BIOTIC AND ABIOTIC STRESS DISTINCTLY DRIVE THE PHYLLOSPHERE MICROBIAL COMMUNITY STRUCTURE

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SEP 13, 2023

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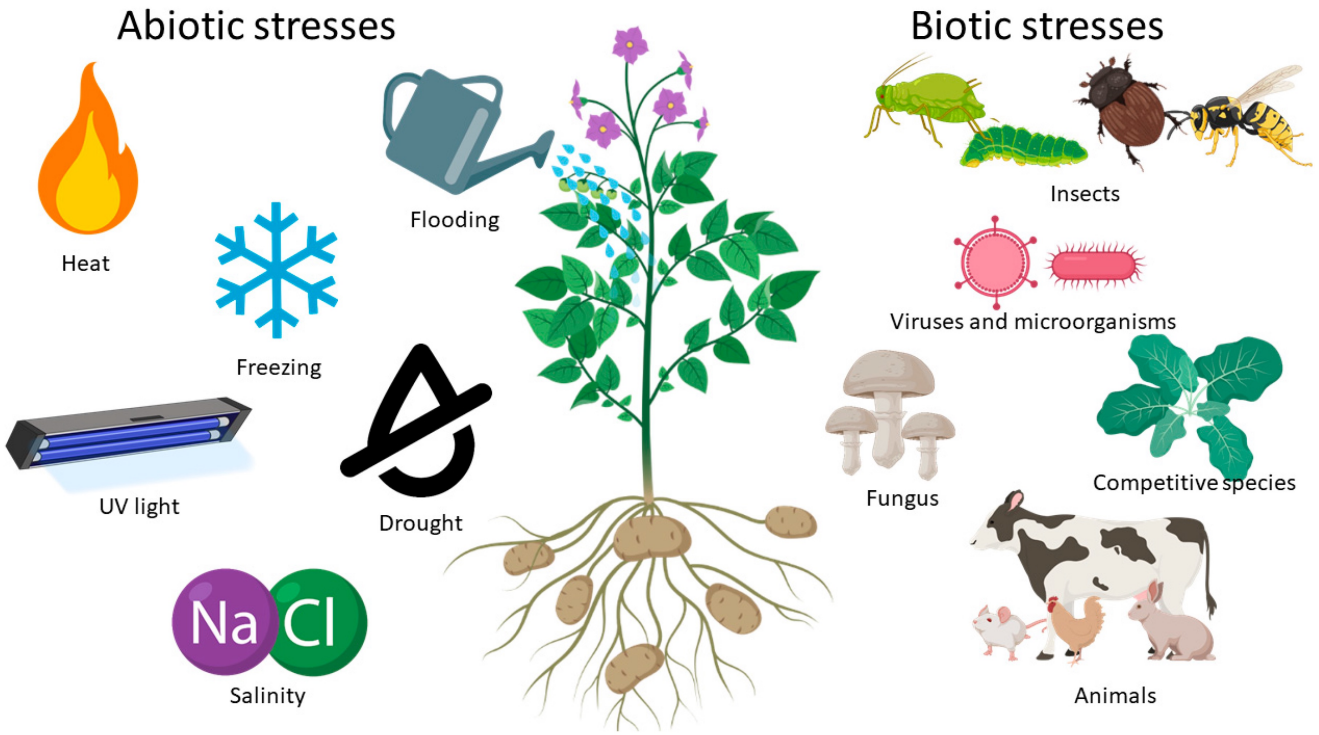
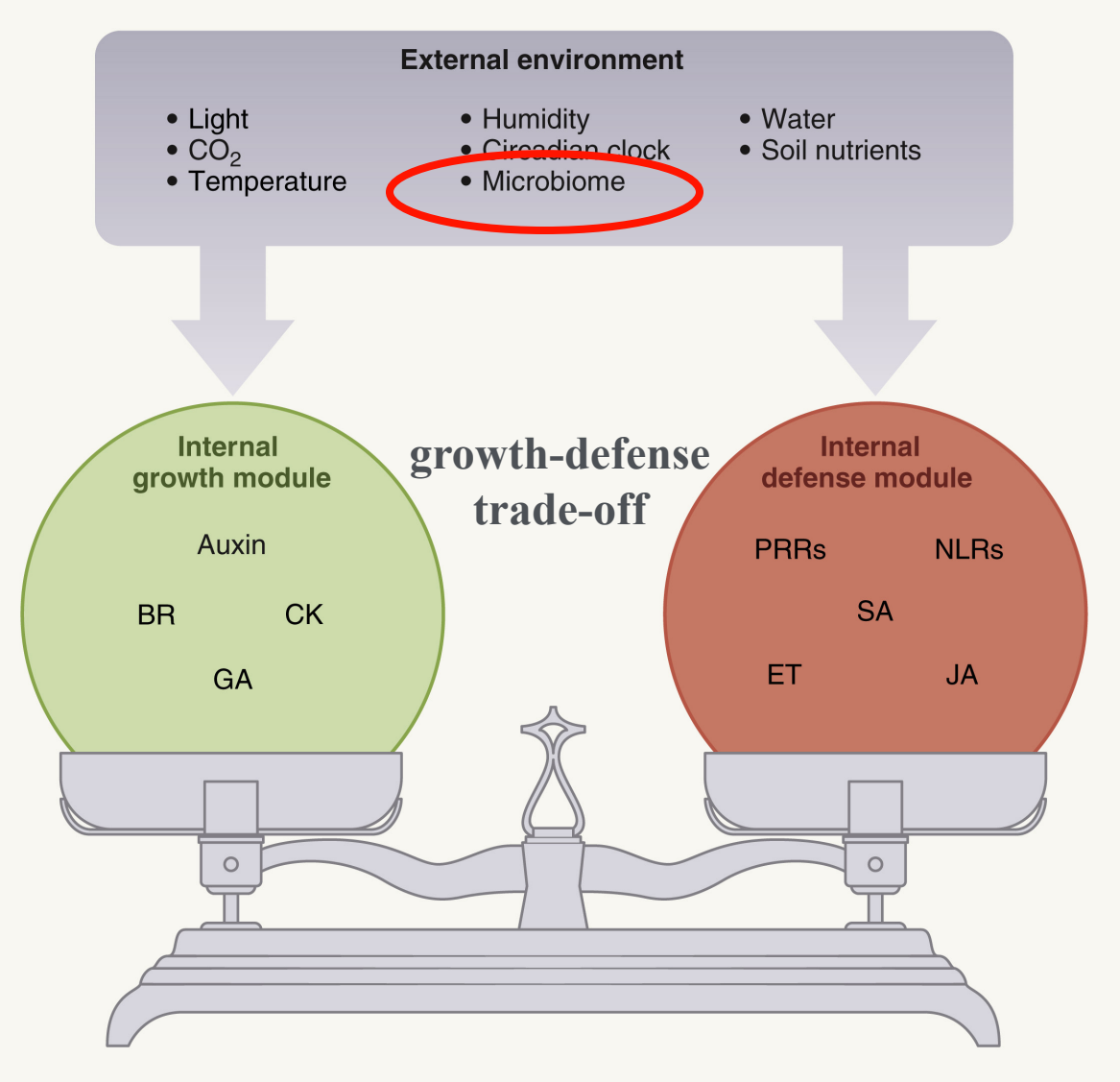
Can plants grow and defend well at the same time?

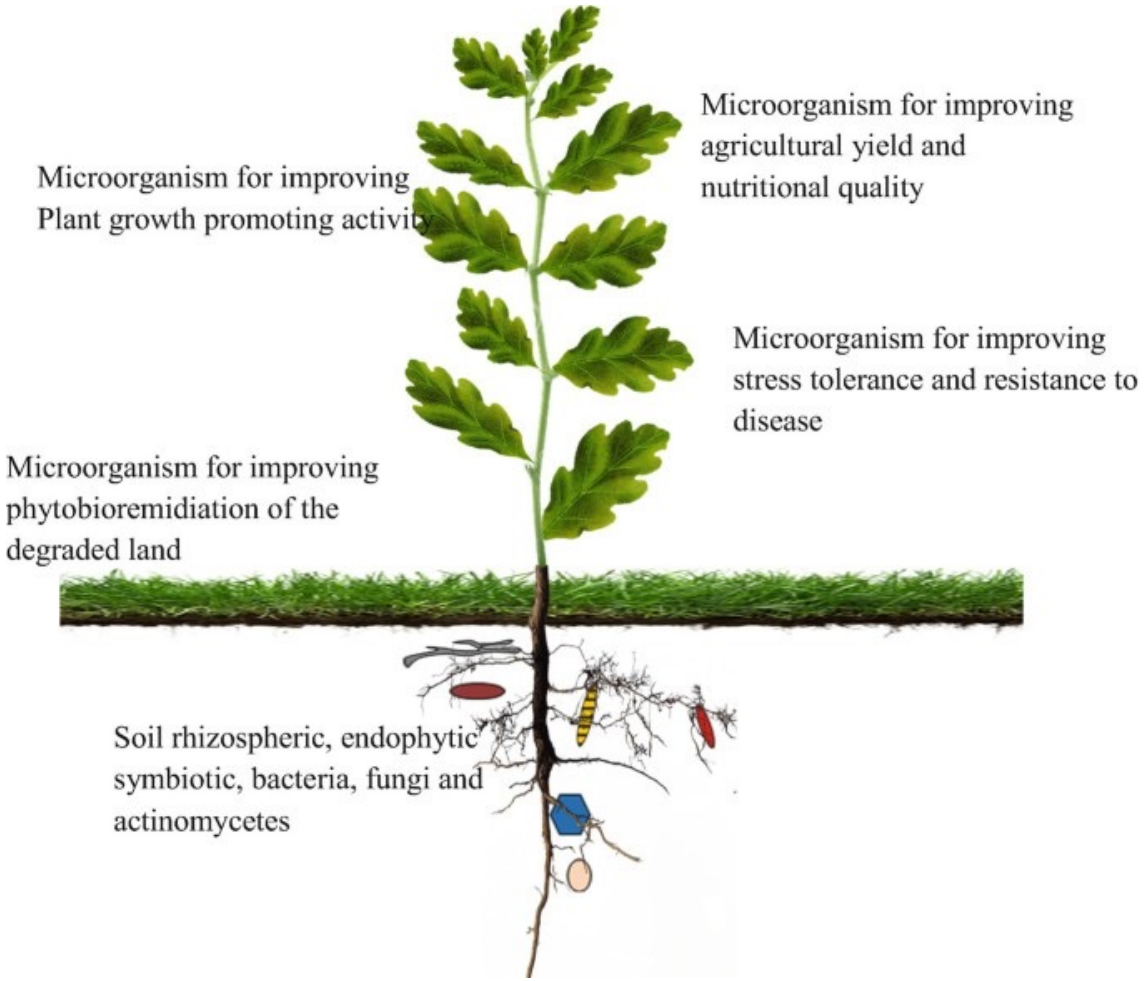


Paramo L. et. al. 2020



He Z. et. al. 2022

Microbial communities play a diverse role in plant health



Dubey et. al. 2019

Microbial ecology and functional diversity of natural habitats

Nitrogen fixation by phyllosphere bacteria associated with higher plants and their colonizing epiphytes of a tropical lowland rainforest of Costa Rica

Michael Fürnkranz, Wolfgang Wanek, Andreas Richter, Guy Abell, Frank Rasche & Angela Sessitsch

The ISME Journal **2**, 561–570 (2008) | Cite this article

Role of Dominant Phyllosphere Bacteria with Plant Growth–Promoting Characteristics on Growth and Nutrition of Maize (*Zea mays* L.)

Vahid Alah Jahandideh Mahjen Abadi, Mozhgan Sepehri, Hadi Asadi Rahmani, Mehdi Zarei, Abdolmajid Ronaghi, Seyed Mohsen Taghavi & Mahdieh Shamshiripour

Journal of Soil Science and Plant Nutrition **20**, 2348–2363 (2020) | Cite this article

Plant Biol (Stuttg). 2014 May;16(3):586-93. doi: 10.1111/plb.12082. Epub 2013 Aug 16.

Community structures of N2 -fixing bacteria associated with the phyllosphere of a Holm oak forest and their response to drought

L Rico [1], R Ogaya, J Terradas, J Peñuelas

Affiliations + expand

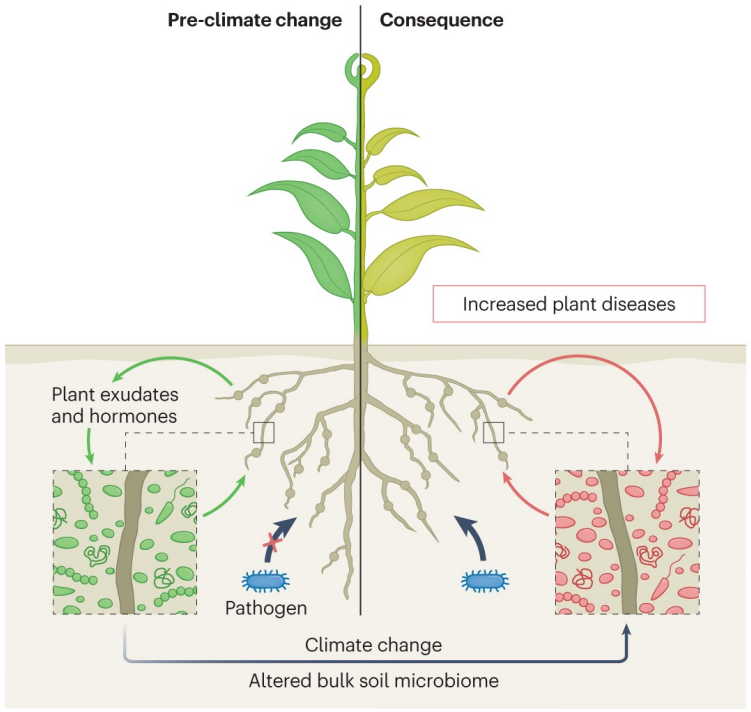
PMID: 23952768 DOI: 10.1111/plb.12082

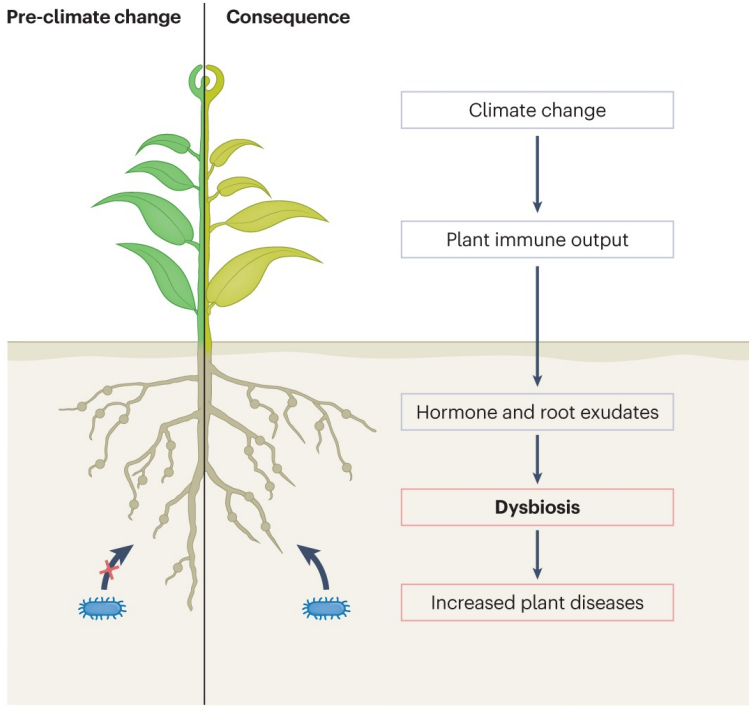
Bacterial Ice Nucleation: A Factor in Frost Injury to Plants 1 FREE

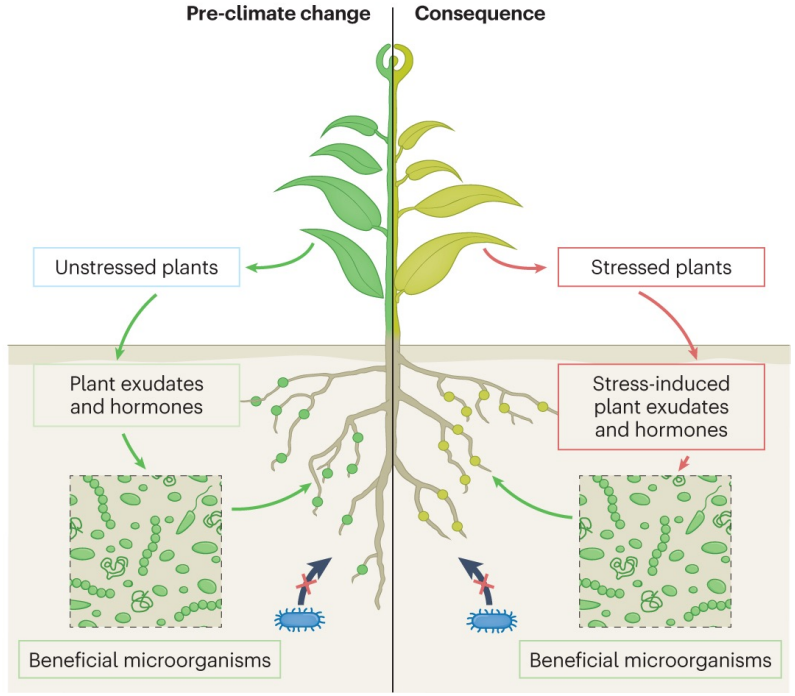
Steven E. Lindow, Deane C. Arny, Christen D. Upper

Plant Physiology, Volume 70, Issue 4, October 1982, Pages 1084–1089,

Climate change induce unpredictability in microbial community structure/function and disease outcome

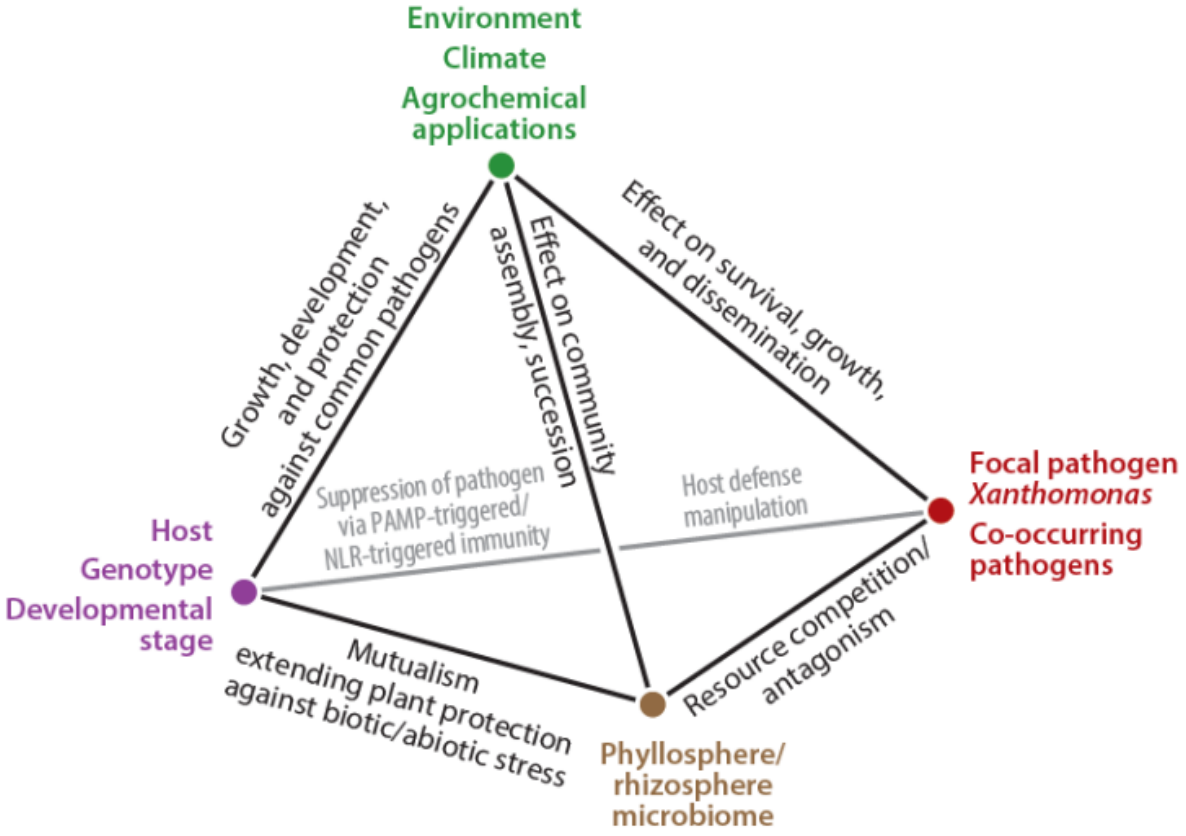




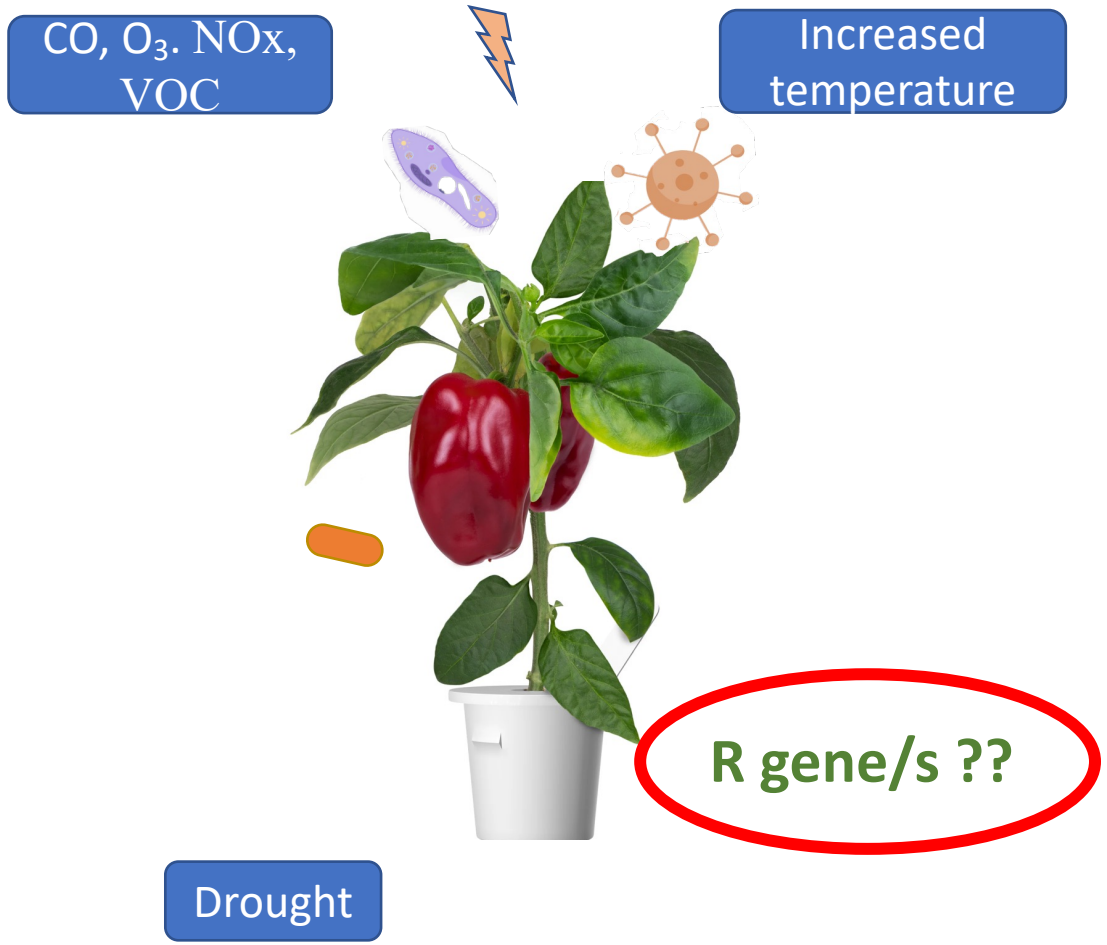


Singh, B.K. et al. 2023

How would plants and associated microbes respond to climate change and emerging pathogens?

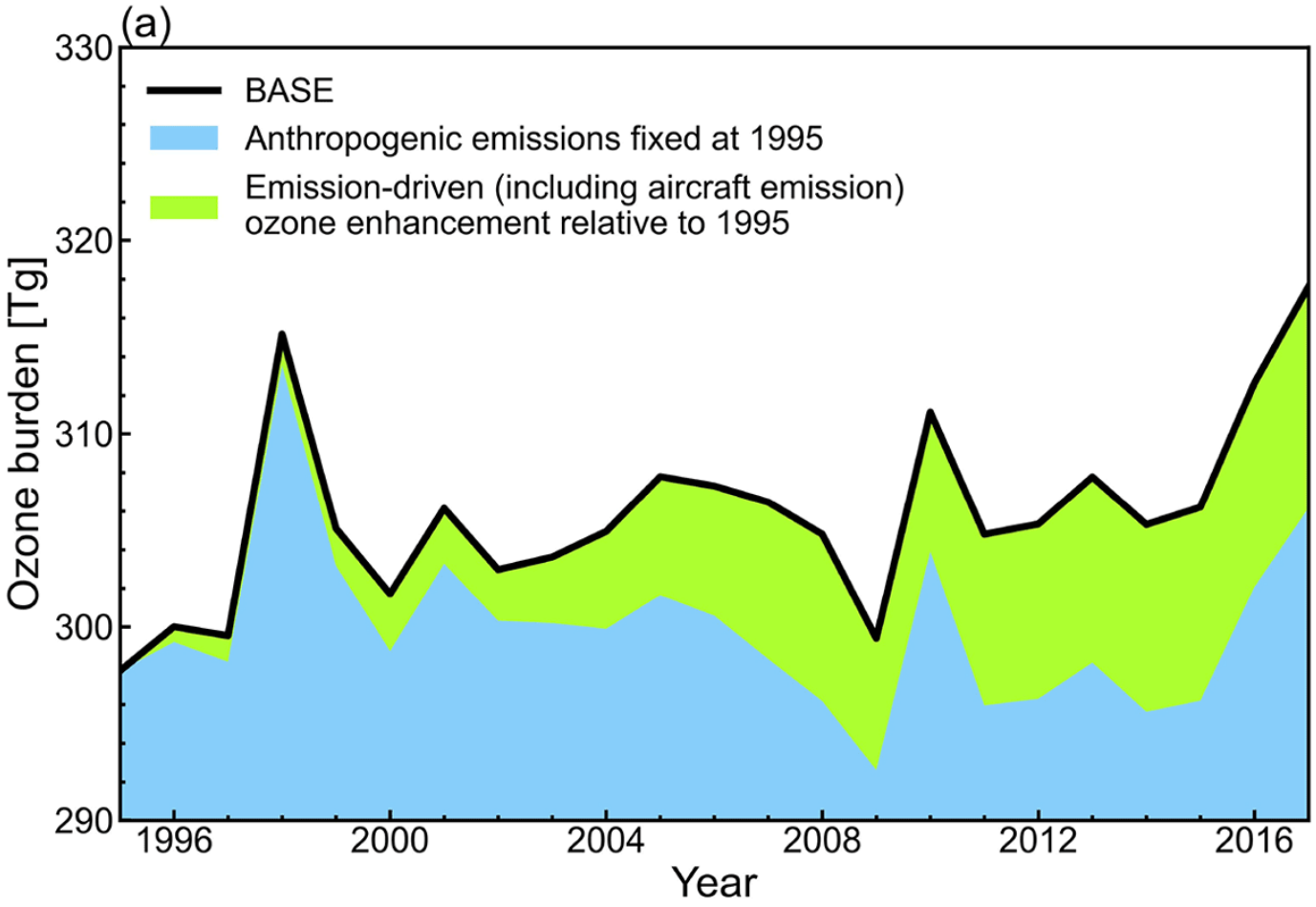


Potnis, N., 2020



ABA ⟷ **SA, JA,ET**

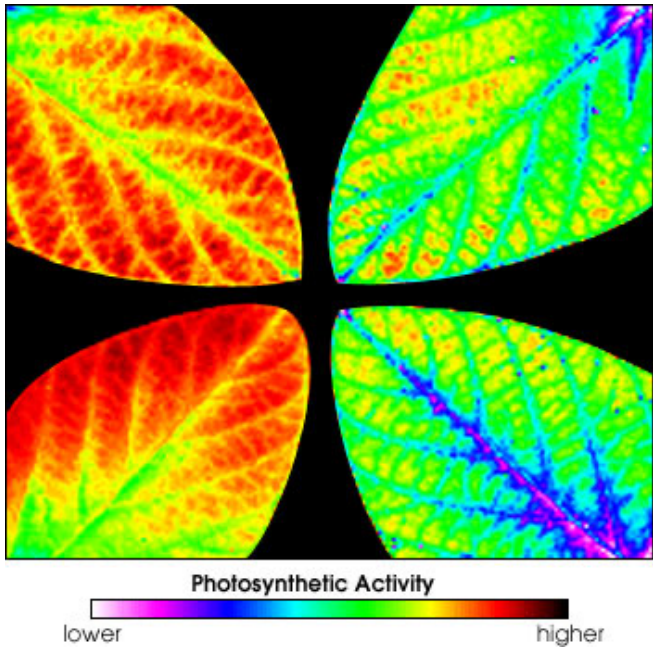
Tropospheric ozone levels is being increased around the globe



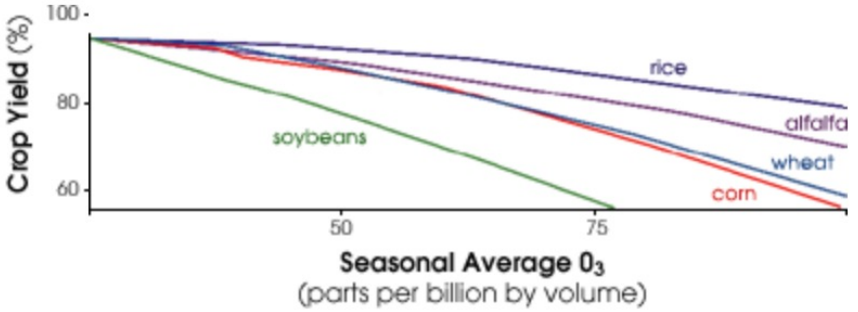
Wang et al. 2022

Tropospheric ozone is considered a major air pollutant having negative effects on plant growth and productivity.

(Photograph courtesy earthobservatory.nasa.gov; photo by Gerald Holmes)

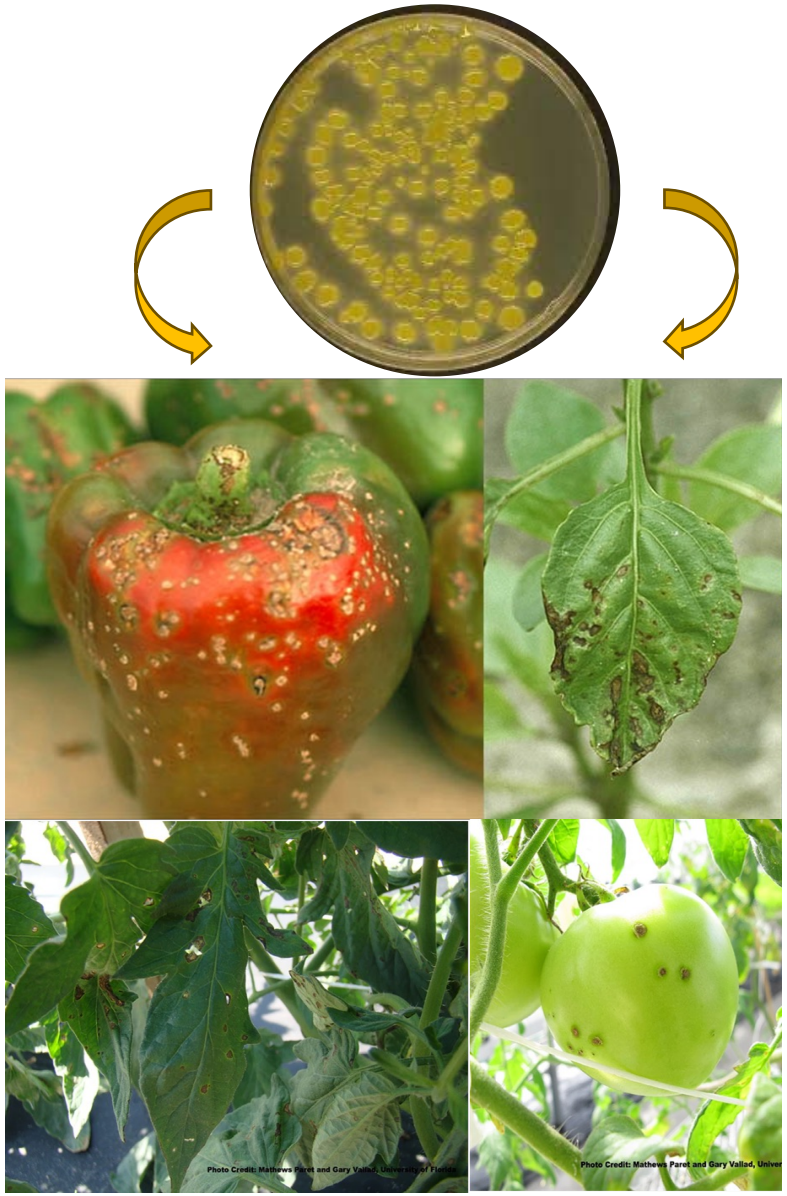


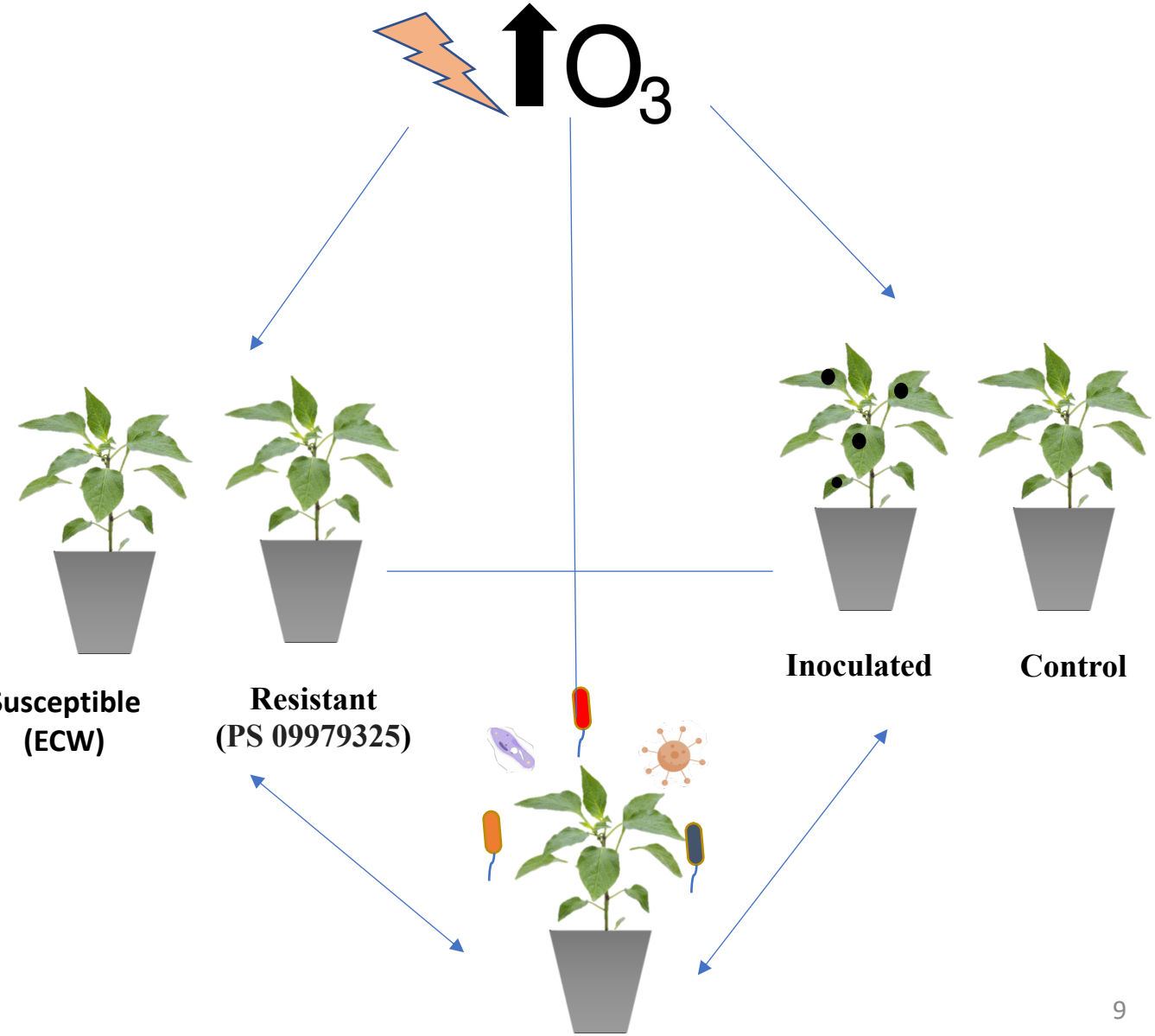
Kim, M.S. et al., 2001,



Chameides et al., 1999

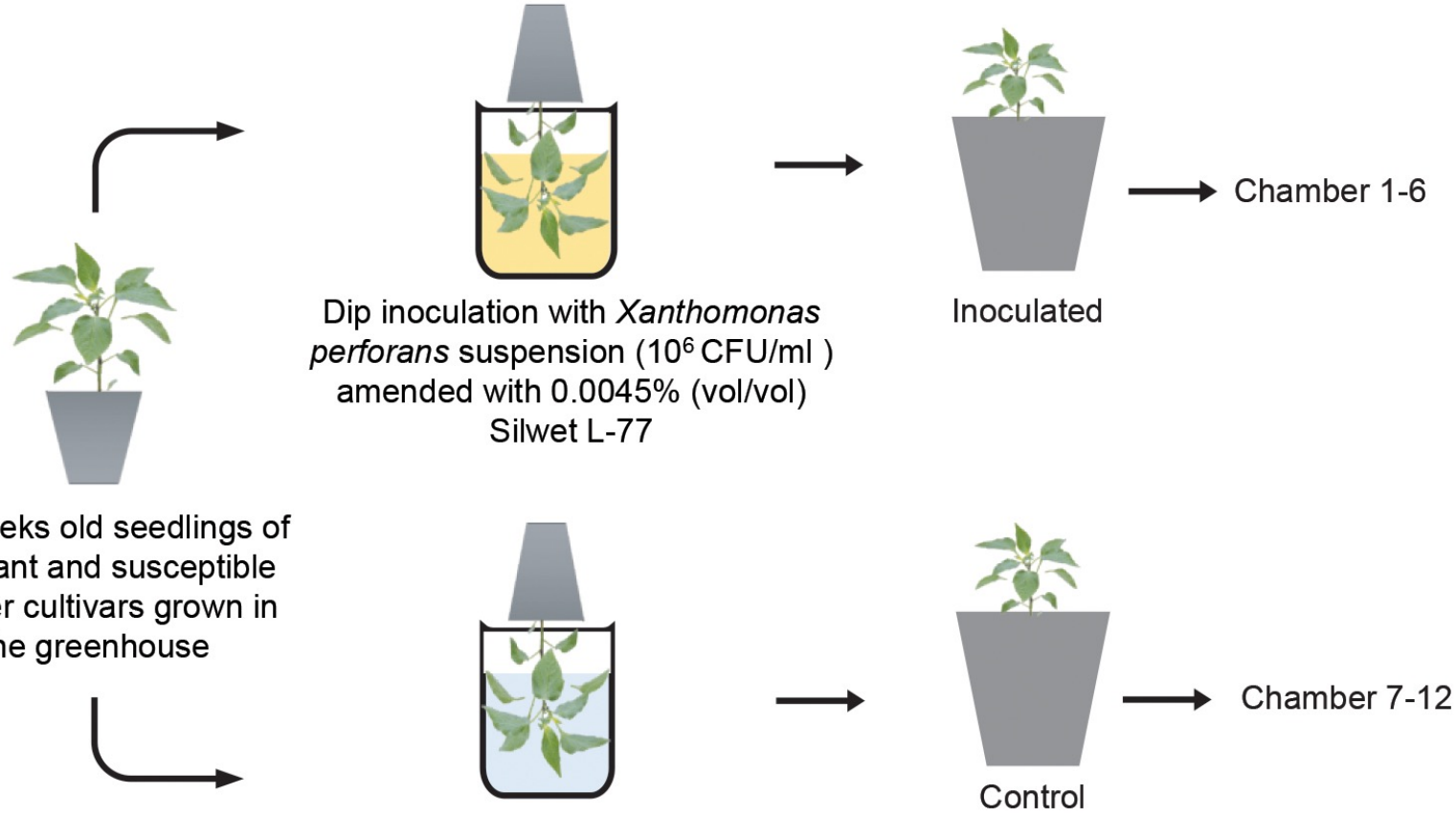
Model system: *Xanthomonas* sp. pathogenic in tomato and pepper (Bacterial leaf spot pathogen)



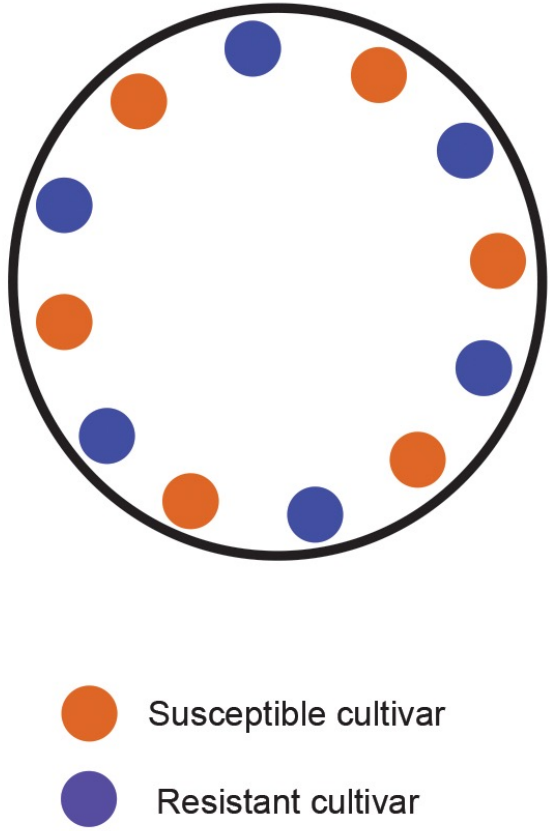


Experimental design

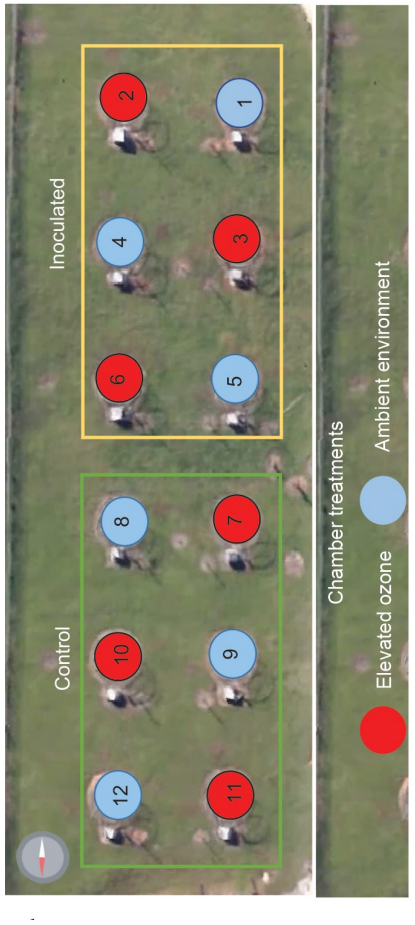
D

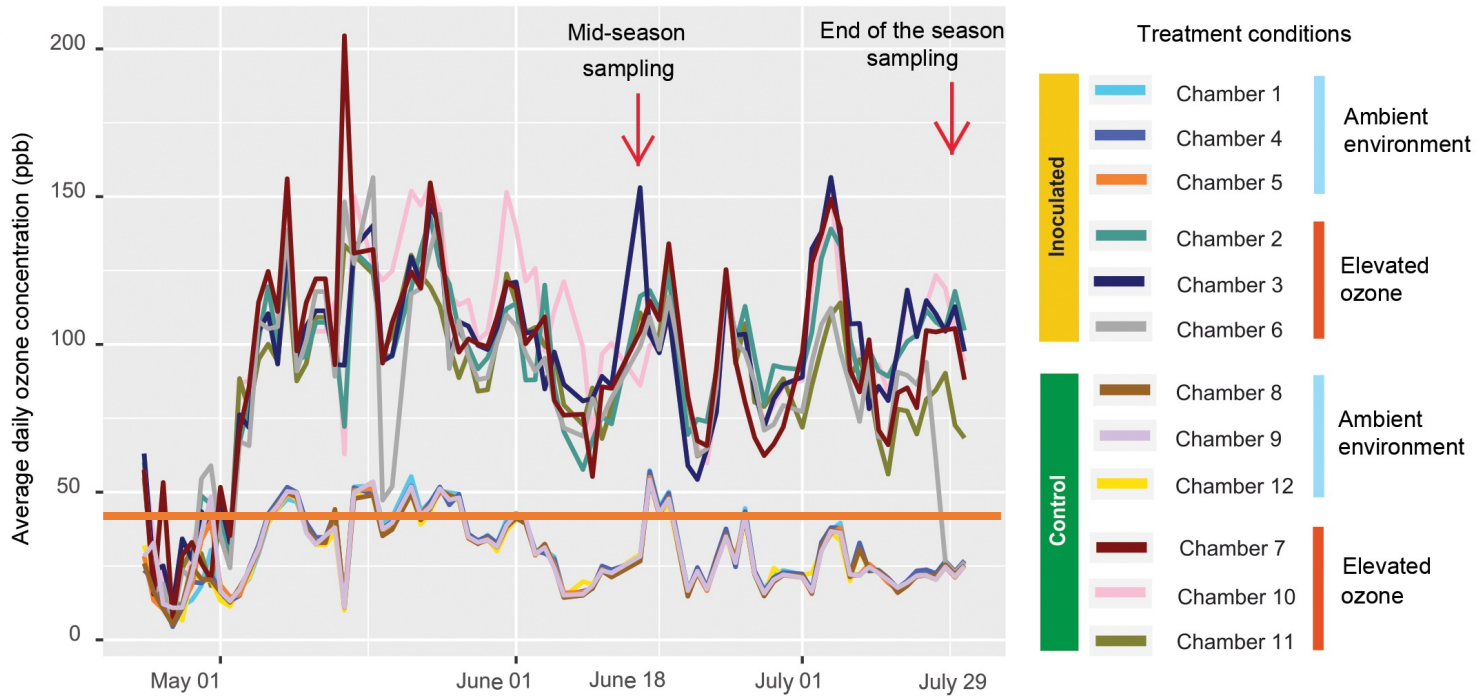


E



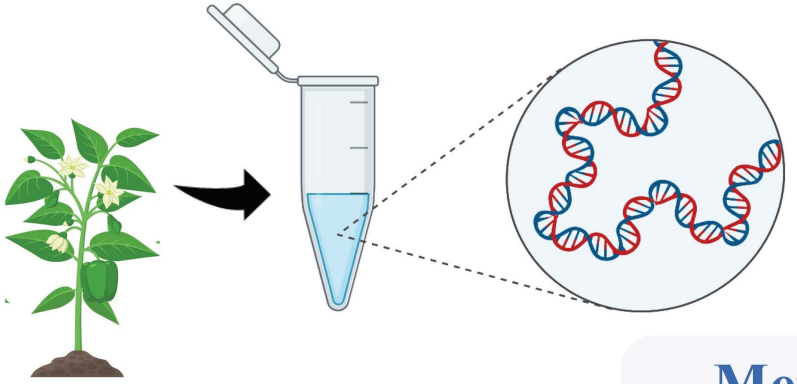
Experimental design



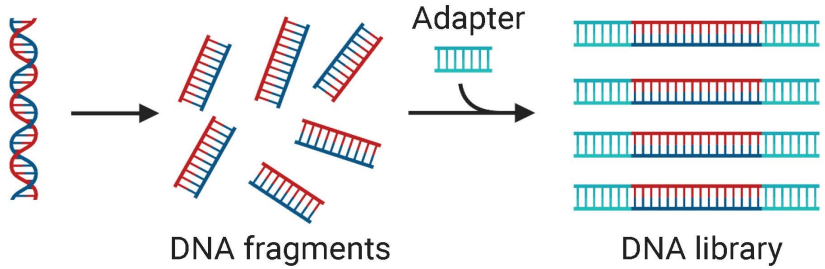


Methods and shotgun metagenomics workflow

Step 1:
DNA extraction

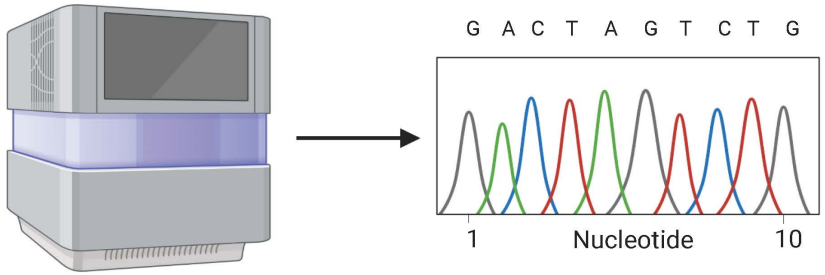


Step 2:
Library preparation

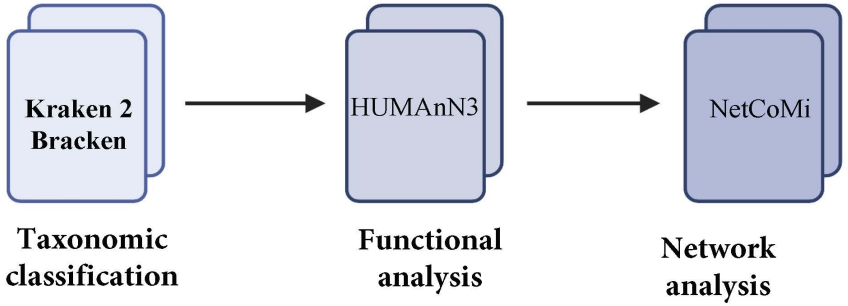


Metagenomic DNA extraction and analysis Workflow

Step 3:
Sequencing



Step 4:
Analysis



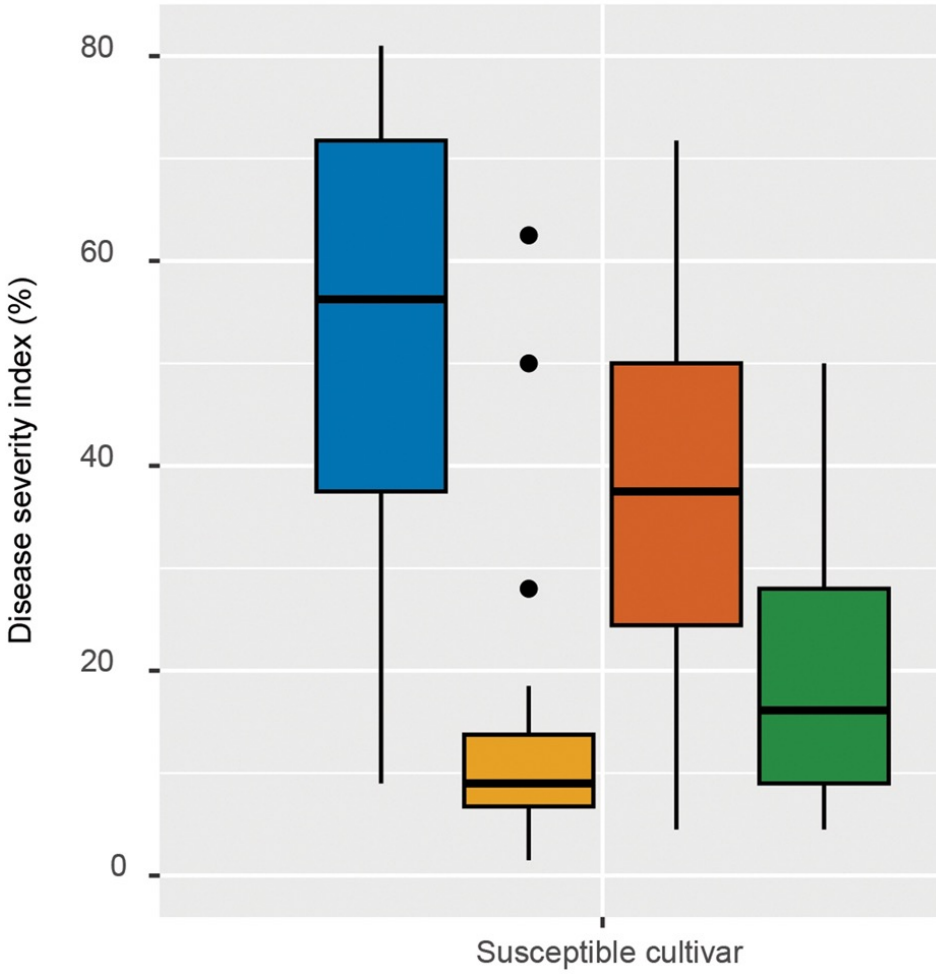
Hypothesis

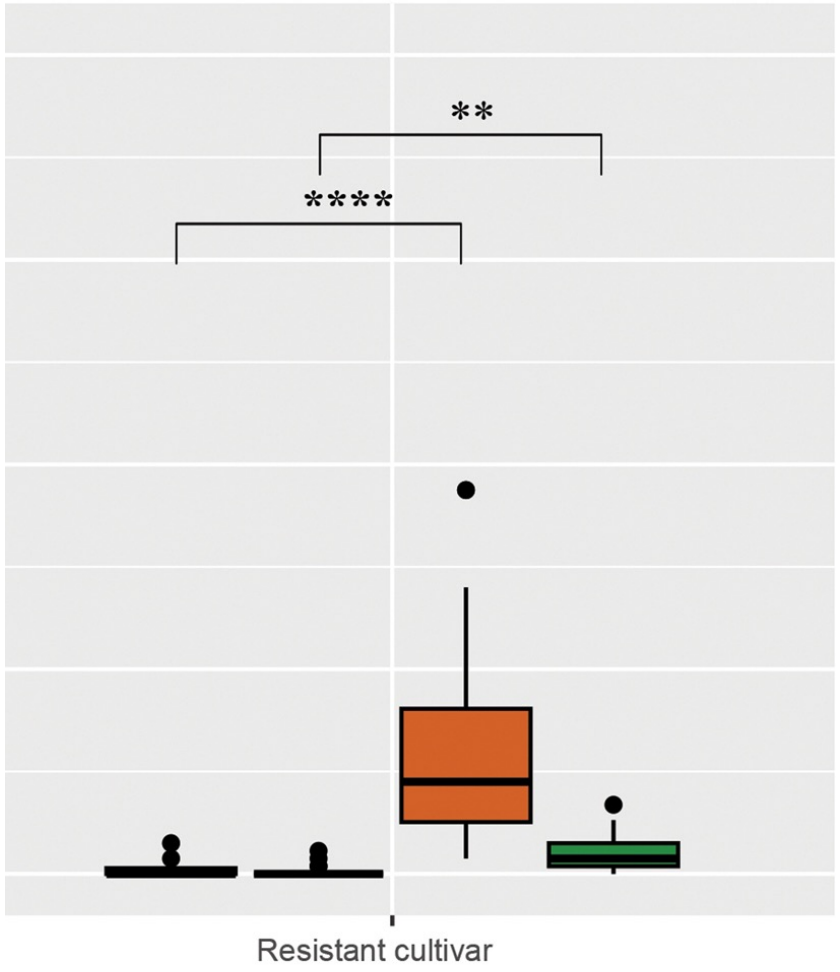
Presence of elevated **O_3 will increase overall susceptibility of pepper** to bacterial spot xanthomonads, even on the resistant cultivar.

Phyllosphere microbial communities will show **alterations in both taxonomic and functional profiles and altered seasonal dynamics** in response to altered O_3 levels, regardless of the cultivars.

Establishment of **disease would disrupt seasonal dynamics** of the phyllosphere microbiome, and this effect will be stronger in the environments that support high disease pressure.

Elevated O_3 exacerbates bacterial spot disease severity on the resistant cultivar but has no effect on the susceptible cultivar





Ambient environment

Mid-season

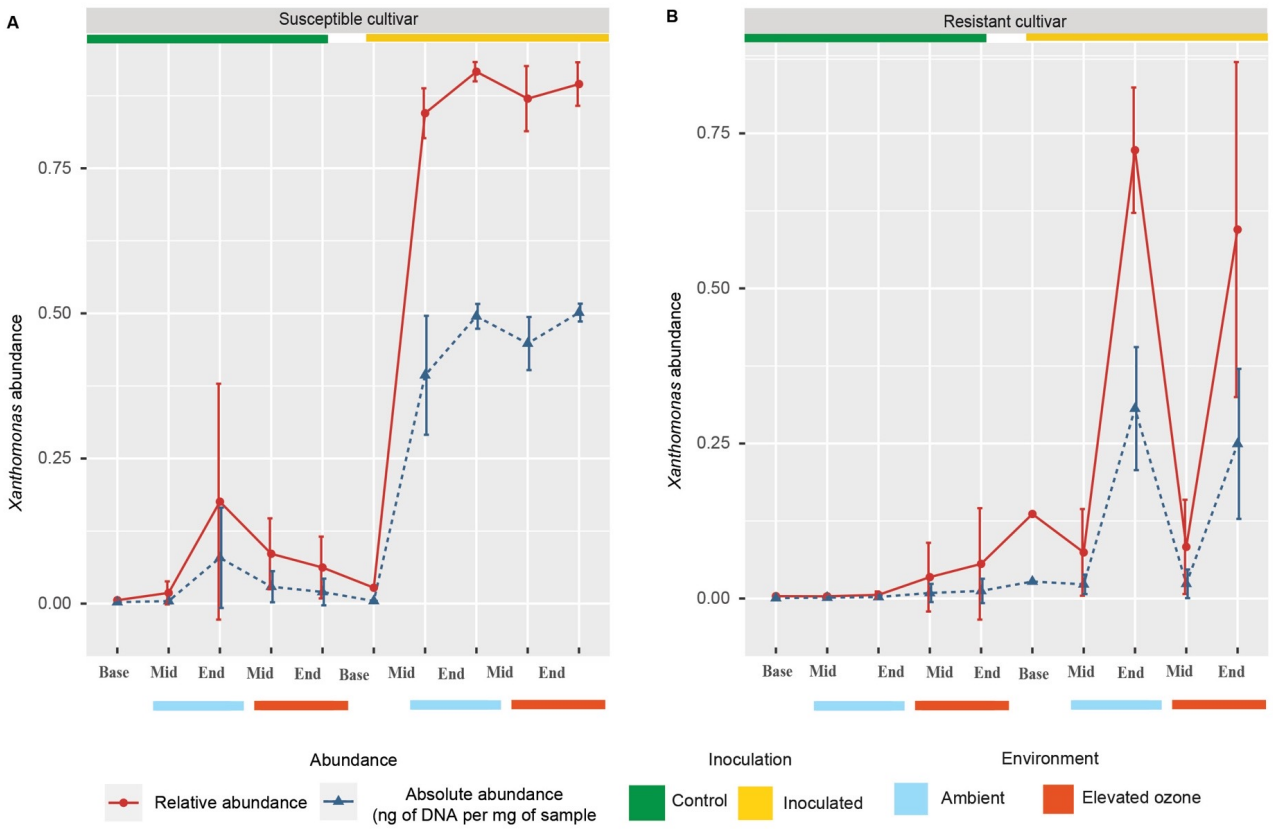
End of season

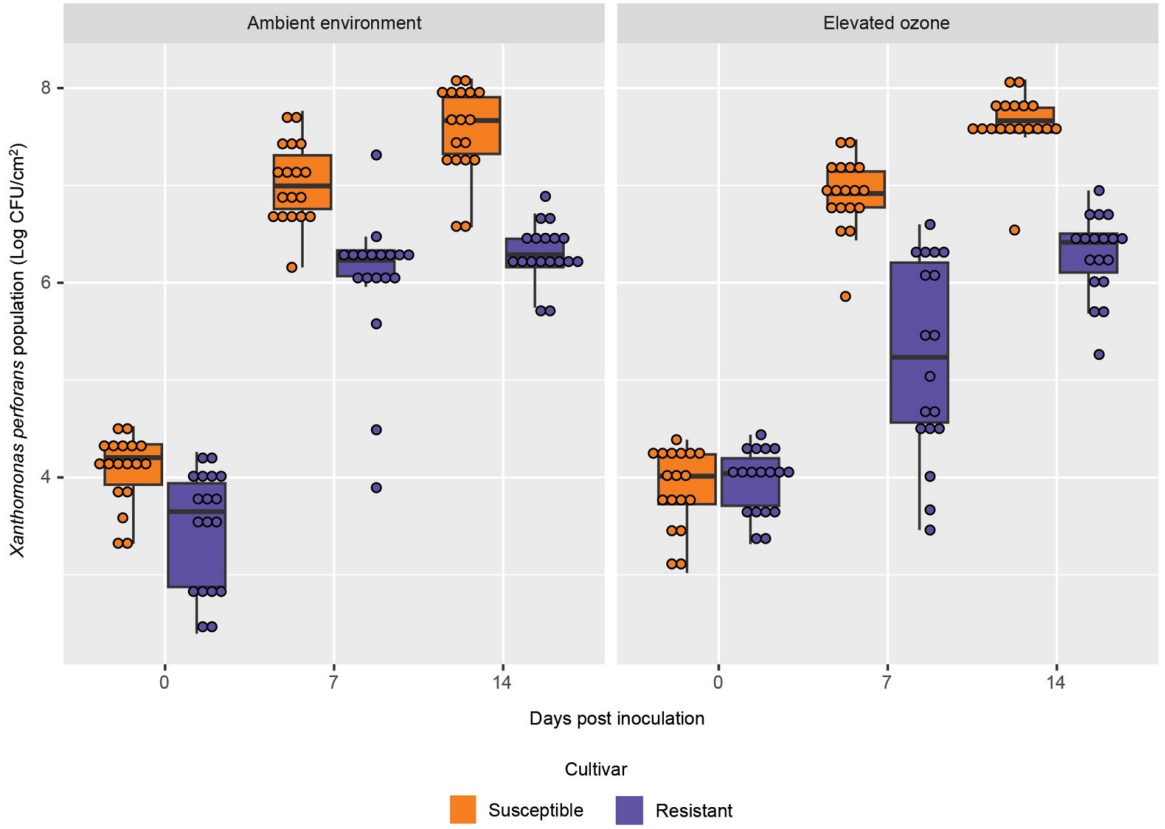
Elevated ozone

Mid-season

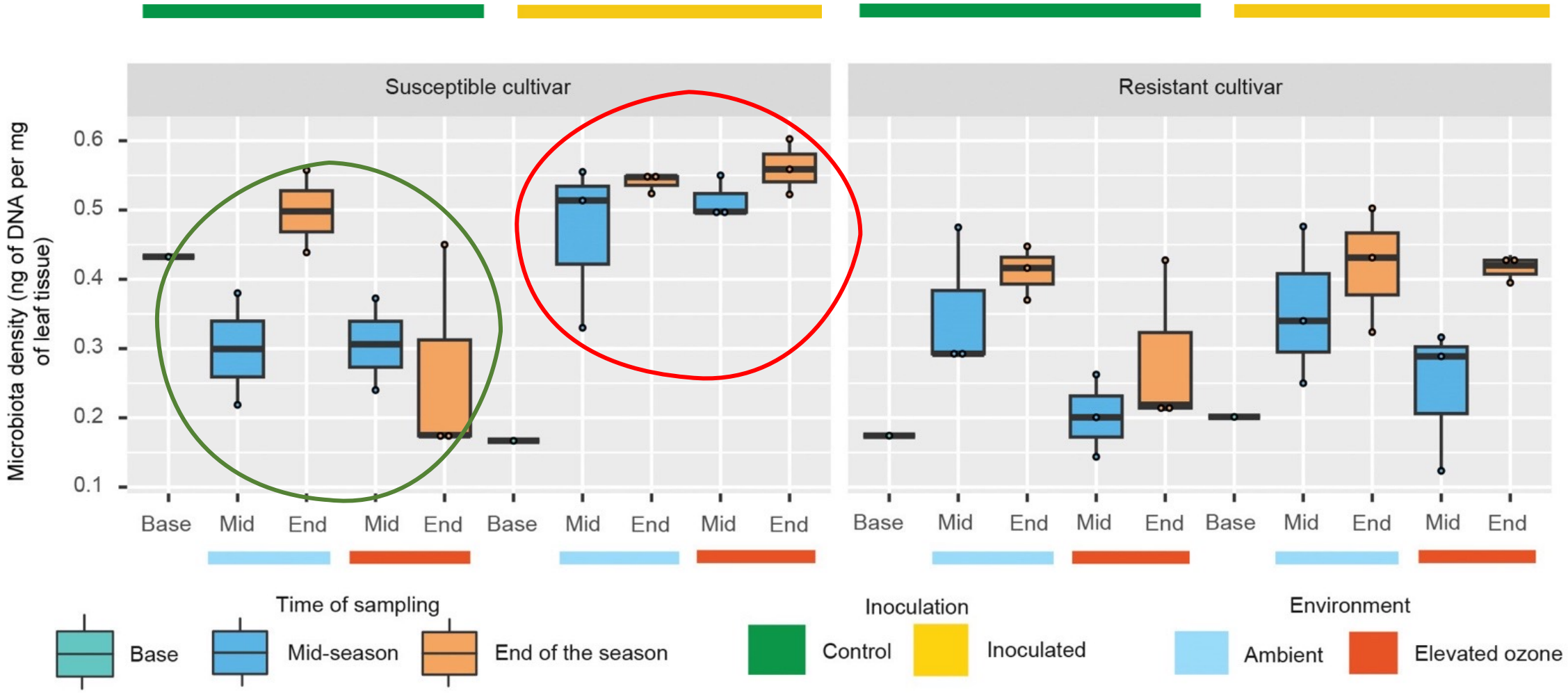
End of season

Elevated O_3 doesn't have the influence on *Xanthomonas* population in both the cultivars



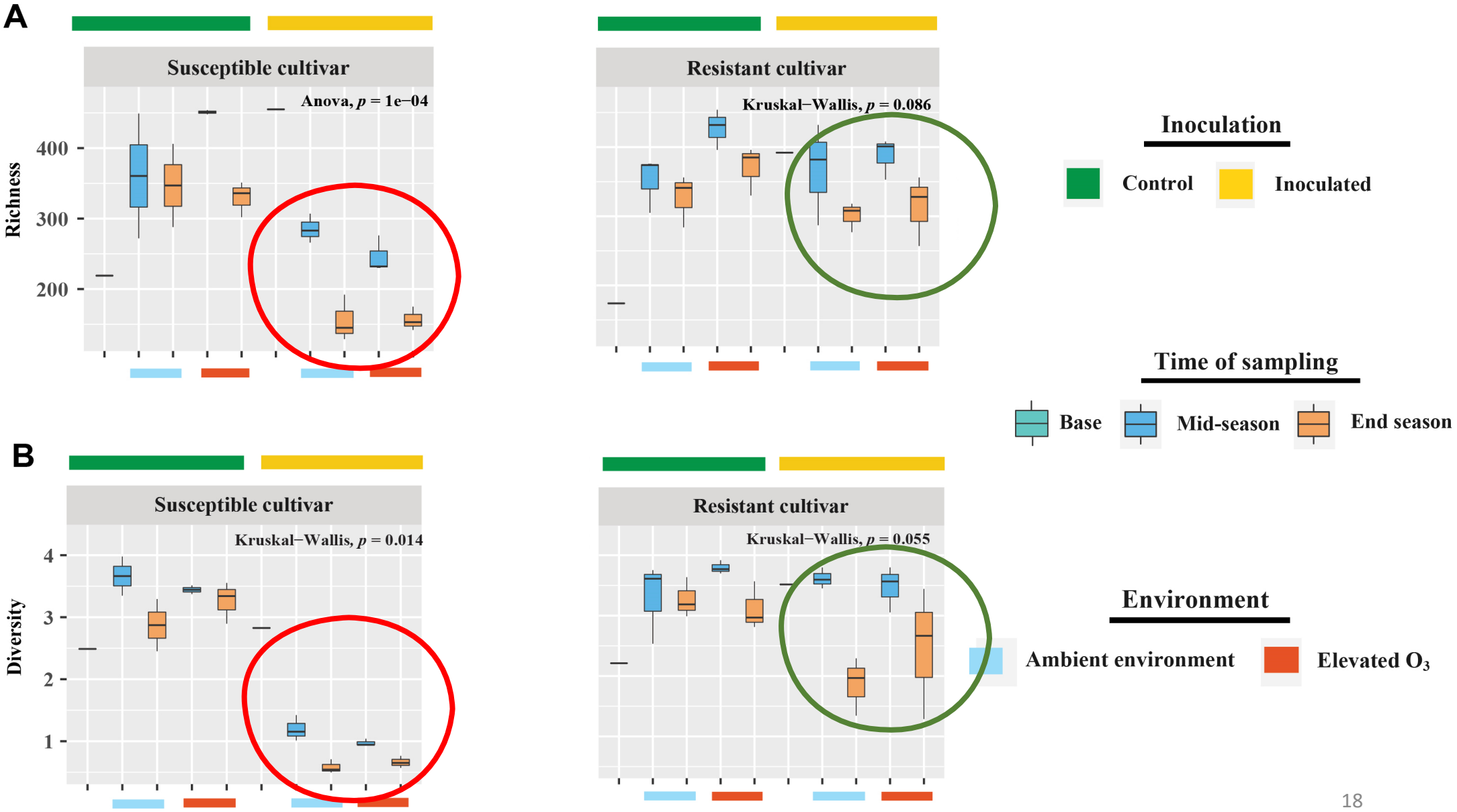


The effects of elevated O_3 on disease outcomes are not fully explained by changes in microbiota density and abundance

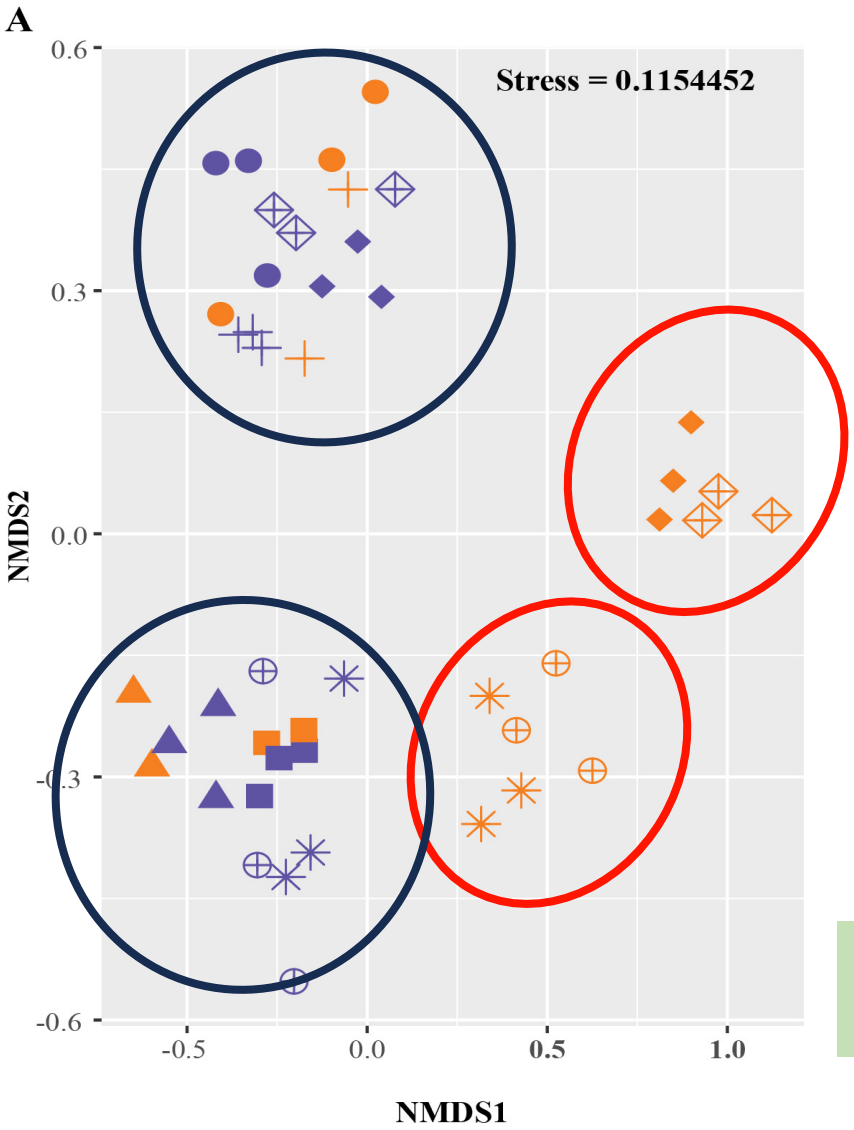


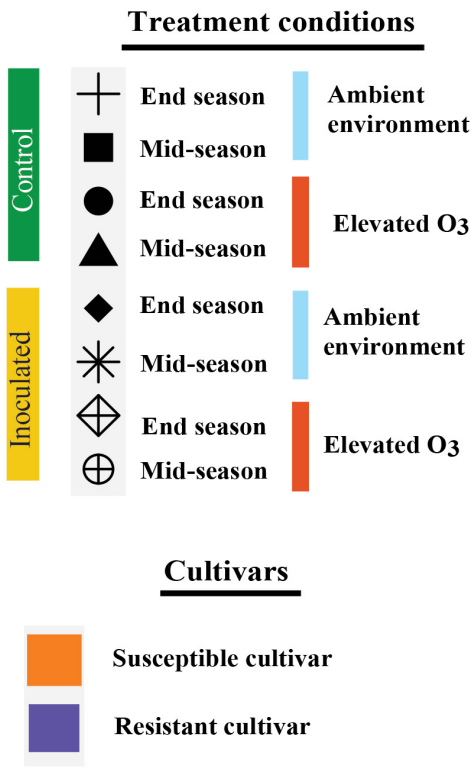
Bacterial diversity and richness increases upon exposure to field conditions

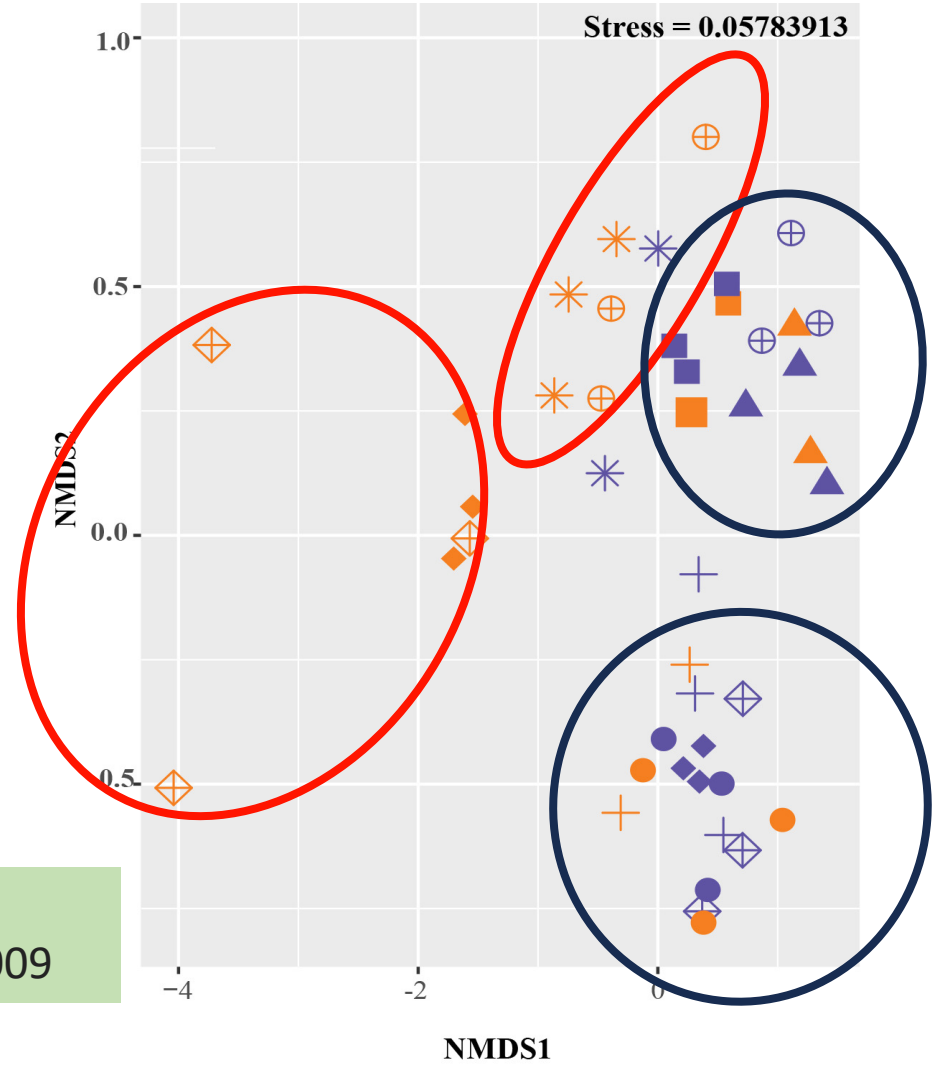
Elevated O_3 has little impact on microbial diversity and richness



Microbial community structure was significantly affected by inoculation and time of sampling

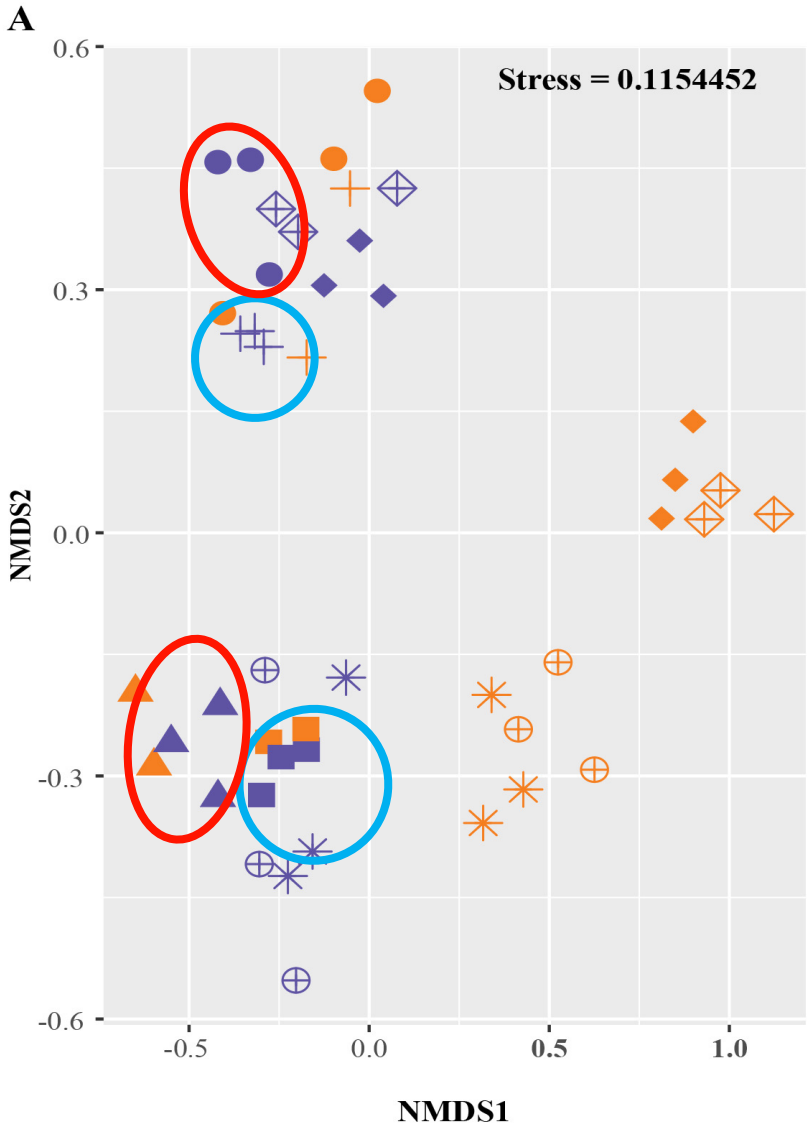




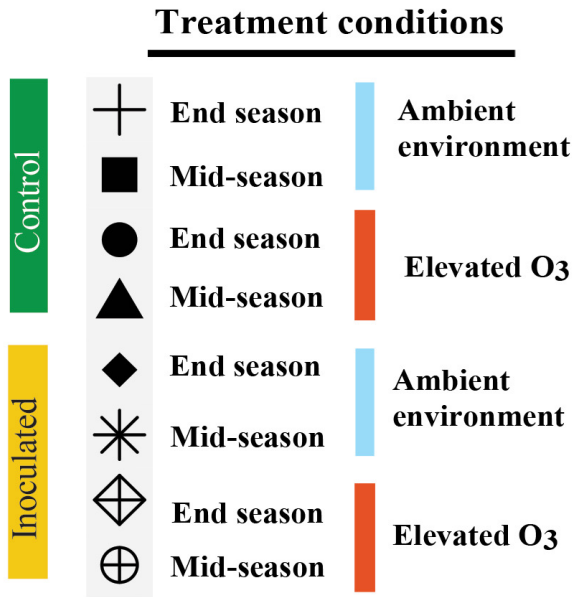


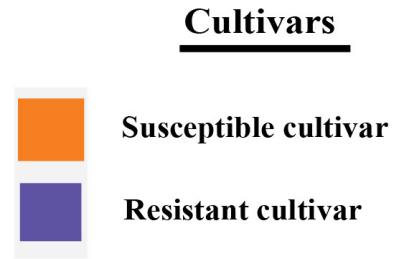
Time : $R^2 = 0.10$, $p = 0.0009$
Inoculation: $R^2 = 0.25$, $p = 0.0009$

Elevated O_3 changes microbial community structure on resistant cultivars in the absence of pathogen

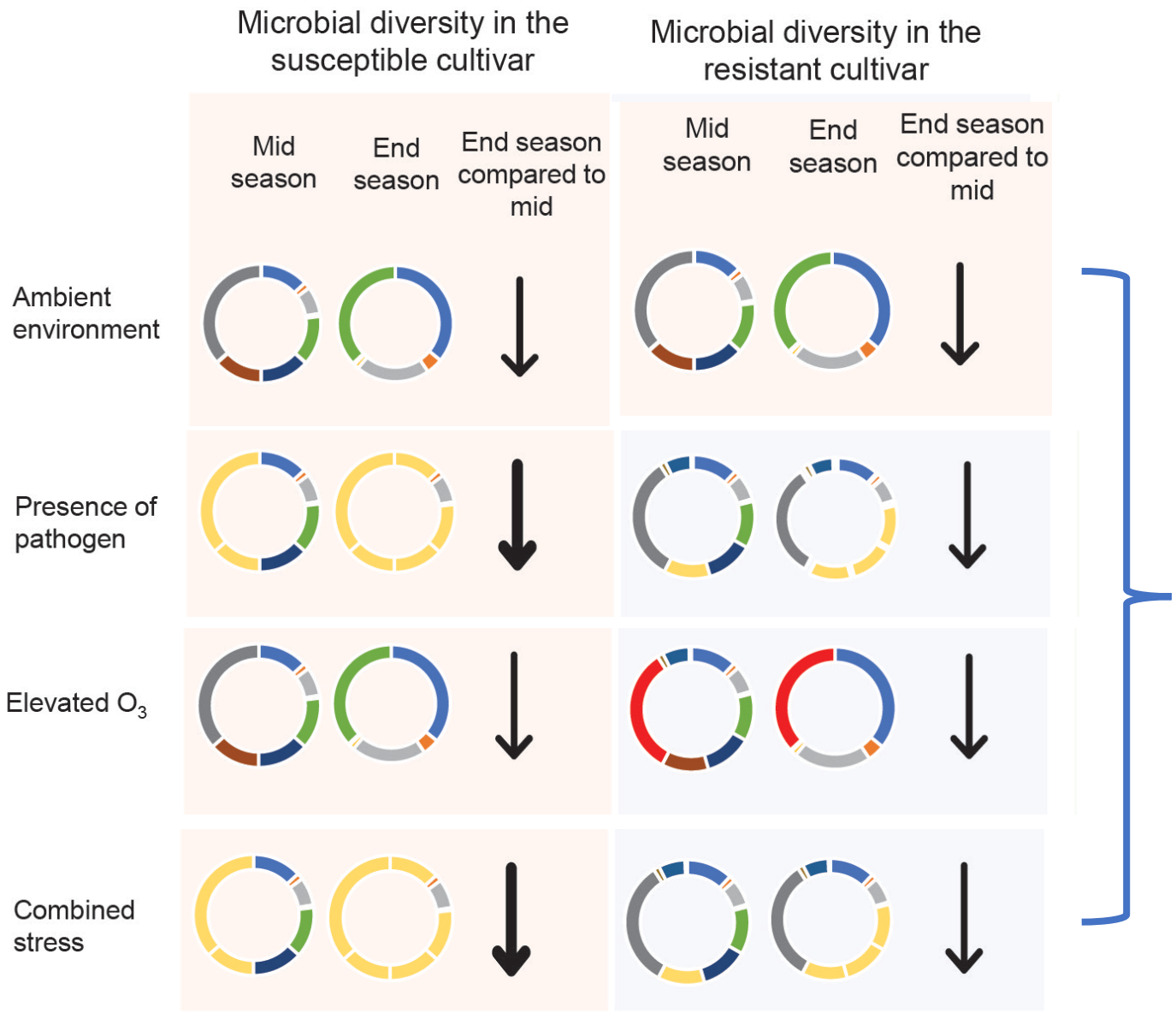


($R^2 = 0.14$, $p = 0.02$)



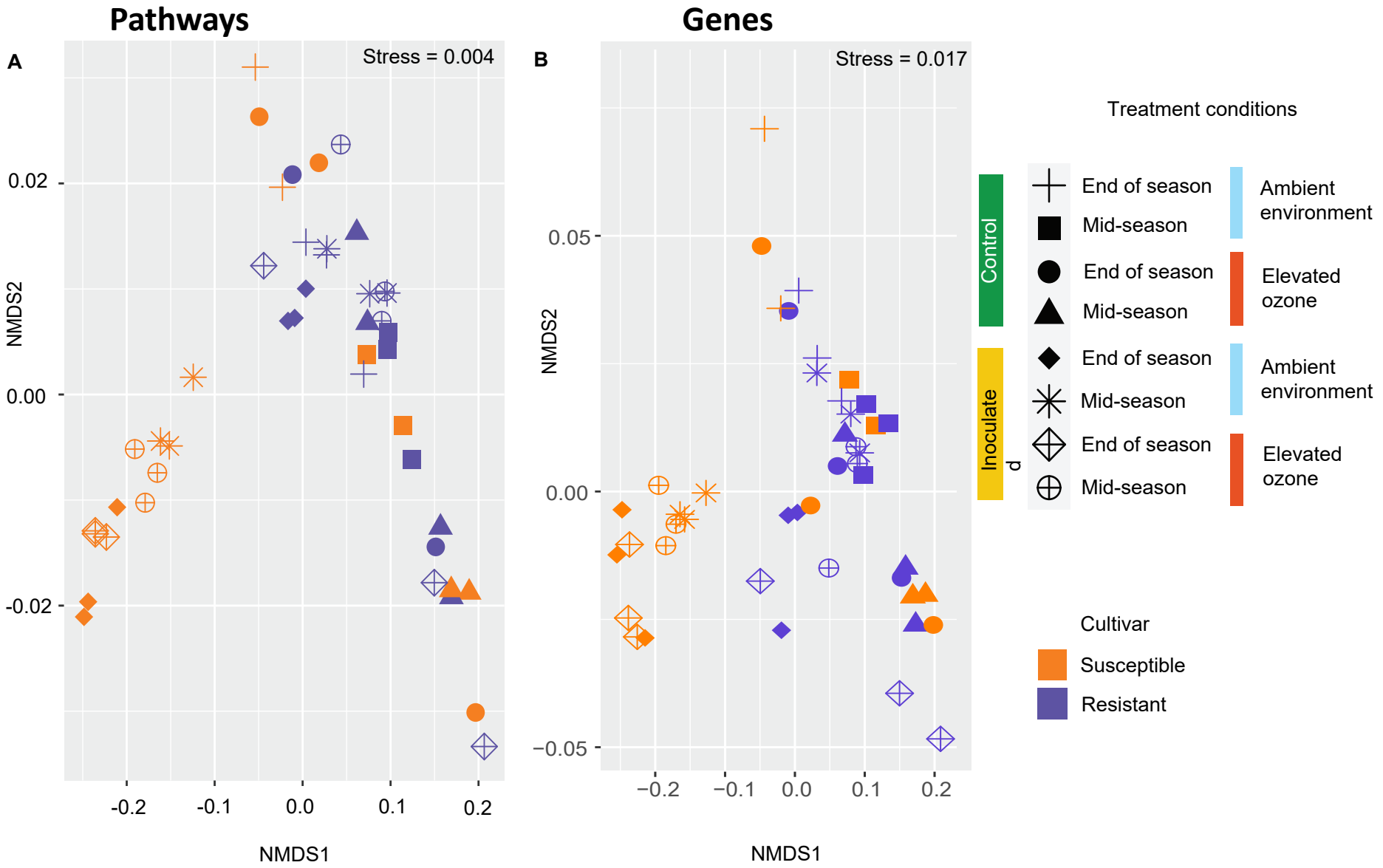


Summary: Influence of environment, pathogen and host resistance in microbial community structure

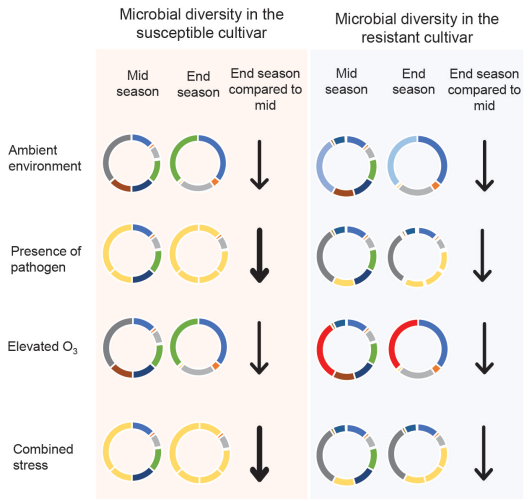


Does the observed taxonomic differences reflect niche-specific microbial functions ?

Phyllosphere microbial communities with different taxonomical compositions shows functional redundancy.



Summary: Influence of environment, pathogen and host resistance in microbial community function



Microbial functions enriched in both the cultivars

Biosynthesis of amino acid
Defense pathways

Carbohydrate metabolism
Defense pathways
Exopolysaccharide pathways

β-oxidation
O_2 independent respiration
DNA repair
Pathways against O_2 stress

Purine nucleotide production and degradation

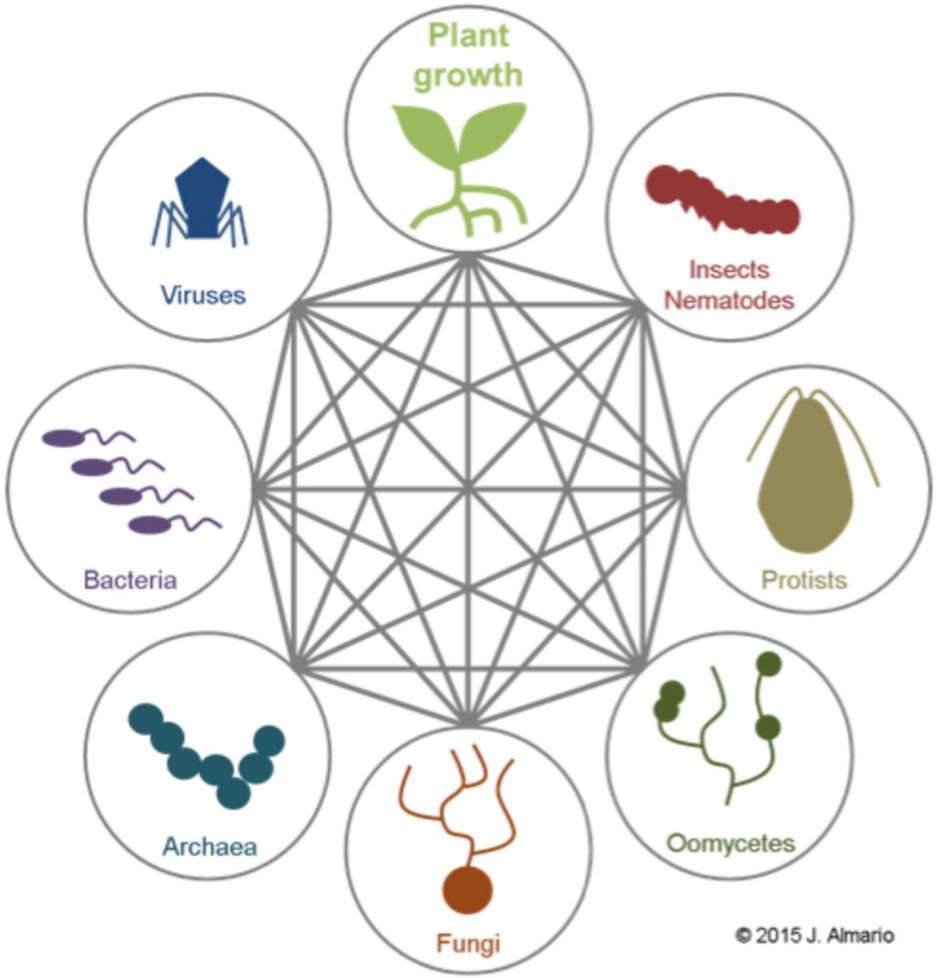
Overall community function

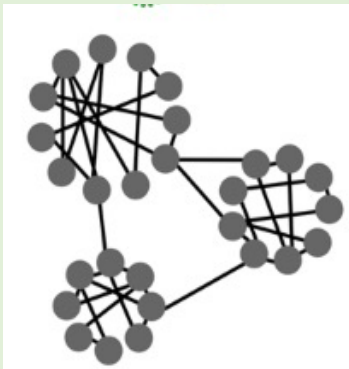
Influence of seasonal succession on community function in the ambient environment, yet functional resilience in the presence of single or combined stress.

How does the biotic and abiotic stress influence the microbial association?

Source:WUR https://www.wur.nl/en/article/microbial-interactions-between-green-microalgae-neochloris-oleoabundans-and-hypothesised-symbionts.htm

Microbial network analysis helps to explore co-occurrence patterns of the microbial communities



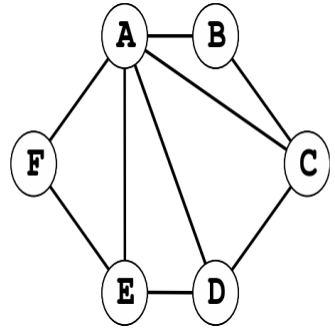


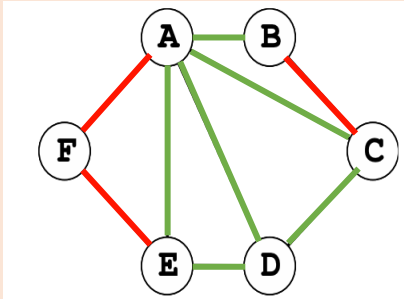
Modularity ↑

modularity have dense connections between the nodes within modules

Average path length ↓

average number of steps which would be required to reach from one node to another





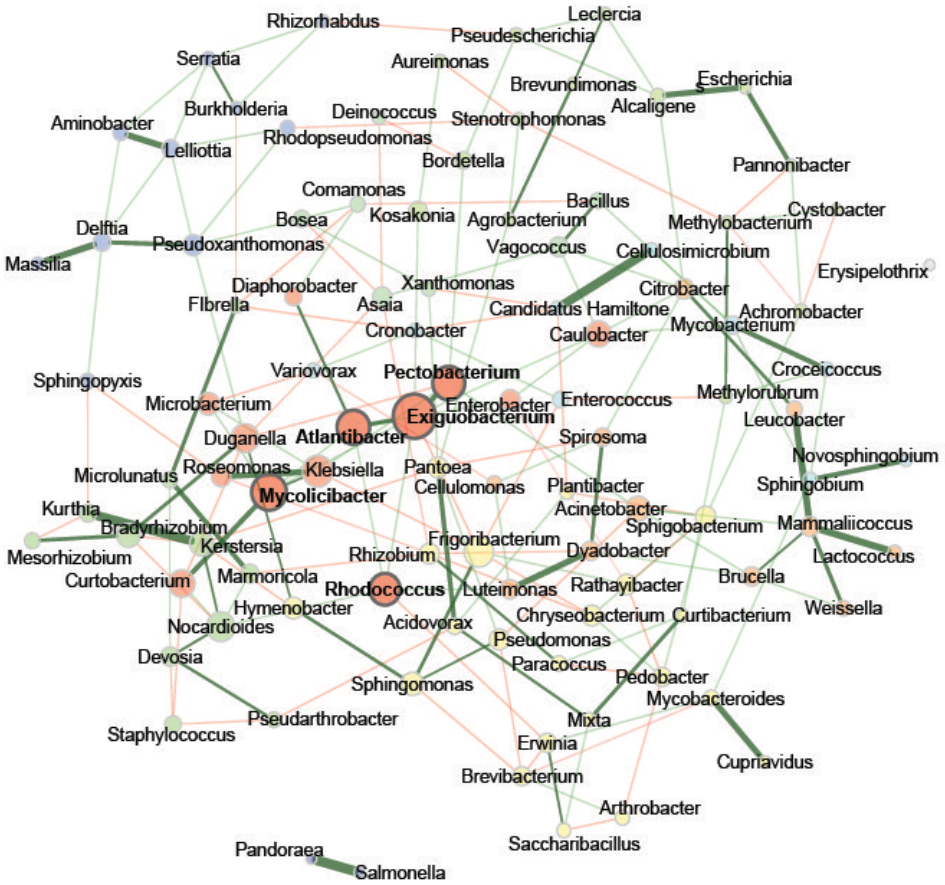
Positive edge percentage ↑

proportion of positive edges in the network

Source: CEPLAS

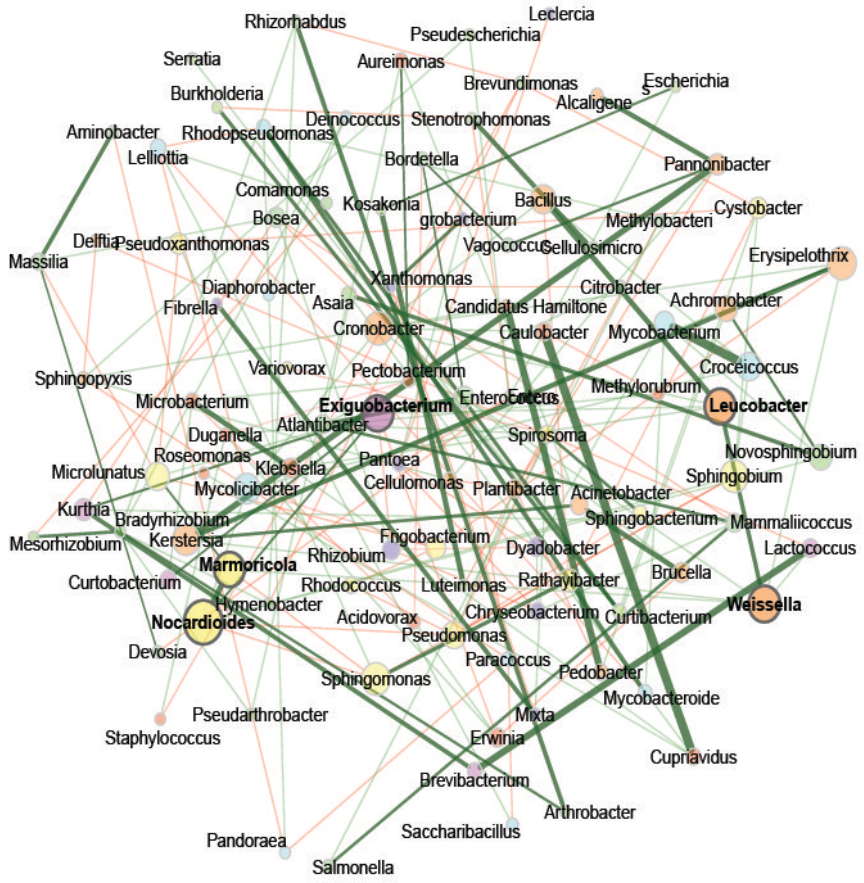
Abiotic stress destabilizes microbial network

Ambient environment



Modularity ↑
Positive edge %
Average Path length ↓

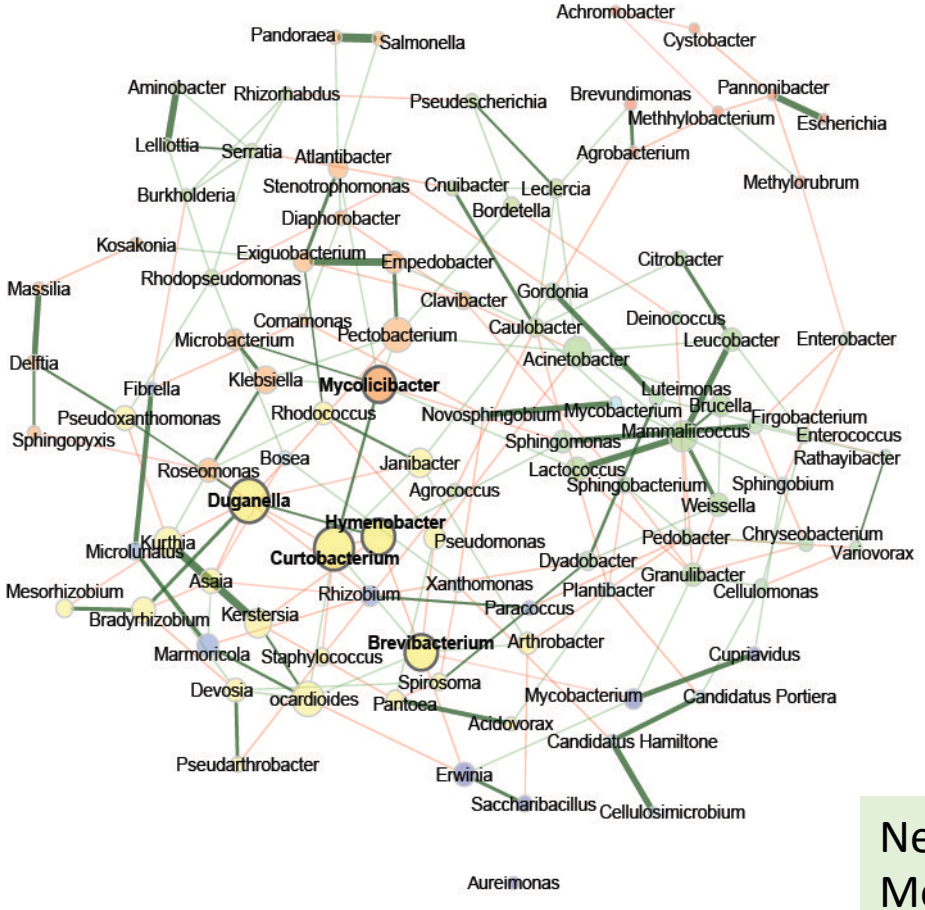
Elevated ozone



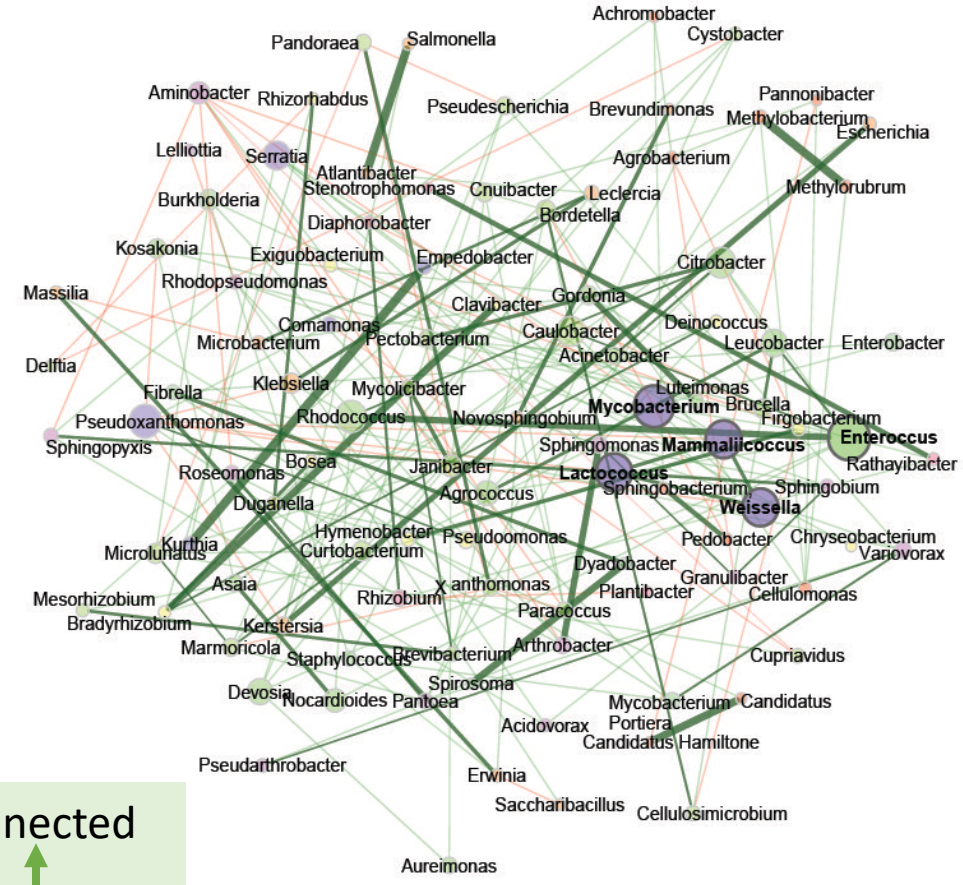
Network: Random
Modularity ↓
Positive edge %
Average Path length ↑

Pathogen infection is associated with microbial communities showing positive and stable interactions

Ambient environment and control plants



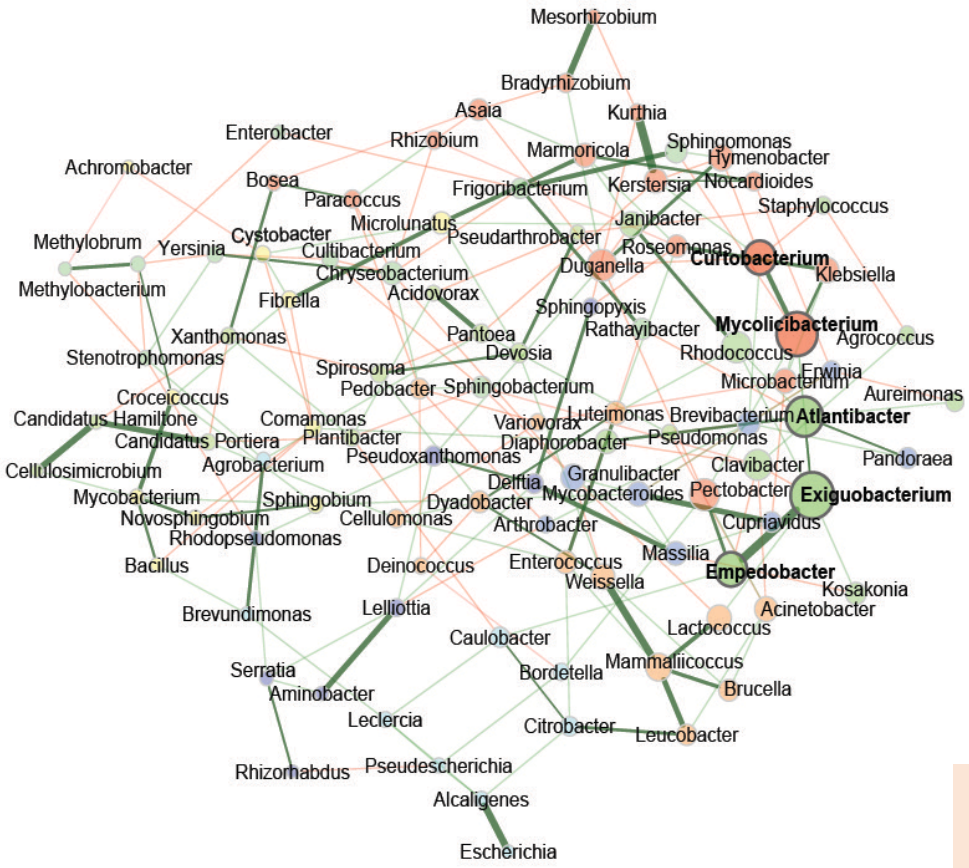
Ambient environment and inoculated plants



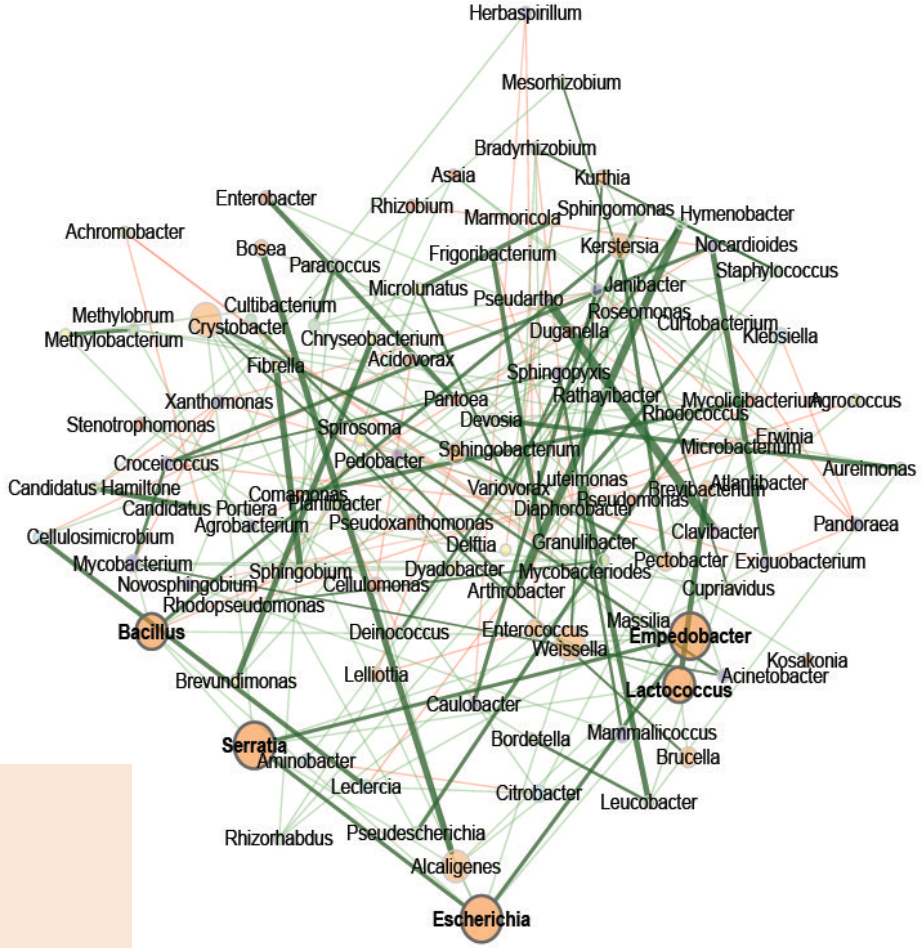
Network: Highly connected
Modularity ↑
Positive edge %
Average Path length ↓

Microbial network topology is altered under combined pathogen and ozone stress.

Ambient environment and control plants

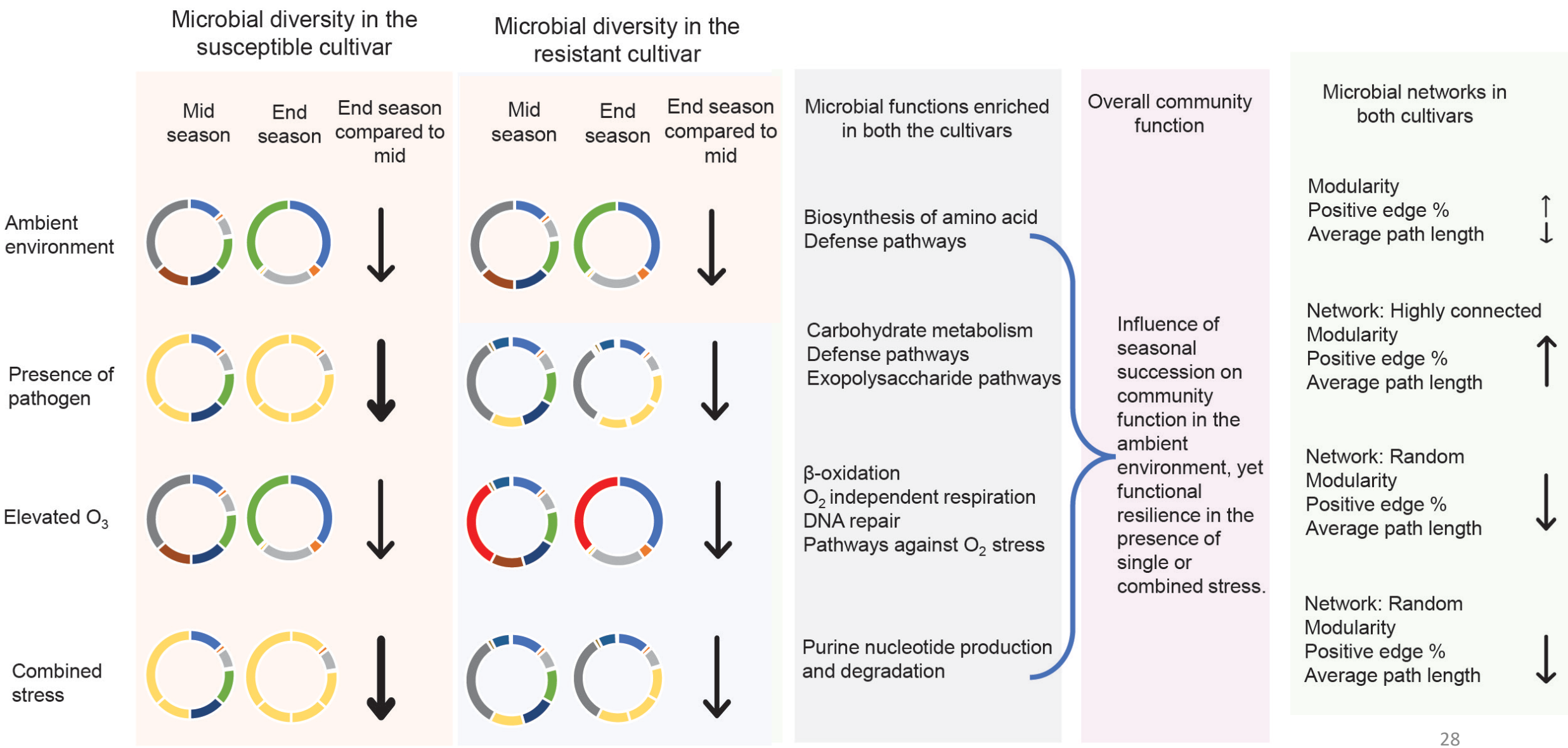


Elevated ozone and inoculated plants



Network: Random
Modularity
Positive edge %
Average Path length

Overall summary



Take home message, inferences and future directions

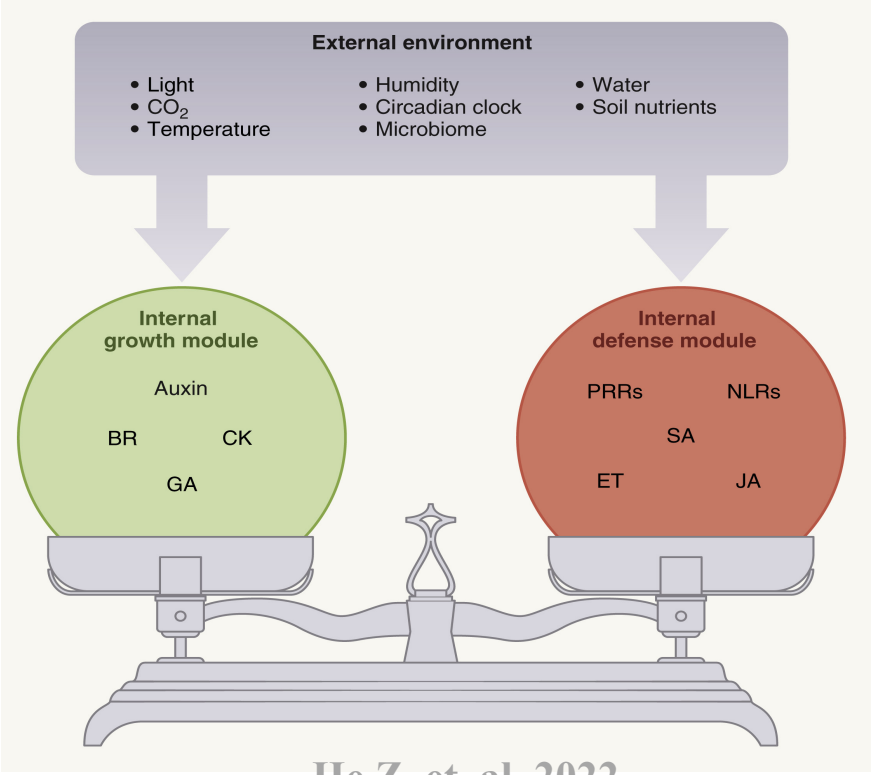
The host defense is likely to be compromised in the face of climate change

Altered host defense in the altered environment?

Is the pathogen being more aggressive with the change in the environment?

Loss of microbiota mediated protection?

Altered interaction among the community members



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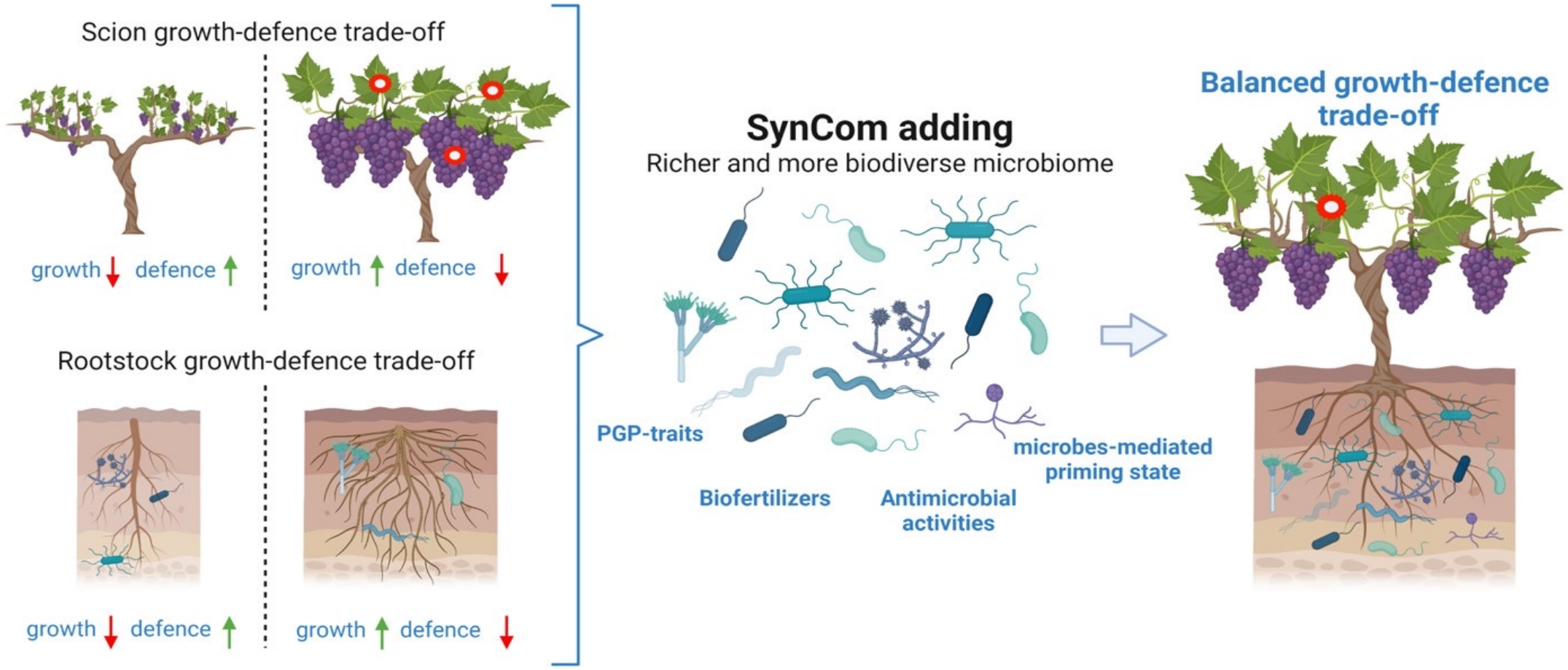
Microbial interactions can be restored by adding SynCom to balance the growth-defense trade-off ??



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Acknowledgement

Dr. Neha Potnis

Dr. Courtney Leisner

Dr. Alvaro Sanz-Saez

<u>Potnis lab members</u>

Amanpreet Kaur

Bijaya Subedi

Kylie Weis

Ivory Russel

Palash Ghosh

Sivakumar Ramamoorthy

<u>Past lab member</u>

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Xanthomonas infection and ozone stress distinctly influence the microbial community structure and interactions in the pepper phyllosphere

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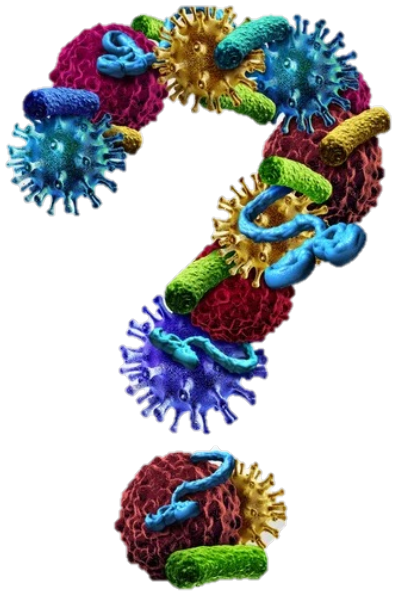
https://doi.org/10.1038/s43705-023-00232-w



https://nehapotnis.wixsite.com/potnislab/

https://github.com/Potnislab/

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