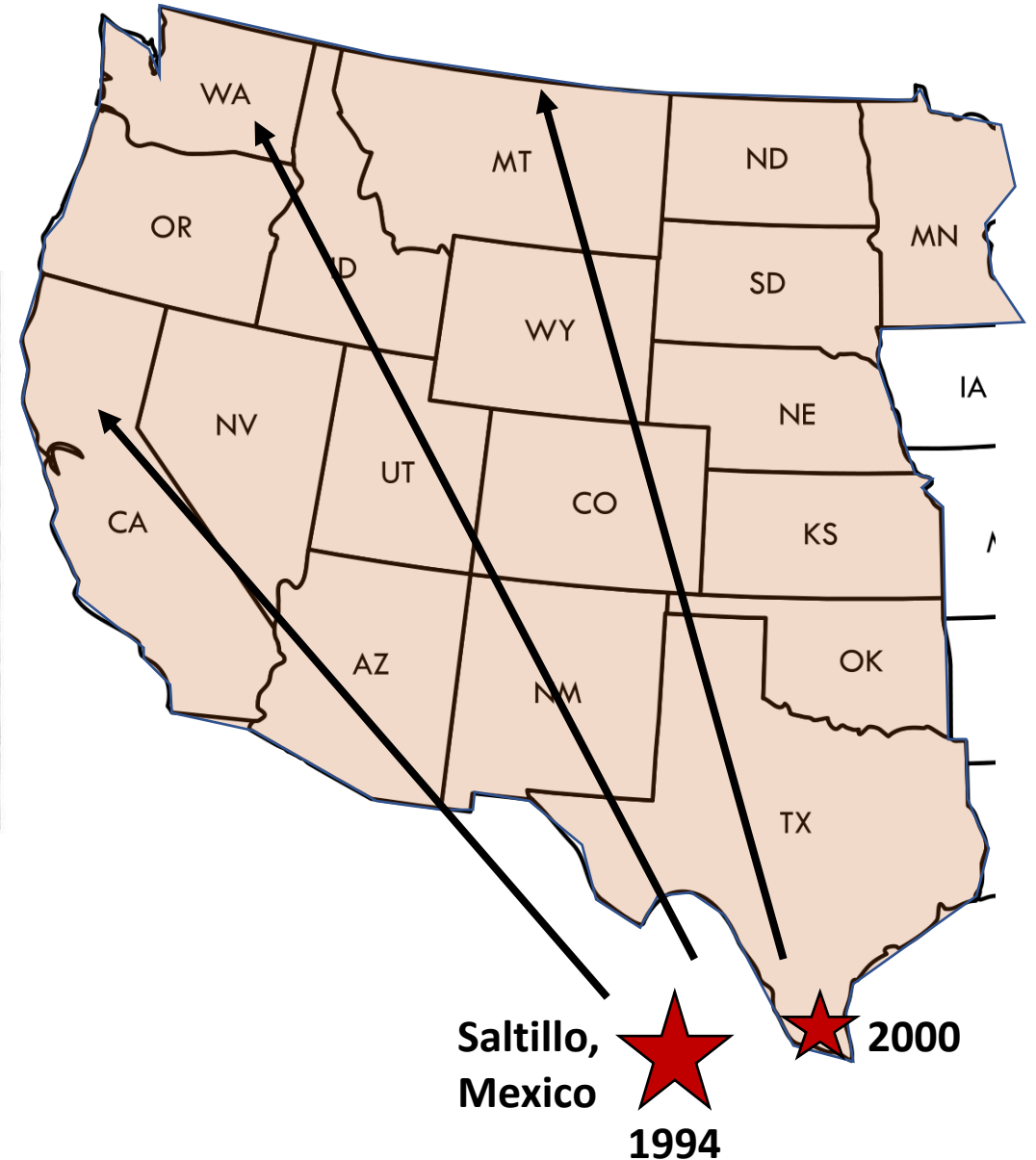
Ca. *Liberibacter solanacearum* and psyllids in native nightshades

The pathogen: *Candidatus Liberibacter solanacearum* (CLso)



Haapalainen, M. (2014). *The Annals of Applied Biology*, 165(2), 172–198

Butler et al. 2012, *Terr. Arthropod Rev.* 5 87-111



CLso is transmitted by the potato psyllid (*Bactericera cockerelli*).

The potato psyllid is native to North America, feeding on plants in the nightshade family.



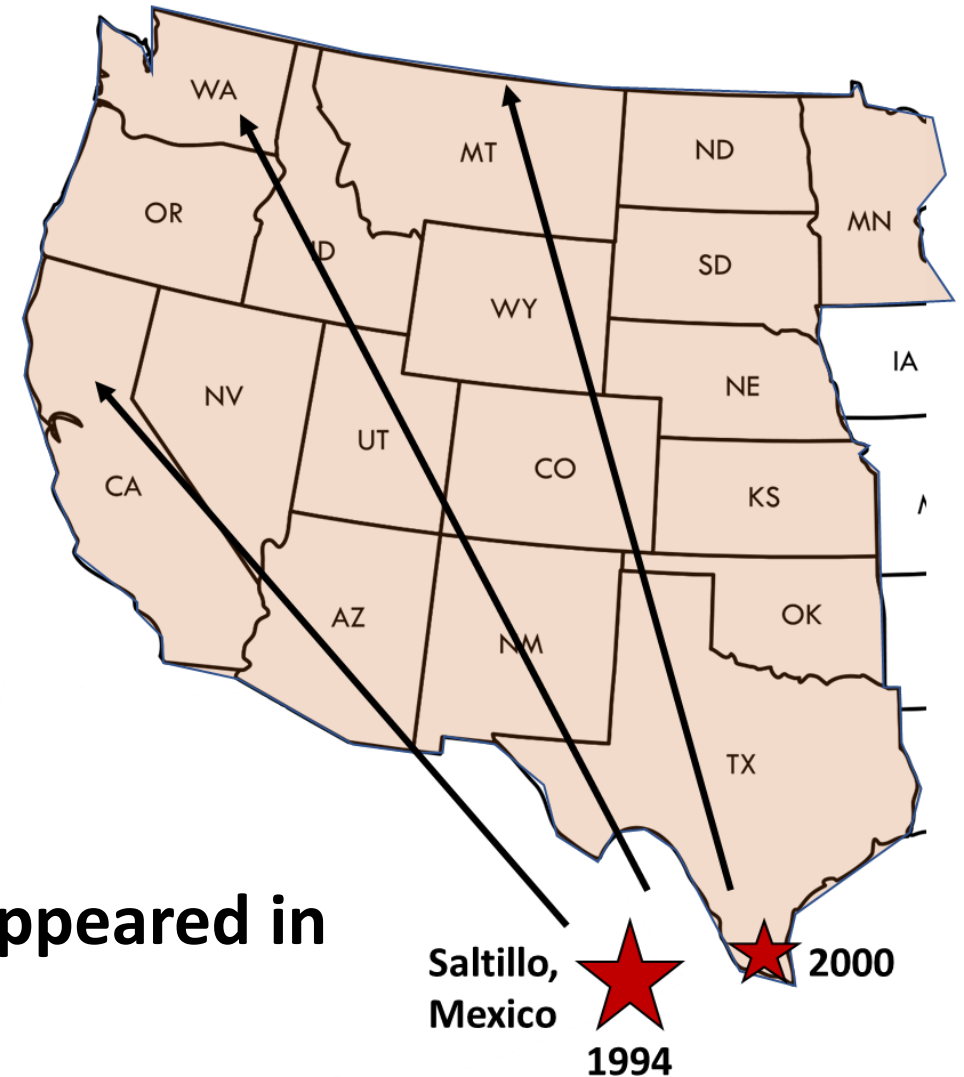
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Somehow...CLso has only recently emerged as a plant-infecting organism

BUT...



Is this really the first time CLso appeared in North America?

Becoming a detective: Discovery and characterization of CLso in herbarium samples of wild plants ranging from three to over 100 years old

Solanum elaeagnifolium



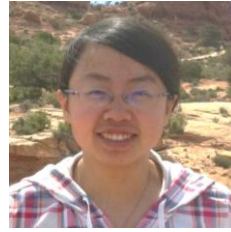
Solanum umbelliferum



Solanum americanum



UCR Herbarium: Dr. Andrew C. Sanders



Dr. Penglin Sun

Documented as non-crop hosts for the potato psyllid vector in Southern California, U.S.A.

→ 72 herbarium specimens screened for CLso by amplifying conserved regions of the 16S ribosomal RNA gene

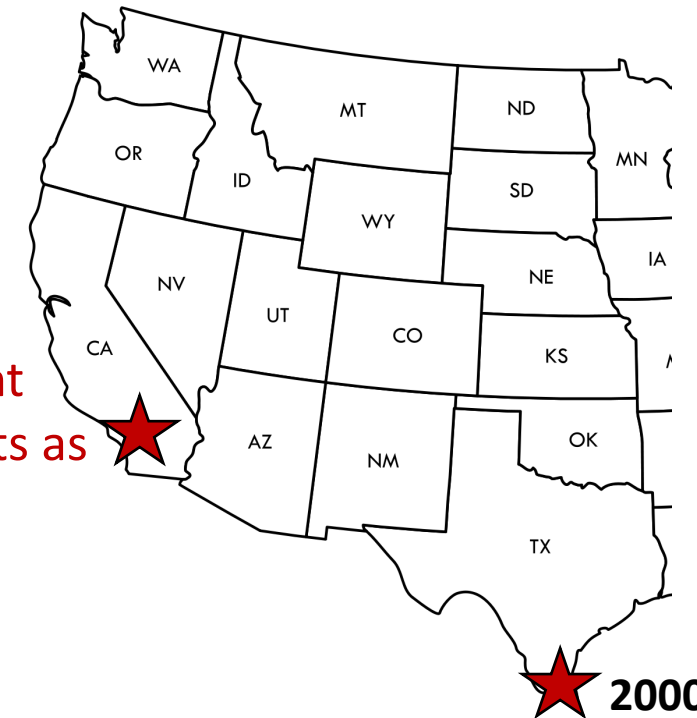
Knowlton, G. F., Thomas, W. L. *J. Econ. Entomol.* 27, (1934)
Wallis, R. L. *J. Econ. Entomol.* 44, (1951)
Wallis, R. L. *U.S. Dept. of Agriculture*, (1955)



We detected CLso in five *Solanum umbelliferum* samples

1. 2016 (Herbarium 61)
2. 2011 (Herbarium 59)
3. 1999 (Herbarium 54)
4. 1995 (Herbarium 51)
5. **1970 (Herbarium 46)**

(2000) Zebra chip disease first detected in US (Texas)



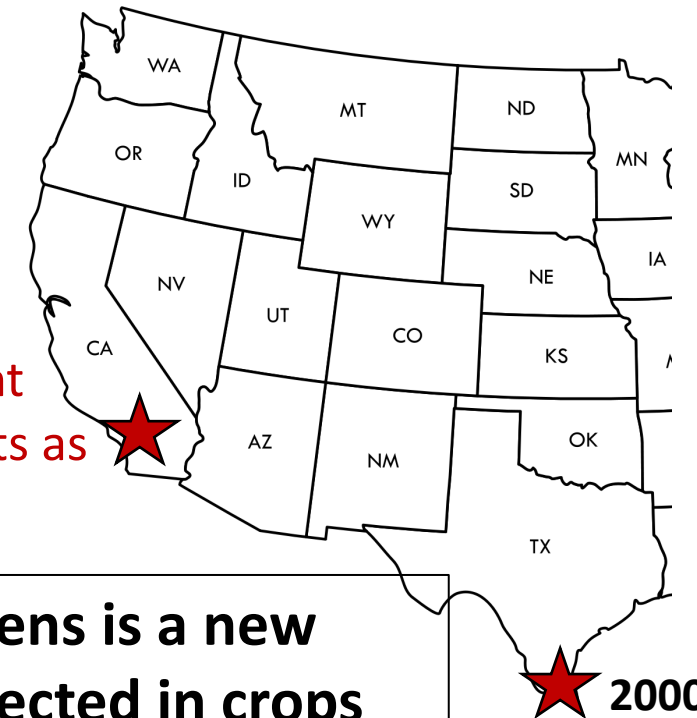
Putative causal agent present in wild plants as early as 1970



We detected CLso in five *Solanum umbelliferum* samples

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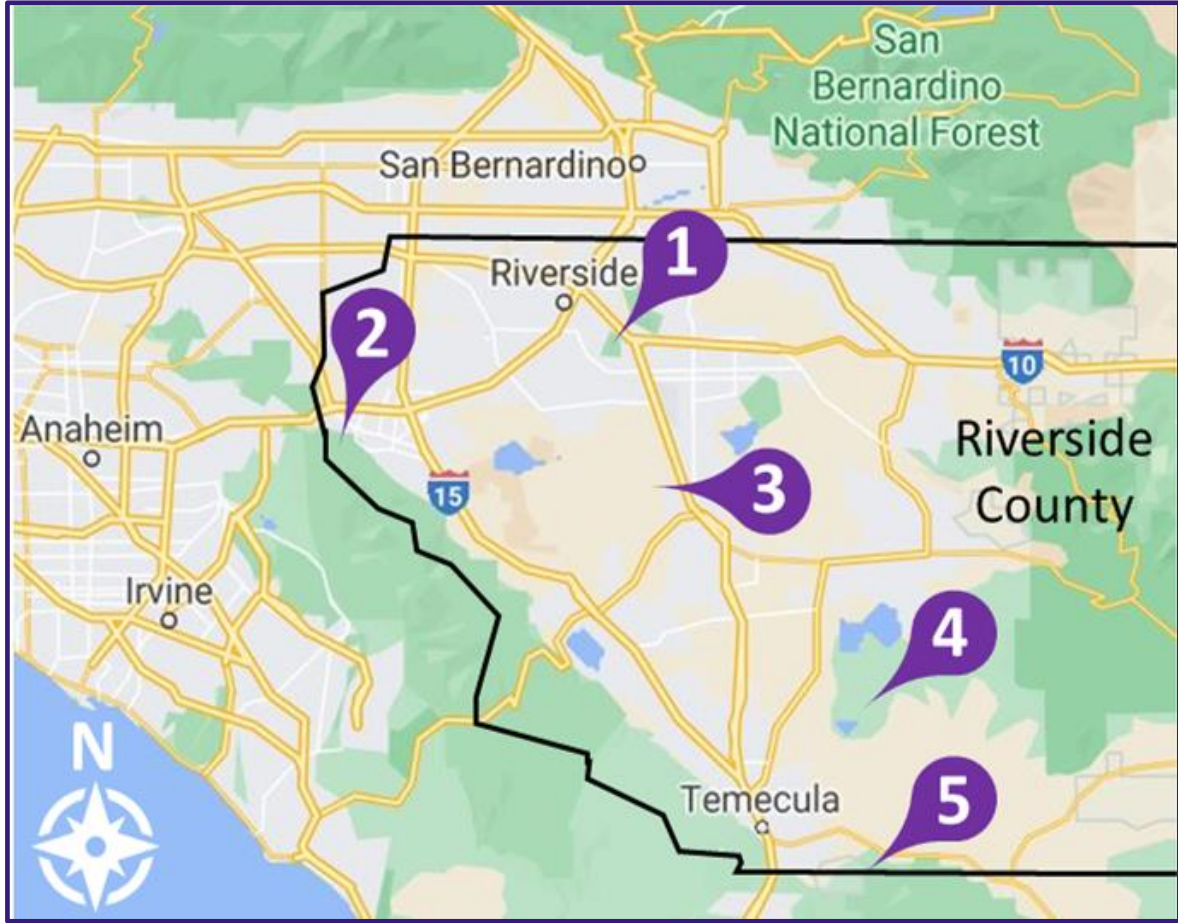
(2000) Zebra chip disease first detected in US (Texas)



Putative causal agent present in wild plants as early as 1970

The CLso in herbarium specimens is a new variant (haplotype), never detected in crops
 → now named CLso G

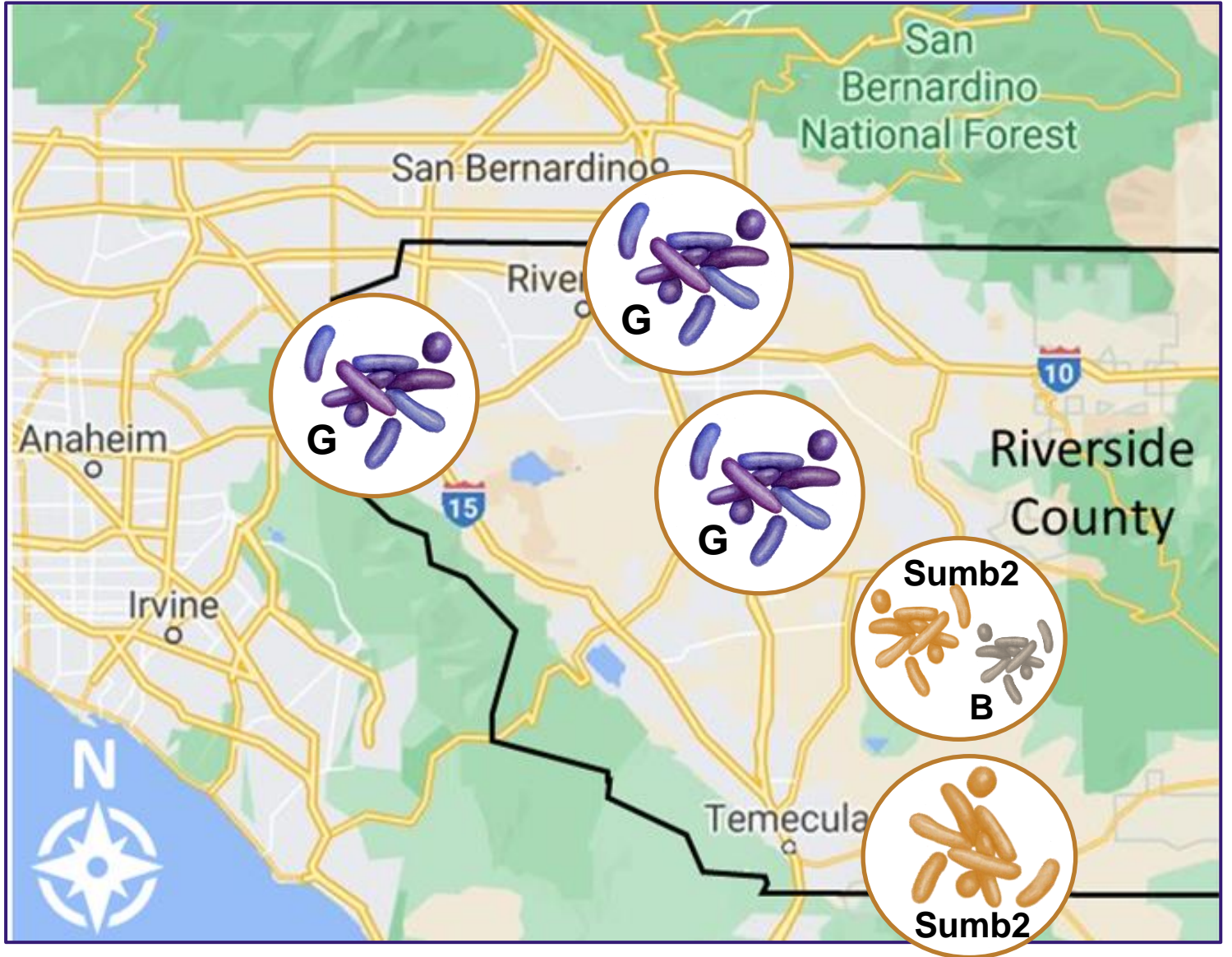
What about contemporary *S. umbelliferum* populations?



- 1. Sycamore Canyon Park
- 2. Original herbarium population (Corona, CA)
- 3. Motte Rimrock UC Reserve
- 4. Shipley Skinner Multispecies Reserve
- 5. Emerson Oaks UC Reserve

Sleuthing results:

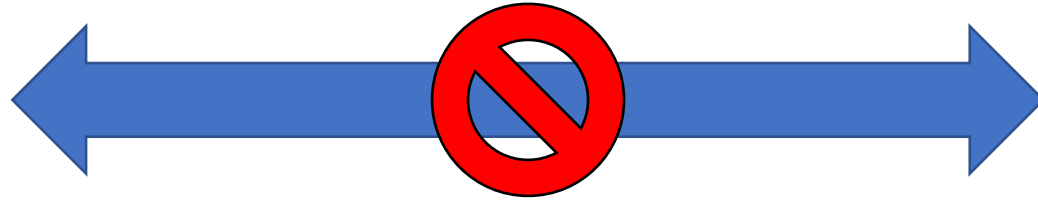
- We found haplotype G in three populations
- We found *another novel haplotype* (“Sumb2”) in the two southernmost populations
- We only found a crop-associated haplotype (B) in *one plant* (in co-infection with “Sumb2”)



CLso haplotypes G, "Sumb2"

Why is this tale different from the story of viruses in wild squash?

CLso haplotypes B, A



Wild nightshade

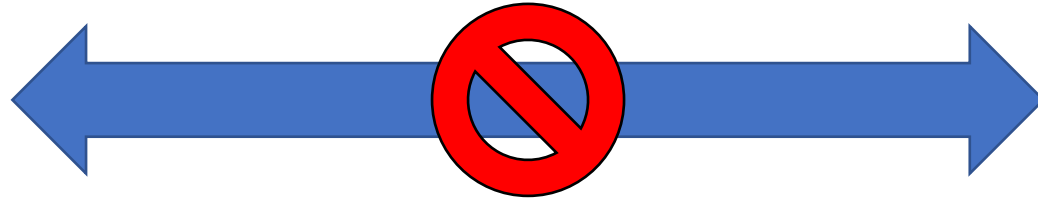
Crops (tomato/potato)

CLso haplotypes G, Sumb2



Wild nightshade

Why is this tale different from the story of viruses in wild squash?



What we thought was one vector species is actually 3 species with very particular host preferences (crop vs. native plants)!

CLso haplotypes B, A



Crops (tomato/potato)

Conclusions

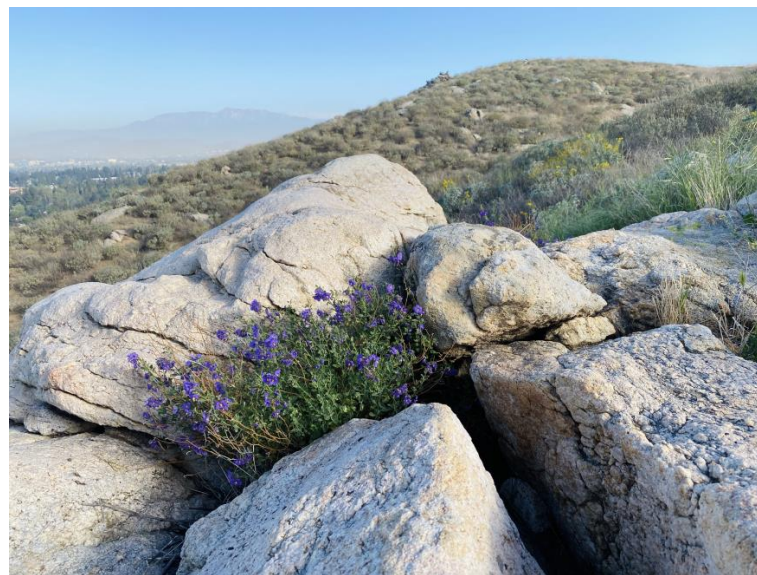
Aphid- and whitefly-transmitted viruses in summer drought tolerant native perennials



Crop-associated viruses frequently spill over to infect wild plants

Crop viruses can modify wild host performance and species interactions

Ca. *Liberibacter solanacearum* and psyllids in native nightshades



Historical specimens are valuable resources for studying pathogen evolution

Vector population structure & behavior underlie pathogen transfer (or lack thereof) across agroecological interfaces

Acknowledgements

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Current Mauck lab members:

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Penguin Sun
Natalie Chan

Mauck laboratory Fall 2023



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CA-R-ENT-5244-CG

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