ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

Svelare l'interazione tra il microbioma della rizosfera ed i geni delle piante per una agricoltura sostenibile

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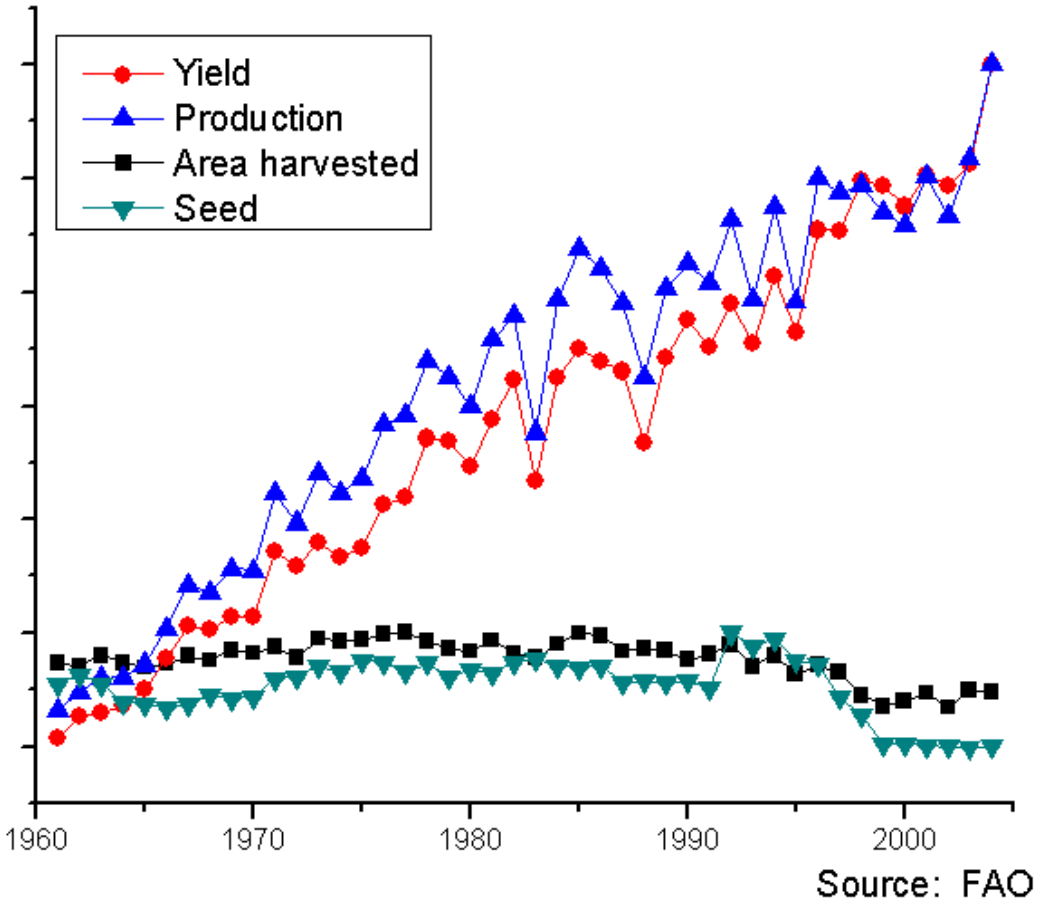
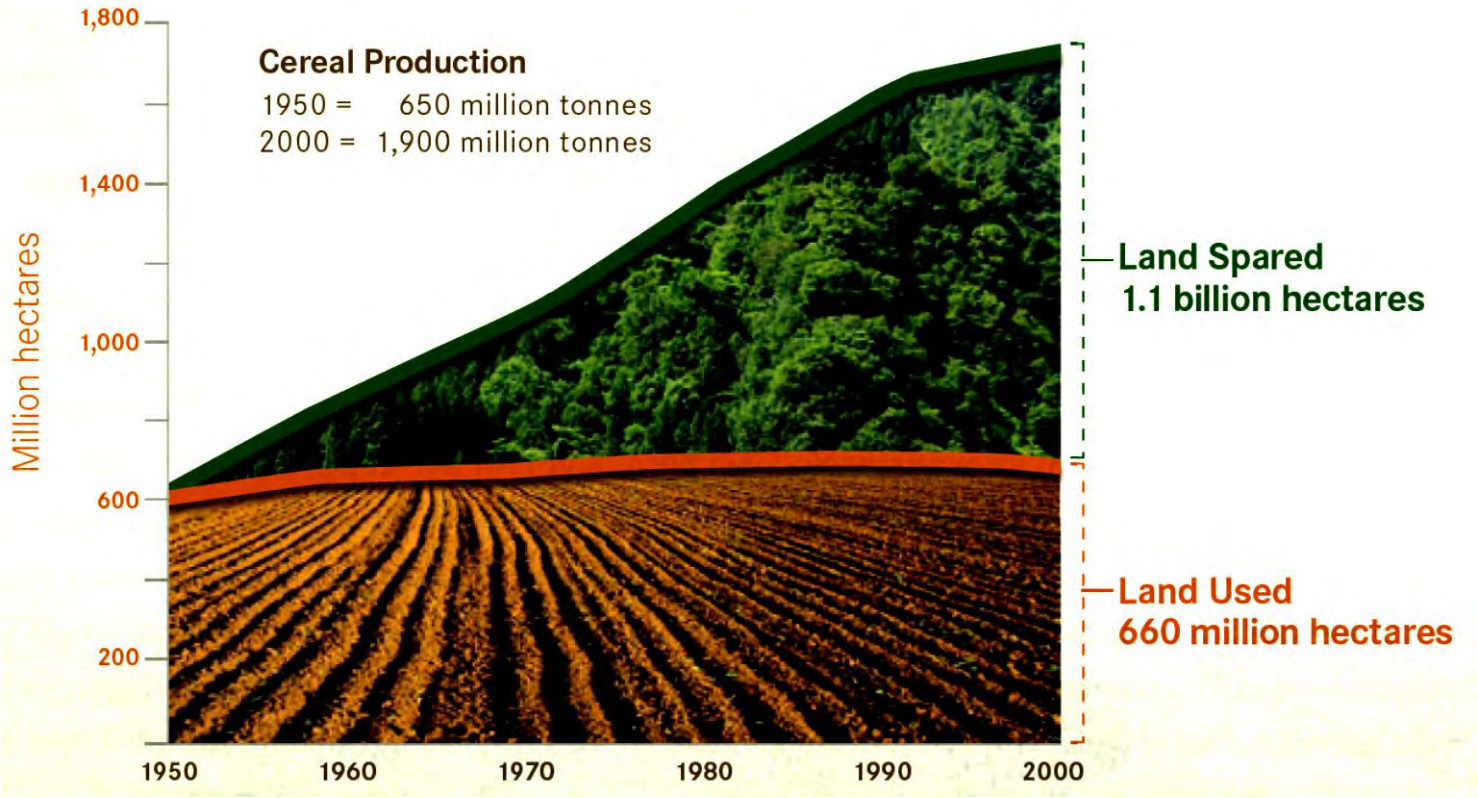
Centro Healthy Planet - Microbioma e la salute dell'uomo, degli organismi viventi e del Pianeta, 20 novembre 2023

Sommario

- Interazioni pianta-microbiota
- Ruolo del microbiota del suolo
- Il microbiota come «*Fenotipo esteso*» della pianta
- I geni delle piante influenzano il microbiota della radice
- Progetti
  - Microbiota della vite e agrofarmaci a base di rame
  - Effetto di specie e cultivar sul microbiota del frumento
  - Wish-roots - usare la genetica delle piante per migliorare la salute del suolo
- Prospettive

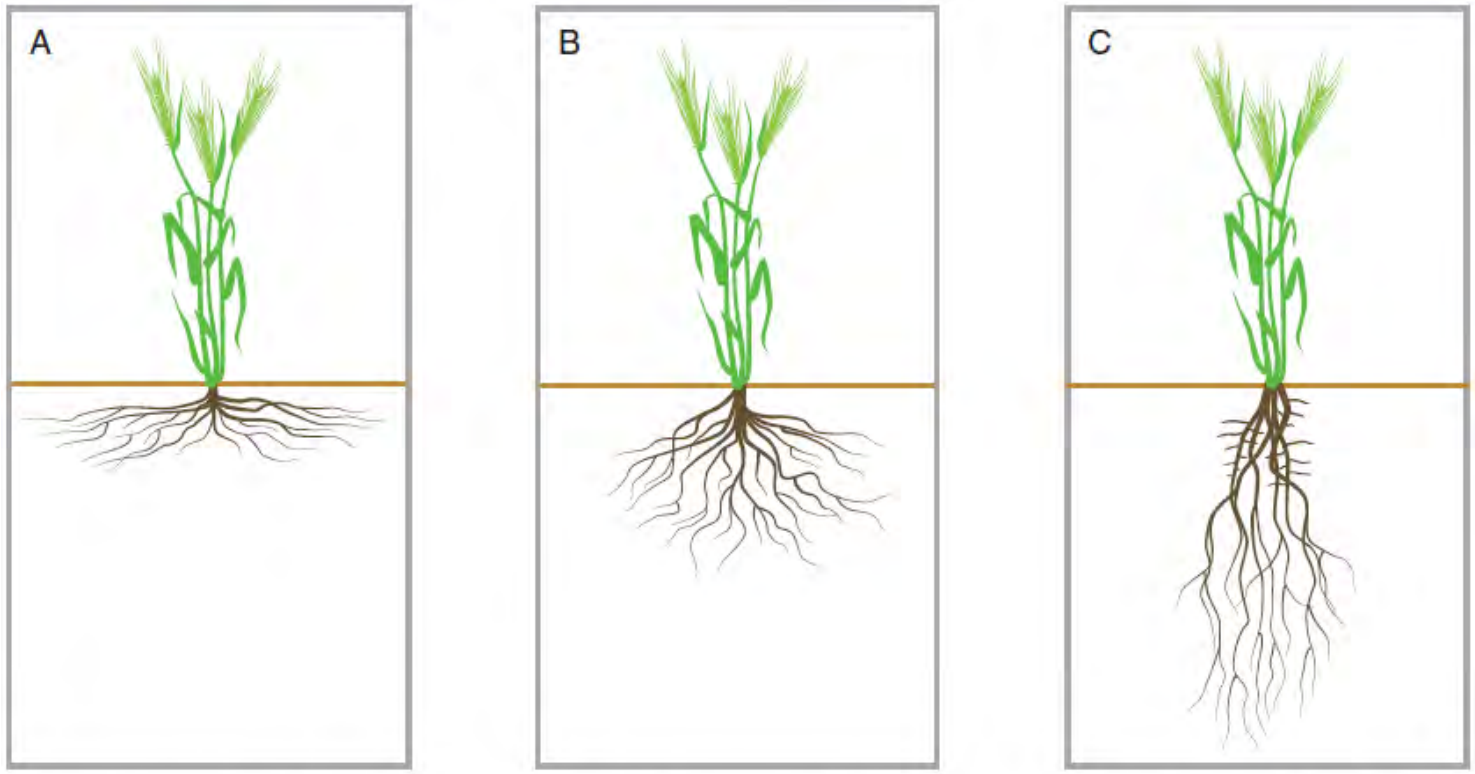
Yield, cultivated area and sustainability





The rhizosphere – an important and little investigated environment

Should we add “root microbiome” to current breeding objectives?



Topsoil foraging for P

Intermediate response for K

Steep, cheap and deep for N

+ rhizobiome composition or diversity???

White et al. 2013. Ann Bot

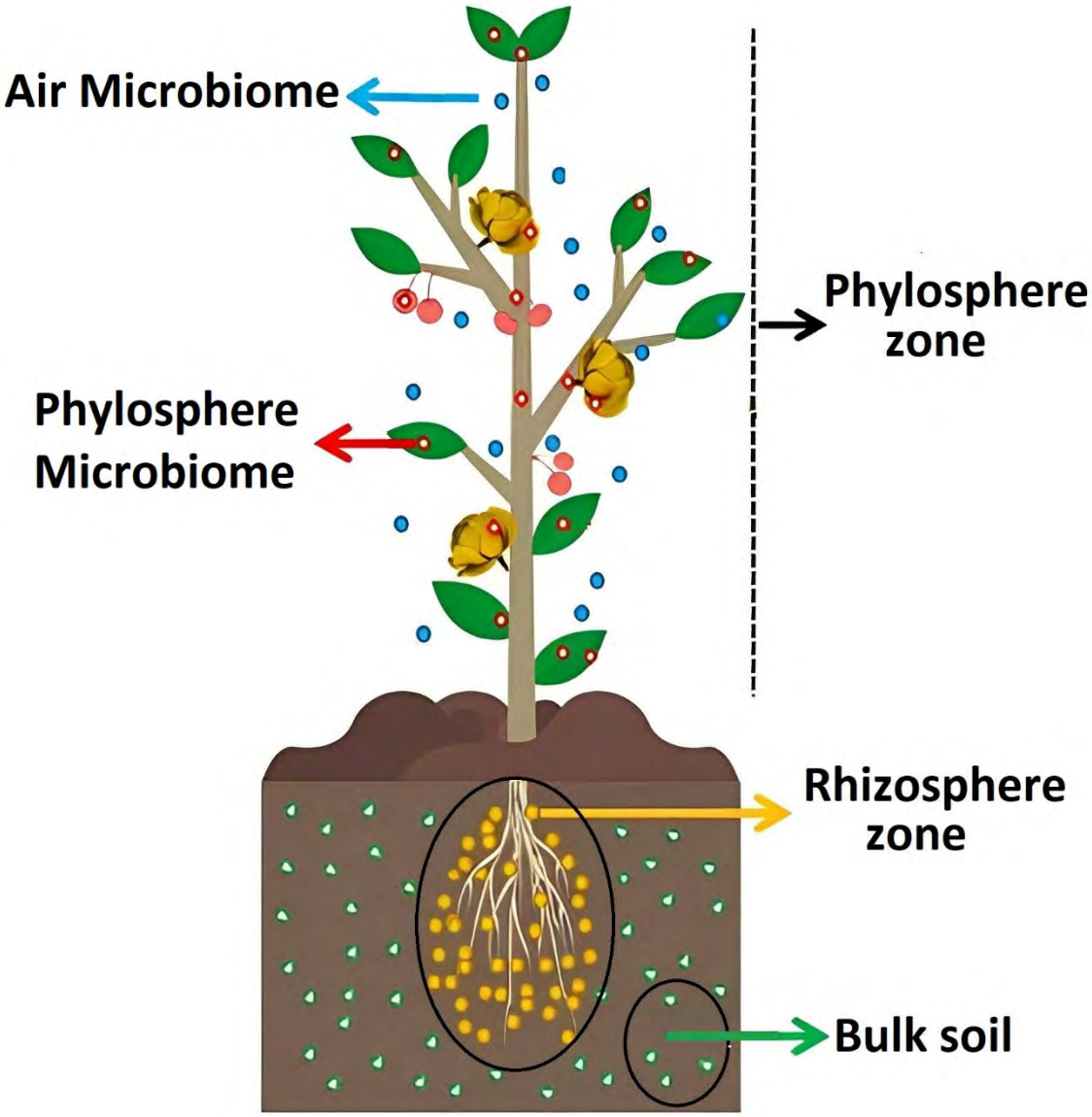
Plant-Microbiome Interactions

- Microbes inhabit rhizosphere, phyllosphere and endosphere
- Rhizosphere - soil region close to roots and influenced by root exudates
- Phyllosphere - aboveground plant organs, such as leaf, stem, flower and fruit
- Endosphere – environment inside plant organs and tissues, or even within cells
- Microbiome changes significantly…

between compartments, rhizosphere diversity is higher than endosphere and phyllosphere

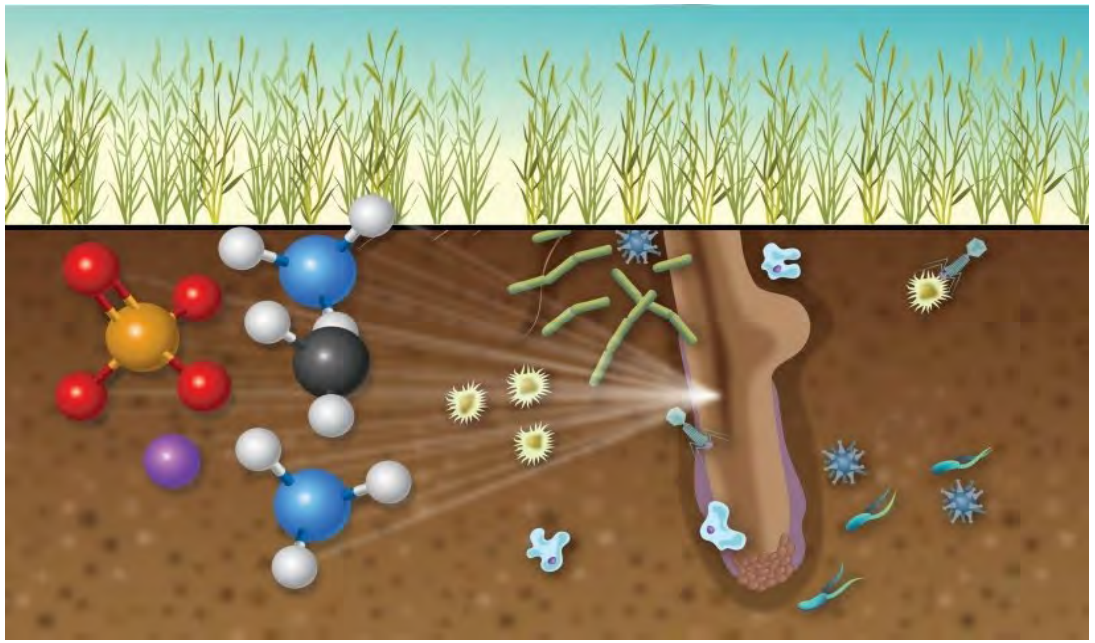
and

according to plant developmental stages, soil environments and genotypes



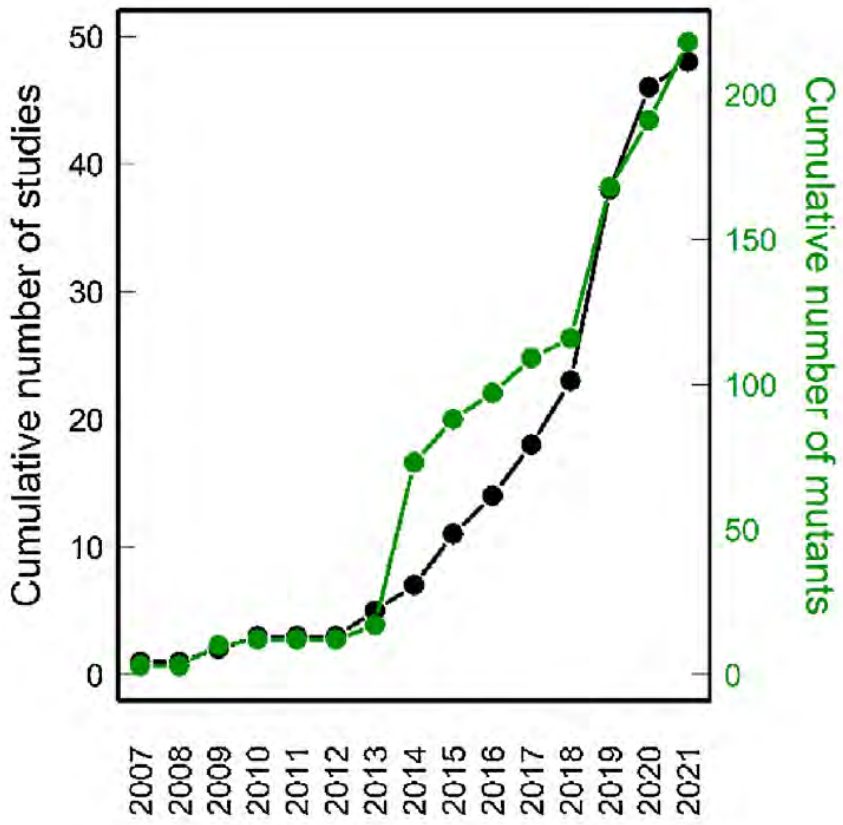
Plant-Microbiome Interactions

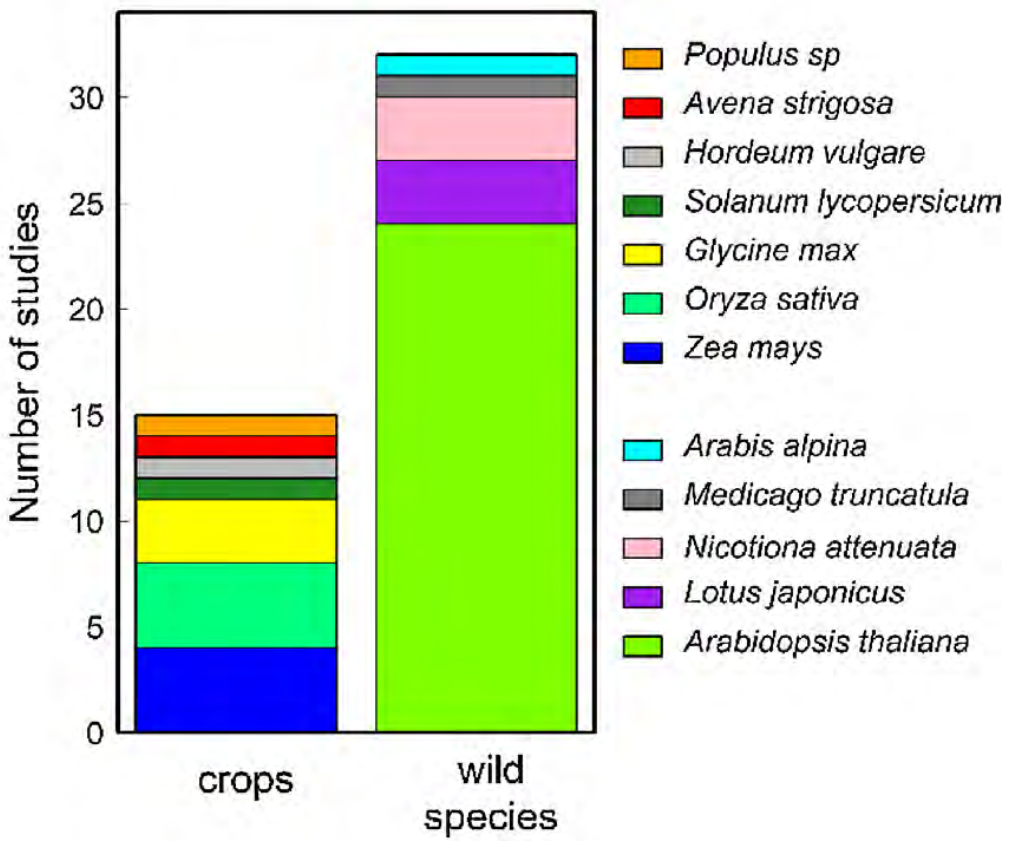
- Interactions can be beneficial, phytopathogenic or even neutral for the plant:
  - Enhanced nutrient and water absorption
  - Protection from parasites
  - Tolerance to abiotic stresses
  - Long term effects on soil fertility
  - Affect carbon storage



- Plants are estimated to use ~20% of their photosynthesized carbon to make root-derived organic molecules, stimulating the formation of distinctive root microbiota from surrounding soil
- Selection of appropriate farming practices and plant breeding can lead to improve plant-microbiome interactions and consequently it will increase the benefit of plant microbiota

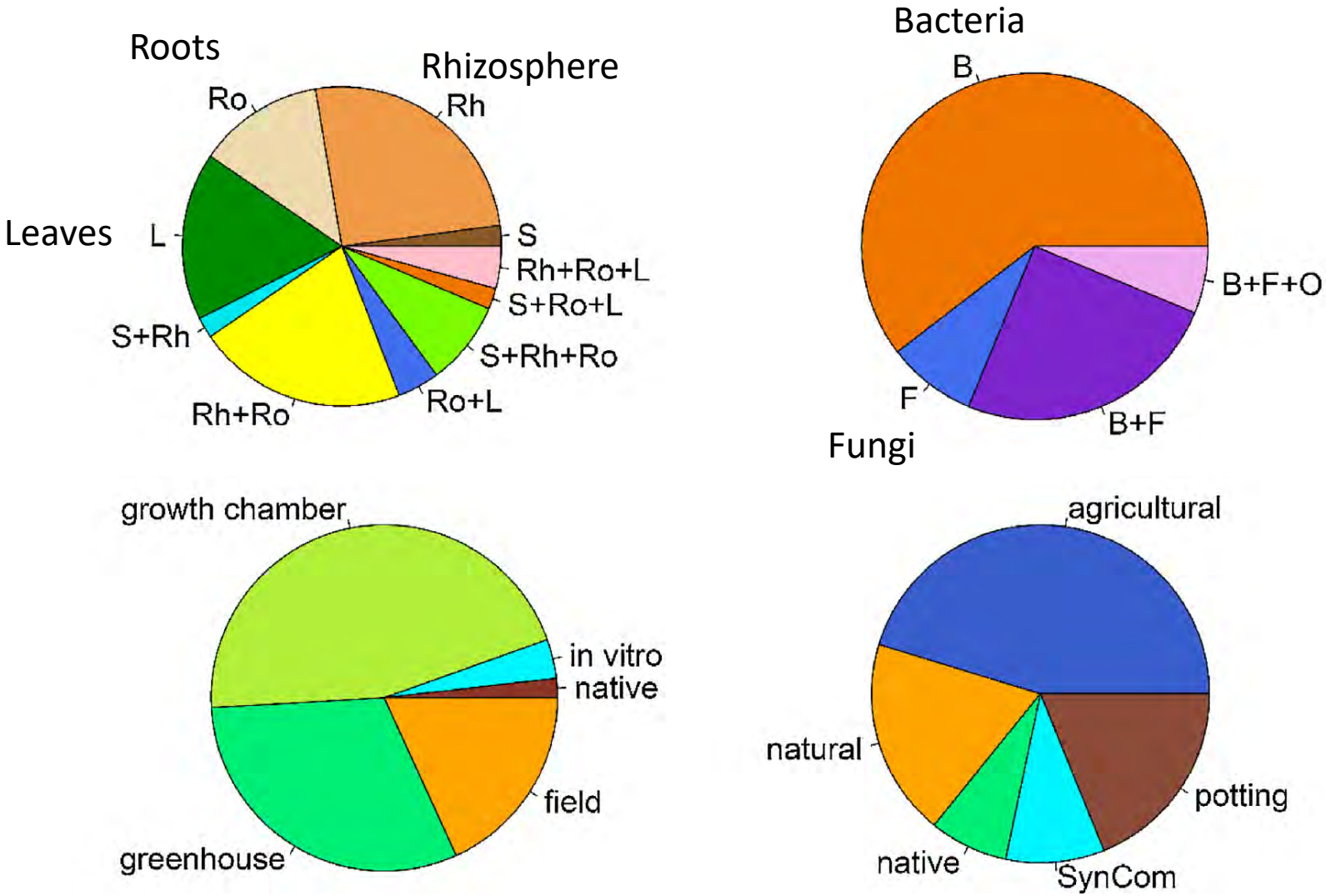
Studies about microbiome-plant genetics interactions using genomics (1/2)





Bergelson et al 2021 Current Opinion in Biotechnology 70:167–173

Studies about microbiome-plant genetics interactions using genomics (2/2)



Bergelson et al 2021 Current Opinion in Biotechnology 70:167–173

Has plant genotype any effect on plant soil microbiome in the field? Yes! But we have to be accurate

PNAS

Diversity and heritability of the maize rhizosphere microbiome under field conditions

Jason A. Peiffer[a,1,2], Aymé Spor[b,c,1,3], Omry Koren[b,c], Zhao Jin[b,c], Susannah Green Tringe[d], Jeffery L. Dangl[e,f,4], Edward S. Buckler[a], and Ruth E. Ley[b,c,4]

[a]Department of Plant Breeding and Genetics, [b]Department of Microbiology, and [c]Department of Molecular Biology and Genetics, Cornell University, Ith NY 14853; [d]Department of Energy, Joint Genome Institute, Walnut Creek, CA, 94598; and [e]Howard Hughes Medical Institute, Department of Biology, Curriculum in Genetics and Molecular Biology, and [f]Department of Microbiology and Immunology, Carolina Center for Genome Sciences, University of N Carolina, Chapel Hill, NC 27599

Contributed by Jeffery L. Dangl, February 15, 2013 (sent for review January 10, 2013)

PNAS

Large-scale replicated field study of maize rhizosphere identifies heritable microbes

William A. Walters[a], Zhao Jin[b,c], Nicholas Youngblut[a], Jason G. Wallace[d], Jessica Sutter[a], Wei Zhang[b], Antonio González-Peña[e], Jason Peiffer[f], Omry Koren[b,g], Qiaojuan Shi[b], Rob Knight[d,h,i], Tijana Glavina del Rio[j], Susannah G. Tringe[j], Edward S. Buckler[k,l], Jeffery L. Dangl[m,n], and Ruth E. Ley[a,b,1]

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We found a small but significant fraction of variation in microbial diversity (both α- andβ-diversity) that could be attributed to host genetics.

2013

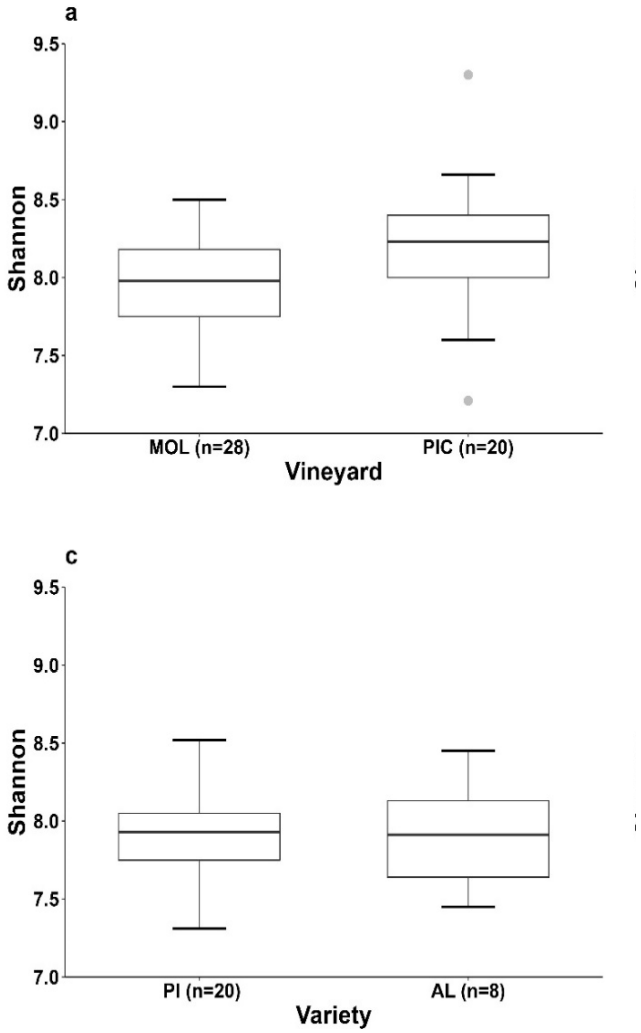
heritability of individual rhizosphere OTUs was lower than for most traditional agronomic traits (0.15–0.25, whereas the heritability of plant yield is around 0.3 and flowering time can be 0.9 or higher).

2018

Rhizosphere microbial (alpha)-diversity in grapevine: No dfference between farms and cultivars

- Real field conditions, Emilia Romagna
- Two Farms, two cultivars
- 16S and ITS amplicon sequencing (ILLUMINA)
- Alpha diversity using Shannon index
- No differences between vineyards for both bacteria and fungi (Kruskal-wallis test)
- No difference between cultivars (Pignoletto and Alionza) in Molinari vineyard
- Overall:

Bacterial S-Index > Fungal S-index



Alpha diversity for a) 16S in two vineyards, b) ITS in two vineyards, c) 16S in MOL, d) ITS in MOL

Shahpari et al. submitted

Discussion and conclusion

- Alpha diversity using Shannon index was higher in bacteria rather than fungi in both Molinari and Picozzi vineyards
- The environment shaped significantly communities but not diversity
- Rootstock genotype has a lower effect than environment
- *Proteobacteria* and *Ascomycota* were dominant phyla in vineyard soil
- At the experiment conditions, we did not see any significant impact of Cu concentrations on microbiome diversity

The Influence of Different Wheat Genotypes and Species on Rhizospheric and Endophytic Bacterial Communities

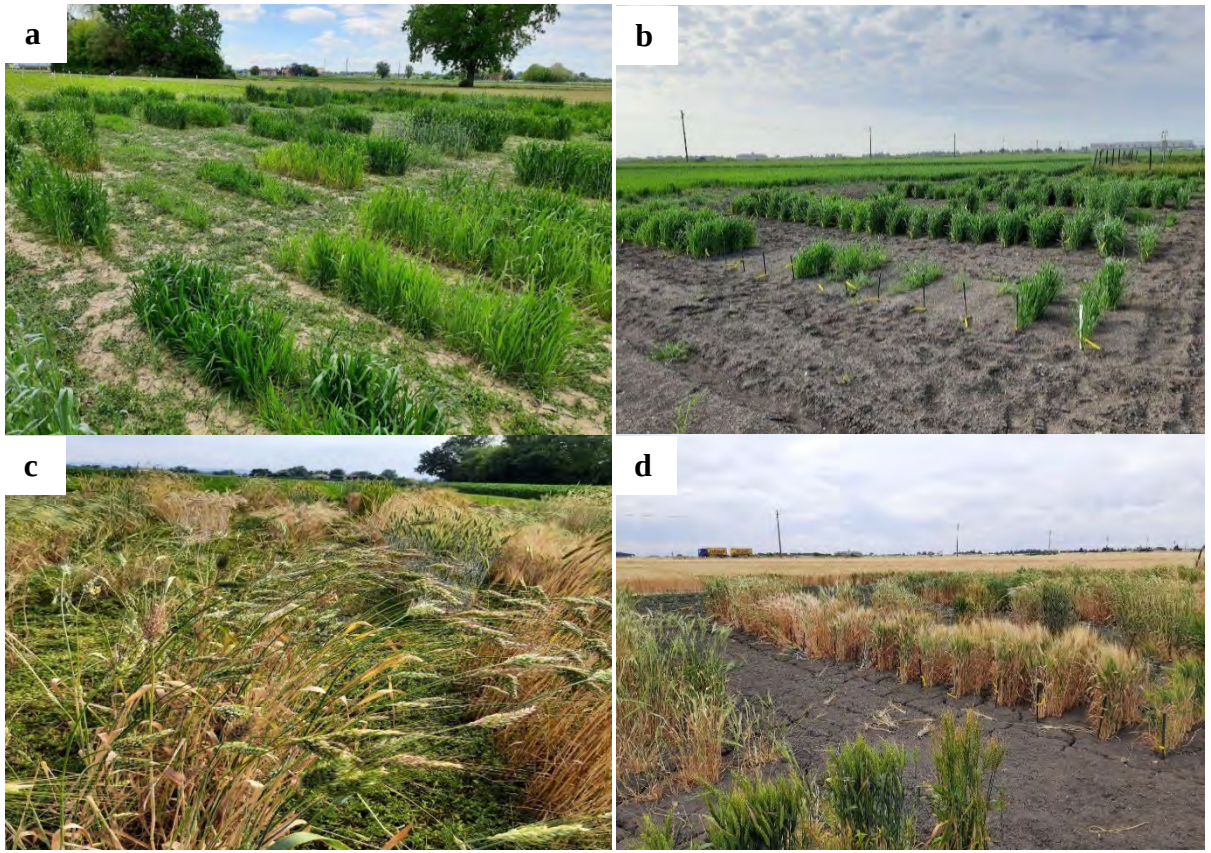
Factors

- Wheat species
- Wheat genotype (= cultivar)
- Field management (minimum tillage vs. conventional management)
- Soil type (rhizospheric vs bulk)

Rhizosphere/bulk soil and root endosphere sampling

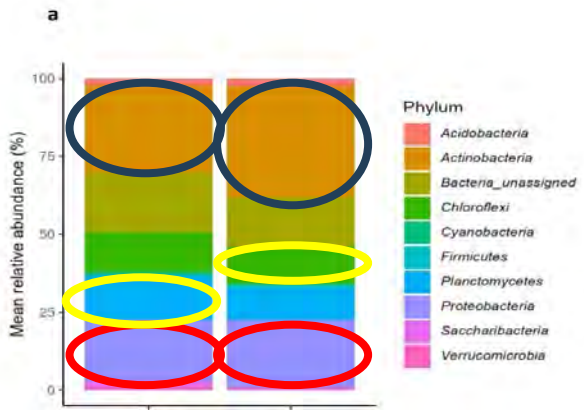
- Collection of 800 rhizosphere/bulk soil root endosphere samples

  - 30 genotypes
  - Two developmental stages
    - First node (Zadoks growth scale 31-33)
    - Beginning of ripening (Zadoks growth scale 87-91)
  - Two fields
  - Rhizosphere/bulk soil collection
    1. For each replication: three plants pulled out randomly using a sterilized shovel
    2. Shake gently and collect loose soil (0-10 cm of the field) = bulk soil
    3. Rhizosphere soil attached to roots collected by shaking vigorously the roots for 30s in sterilized plastic bags and stored in -80 °C
  - Root endosphere
    - Roots collected in Falcon tube and immediate surface sterilization followed in laboratory and stored in -80 °C

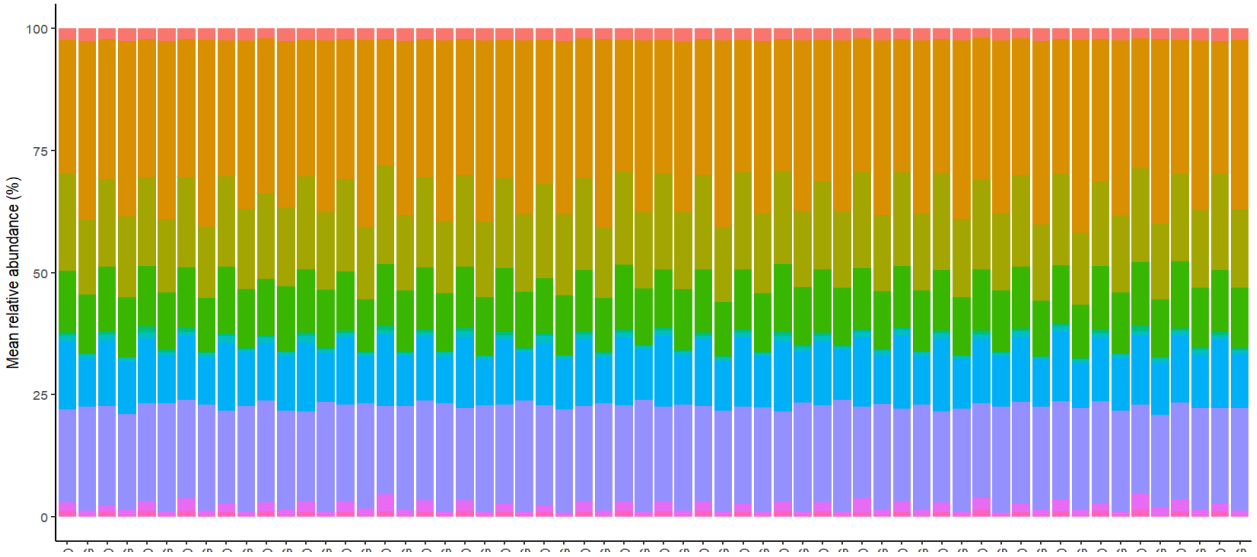


Analysis of taxonomic distribution of wheat rhizospheric samples

- Taxonomic distribution:
  - Field, Species_Field, and Genotype_Field at **phylum** and **family** levels
  - Only groups with relative abundances ≥ 1.0% are reported



- Most frequent phyla:
  - BO field: *Actinobacteria* (28.02%), *Proteobacteria* (19.59%) and *Planctomycetes* (13.70%)
  - FG field: *Actinobacteria (35.65%), Proteobacteria (21.61%) and Chloroflexi (12.02%)*



- Some of the most frequent family:
  - *Microbacteriaceae, Rhodospirillaceae, Streptomycetaceae*

WISH-ROOTS
Making soil health a breeding target

Tuning the wheat root microbiome to improve soil health and optimize rhizosphere nitrogen cycling and availability

EJP project

- **20 wheat cultivars**
- **6 environments (Europe, China e South Africa)**
- **Root and soil traits (including microbiome)**
- **3 years**

Acknowledgements

DISTAL - University of Bologna, Italy
Roberto Tuberosa
Marco Maccaferri
Armin Shahpari
Matteo Bozzoli
Cristian Forestan
Giovanni Burgio
Ilaria Braschi
Matteo Brecchia
Diana Di Gioia
Daniele Alberoni

CREA CI FOGGIA
Nicola Pecchioni

John Innes Centre UK
Maria-Hernandez Soriano

University of Nottingham
Malcolm Bennett, Riccardo Fusi

University of Bonn
Frank Hochholdinger