

Comparative Genomics of Mycorrhizal Symbiosis and Wood Decay in Forest Ecosystems

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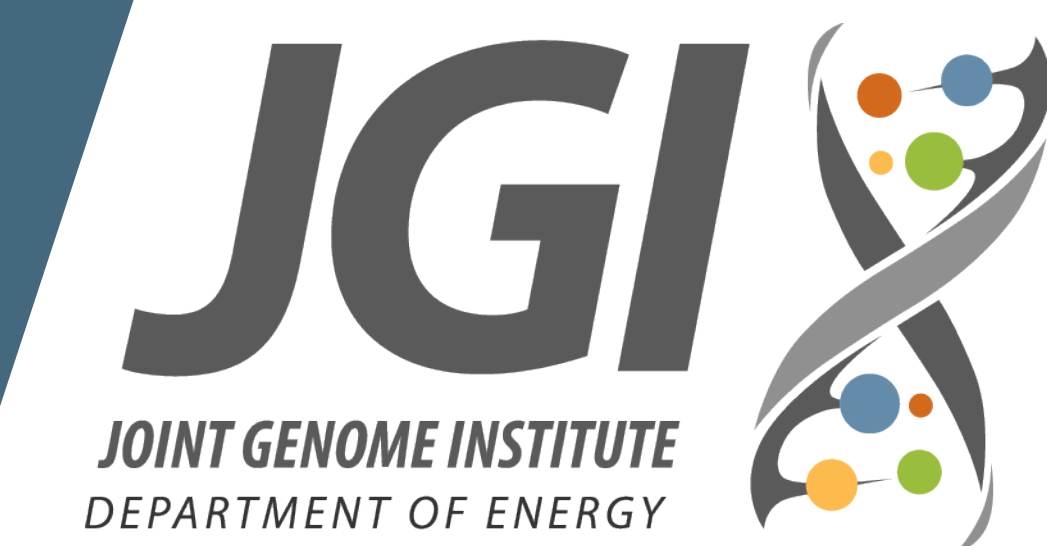
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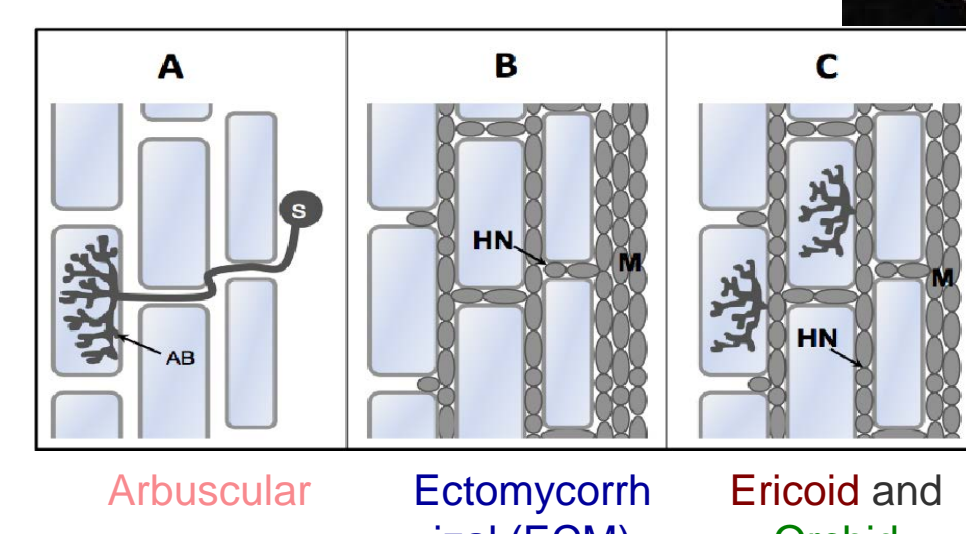
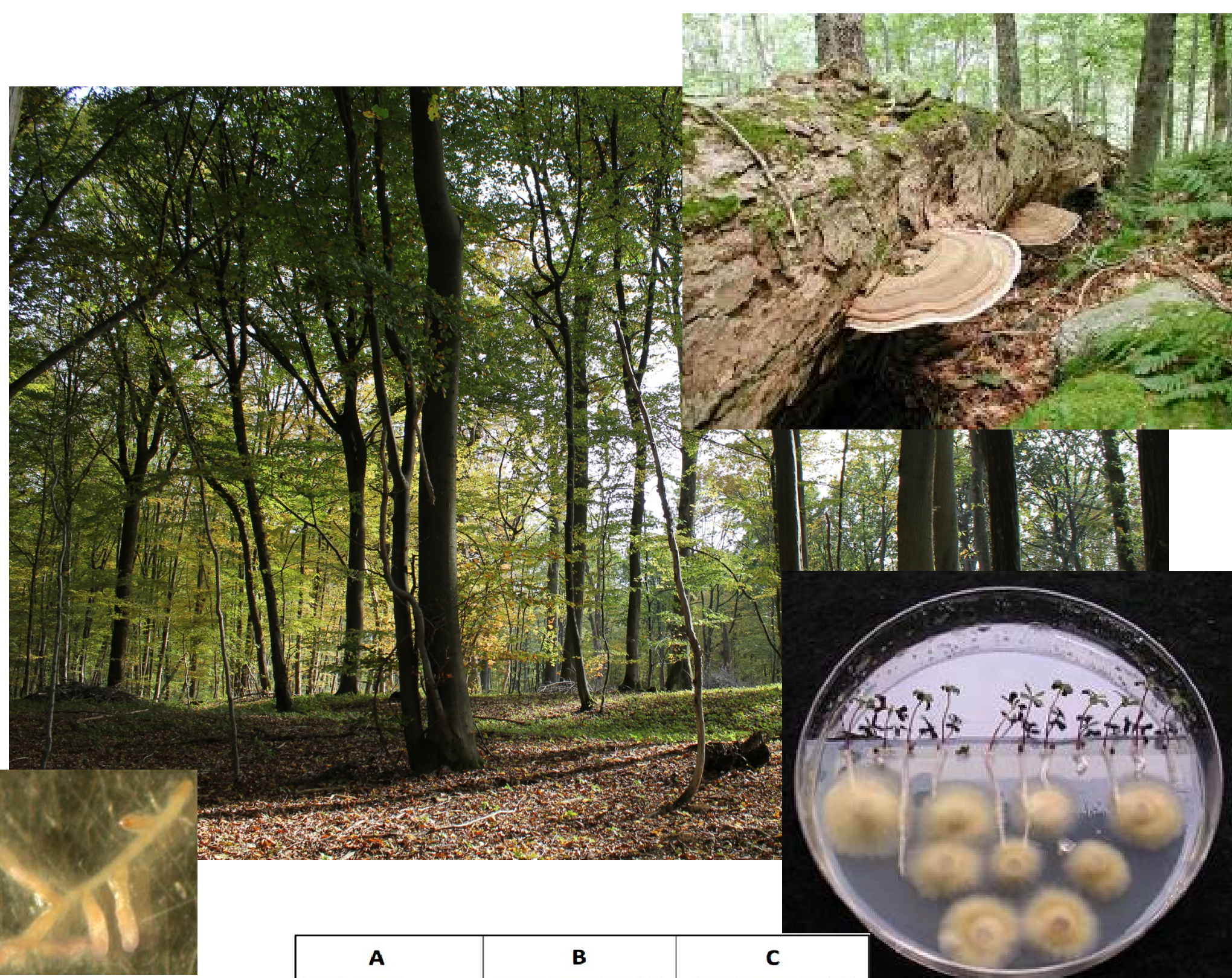
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ABSTRACT

Forests, very important and complex ecosystems, depend on tree-microbial associations above and below ground. Understanding molecular mechanisms of associations between trees and fungi in forests requires a novel, community-driven, multi-disciplinary approach based on genomics and ecological data and tools. Here we propose a three-way approach to strengthen collaboration between our institutions, LBNL and INRA, and with a larger scientific community on exploration of associations between trees and fungi in forests to create a basis for understanding forest ecology and management strategies.

CO₂ release from wood decay



C capture in mycorrhizal roots

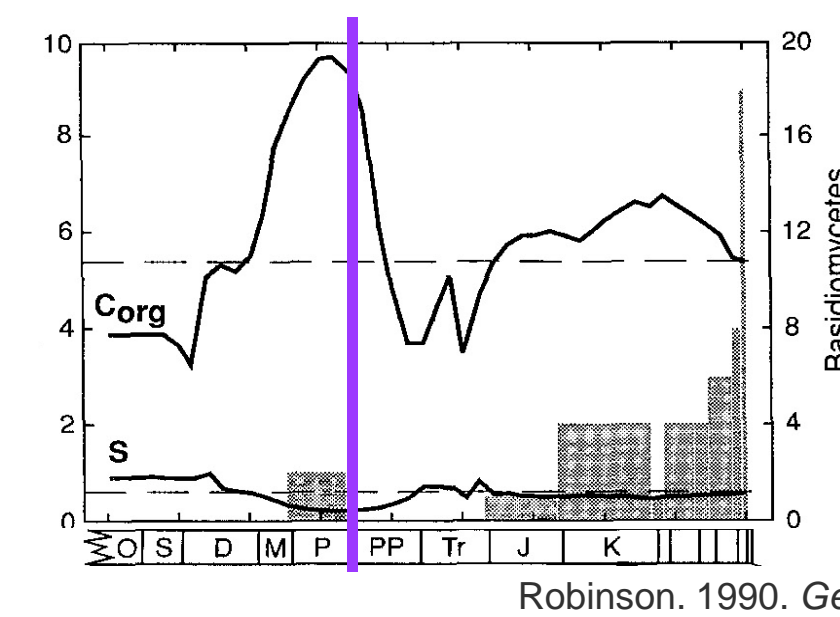
Types of mycorrhizae

OBJECTIVES

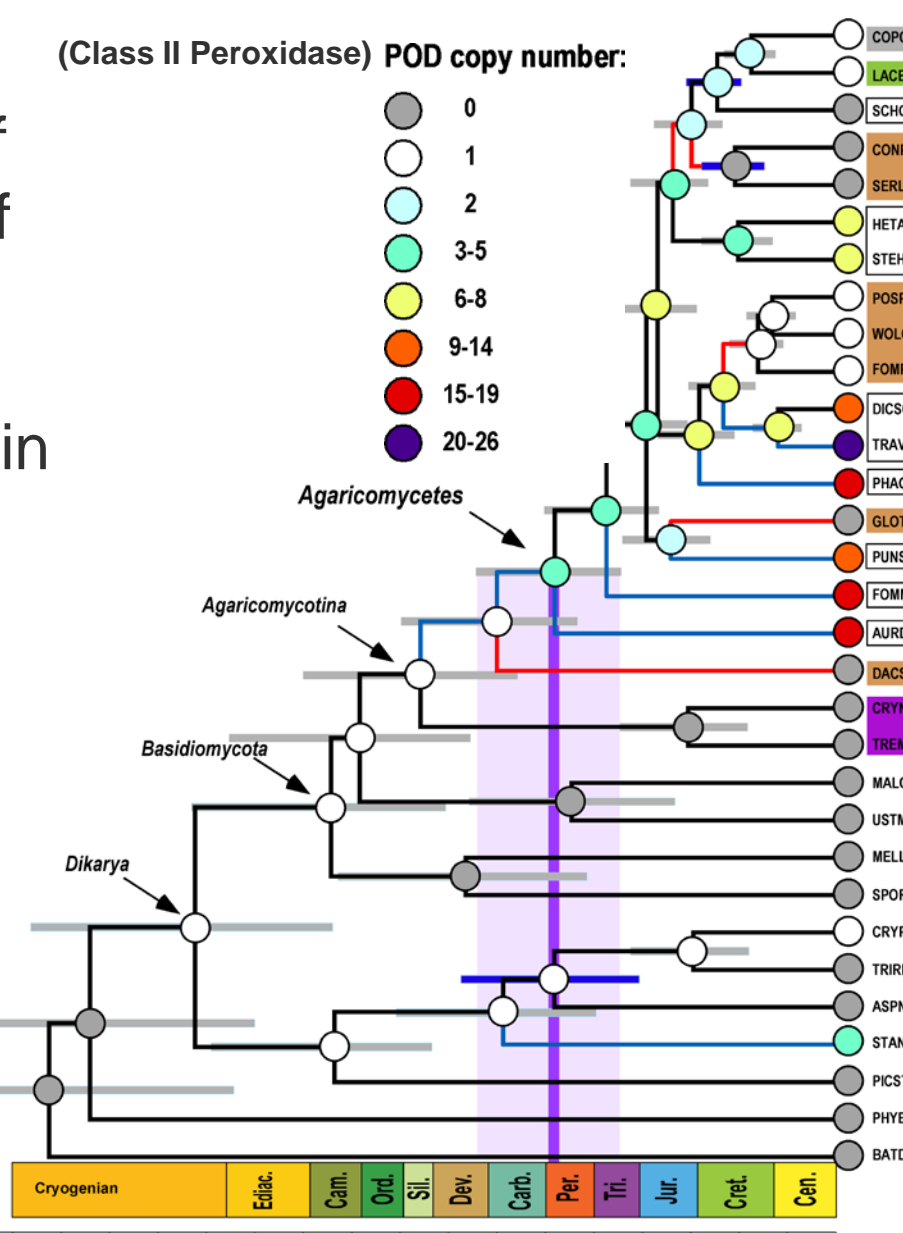
1. Strengthen collaboration between INRA and JGI (LBNL) in analysis of multi-dimensional datasets on tree-microbial interactions within the context of forest ecology and management. Establish regular communication and working visits to exchange data and tools, experimental and computational techniques, and general expertise developed in each laboratory. Collaboration between these two leading institutions will facilitate interactions between larger scientific communities on both sides of the Atlantic Ocean.
2. Organize, coordinate, and attend several workshops to maximize the number of researchers from different disciplines to develop new resources and strategies in the framework of forest ecosystems, its microbial components, and interactions. Support younger researchers from both laboratories to participate in and present their research at these meetings.
3. Provide training opportunities and support for young researchers in both groups to learn new techniques developed at partner labs, to explore new research environments, and develop new collaborations for better interpretation of data and design of future experiments. Training abroad will facilitate exchange of different approaches offered by American and European scientific schools.

LARGE-SCALE GENOMICS STUDIES

Sequencing and analysis of 40+ genomes of wood decay fungi is in progress. Comparative analysis of the first dozen revealed a comprehensive catalog of enzymes involved in plant biomass degradation. Evolutionary analysis suggested that the ancestral wood decay fungus may have caused the sharp decline in the rate of C_{org} burial at the end of the Permo-Carboniferous. (Floudas et al., Science. 2012)



Robinson. 1990. Geology 15: 607-610.



Mycorrhizal Genomics

#	Names	Assembly length	# genes
1	Arantia muscaria Koide v1.0	40,699,759	18,153
2	Boletus edulis v1.0	46,637,611	16,933
3	Cenococcium geophilum 1.58.v2.0	177,557,160	14,748
4	Chromococcus venosus 120613-1.v1.0	126,036,033	17,986
5	Cortinarius glaucopus AT 2004.276.v2.0	63,450,306	20,377
6	Gyrodont luteus BX v1.0	43,048,674	11,779
7	Hebeloma cylindrosporum h7.v2.0	38,226,047	15,382
8	Laccaria amethystina LaAM-08-1.v1.0	52,197,432	21,066
9	Laccaria bicolor v2.0	60,707,050	23,130
10	Meliniomyces bicolor E.v2.0	82,384,847	18,619
11	Meliniomyces variabilis F.v1.0	55,857,776	20,389
12	Morchella conica CCRA5932.v1.0	48,213,273	11,600
13	Oidiodendron maus Zn.v1.0	46,426,256	16,703
14	Paxillus involutus ATCC 200175.v1.0	58,301,126	17,968
15	Paxillus rubicundulus Ve08.2h10.v1.0	53,011,005	22,065
16	Piloderma croceum F.1598.v1.0	59,326,866	21,583
17	Pisolithus microcarpus 441.v1.0	53,027,657	21,064
18	Pisolithus tinctorius Marz 270.v1.0	71,007,534	22,701
19	Rhizophagus irregularis DAOM 181602.v1.0	91,983,792	30,282
20	Sclerotinia citrinum Fouq A.v1.0	56,144,862	21,012
21	Sebacina vermifera MAFF 305830.v1.0	38,094,242	15,312
22	Suillus brevipes v1.0	51,712,595	22,453
23	Suillus luteus UPL-Shi-Lm8n1.v1.0	37,014,302	18,316
24	Terfezia boudieri S1.v1.0	63,234,673	10,200
25	Tricholoma matsutake 945.v3.0	175,759,688	22,895
26	Tuber magnatum v1.0	192,781,443	9,433
27	Tuber melanosporum from Genoscope	124,945,702	7,496
28	Tulasnella calospora AL134D.v1.0	62,392,858	19,659
29	Wilcoxina mikolae CBS 423.85.v1.0	117,288,895	13,093

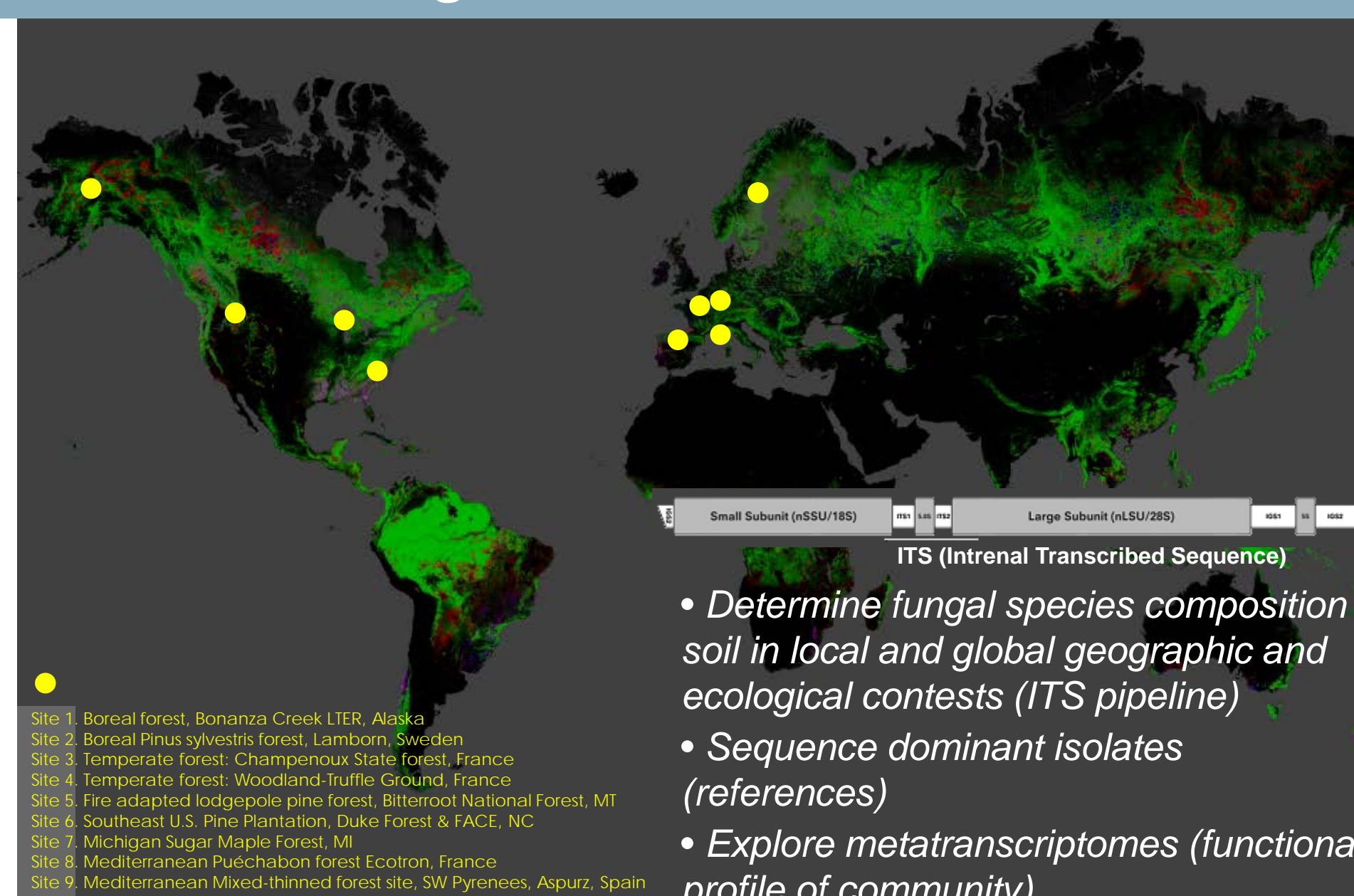


Genomes of 30+mycorrhizal fungi are being sequenced by JGI to study evolutionary origins and mechanisms of interactions with plants. Transcriptomics of model systems is the next step.

Piloderma croceum-Quercus robur

Hebeloma cylindrosporum-Pinus pinaster

Ecogenomics of Forest Soil



- Determine fungal species composition in soil in local and global geographic and ecological contexts (ITS pipeline)
- Sequence dominant isolates (references)
- Explore metatranscriptomes (functional profile of community)

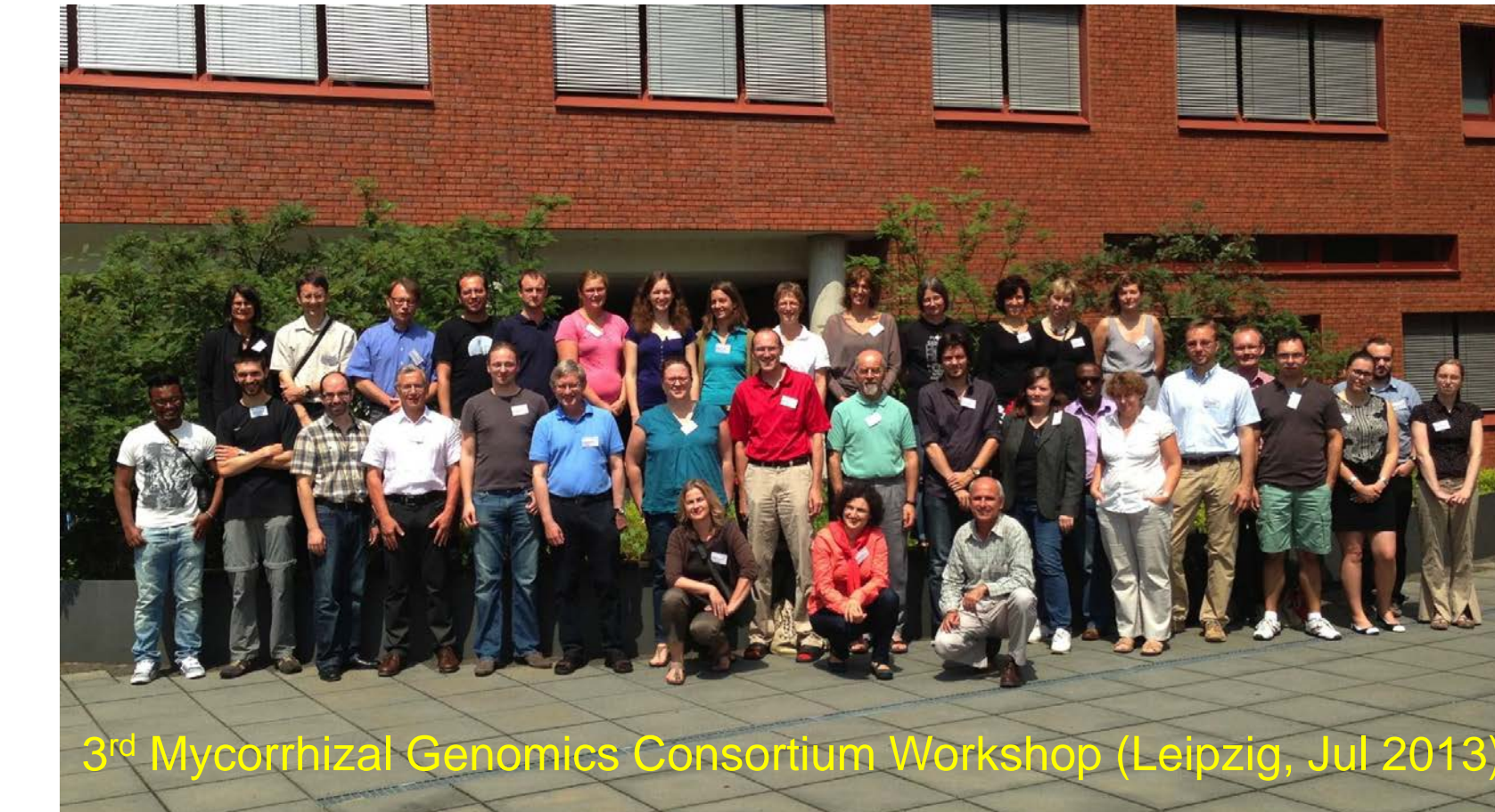
ACHIEVEMENTS

Research Community Building and Training

We organized four Mycorrhizal genomics workshop in Europe (Nancy, France-2012; Leipzig, Germany 2013; Seville, Spain 2014) and several in USA (New Haven, CT (August 2012), Pacific Grove, CA (March 2013), Austin, TX (Aug 2013), Walnut Creek, CA (March 2014)). In March 2014 Grigoriev's lab with FBF support hosted a bioinformatics engineer from INRA Emmanuelle Morin for annotation of INRA sequenced genomes.



Emmanuelle Morin from INRA at JGI/LBL



3rd Mycorrhizal Genomics Consortium Workshop (Leipzig, Jul 2013)

Several new international collaborations started in 2013-2014:

- US-Bonito et al. (2014) Comparative genomics of early diverging terrestrial fungi and their bacterial endosymbionts JGI CSP #1450 (2014) (with INRA-Nancy)
- Duplessis et al. (2014) Combined population genomics and transcriptomics to decipher the molecular bases of virulence and host adaptation in the poplar leaf rust fungus *Melampsora larici-populina* JGI CSP #1450 (with INRA-Nancy)
- Taylor et al. (2014) Fungal response to global change: adaptive genes and rates of mutation and recombination. JGI CSP #1462 (with Paris-Sud University)
- Rosso et al. (2013) Survey of lignocellulolytic capabilities over the order Polyporales JGI CSP #999 (with Aix-Marseille University, Université de Lille and INRA-Nancy)
- Martin et al. (2013) *Mycorrhizal Genomics Initiative: Exploring the Symbiotic Transcriptomes*. JGI CSP #978 (with INRA-Nancy and INRA-Paris)
- Kema G et al. (2013) *Deciphering the Interactome of Dothideomycete-bioenergy crops*. JGI CSP #983 (with – INRA-Paris)
- De Vries et al. (2013) Mining the diversity of *Aspergillus* and related species to improved biomass utilization JGI CSP #985 (with Aix-Marseille University)

Key Publications (2012-2014)

- Grigoriev IV et al (2014) MycoCosm portal: gearing up for 1000 fungal genomes. *Nucleic Acids Res.* 42(1):D699-704.
- Grigoriev IV (2013) A changing landscape of fungal genomics. In: *The Ecological Genomics of Fungi* (Ed F. Martin), John Wiley & Sons, Inc, Hoboken, NJ. pp 3-20.
- Grigoriev IV (2013) Fungal Genomics for energy and environment. In: *Genomics of Soil- and Plant-Associated Fungi*, Soil Biology 36 (Eds B. Horwitz, P.K. Mukherjee, M Mukherjee, C.P. Kubicek), Springer Berlin Heidelberg. pp. 11-28.
- Tisserant E, et sl., Grigoriev IV, Corradi N, Roux C, Martin F. (2013) Genome of an arbuscular mycorrhizal fungus provides insight into the oldest plant symbiosis. *Proc Natl Acad Sci U S A.* 110(50):20117-20122.
- Binder M, Justo A, Riley R, Salamov A, López-Giráldez F, Sjökvist E, Copeland A, Foster B, Sun H, Larsson E, Larsson KH, Townsend J, Grigoriev IV, Hibbett DS. (2013) Phylogenetic and Phylogenomic overview of the Polyporales. *Mycologia*. 2013 Aug 11. [Epub ahead of print]
- Morin E, et al., Grigoriev IV, Martin F. (2012) Genome sequence of the button mushroom *Agaricus bisporus* reveals mechanisms governing adaptation to a humic-rich ecological niche. *Proc Natl Acad Sci U S A.* 109(43):17501-6.
- Floudas D, et al., Martin F, Cullen D, Grigoriev IV, Hibbett DS (2012) The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science.* 336(6089):1715