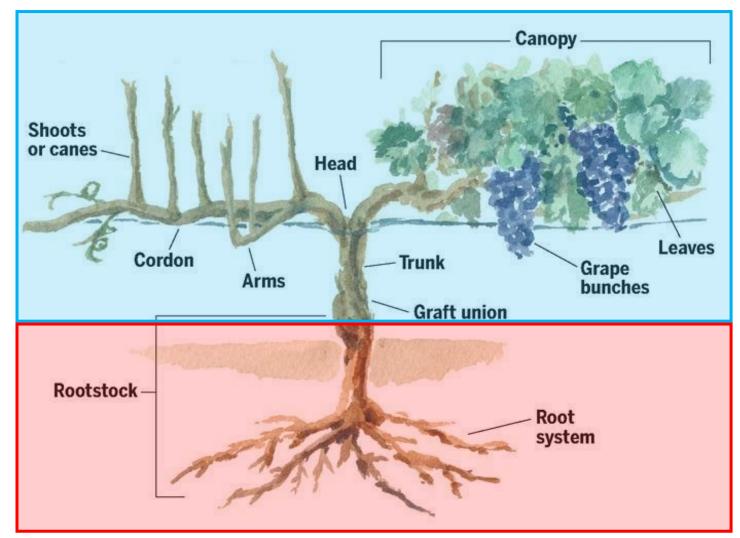
From roots to shoots, the impact of grafting on Vitis microbiota

Joel Swift Miller Lab Grape and Wine Symposium March 9th, 2022



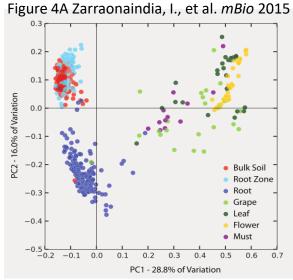
 I am interested in how the root system (Rootstock) impacts the shoot system (Scion) of grape vines.



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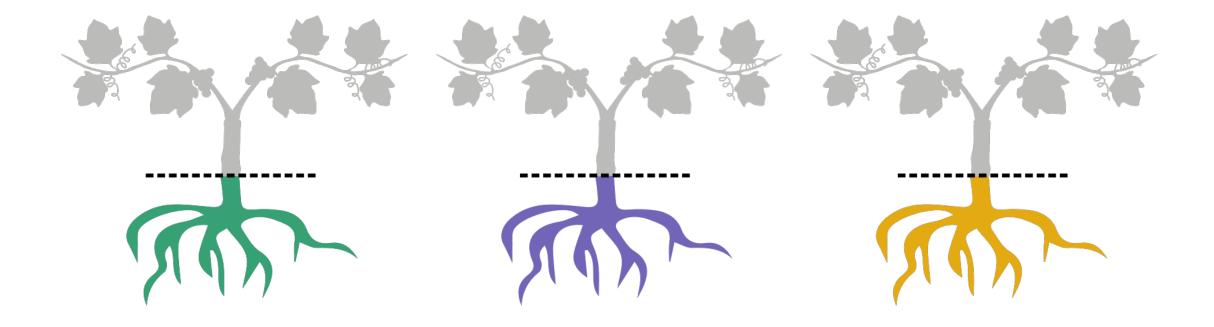
Microorganisms and grapes - What do we know?

• Grapevine compartments have distinct bacterial fungal communities^{1,2}.



- Grape microbiota are influenced by a number of environmental factors (e.g. soil type, climate, terrain)^{3,4}.
- Grafting while ubiquitous in viticulture is under explored, to date studies have only examined microbiota of the roots in relation to grafting^{5,6}.
 - 1. Zarraonaindia, I., et al. *mBio* 2015
 - 2. Liu, D. and Howell, K. Env Microbiol 2021
 - 3. Burns, K. N., et al. Soil Biol Biochem 2015
 - 4. Bokulich, N. A., et al. PNAS 2014
 - 5. Marasco, R. et al. Microbiome 2018
 - 6. D'Amico, F. D. et al. Front Microbiol 2018

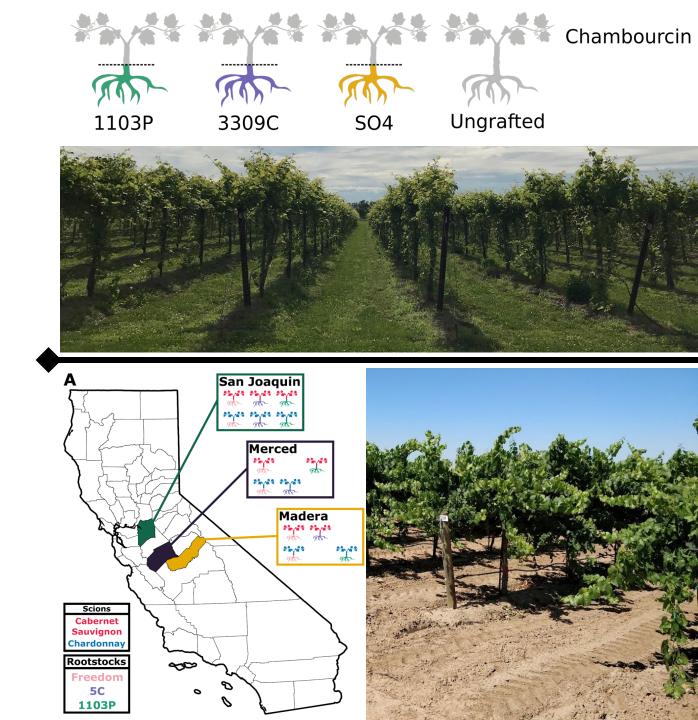
To build a complete picture of how root system genotypes control microbiota of the plant will require sampling above and below ground.

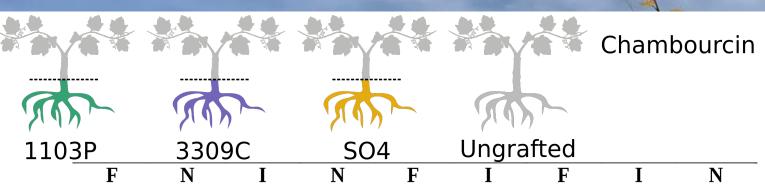


Research Outline

- Southwest Missouri
 - 2018 Harvest

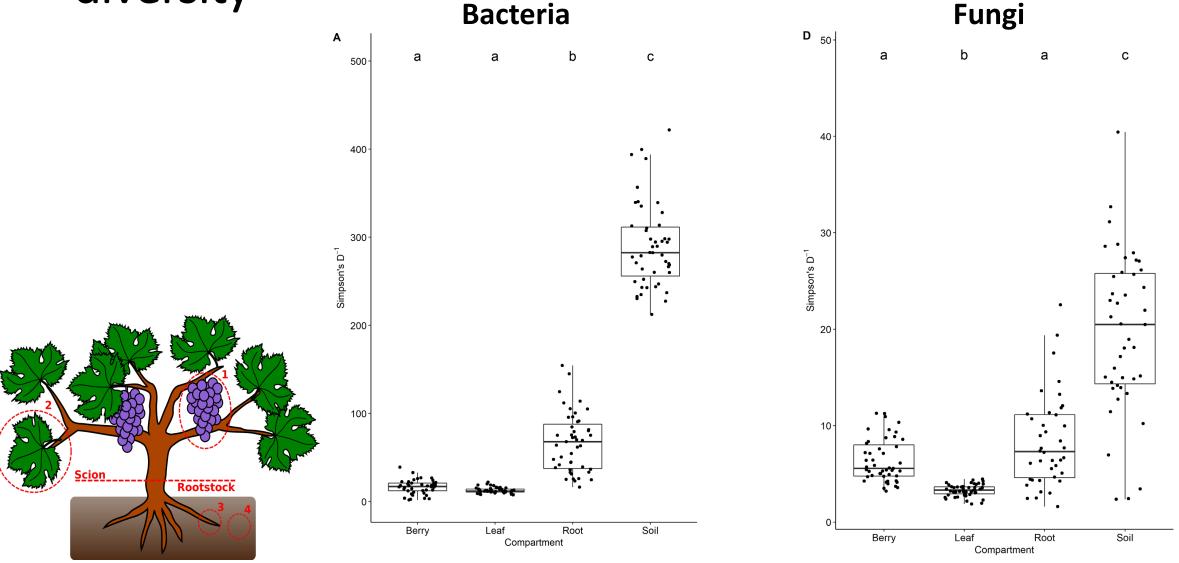
- Central Valley California
 - Multiple time points, years, and vineyards



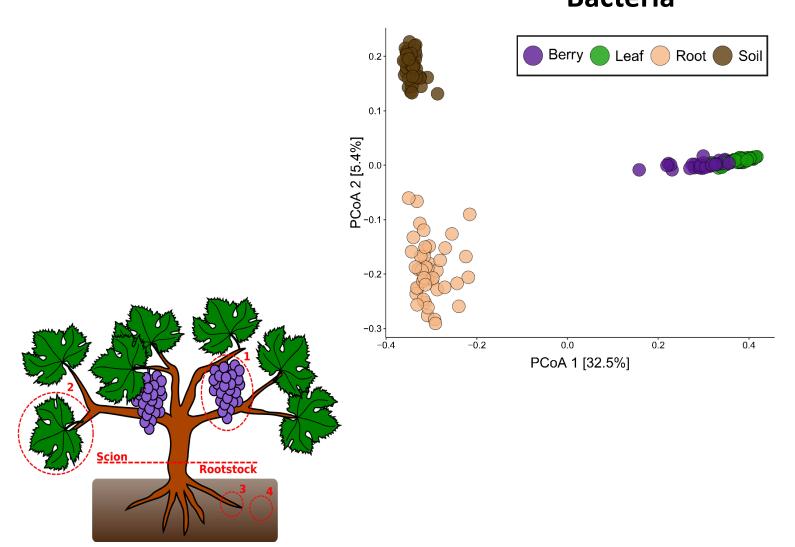




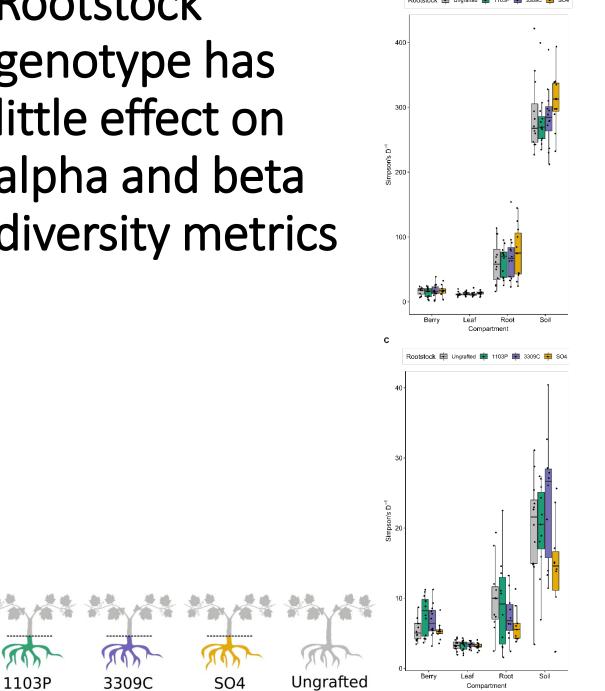
Grapevine compartments exhibit varying levels of diversity Bacteria



Grapevine compartments harbor distinct microbiota



Rootstock genotype has little effect on alpha and beta diversity metrics



А



Phytopathology • 2018 • 108:1429-1442 • https://doi.org/10.1094/PHYTO-03-18-0098-R

Etiology

Grape Sour Rot: A Four-Way Interaction Involving the Host, Yeast, Acetic Acid Bacteria, and Insects

Megan E. Hall,[†] Gregory M. Loeb, Lance Cadle-Davidson, Katherine J. Evans, and Wayne F. Wilcox

First and fifth authors: Section of Plant Pathology and Plant-Microbe Biology, School of Integrative Plant Science, and New York State Agricultural Experiment Station, Cornell University, Geneva 14456; second author: Department of Entomology, New York State Agricultural Experiment Station, Cornell University; third author: United States Department of Agriculture–Agricultural Research Service, Grape Genetics Research Unit, Geneva, NY 14456; and fourth author: Tasmanian Institute of Agriculture, University of Tasmania, Hobart, Tas. 7001, Australia.

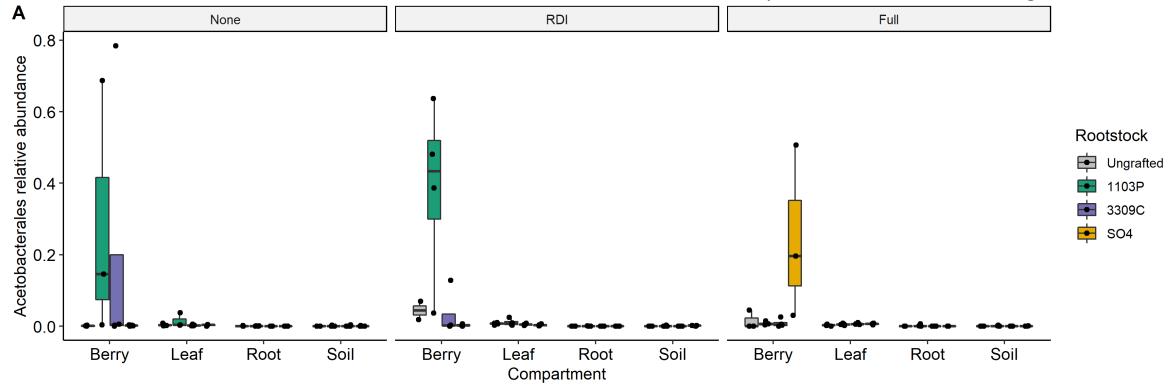
Accepted for publication 28 June 2018.



Damaged host tissue + Yeast + Acetic acid bacteria + Drosophila = Sour Rot

How do rootstocks influence the abundance of *Acetobacterales*?

Compartment x Rootstock x Irrigation *P* = 0.002

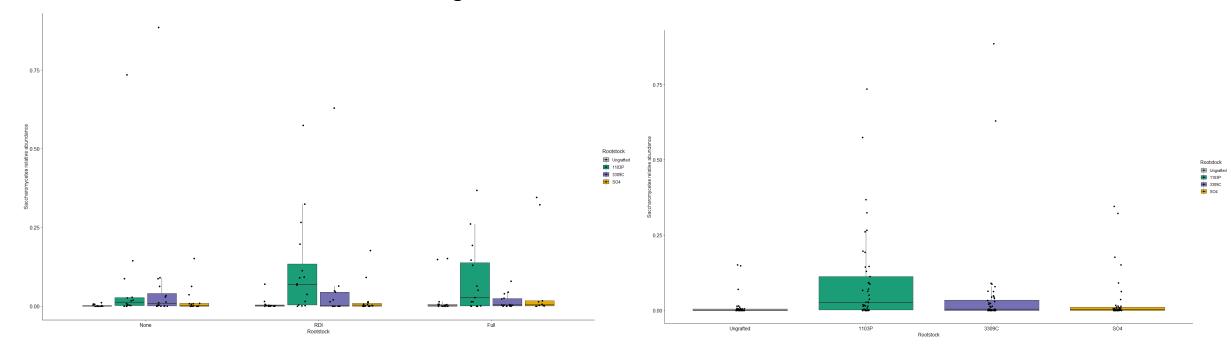


Damaged host tissue + Yeast + Acetic acid bacteria + Drosophila = Sour Rot

How do rootstocks influence the abundance of *Saccharomycetes*?

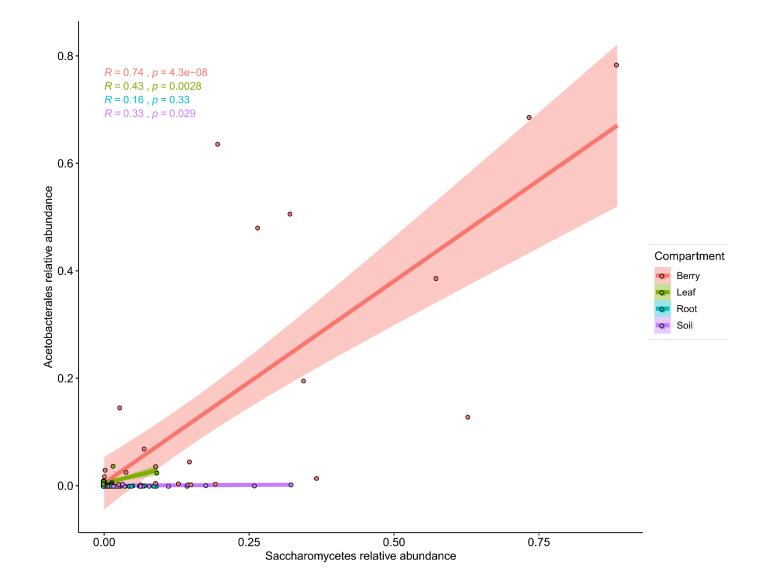
Rootstock x Irrigation P = 0.007

Rootstock P = 0.006



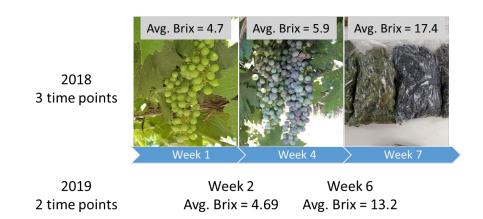
Damaged host tissue + Yeast + Acetic acid bacteria + Drosophila = Sour Rot

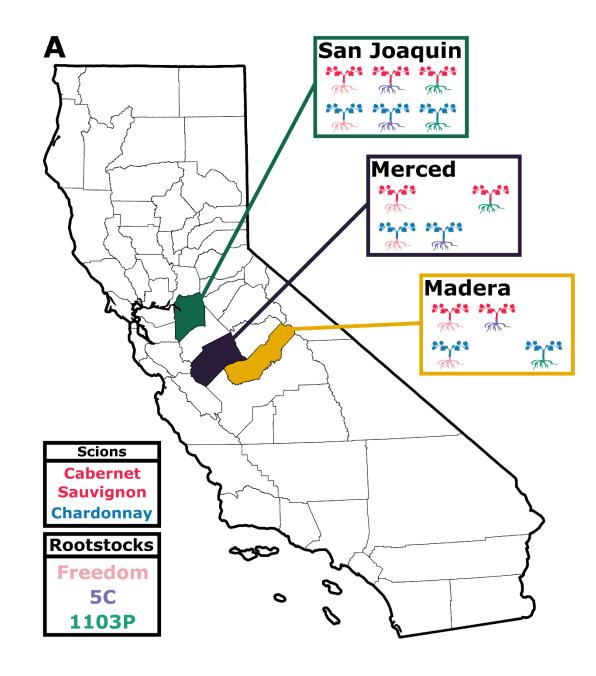
Strong correlation between the relative abundance of *Saccharomycetes* and *Acetobacterales*



Central Valley California

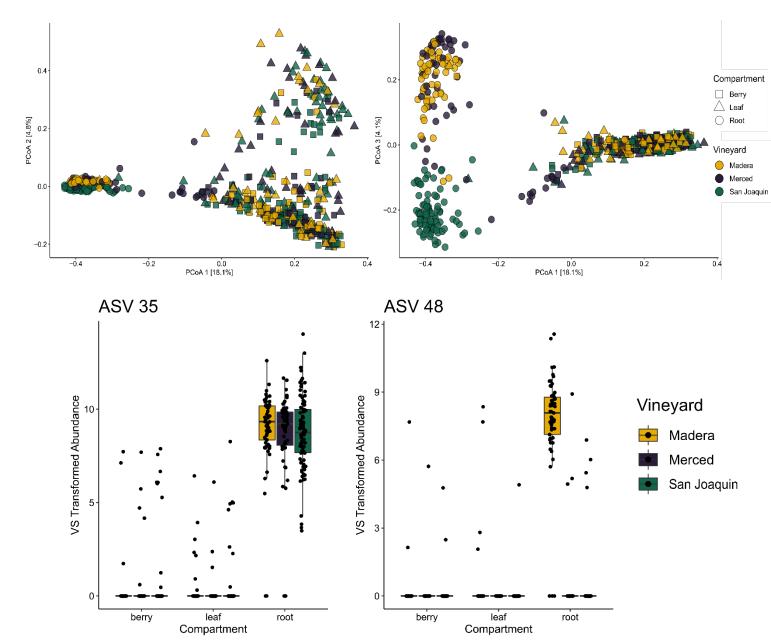
- Three field sites (commercial vineyards) along a N/S transect (~110 miles).
- Collections made across the 2018 and 2019 summer growing season.





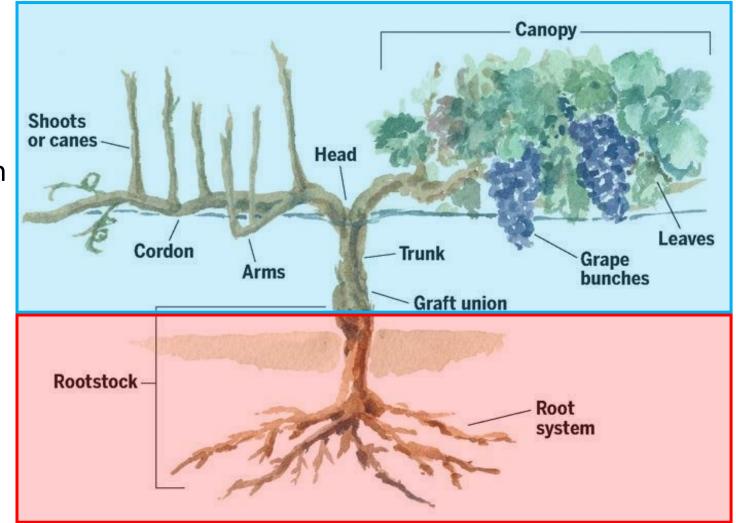
Preliminary results in California

- Vineyard and plant compartment are the largest drivers of bacterial composition.
- Root samples show clustering by vineyard (but not berries or leaves).
- Rootstock genotype had a small but measurable impact on bacterial composition (R² = 0.04).



Takeaways

- Compartments act as distinct habitats with particular suites of microorganisms.
- The influence of rootstock is small on global patterns but specific microorganisms show interesting associations.
- Across vineyards, soil and root microbiota display biogeographic patterning (terroir) while microbiota of the berries and leaves were conserved.



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Collaborating Institutions



Funding



Grape and Wine Institute

