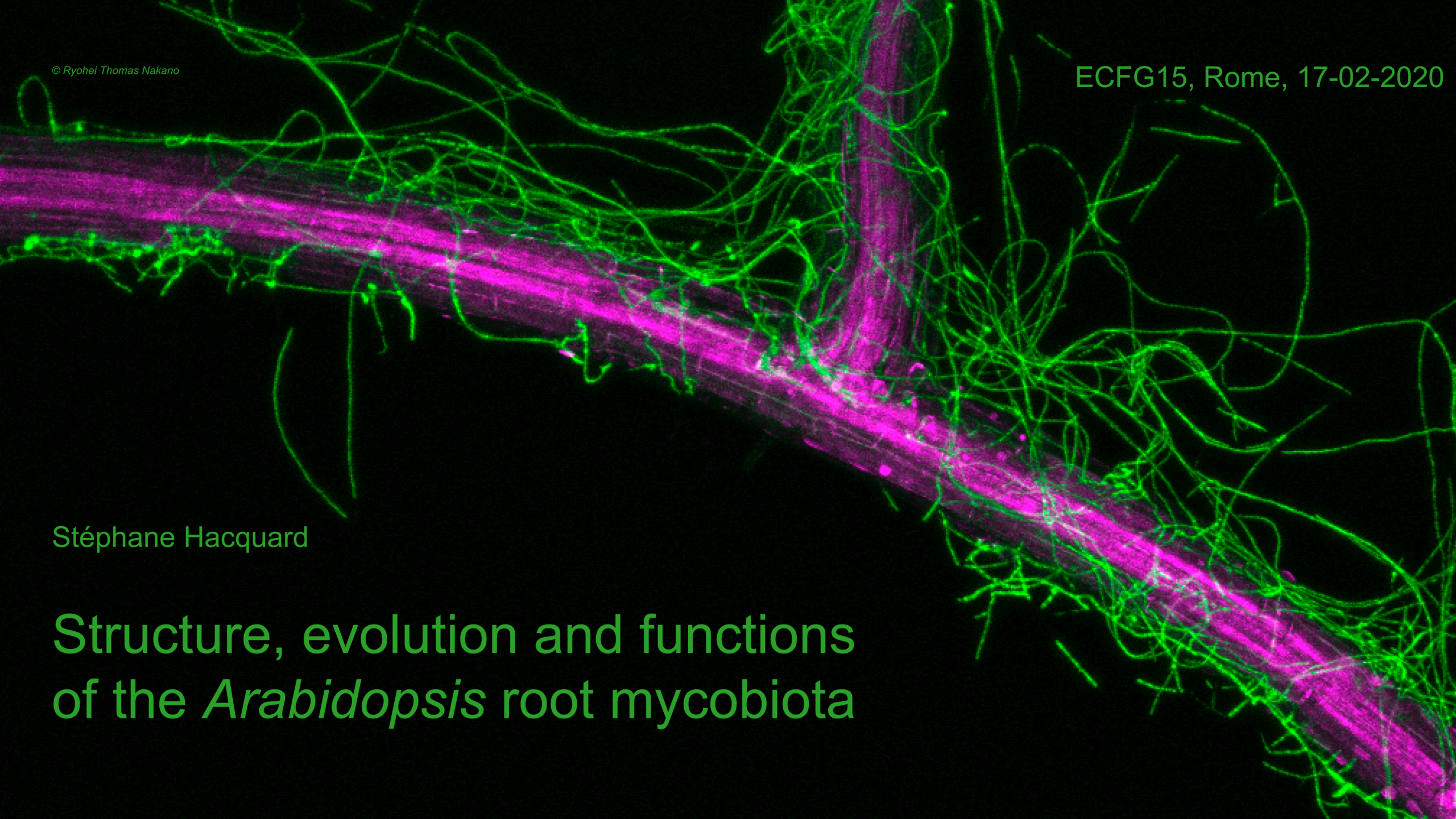

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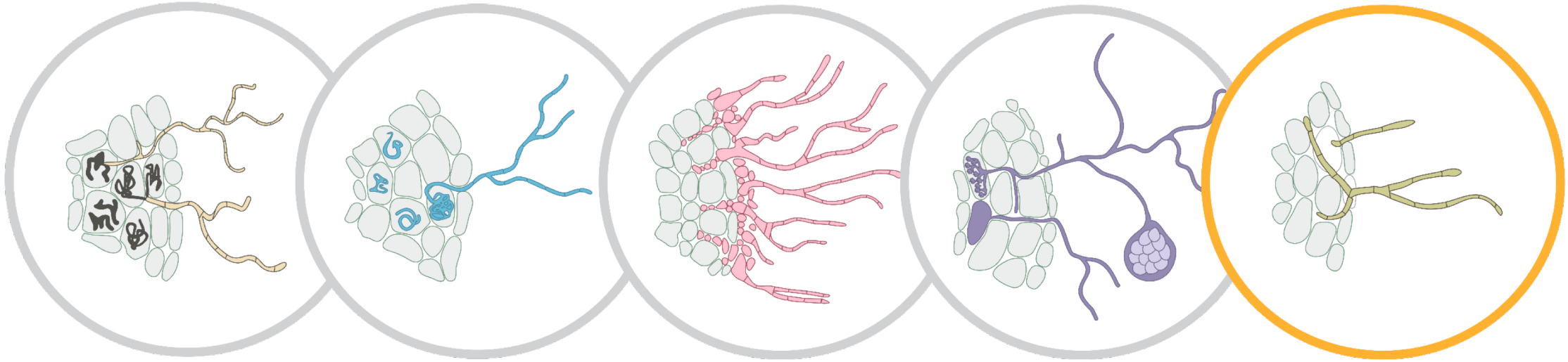
ECFG15, Rome, 17-02-2020

Stéphane Hacquard

Structure, evolution and functions of the *Arabidopsis* root mycobiota

Introduction

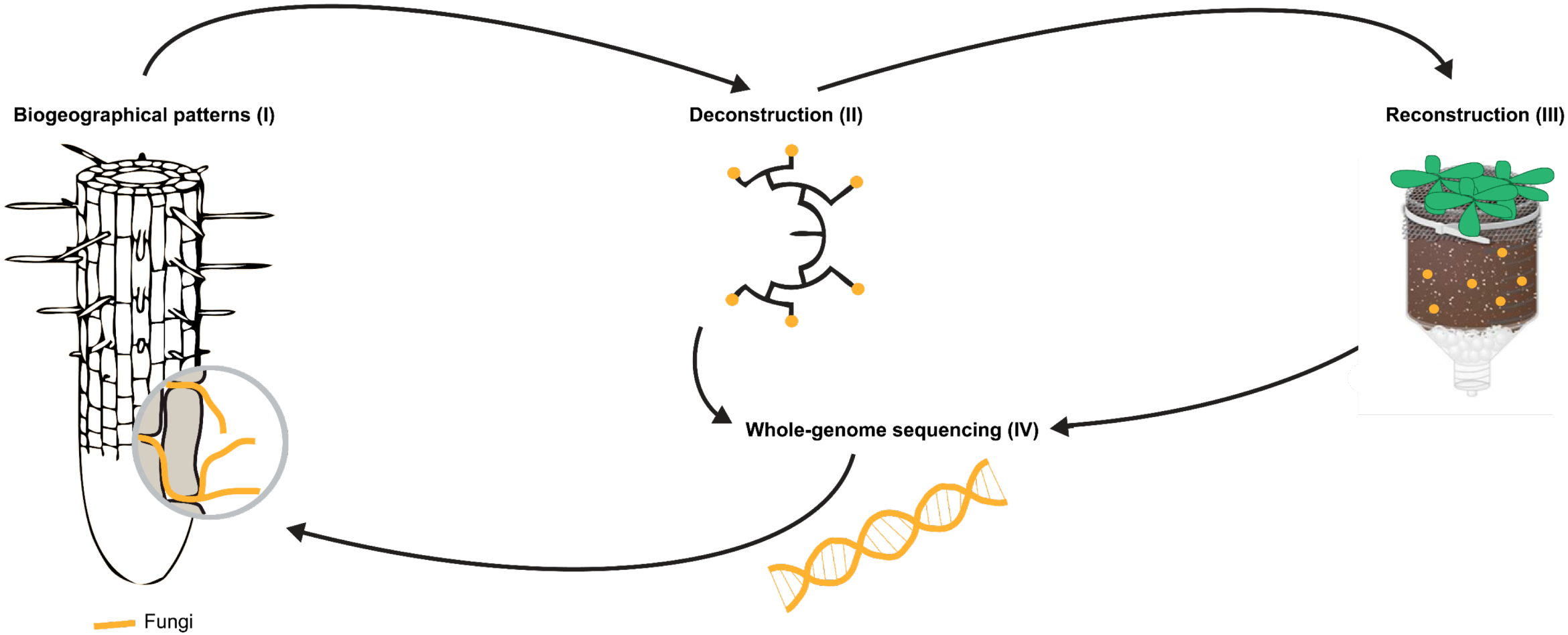


Land plants:	10%*	1.5%*	2%*	72%*	100%

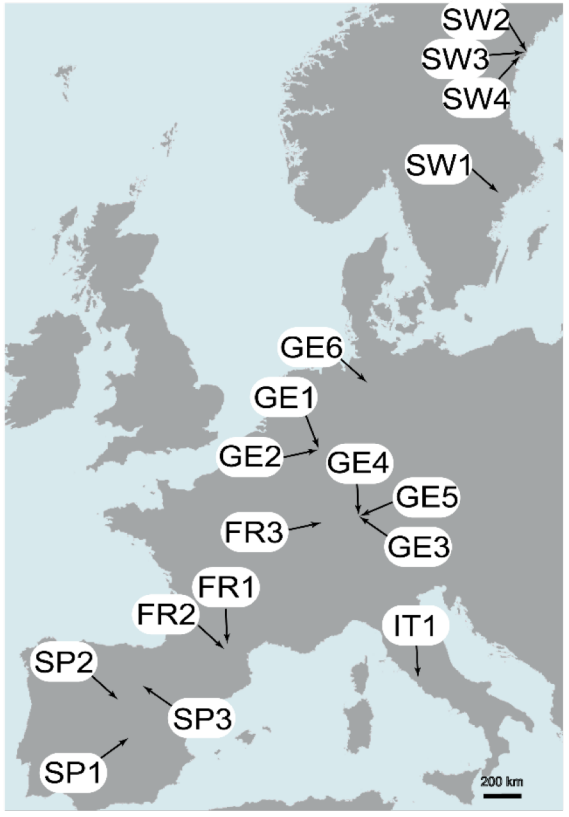
- The majority of vascular plants are mycorrhizal
- Mycorrhizal associations have key roles in maintaining plant productivity in natural and agricultural habitats

*Based on Brundrett and Tedersoo, New Phytologist 2018

Introduction



Continental-scale survey of *A. thaliana* root-associated fungal communities

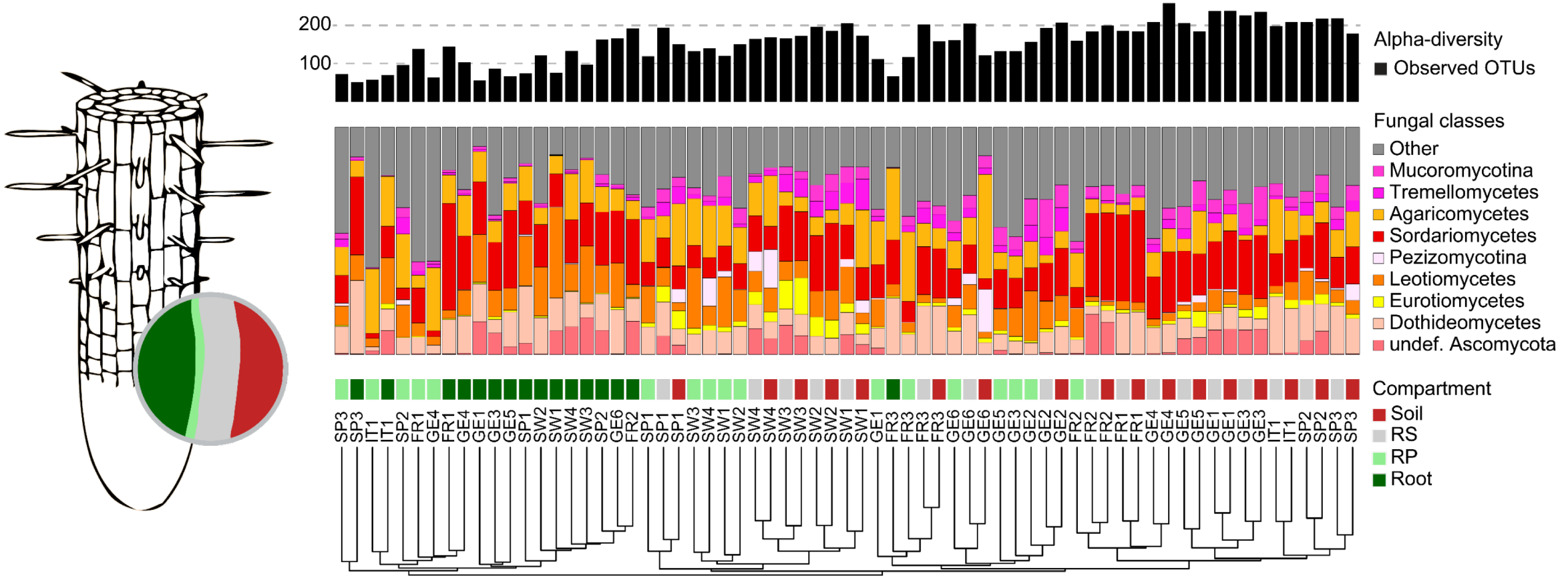


Arabidopsis thaliana

neighboring grasses

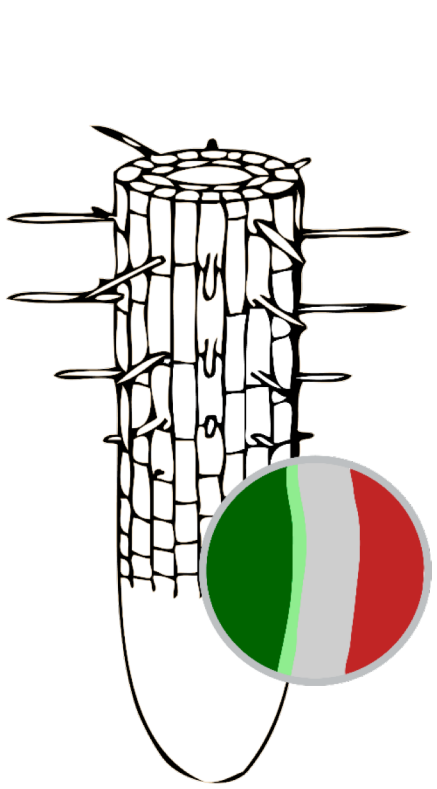
Thiergart et al. Nature Ecology & Evolution 2020

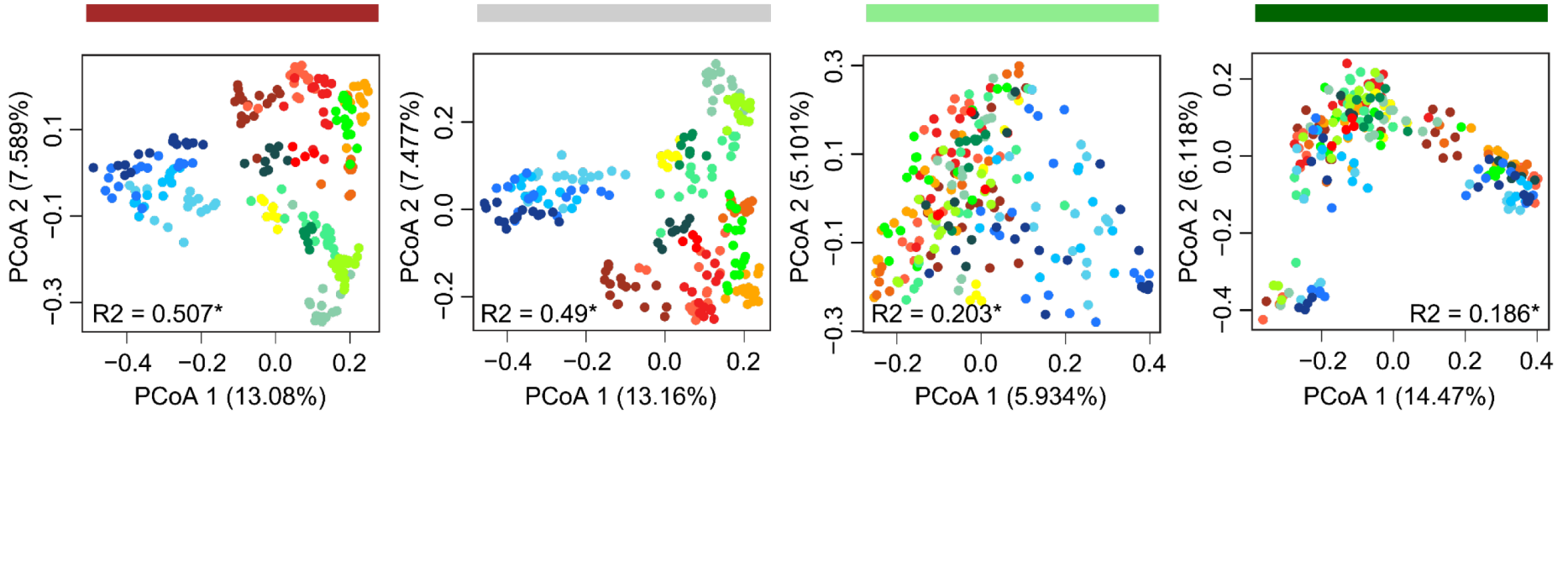
Similarity in endosphere-associated fungal communities across European sites



Thiergart et al. Nature Ecology & Evolution 2020

Strong geographical structuring of fungal communities in soil, but not in roots

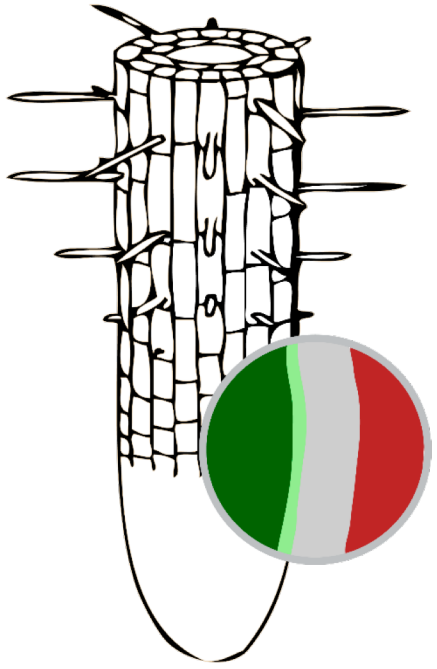


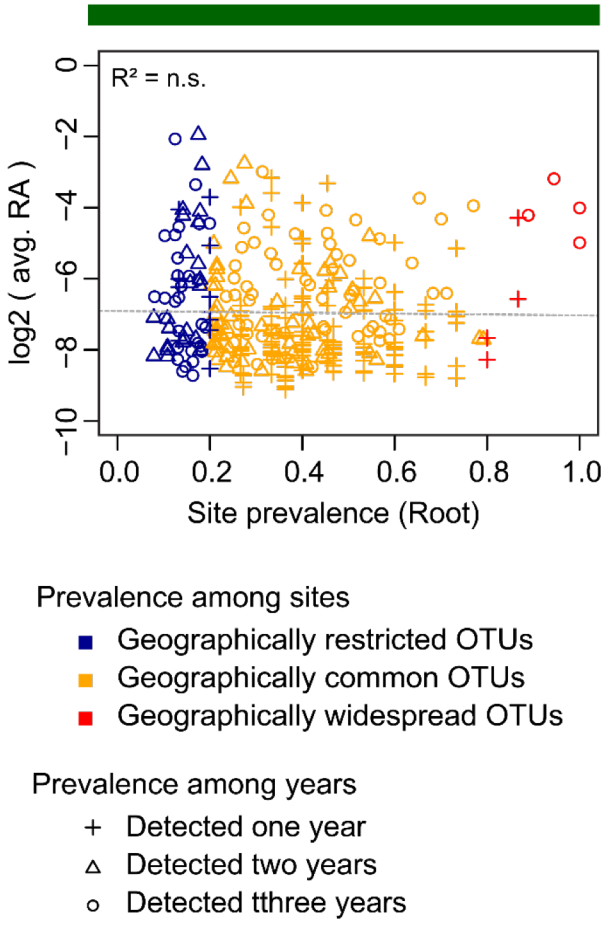


Thiergart et al. Nature Ecology & Evolution 2020

PERMANOVA, *$P < 0.001$

Few geographically widespread fungi consistently colonize roots across sites



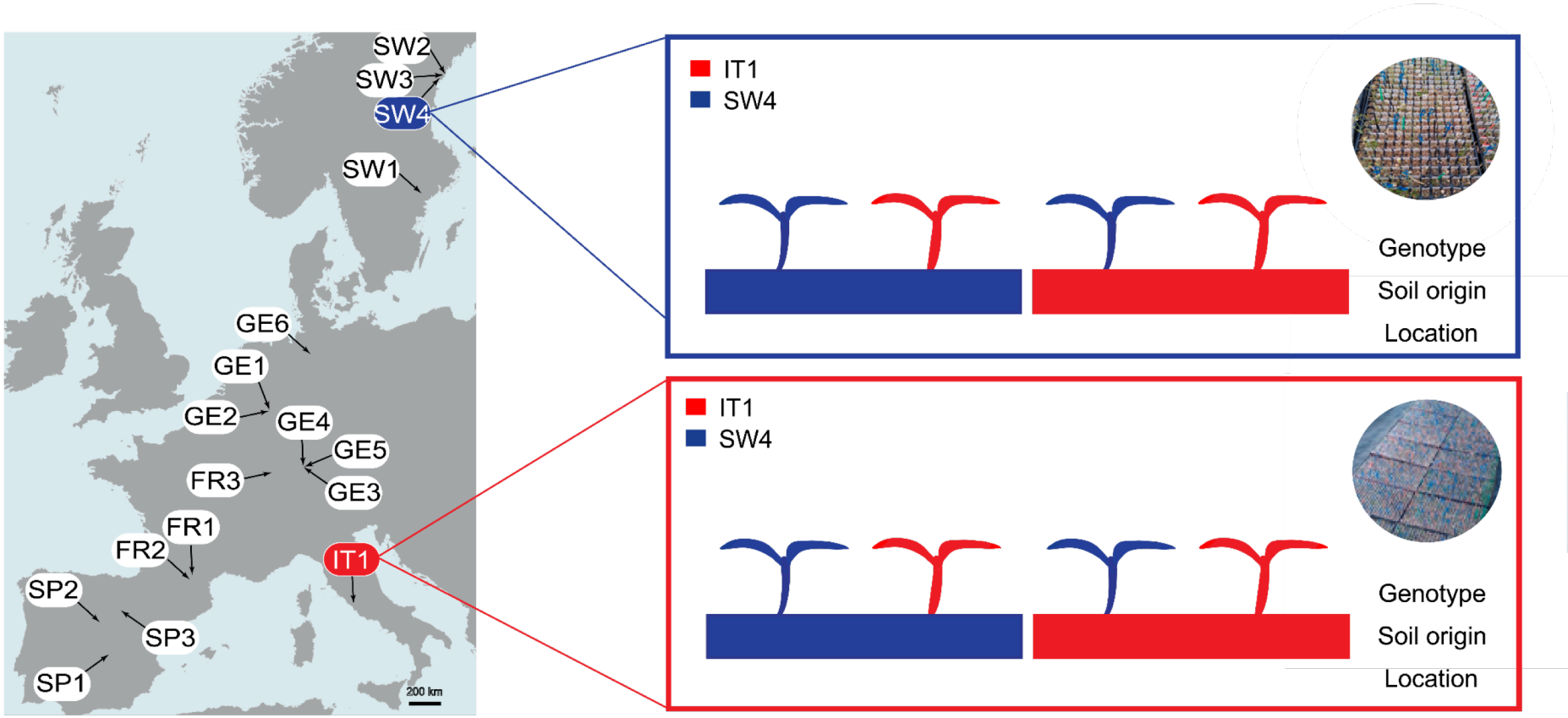


Prevalence among sites
- Geographically restricted OTUs
- Geographically common OTUs
- Geographically widespread OTUs

Prevalence among years
- \+ Detected one year
- △ Detected two years
- ○ Detected tthree years

Thiergart et al. Nature Ecology & Evolution 2020

Uncoupling soil conditions from location in a reciprocal transplant experiment



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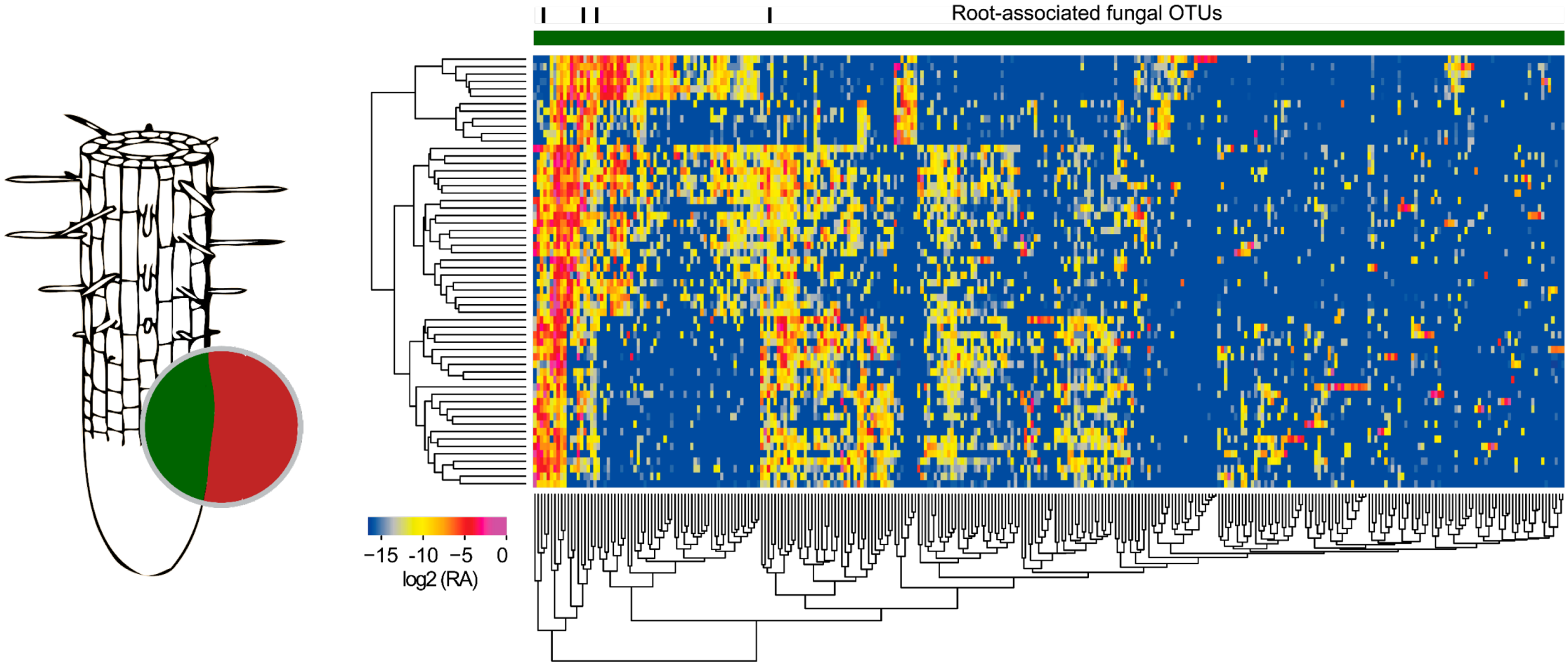
Climate as important as soil origin for root mycobiota differentiation



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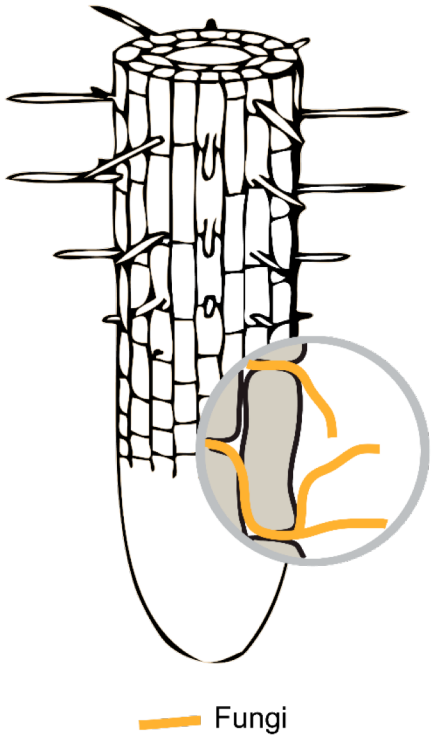
Take home messages (I)

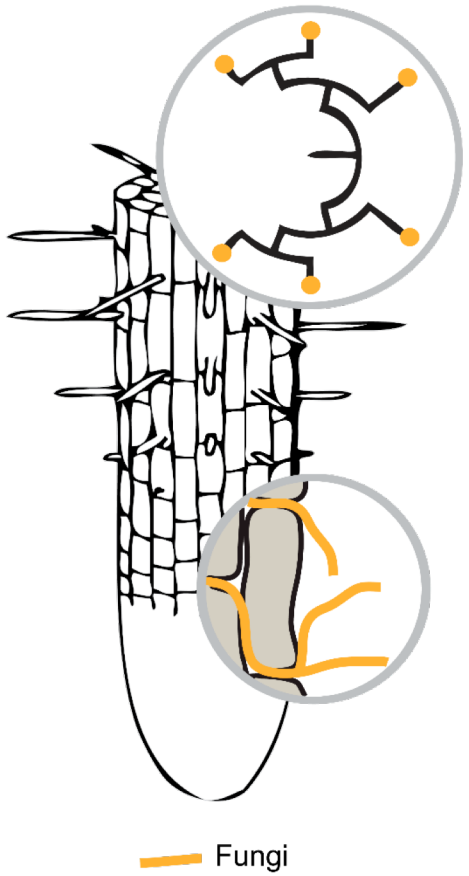
Biogeographical patterns (I)

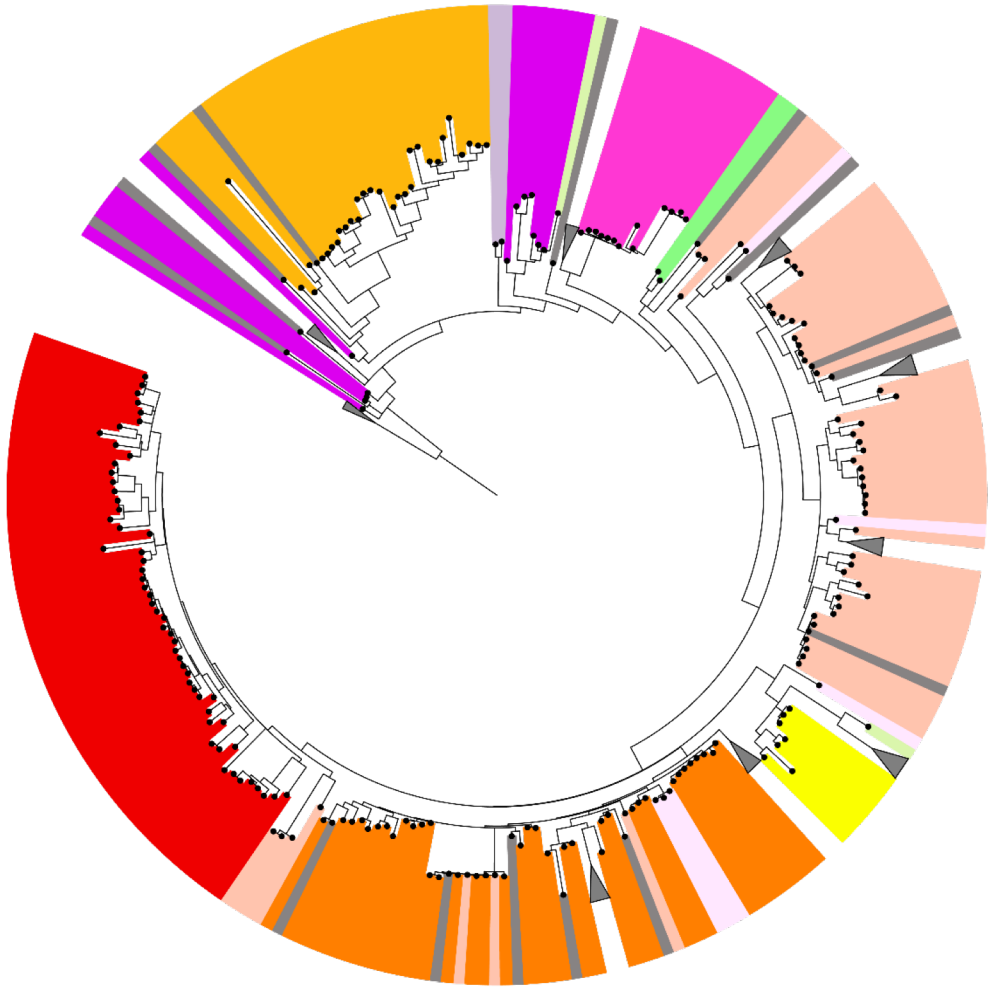


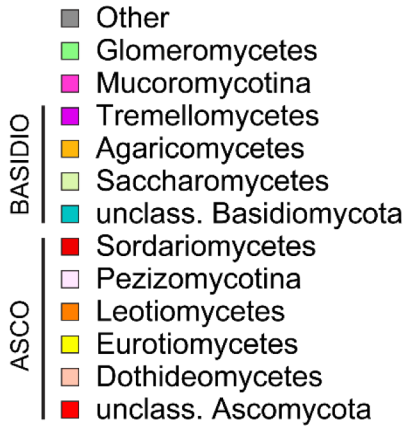
- Less geographical structuring in roots than in soil
- Very few geographically widespread taxa
- Site-specific signatures explained by differences in climate and soil conditions
- Weak influence of the host genotype

Cultured fungi from few sites partly recapitulate the root mycobiota from all sites

488 root-associated fungal isolates
(European transect + CAS)

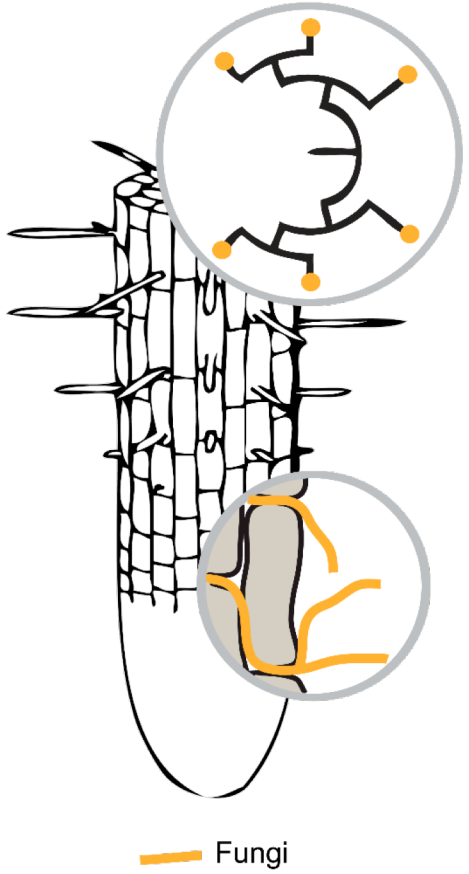


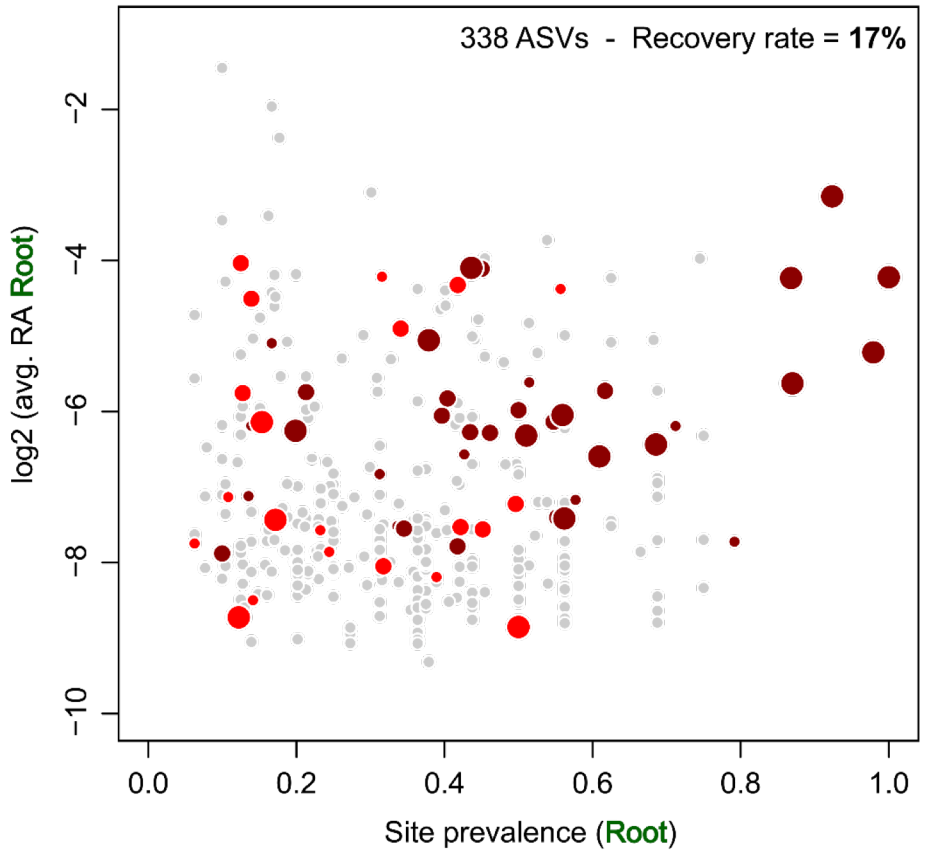




Several abundant and prevalent root mycobiota members can be cultured

488 root-associated fungal isolates
(European transect + CAS)



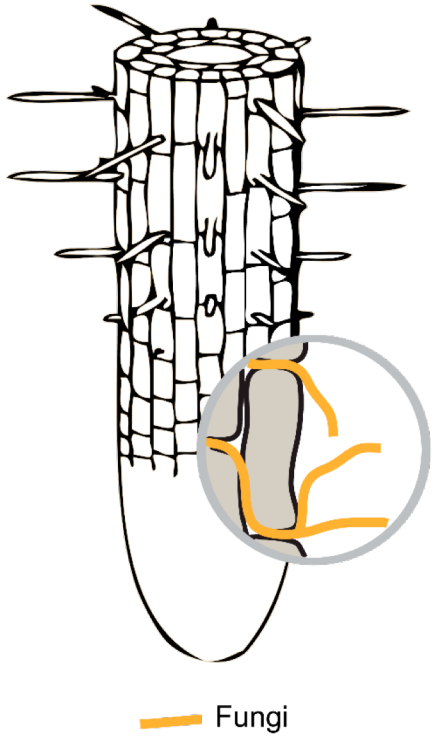


No hit with ASVs (similarity < 97%)
Hit with ASVs (similarity 97-99%)
Hit with ASVs (similarity 100%)

1 isolate
2-10 isolates
>10 isolates

Take home messages (II)

Biogeographical patterns (I)



Fungi

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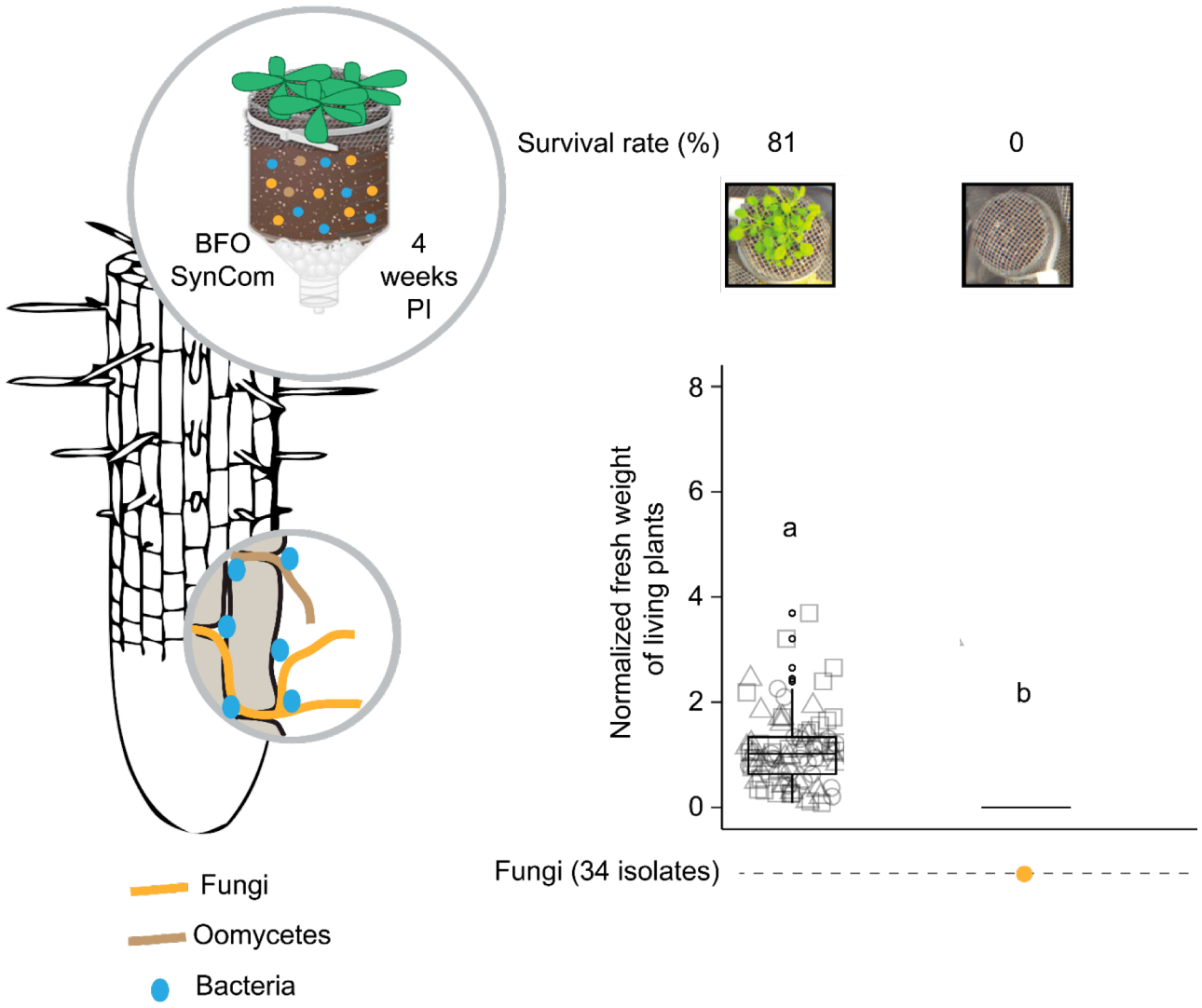
Deconstruction (II)

- Representative isolates available for 17% of the sequence variants detected in roots
- Representative isolates available for 46% of the most abundant and prevalant sequence variants detected in roots

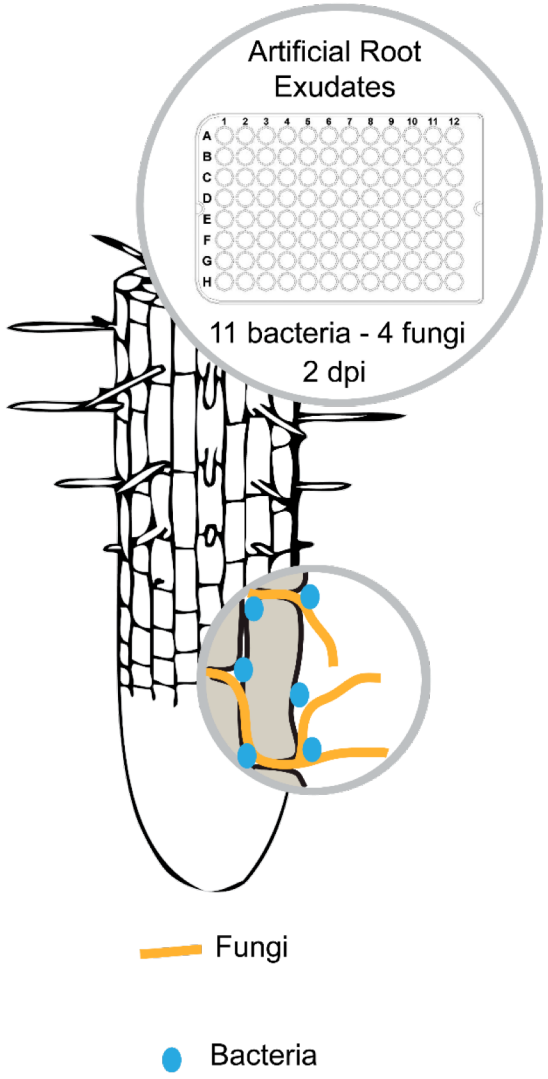
Bacterial commensals maintain fungal balance in roots and promote host health

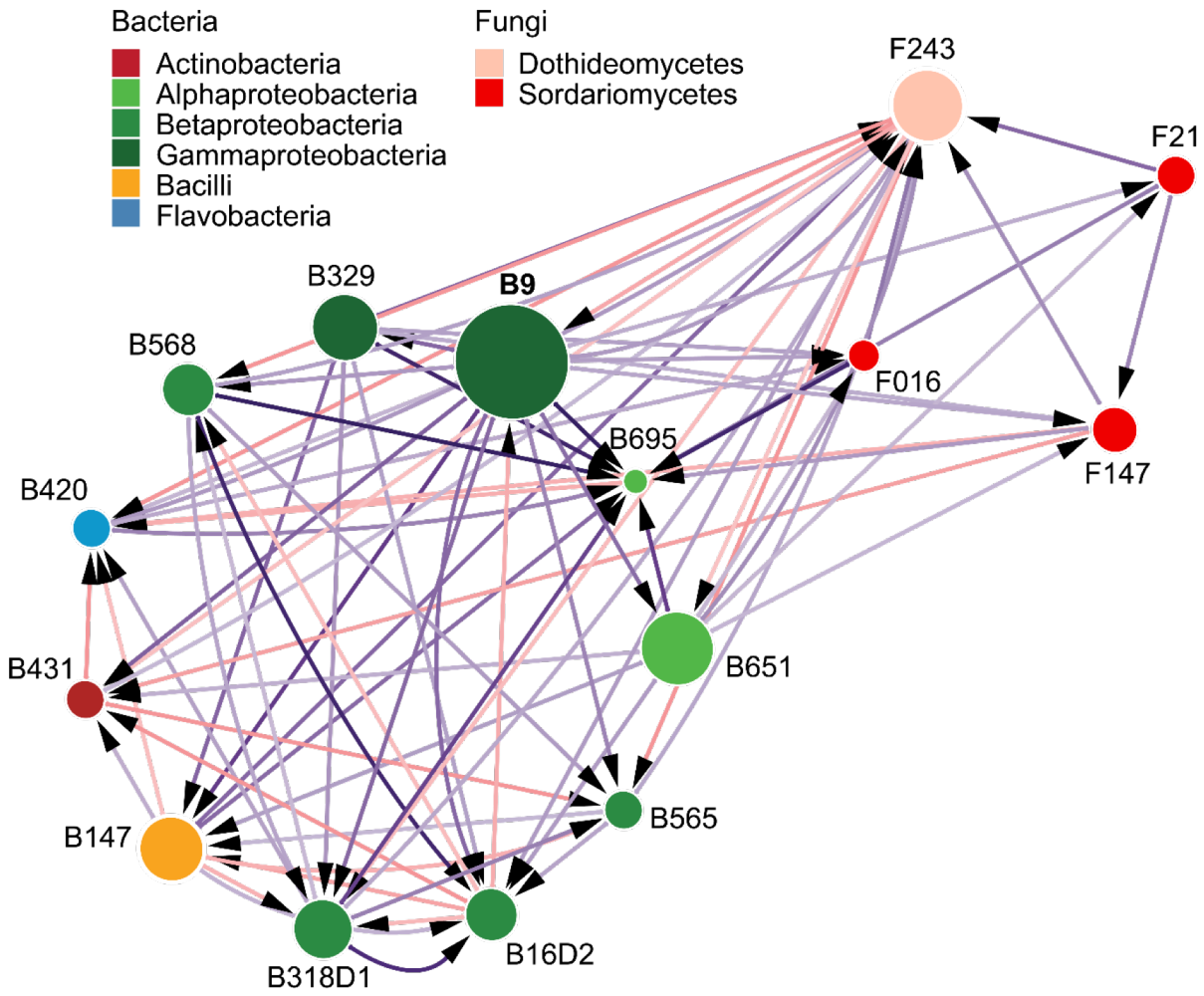


Duran et al. Cell 2018

Kruskal-Wallis with Dunn's post-hoc test, $P < 0.05$

Highly competitive Pseudomonas B9 protects plant from the fungal SynCom

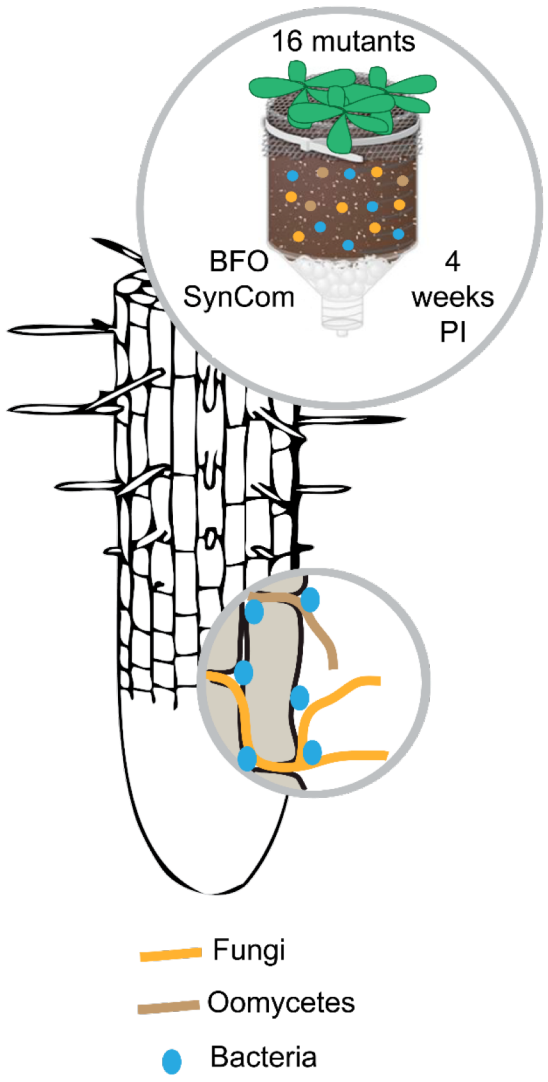


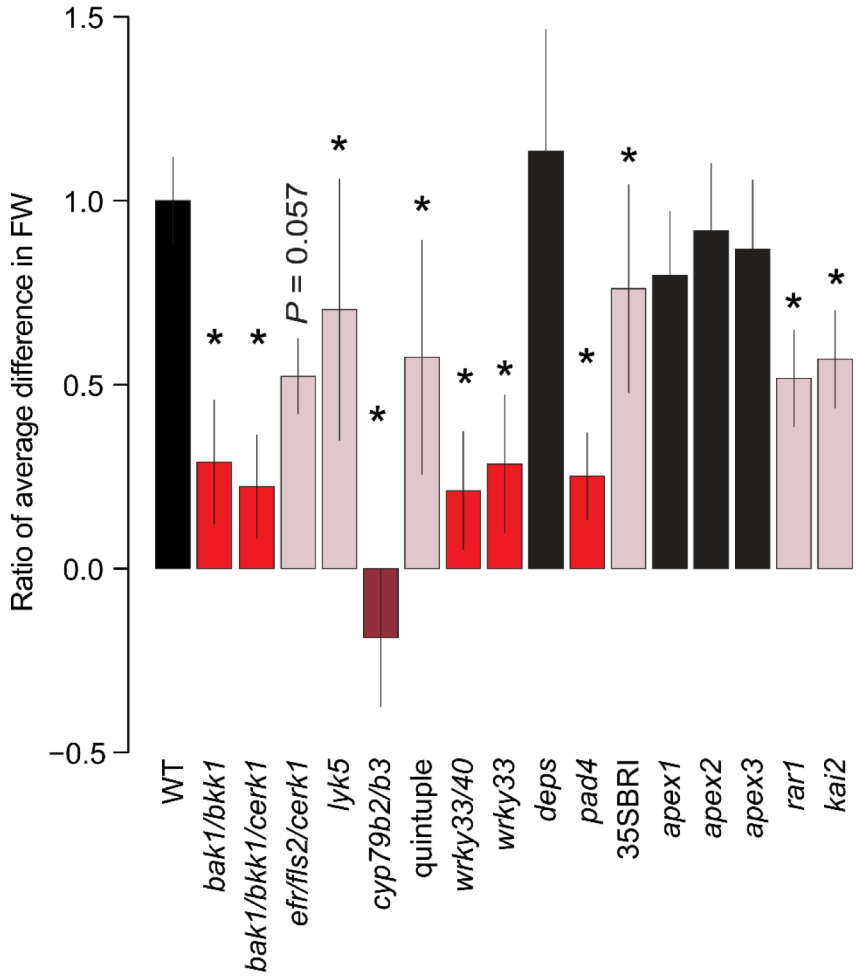


Unpublished - Getzke

Kruskal-Wallis with Dunn's post-hoc test, $P < 0.05$

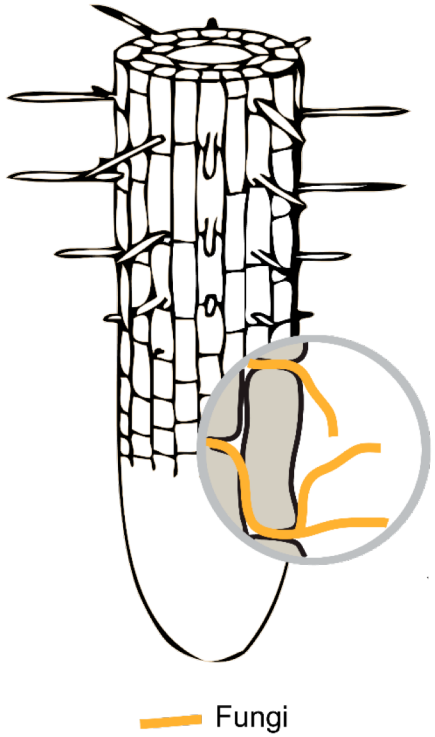
Control of fungal load by host immunity in roots is linked to BFO-mediated PGP





Take home messages (III)

Biogeographical patterns (I)



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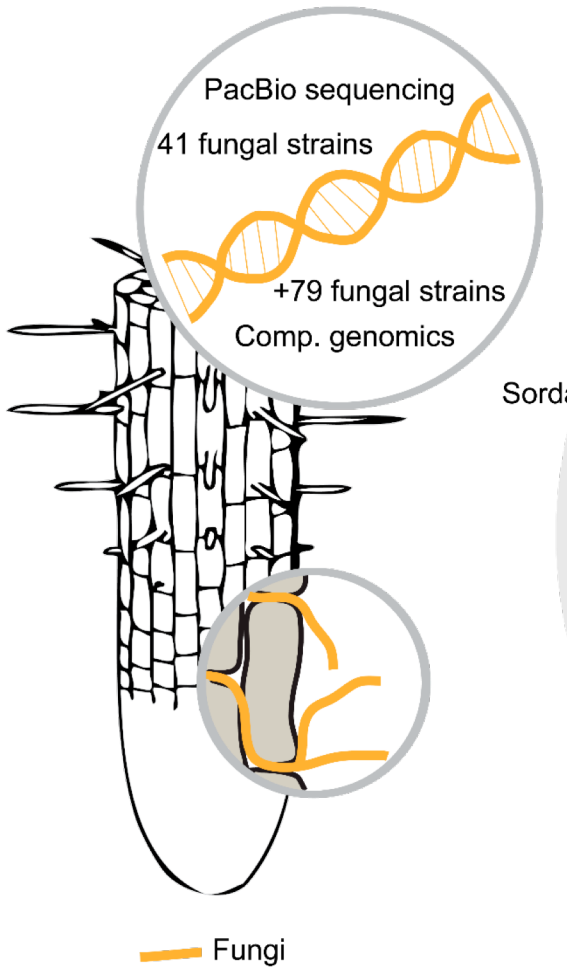
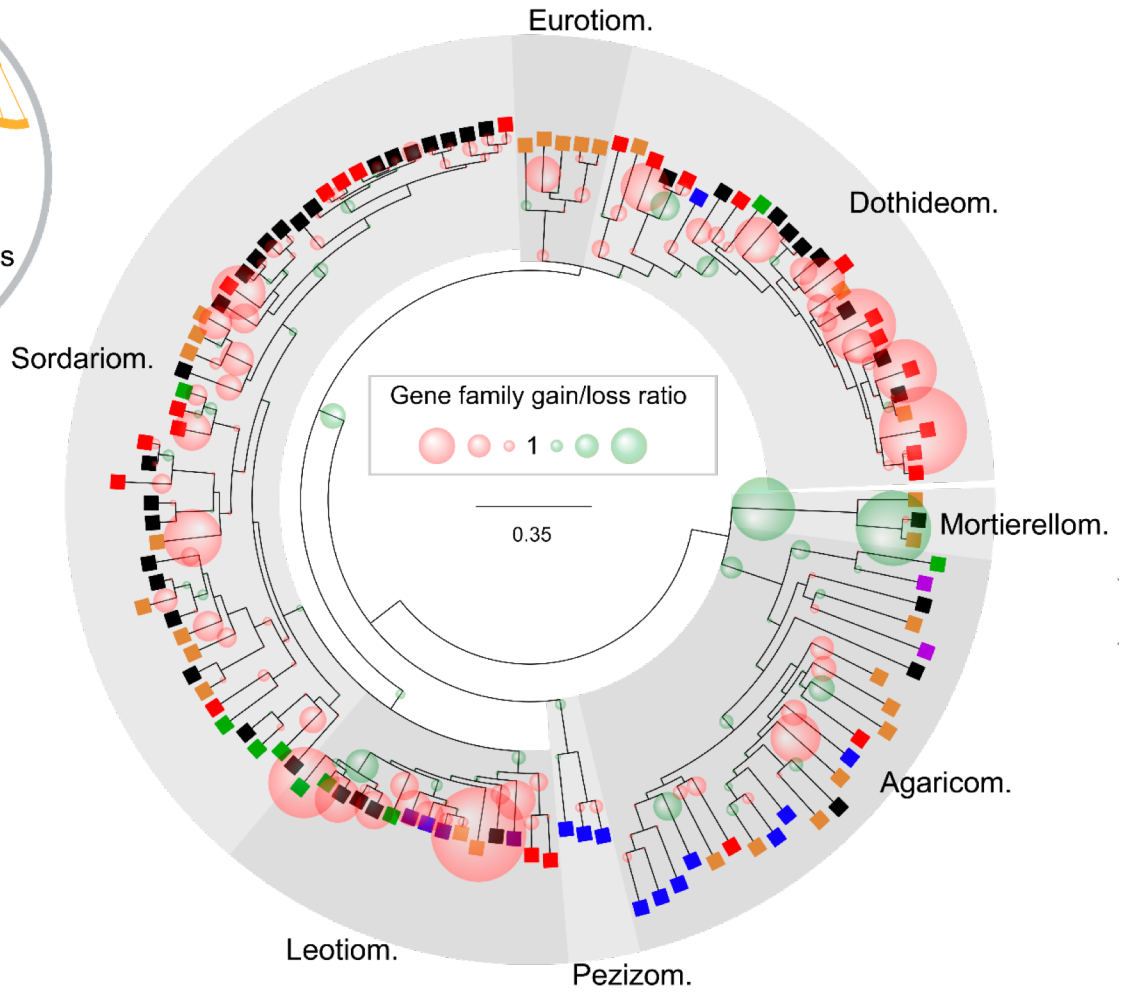
Reconstruction (III)

- Detrimental activity of root-colonizing fungi in a community context
- Bacterial root commensals regulate fungal growth and diversity in plant roots
- Plant innate immune system regulates fungal load in roots and is needed for microbiota-mediated PGP

Fungal endophytes likely evolved from ancestors with diverse lifestyles

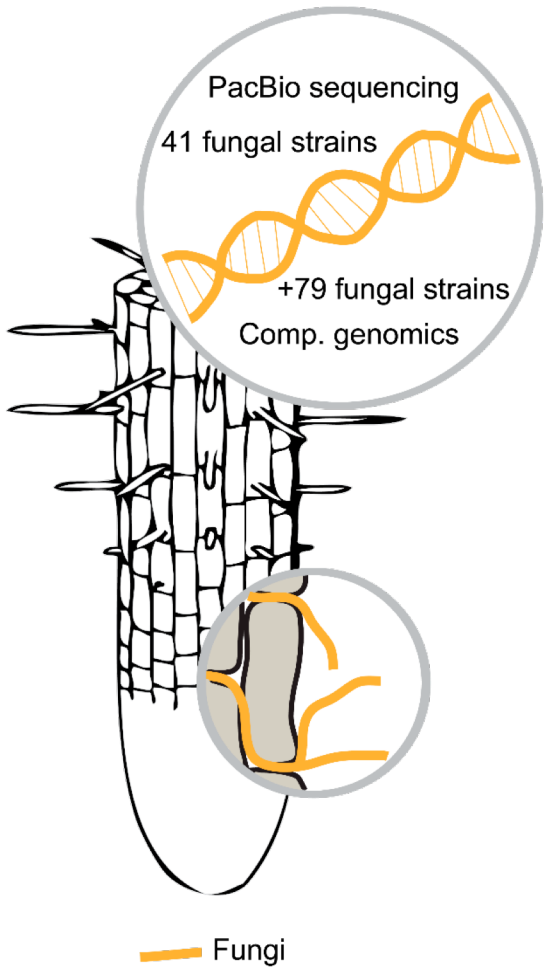


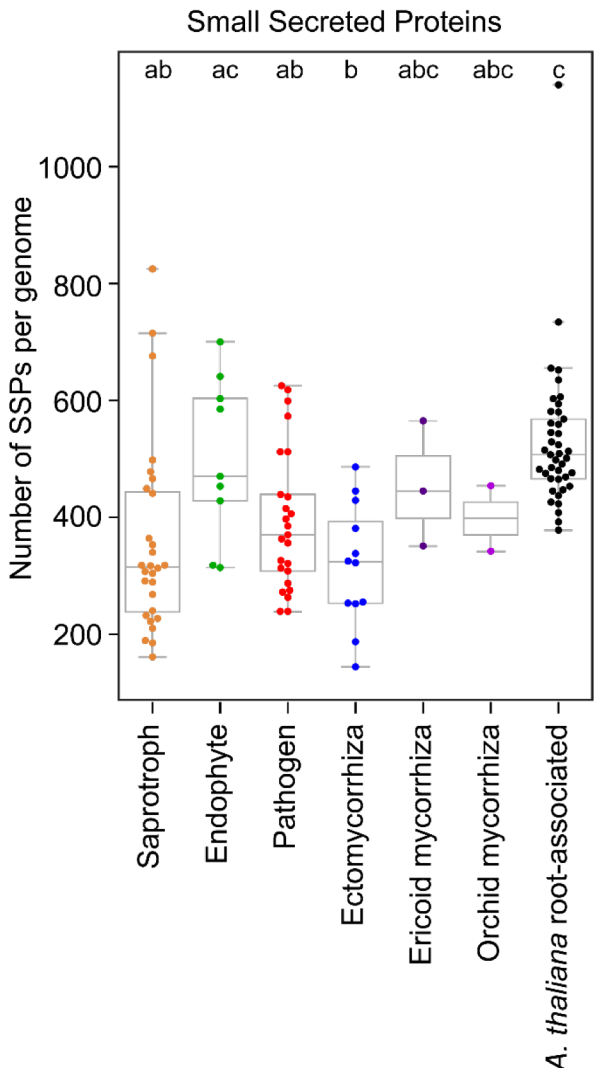


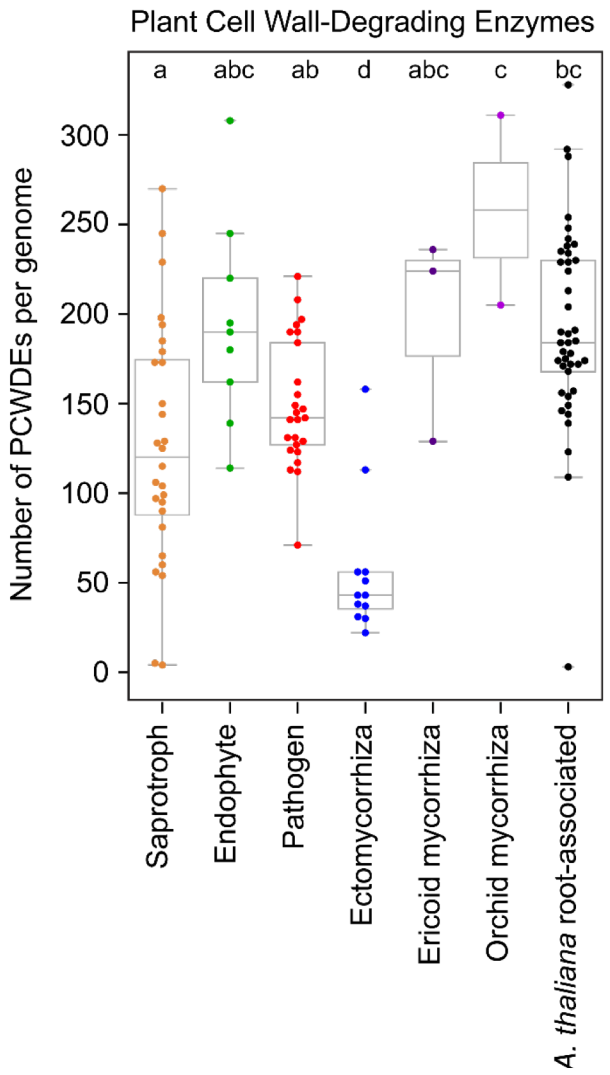
- Saprotroph
- Endophyte
- Pathogen
- Ectomycorrhiza
- Ericoid mycorrhiza
- Orchid mycorrhiza
- *A. thaliana* root-associated

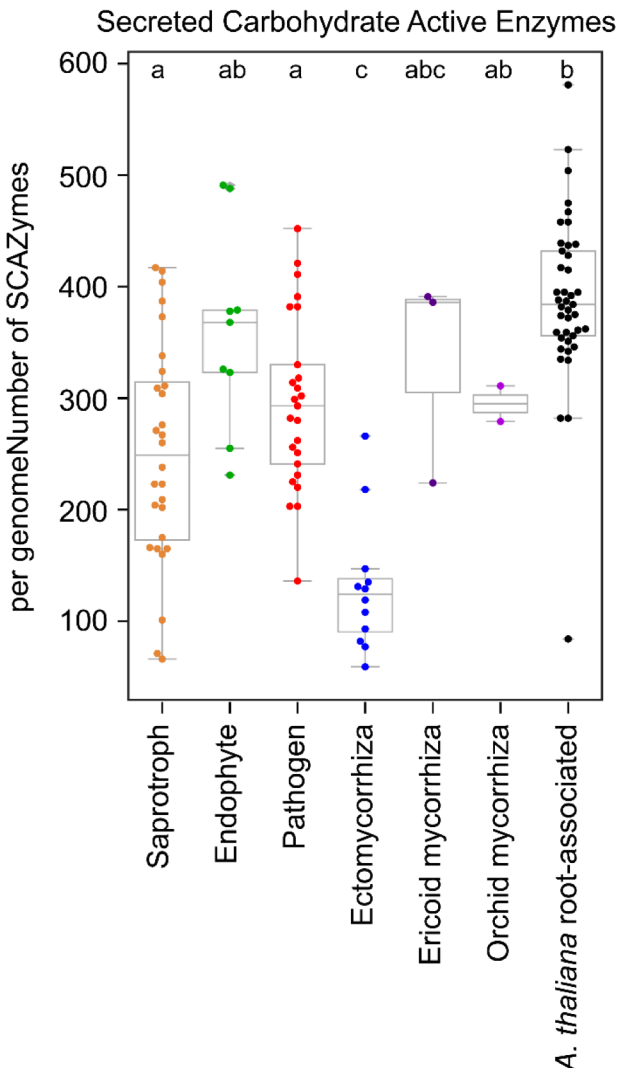
Unpublished - Mesny - Collaborations: Martin, Kohler, Miyauchi (INRA Nancy) - Grigoriev, Barry (JGI) - Henrissat (CNRS Marseille)

Reduction of pathogenic/saprotrophic traits is not a prerequisite for endophytism



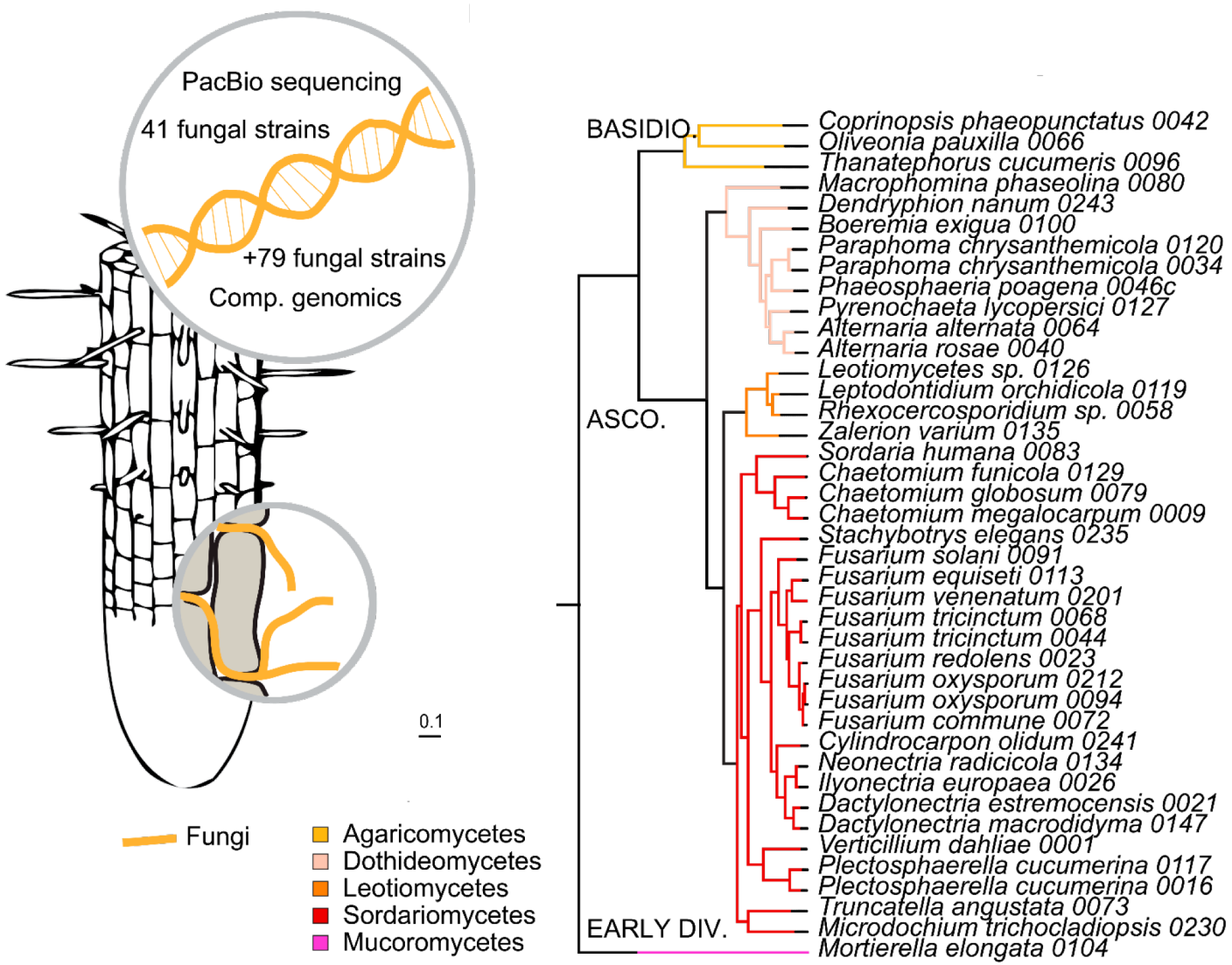






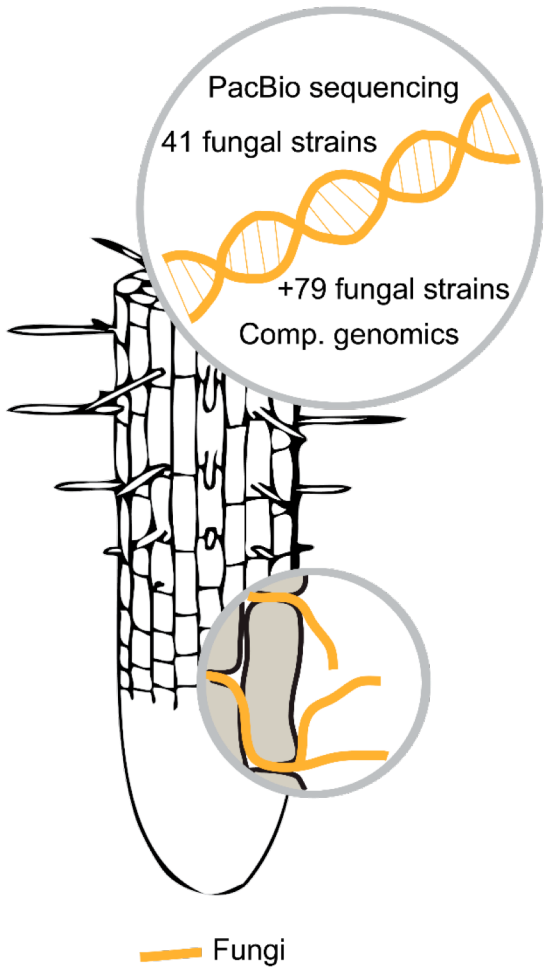
Unpublished - Mesny - Collaborations: Martin, Kohler, Miyauchi (INRA Nancy) - Grigoriev, Barry (JGI) - Henrissat (CNRS Marseille) ANOVA (Counts~Phylogeny*Lifestyle), $P < 0.05$ + TukeyHSD

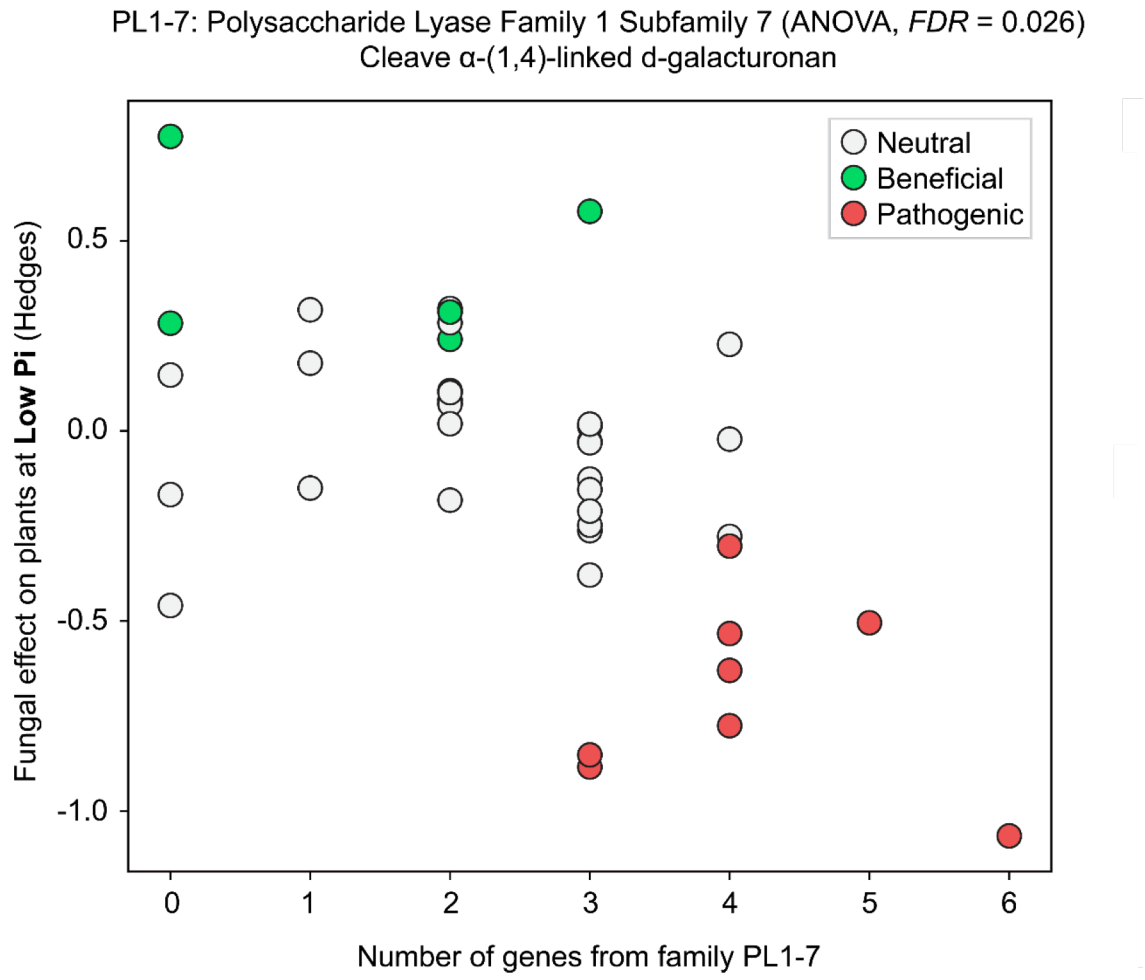
Several detrimental, few beneficial root-associated fungi in mono-associations



Kruskal-Wallis, $P < 0.05$, Dunn's test

Significant association between fungal lifestyle and PL1-7 CAZyme repertoire

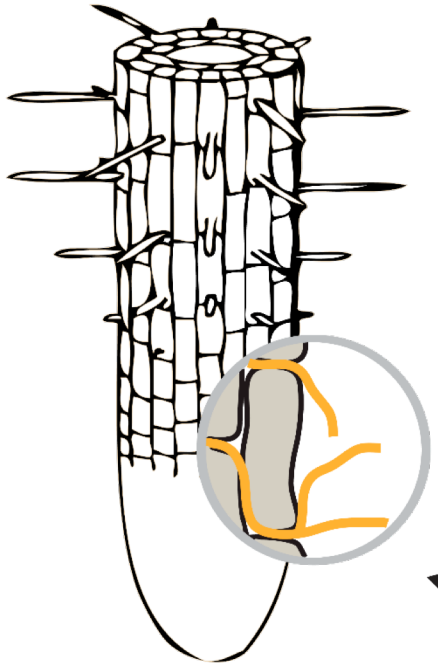




Unpublished - Mesny - Collaborations: Martin, Kohler, Miyauchi (INRA Nancy) - Grigoriev, Barry (JGI) - Henrissat (CNRS Marseille)

Take home messages (IV)

Biogeographical patterns (I)



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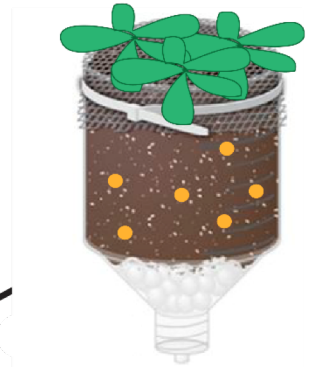
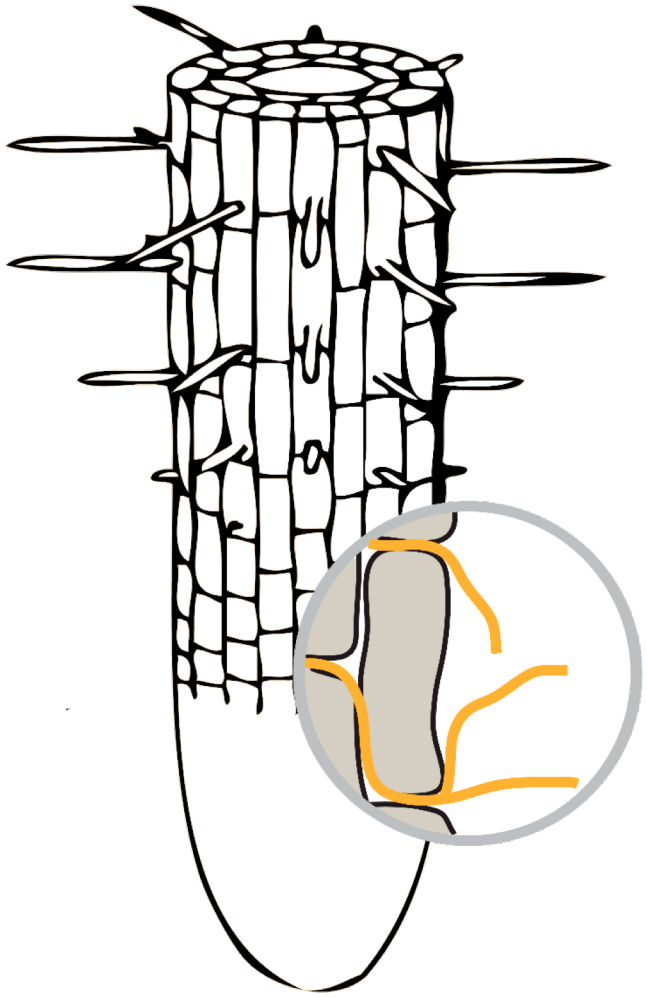


Whole-genome sequencing (IV)

- CAZyme and SSP repertoires of *A. thaliana* root-associated fungi closely resemble those of endophytes, but not of ectomycorrhizal fungi
- Possible link between pectin dissolution of plant cell wall and pathogenicitiy in root-colonizing fungi
- Detrimental activity of root-colonizing fungi in a community context
- Bacterial root commensals regulate fungal growth and diversity in plant roots
- Plant innate immune system regulates fungal load in roots and is needed for microbiota-mediated PGP

General model and conclusions



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MAX-PLANCK-GESELLSCHAFT

Paul Schulze-Lefert
Ruben Garrido-Oter
Bruno Huettel

MAX-PLANCK-GESELLSCHAFT

Jon Agren
Thomas Ellis

UPPSALA UNIVERSITET

Eric Kemen

EBERHARD KARLS UNIVERSITÄT TÜBINGEN

Fabrice Roux

LIPM

Carlos Alonso Blanco

CNB
CENTRO NACIONAL DE BIOTECNOLOGIA

Bernard Henrissat
and co-workers

afmb
architecture et fonction des macromolécules biologiques

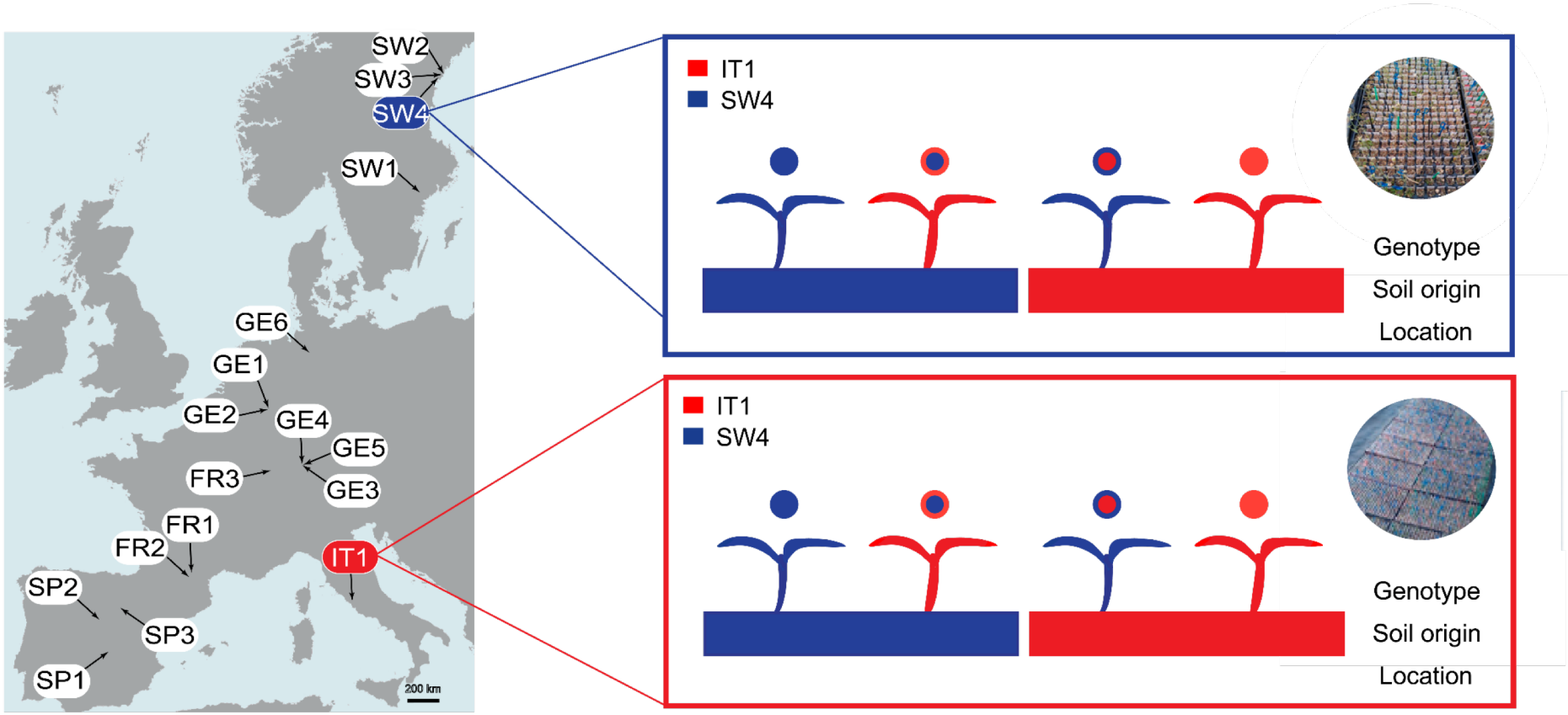
Francis Martin
Annegret Kohler
Shingo Miyauchi

INTERACTIONS
ARBRES-MICROORGANISMES

Igor Grigoriev
Kerrie Barry
Sajeet Haridas

JGI
JOINT GENOME INSTITUTE

Strong local adaptation between the two *A. thaliana* populations



Thiergart et al. Nature Ecology & Evolution 2020