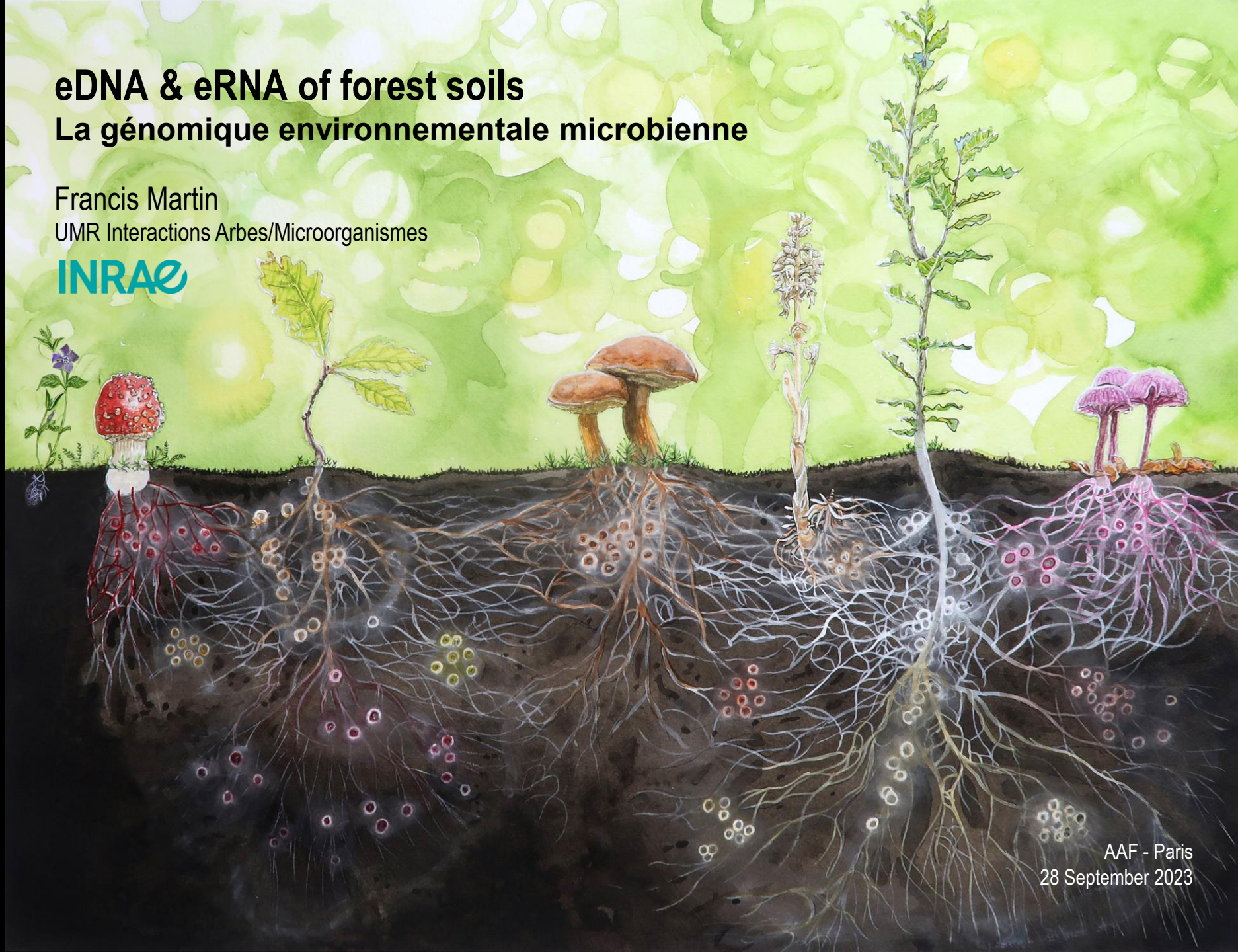


eDNA & eRNA of forest soils

La génomique environnementale microbienne

Francis Martin
UMR Interactions Arbres/Microorganismes

INRAE



AAF - Paris
28 September 2023

Saprotrophs



White rotters



Brown rotters



Litter, soil decayers

Harnessing Large-Scale Genome & Transcriptome Sequencing to Predict Ecological Traits



Symbiotrophs

Ectomycorrhizal fungi



Arbuscular mycorrhizal



Pathogens





eDNA

eRNA

From the Genomes to the Biomes


In highly complex terrestrial ecosystems involving many interacting microbial guilds and plant communities, I believe that a genome-to-ecosystem strategy will provide a better understanding of the respective roles of the thousands of species of wood decayers, soil and litter decomposers, and mycorrhizal species flourishing in soil and roots.

From the Genomes to the Biomes

Limiting Steps

1. Designing efficient protocols for the extraction of soil RNA (eRNA) from eukaryotes & synthesis of cDNAs
2. Large-scale sequencing of fungal reference genomes to map RNA reads (taxonomic affiliation & quantification of transcript levels)
3. Designing a bioinformatic pipeline able to handle terabytes of RNA sequences (assembling transcriptomes & transcript annotations)

Mycorrhizal Genomics Initiative




Home Workshops Data

JGI CSP 2011: Exploring the Genome Diversity of Mycorrhizal Fungi to Understand the Evolution and Functioning of Symbiosis in Woody Shrubs and Trees

Posted on October 4, 2012

PI's: F Martin (INRA-Nancy), D Hibbett (Clark University) & I Grigoriev (DOE JGI)

1000 Fungal Genomes Project
Sequencing unsampled fungal diversity



About Participants Protocols

2426 genomes in JGI MycoCosm
4600 genomes in NCBI database

1000+


2008

nature Vol 452 | 6 March 2008 | doi:10.1038/nature06556

LETTERS

The genome of *Laccaria bicolor* provides insights into mycorrhizal symbiosis

2015

13 species of mycorrhizal symbionts 

Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists



2020

nature COMMUNICATIONS

62 species of mycorrhizal symbionts

ARTICLE

<https://doi.org/10.1038/s41467-020-18795-w> OPEN

Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits

Shingo Miyauchi et al.^{1*}

On September 2023, **>220** species of mycorrhizal symbionts, incl.

- ECM, ectomycorrhizal fungi
- AMF, arbuscular mycorrhizal fungi
- ERM, ericoid mycorrhizal fungi
- ORC, orchid mycorrhizal fungi

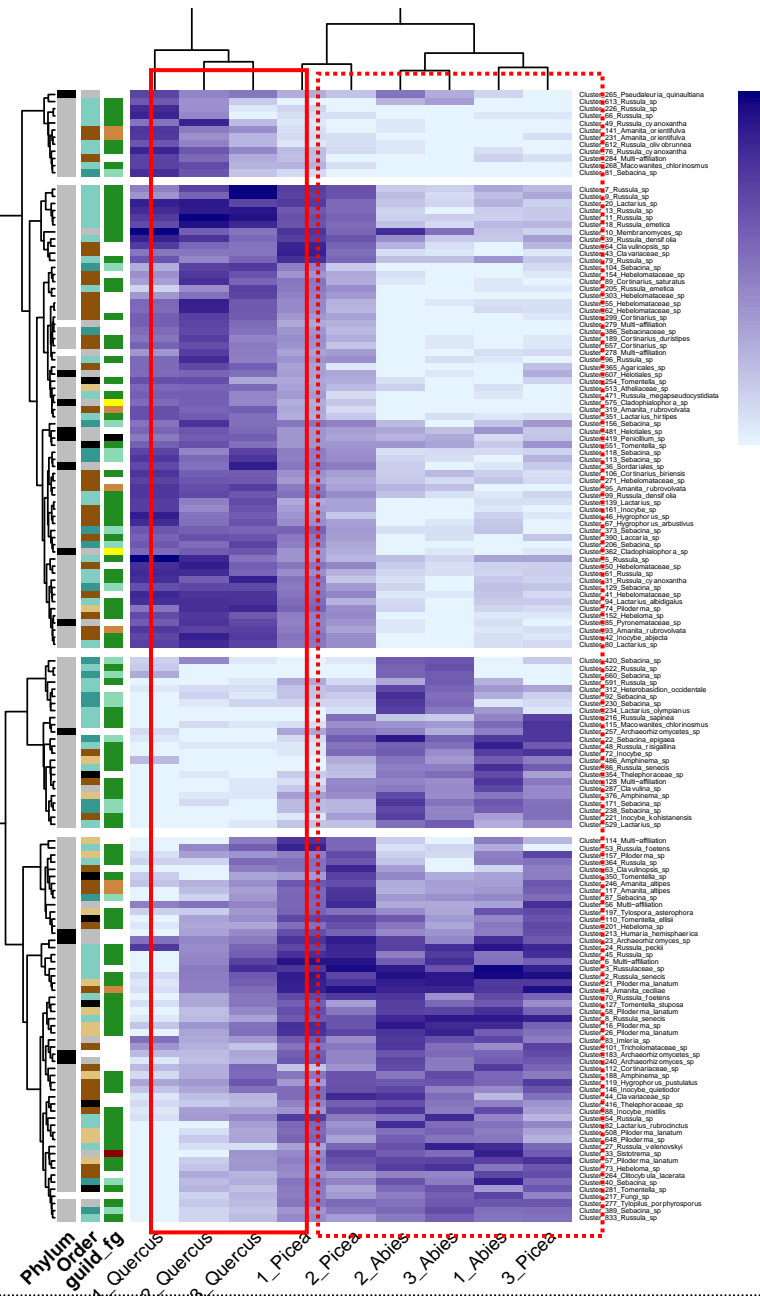


Yulong Xue Shan, Jade Dragon Snow Mountain, Yunnan Province, China

INRAE – Beijing Forestry University – Kunming Institute of Botany
(Profs Y-C Dai, Z-L Yang & G Wu)

Oak – Spruce Fir

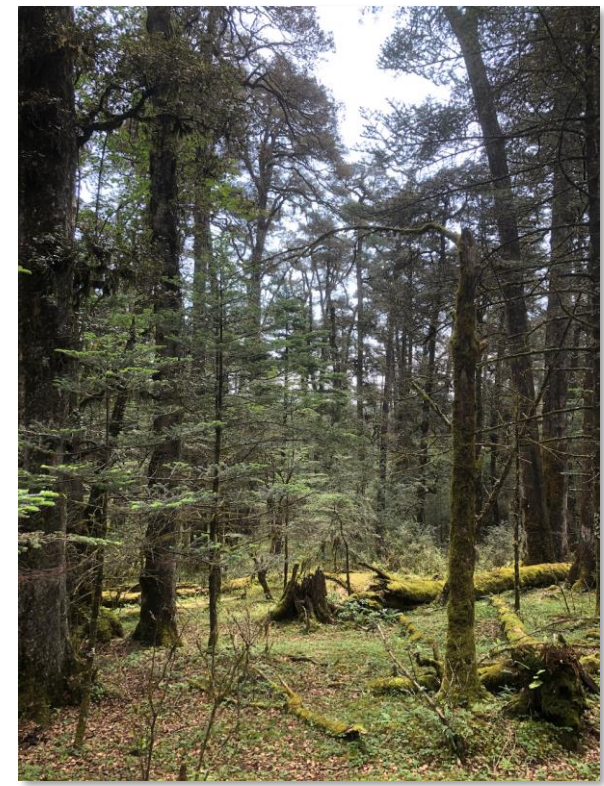
Fungal OTU distribution in soils of old-growth oak, fir or spruce forests



rDNA ITS metabarcoding



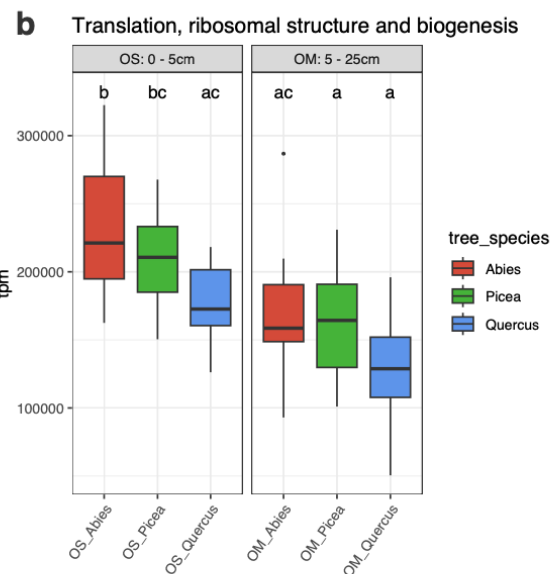
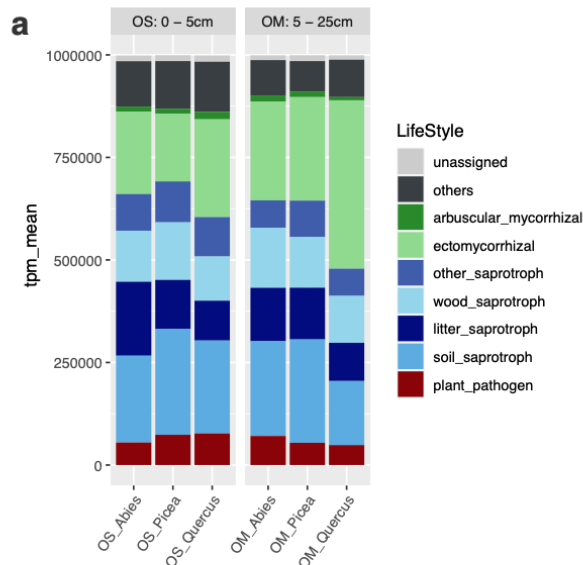
The taxonomic composition within individual functional groups (saprotrophs, symbiotrophs) was highly variable in the oak- or conifer-dominated forests, in terms of the occurrence of OTUs as well as the proportions of OTUs within each functional group. The core fungal microbiome comprised only ~20 % of the total OTUs across all soil samples.



eRNA: metatranscriptomics of soil fungal communities

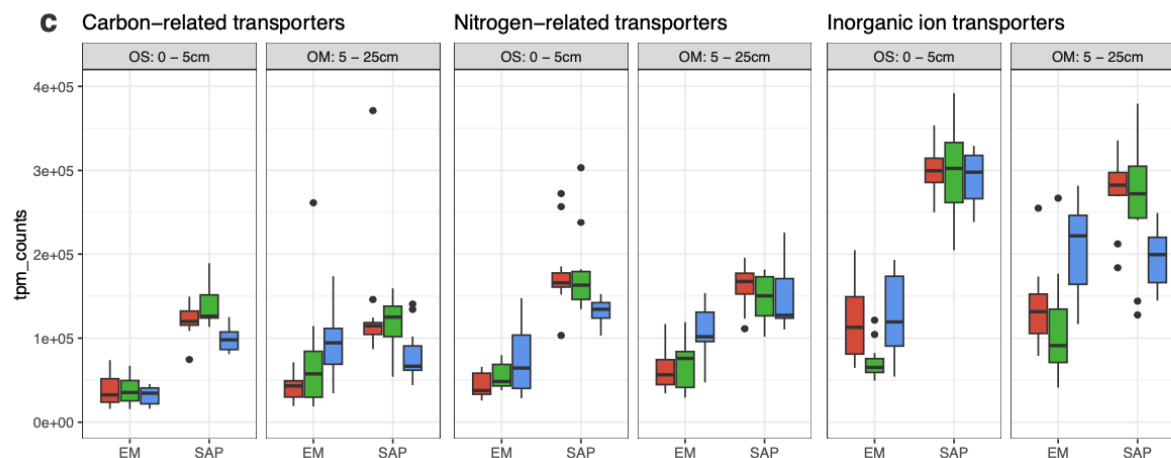
Fungal transcriptional responses to forest associations and soil layers

Relative abundance of transcripts according to the functional fungal guilds

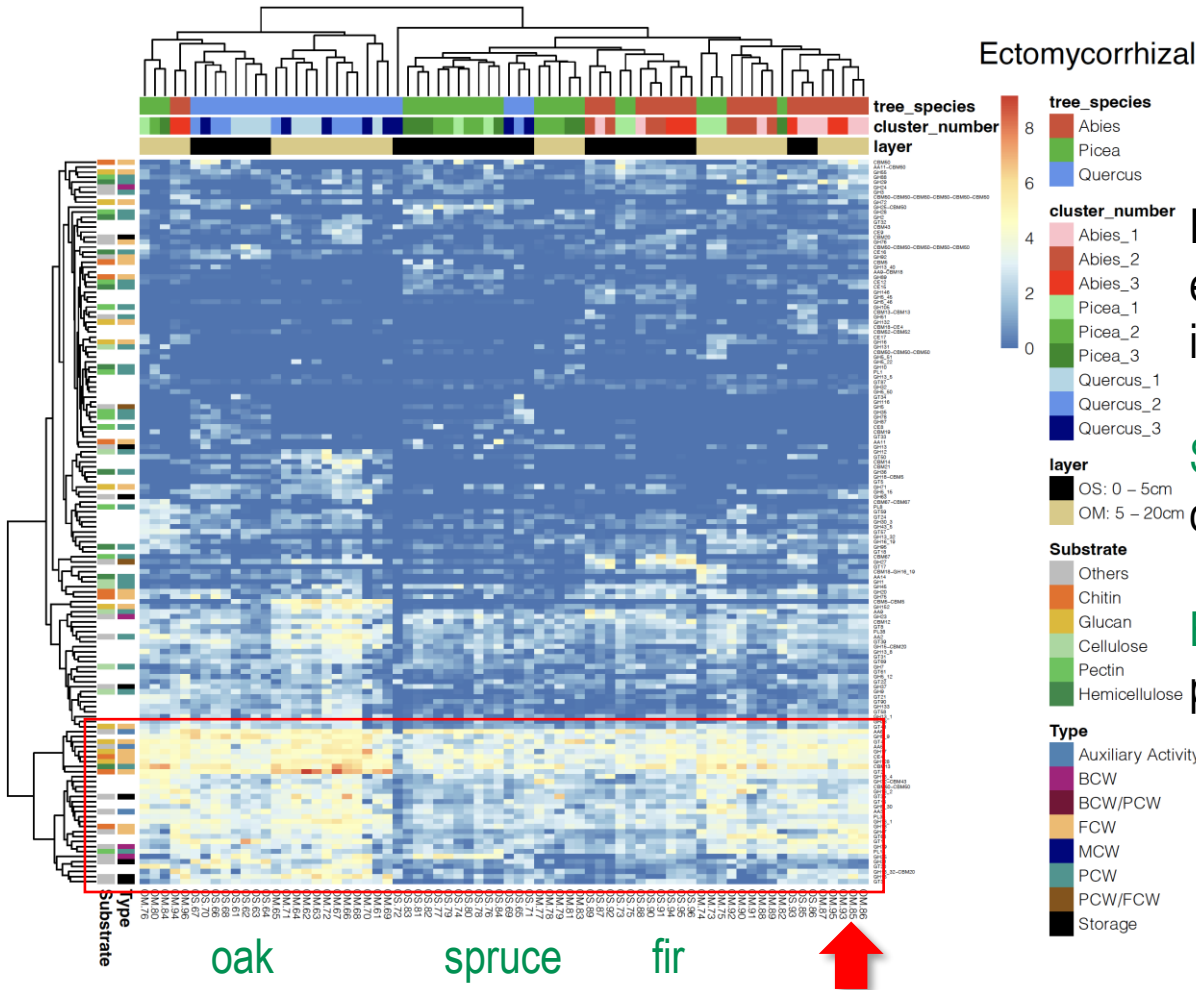


Sum of transcripts coding for the core translational machinery, a proxy for fungal growth rate

Differences in relative transcription levels of genes involved in uptake



CAZyme gene expression *in situ* in forest soils a proxy for the decomposition of soil organic matter



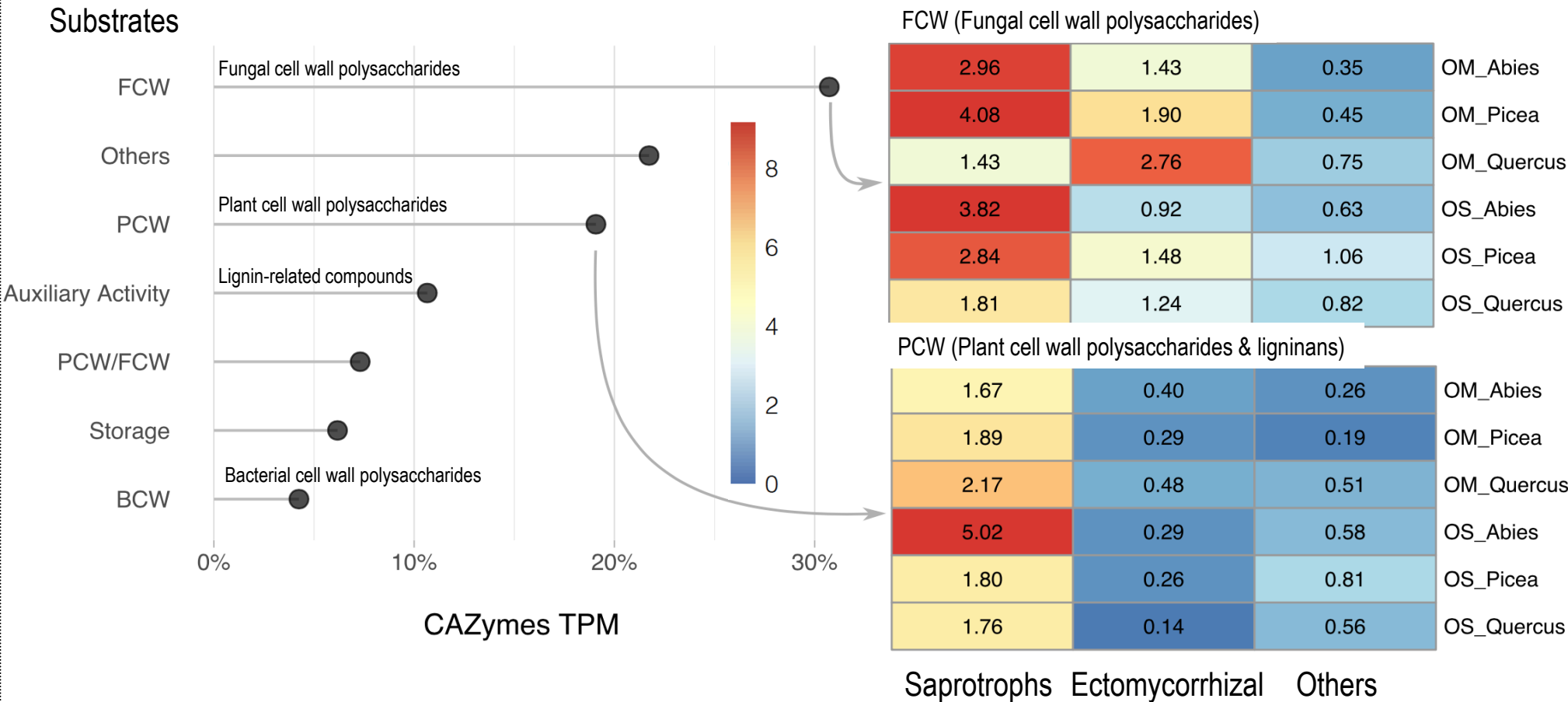
Fine tuning of CAZyme gene expression in either ectomycorrhizal or saprotrophic fungi in oak-, spruce- and fir-dominated forests.

Saprotrophic taxa: plant polysaccharide degradation

Ectomycorrhizal taxa: fungal & bacterial polysaccharide degradation

CAZymes, carbohydrate-active enzymes, e.g. cellulases, hemicellulases, LPMOs, pectinases, lignin peroxidases, laccases

CAZyme gene expression *in situ* in forest soils



Take-Away Points

Stable functional structure despite high taxonomic variability across fungal communities in soils of old-growth montane forests

- Our taxonomic rDNA profiling revealed striking shifts in the composition of the saprotrophic and ectomycorrhizal guilds among the oak-, fir-, and spruce-dominated forests.
- Despite their highly variable taxonomic composition, fungal guilds exhibited remarkably similar functional traits for growth-related and core metabolic pathways across forest associations, suggesting **ecological redundancy**.
- However, we found that the expression profiles of genes related to polysaccharide and protein (SOM) degradation and nutrient transport notably varied between and within the fungal guilds, suggesting **niche adaptation**.



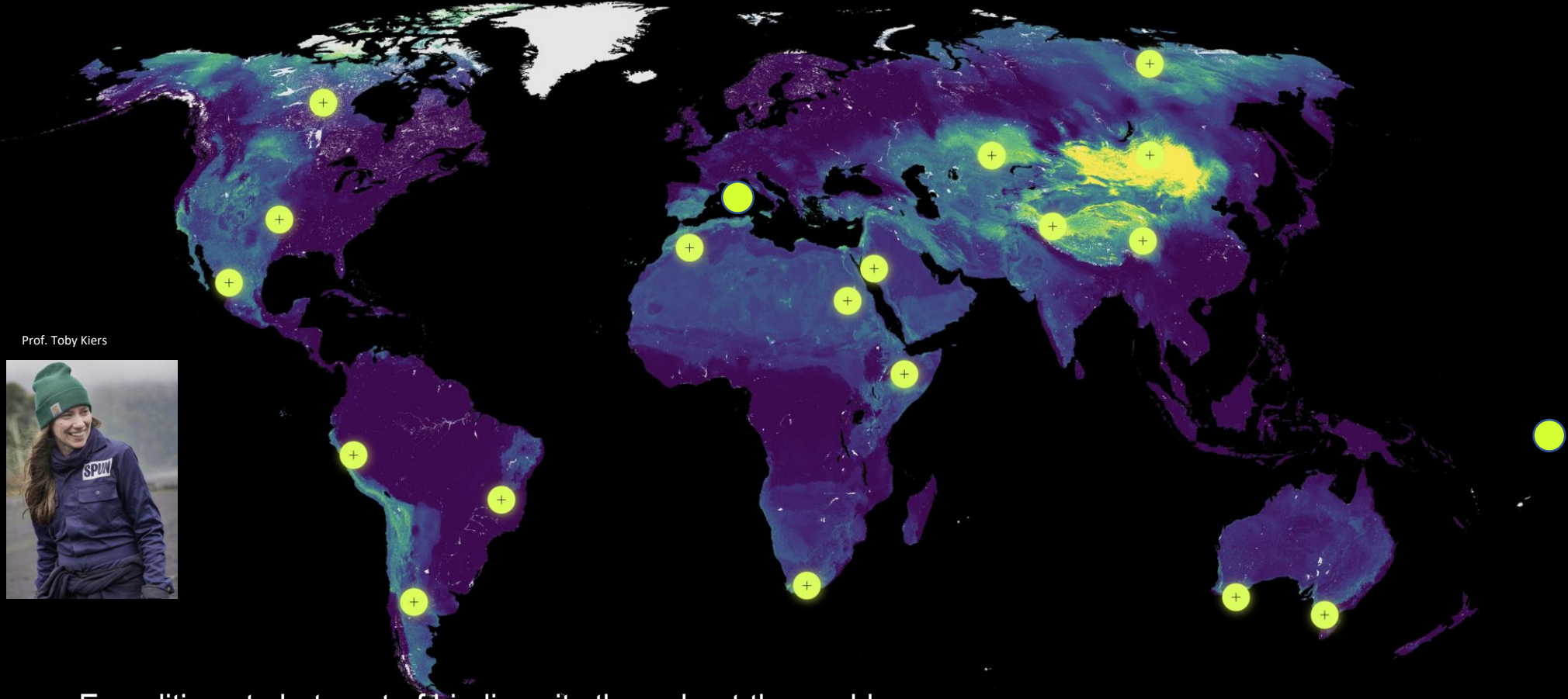


Yunnan Baotai Mountain Forest National Park

Toward >10,000 fungal genomes, incl. 1000 mycorrhizal genomes ...

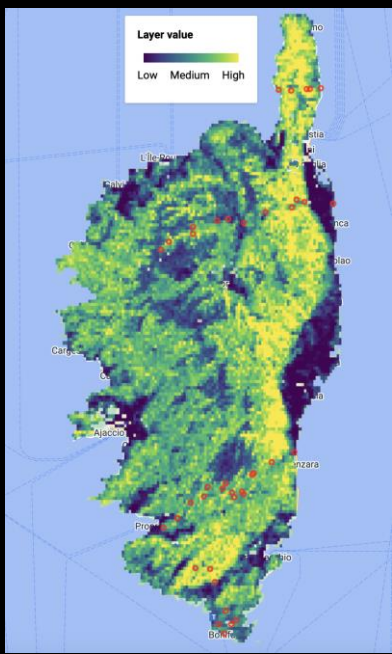
- The current set of sequenced mycorrhizal genomes represents less than **~0.4%** of the ~ 50,000 species of mycorrhizal fungi identified so far. Thousands of additional genomes should be sequenced to unearth the true genetic and functional diversity of this fungal guild.
- Sequencing genomes of mycorrhizal species from poorly known ecosystems (e.g., arctic and tropical biomes) may reveal specific gene sets involved in adaptation to these ecosystems.

SPUN: Society for the Protection of the Underground Networks



Expeditions to hot-spot of biodiversity throughout the world:

- To explore microbiomes in terrestrial ecosystems and their sensitivity to climate change
- To popularize science & team with local communities
- To educate
- To influence policy



SPUN – INRAE – CNBC expedition in Corsica





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Prof. Gang WU



Gang WU



Mycorrhizal Genomics Initiative



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Igor Grigoriev



David Hibbett



Laszlo Nagy