

Contribution of metagenomics (barcoding and metabarcoding) in the study of fungal diversity

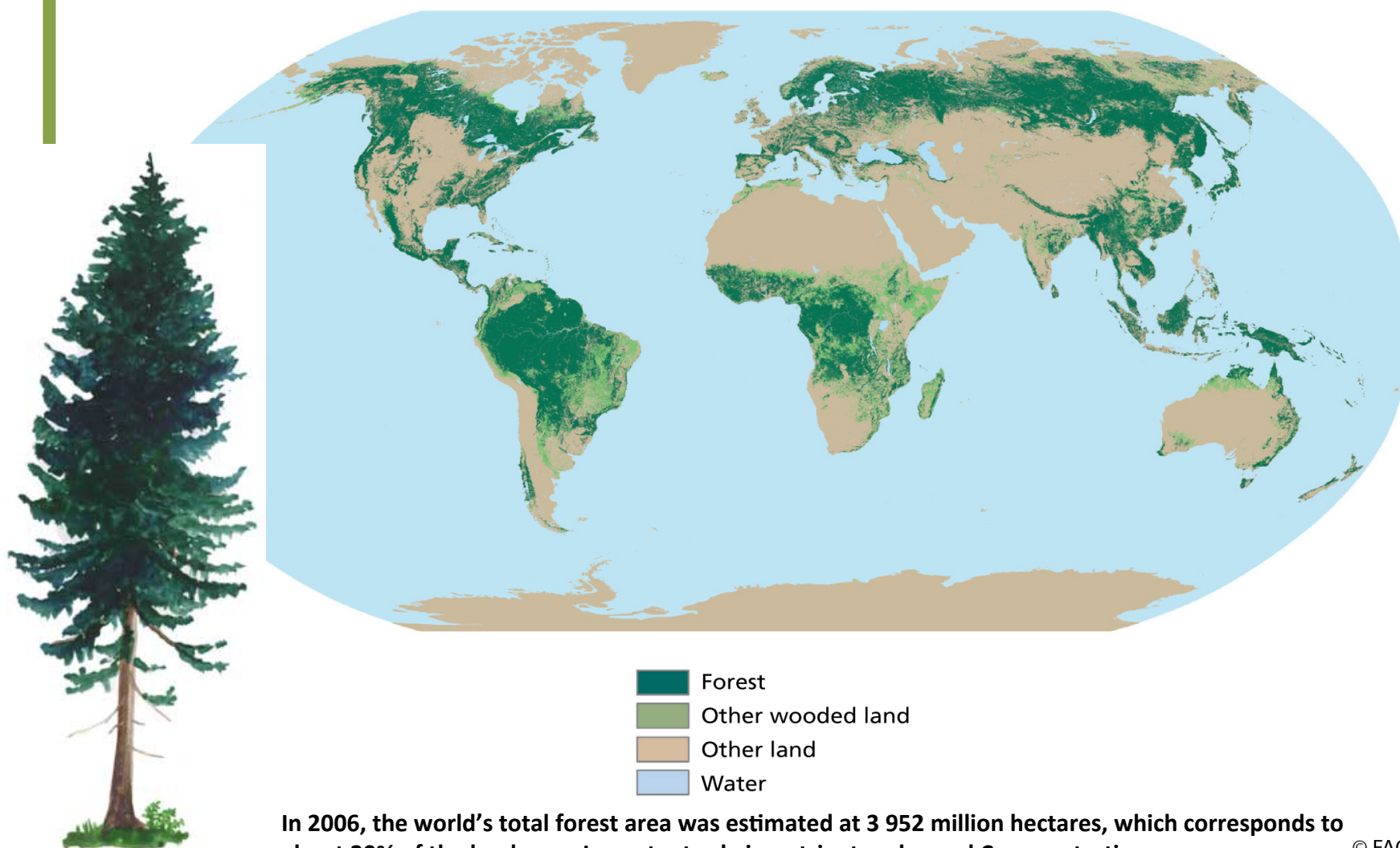
Marc Buée
INRA Nancy, France



UMR 1136 Interactions Arbres - Microorganismes, INRA, Université de Lorraine



The world's forests

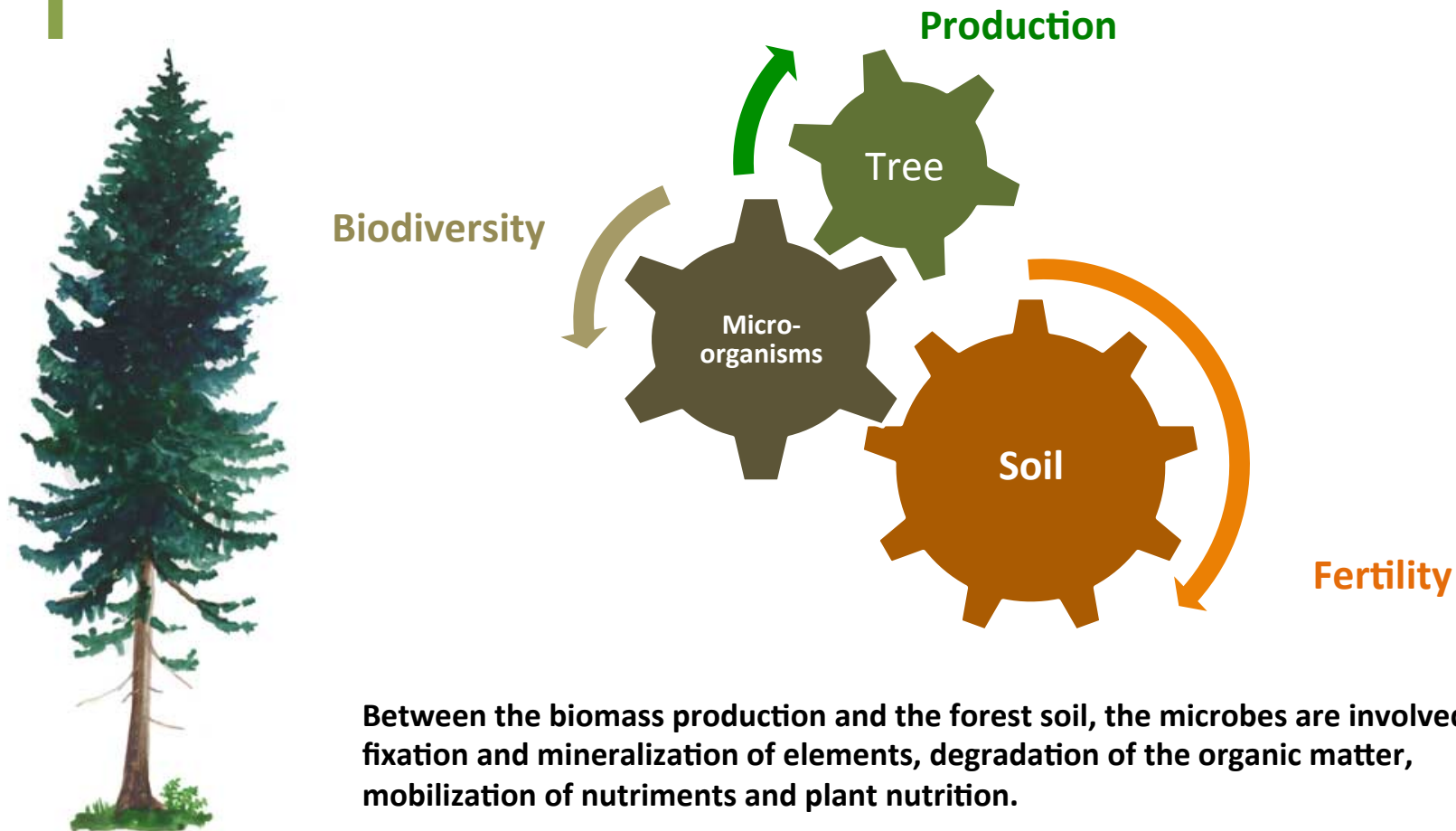


In 2006, the world's total forest area was estimated at 3 952 million hectares, which corresponds to about 30% of the land area. Important role in nutrient cycles and C sequestration.

© FAO 2006

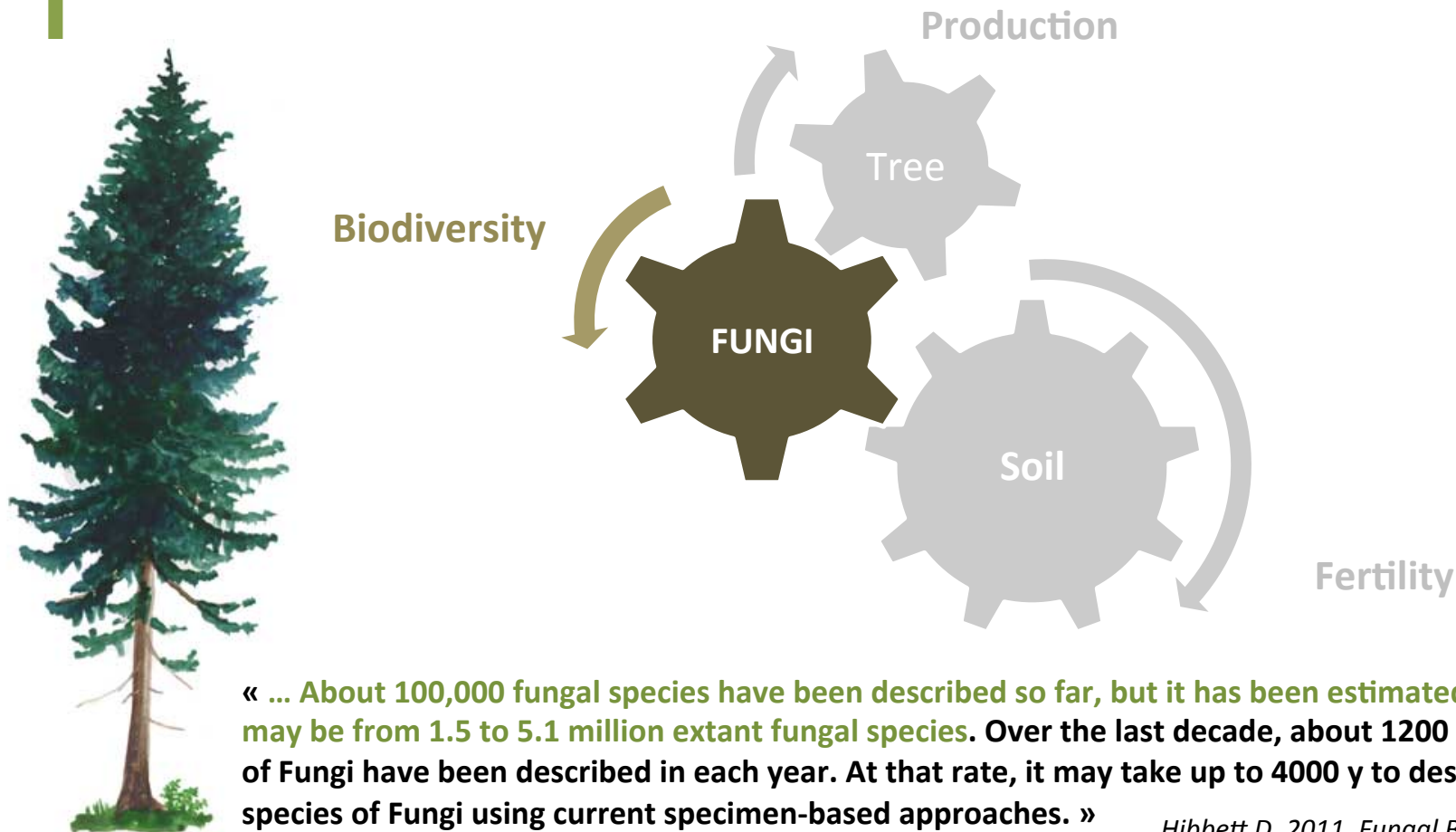
Forest ecosystem functioning

Diversity of microbial communities in the forest ecosystems



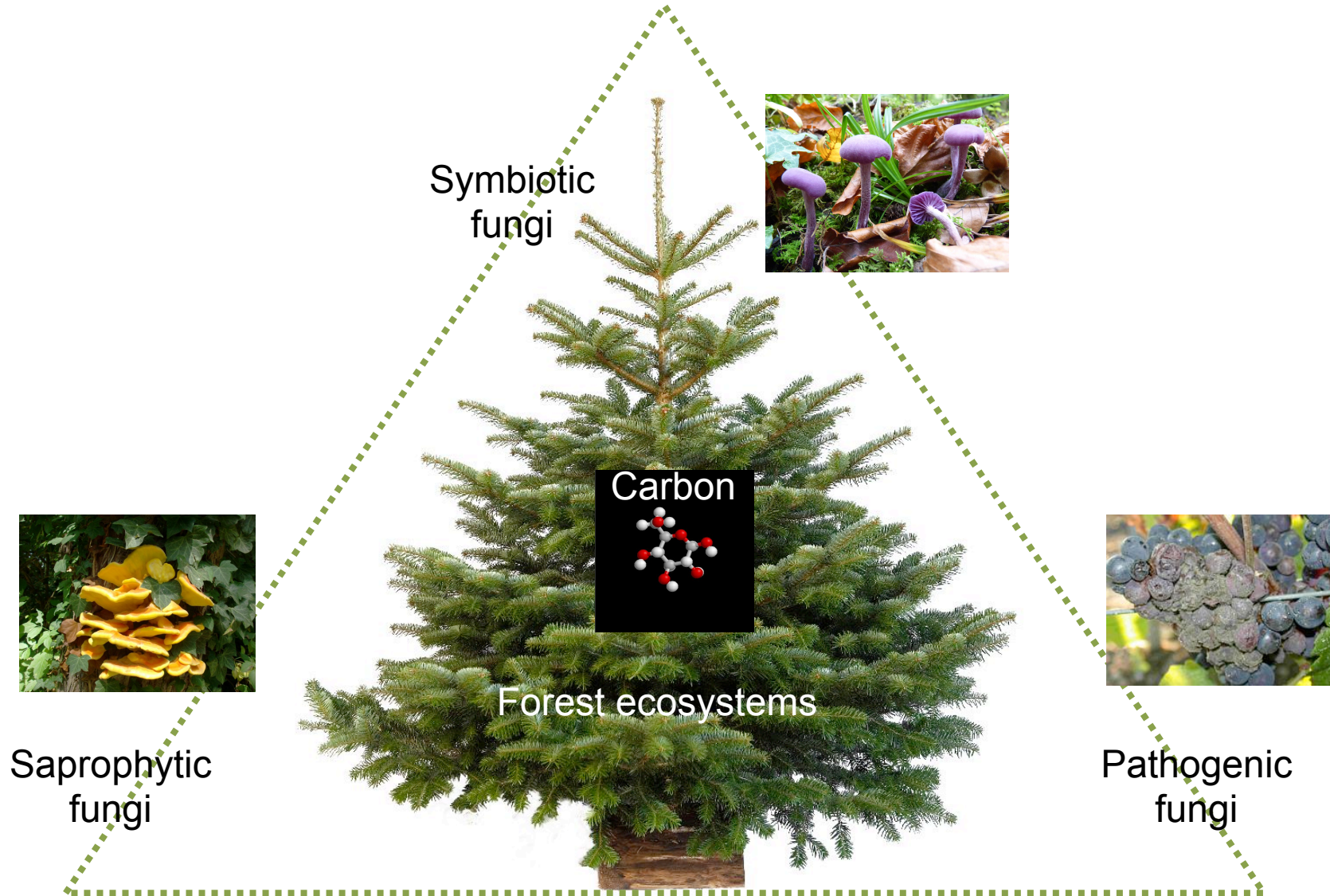
Forest ecosystem functioning

Diversity of fungal communities in the forest ecosystems

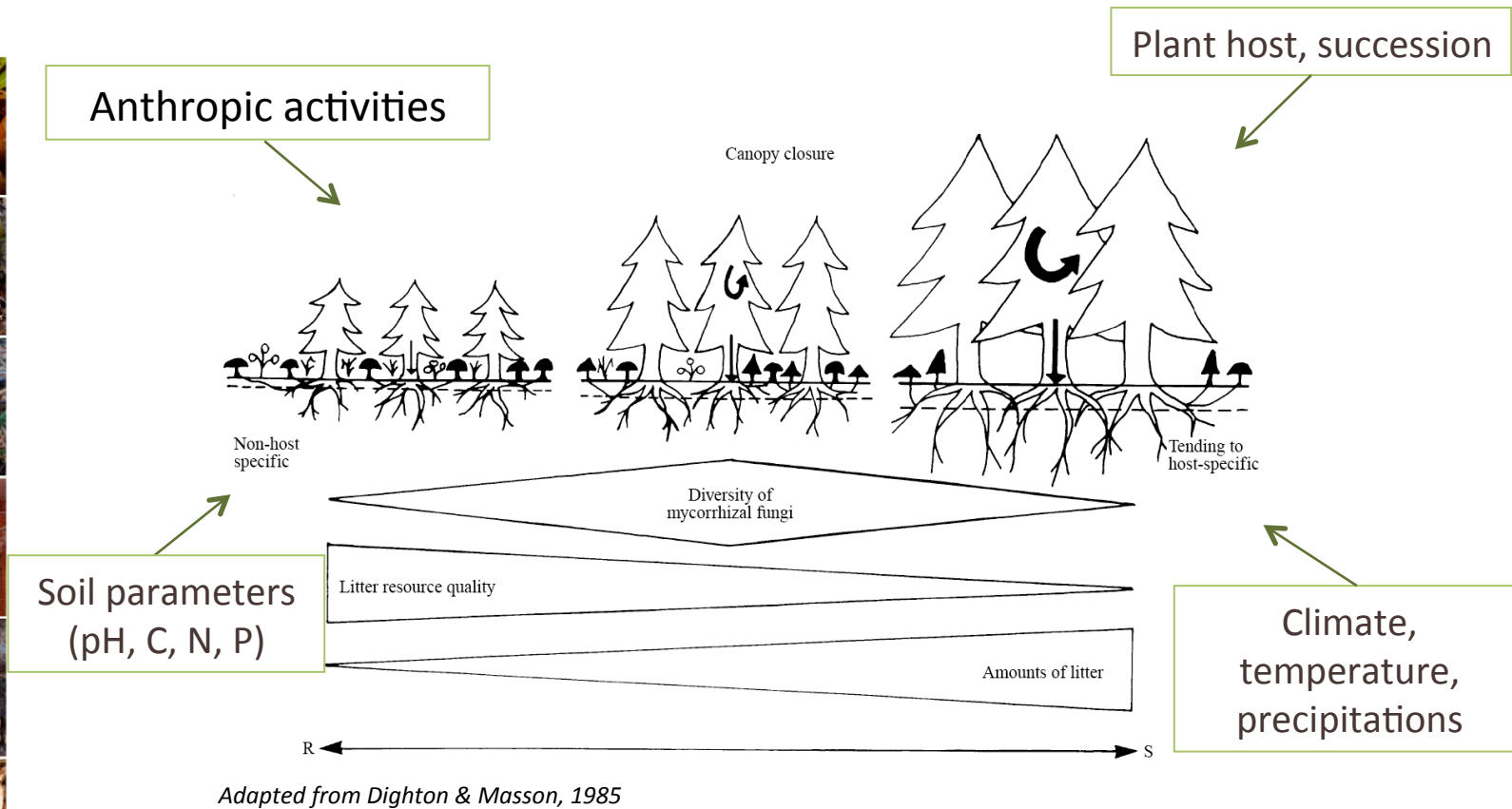


Hibbett D. 2011. *Fungal Biology Reviews*

**Diversity of fungi is linked to diversity of habitats and ecological traits
(mutualistic, saprophytic or pathogenic fungi)**



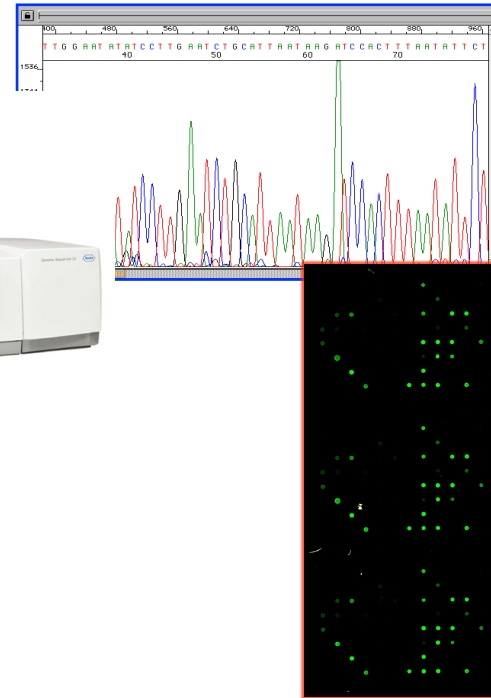
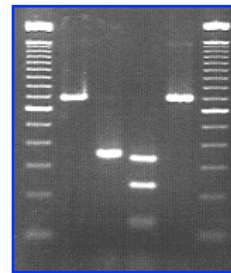
Why this huge diversity?



Soil fungi occur in remarkably species-rich assemblages. One of the prevailing hypotheses to explain this diversity is niche differentiation; by occupying distinct ecological niches within a site, multiple fungal species are able to co-occur.

How investigate this huge diversity ?

From sporocarp inventory to molecular approaches (complementary approaches)



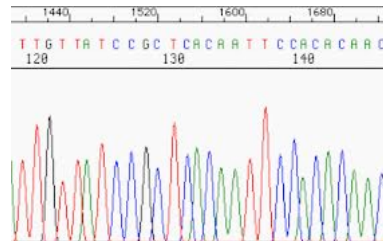
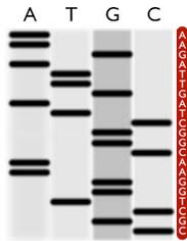
How investigate this huge diversity ?

REVIEW ARTICLE

The molecular revolution in ectomycorrhizal ecology: peeking into the black-box *at the global scale*

The recent improvements in sequencing techniques and bio-informatics make the mark of the second molecular revolution in fungal ecology (meta-barcoding).

Abstract



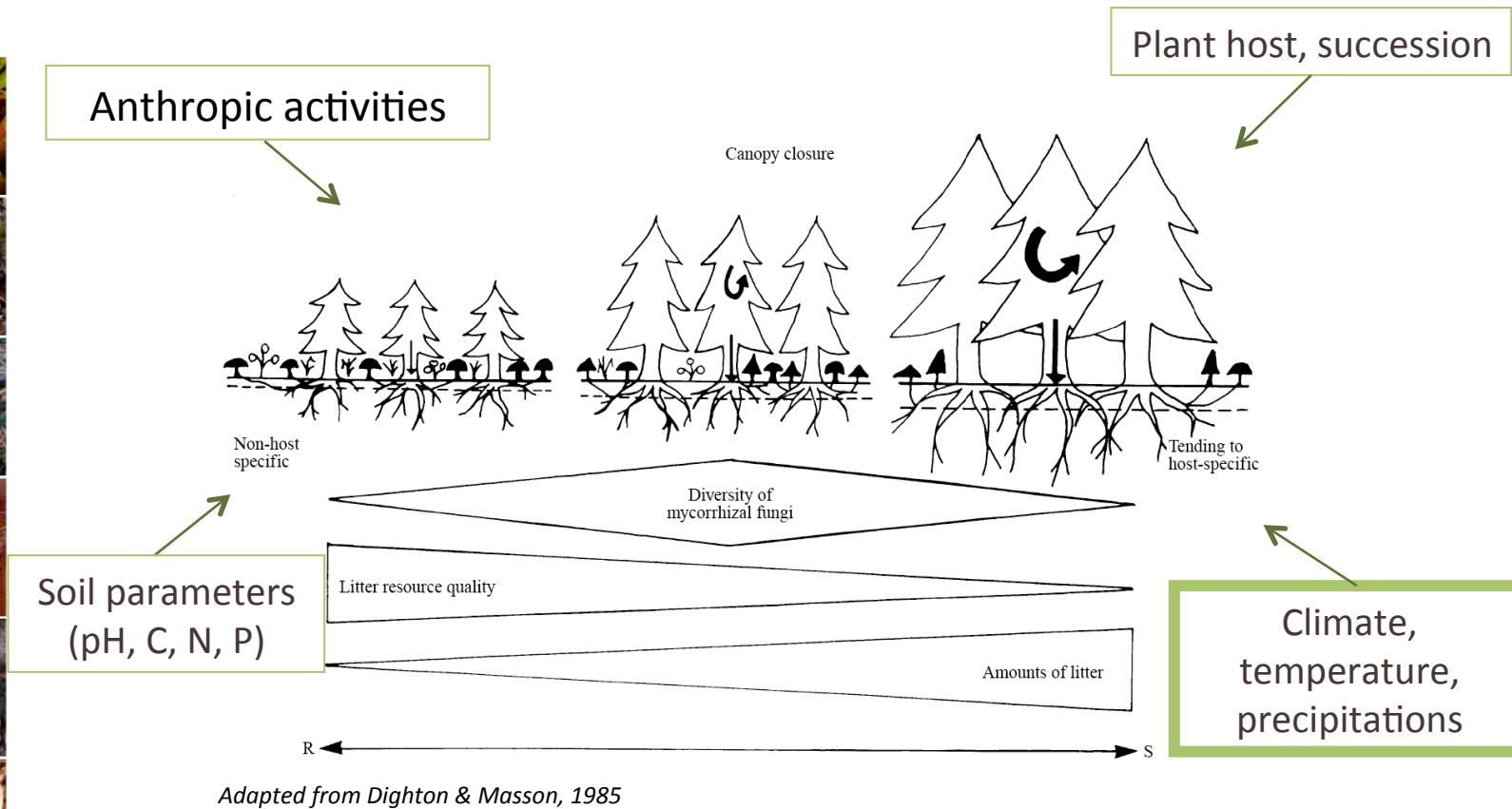
1977
Sanger sequencing

1990
Sequencing with
fluorescence
measurement

1999
Sequencing with capillary
electrophoresis

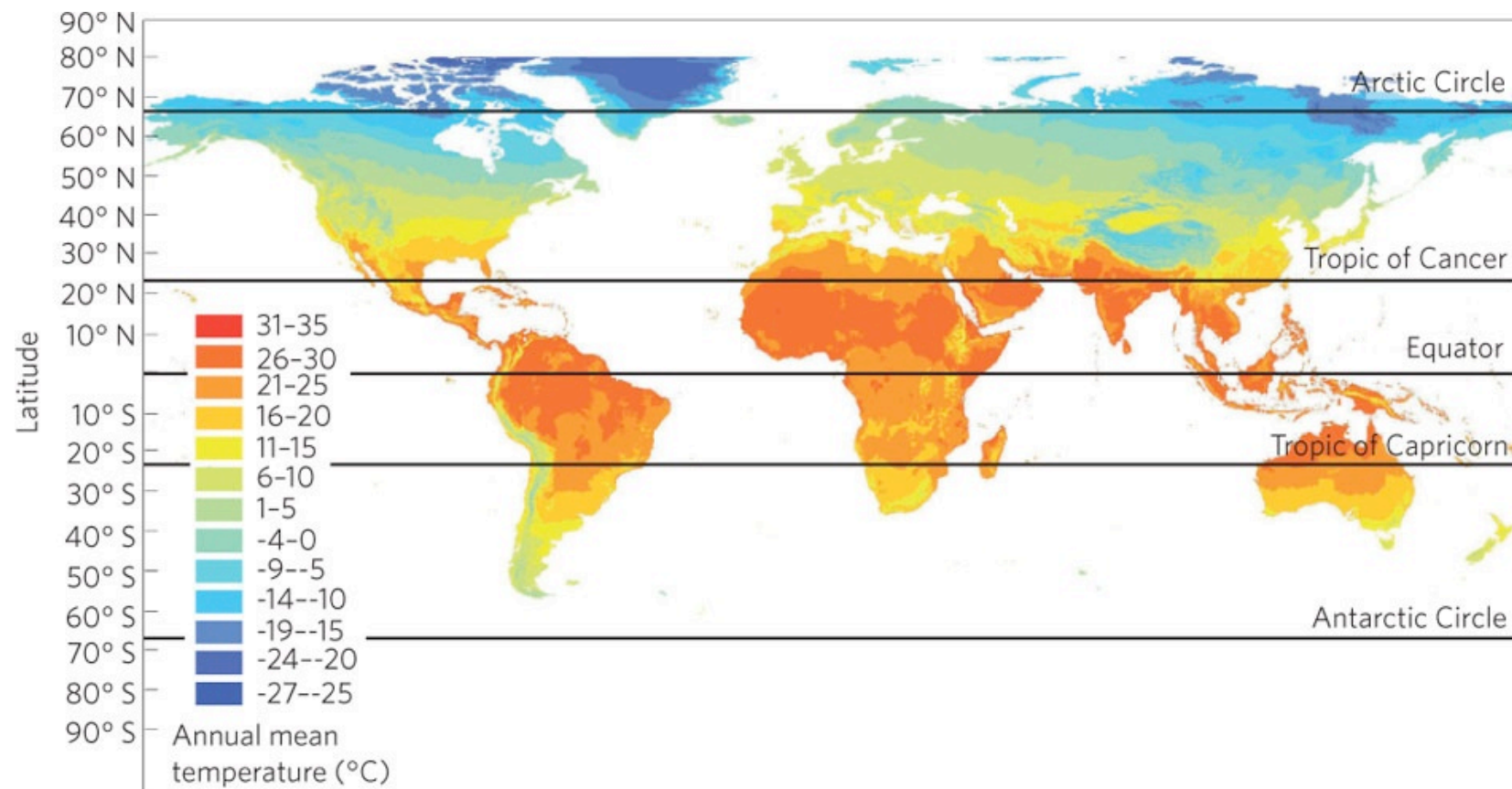
2006-2014
New Generation
Sequencing (NGS)

Why this huge diversity?



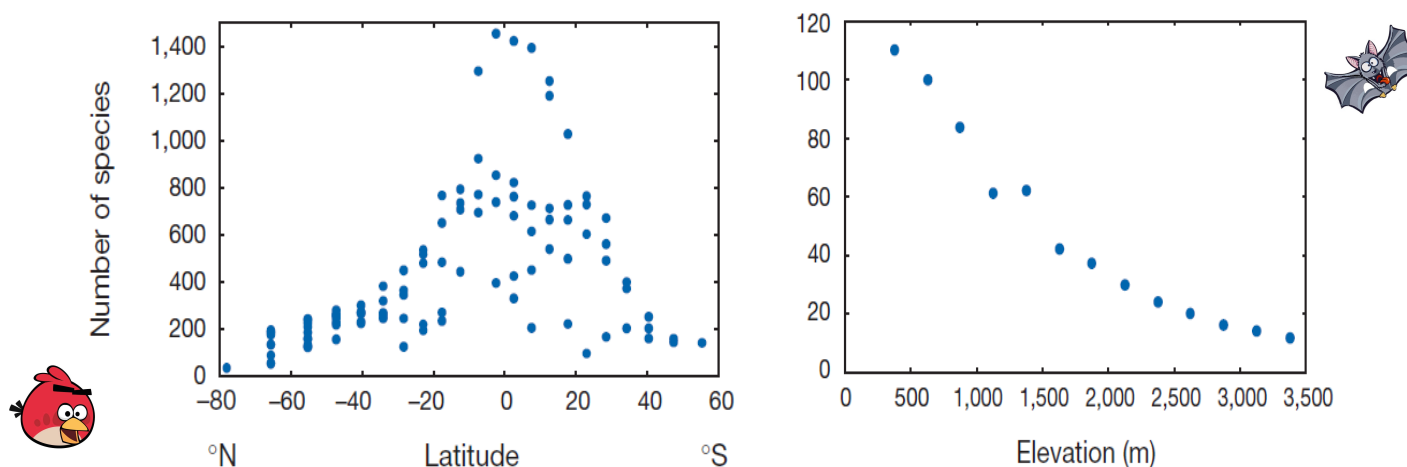
Advantage of New Generation Sequencing (NGS) to investigate unprecedented scale of sampling in fungal ecology... => Use natural climatic gradients to investigate the impact of temperatures and precipitations on fungal diversity and community structure

Are fungi follow the same global distribution pattern than macro-organisms?



Richness and temperature gradients: a biogeographic approach

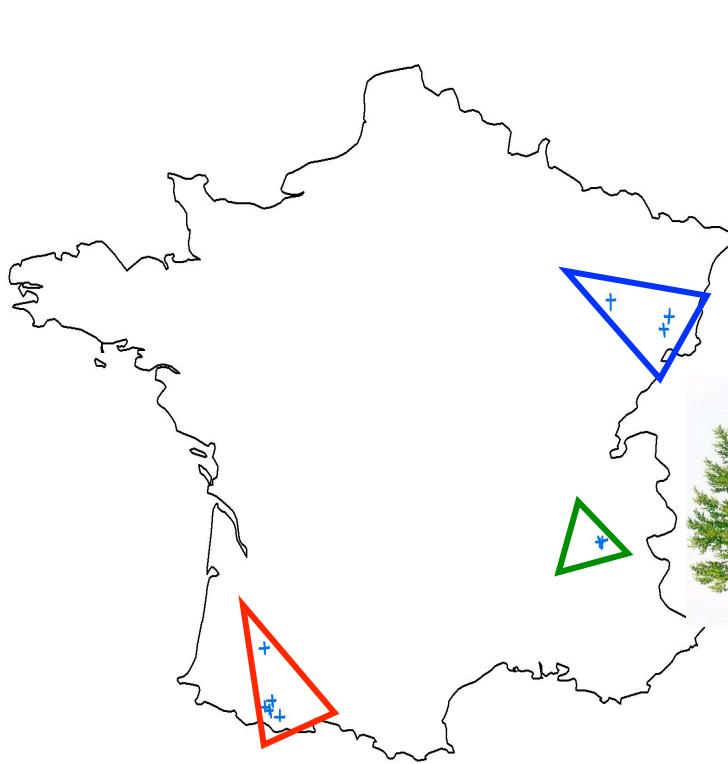
A common pattern in ecology is the latitudinal (and altitudinal) gradient of diversity. These examples with birds and bats show these common patterns : the trend is a lower species richness when moving away from the equator (or when the altitude increases). Positive correlation between energetic (thermic) gradient and richness.



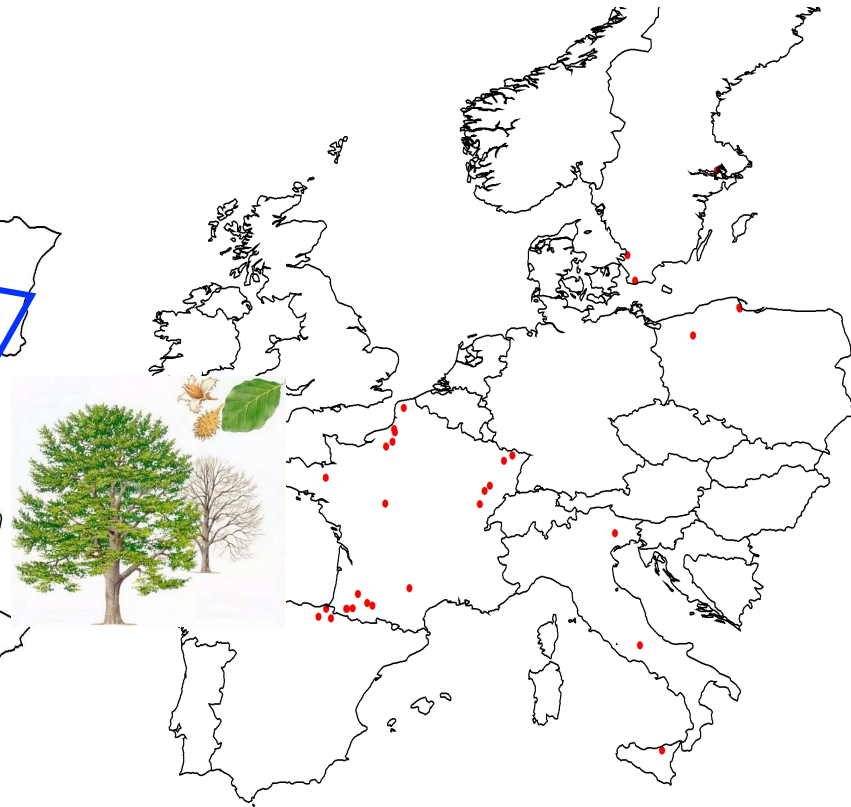
Gaston, 2000 Nature

For fungal communities: numerous controversies (Arnold and Ludzoni, 2007; Amend et al. 2010; Fierer et al. 2011; Bahram et al. 2012; Miyamoto et al. 2014; Tedersoo et al. 2014...)

Ecology of fungal communities in beech forests: Use of NGS (metabarcoding) in a biogeographical approach



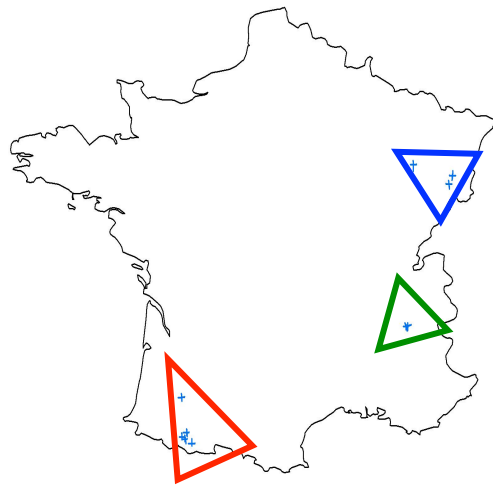
Altitudinal gradients in France



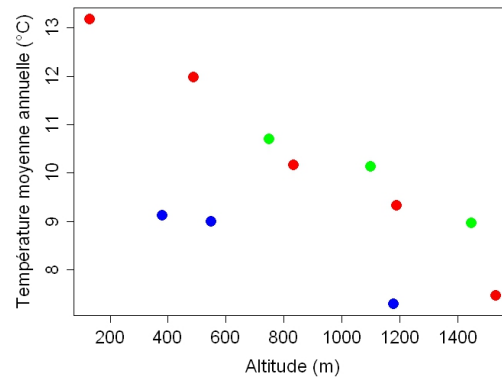
Latitudinal gradient in Europe



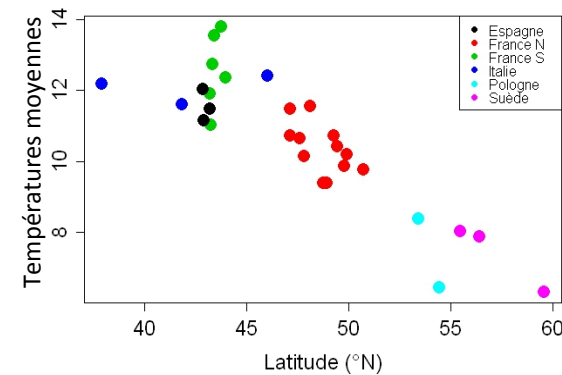
Ecology of fungal communities in beech forests: Use of NGS (metabarcoding) in a biogeographical approach



Altitudinal gradients in France



Latitudinal gradient in Europe



Coince et al. 2013 Fungal Ecology, Coince et al. 2014 PlosOne , Coince et al. (in preparation)



Methods

– Sampling strategy –

495 soil cores for Altitudinal gradients

465 soil cores for Latitudinal gradient (31 sites)

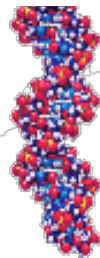
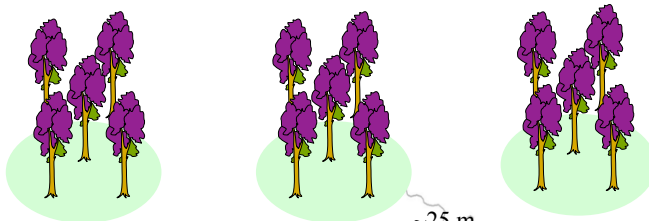
– Roots handling (1 sample = 1 tree = pool of 3 cores)–

– DNA extraction –

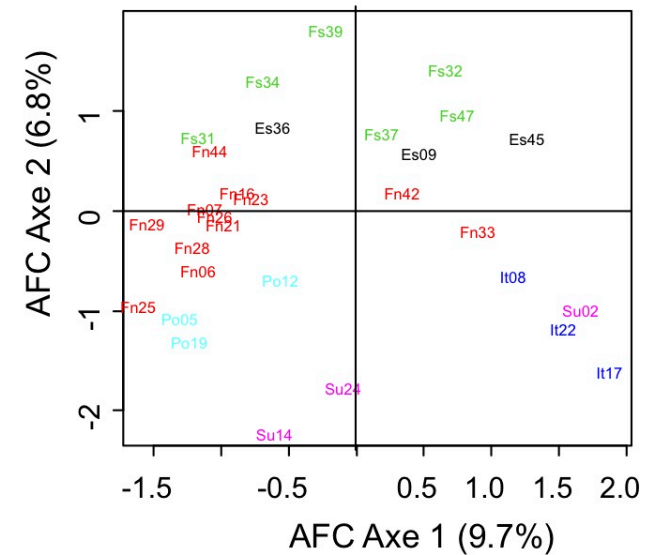
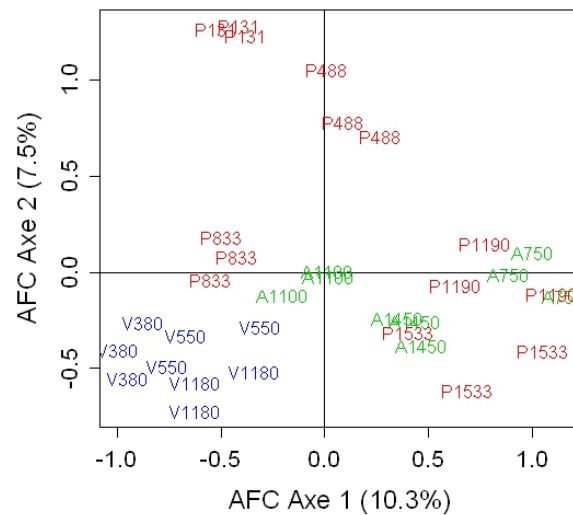
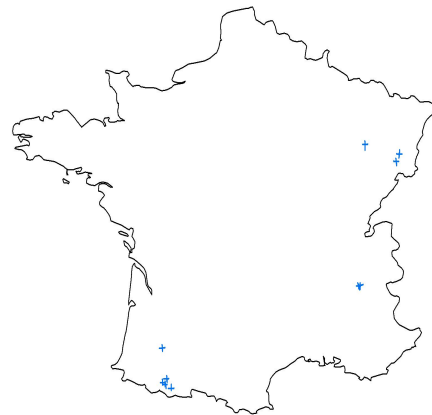
– PCR amplification (ITS1 region) – ITS1F-ITS2 primer pairs

– Amplicons libraries (with molecular tag) and Pyrosequencing –

– Bioinformatic analyses and taxonomic assignment –

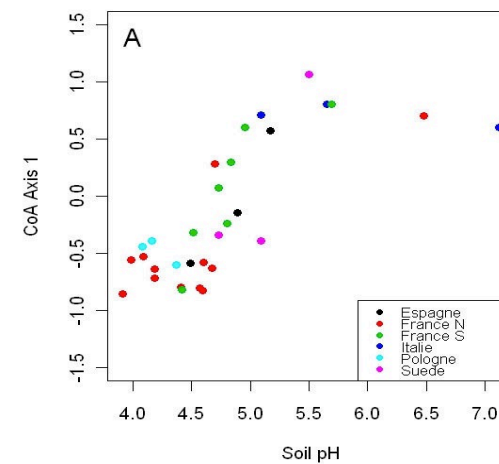
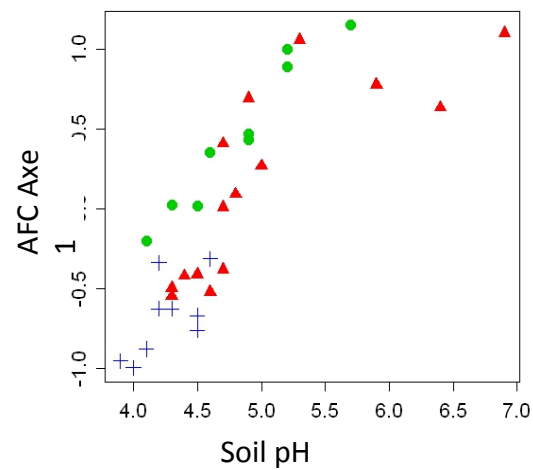
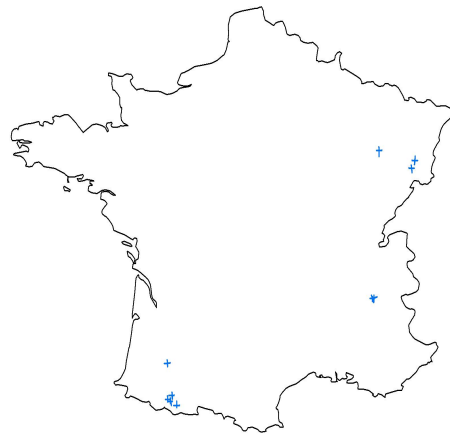


Composition (species assemblage) of fungal communities: a biogeographical approach



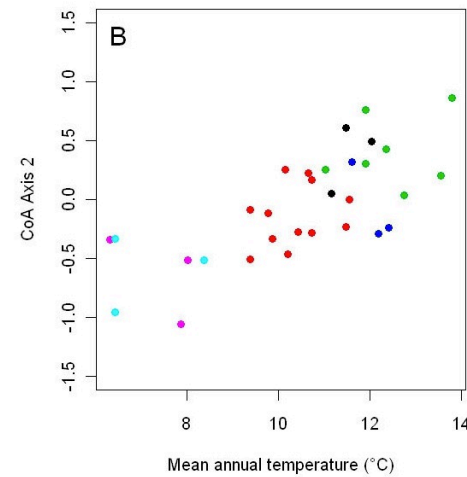
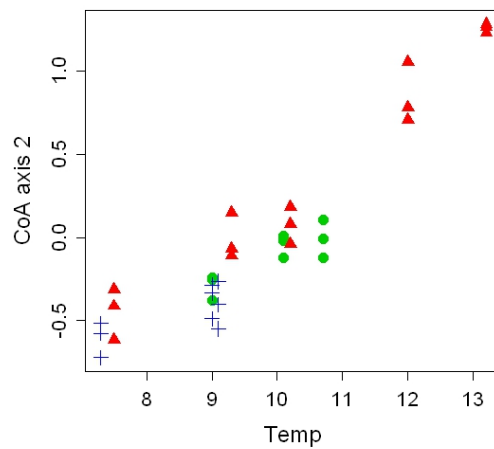
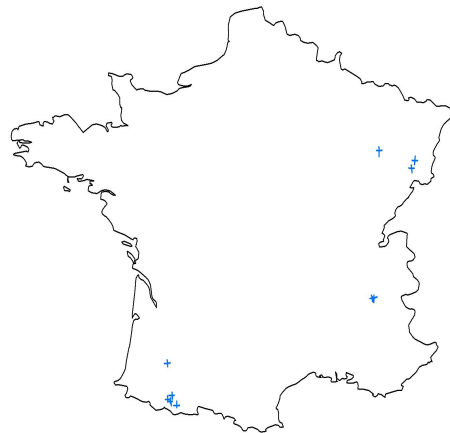
Correspondence analysis (two first axes) – links with environmental parameters?

Composition (species assemblage) of fungal communities: a biogeographical approach



Axe 1 = soil pH in both studies

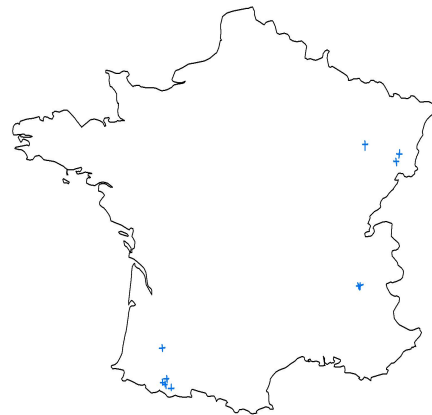
Composition (species assemblage) of fungal communities: a biogeographical approach



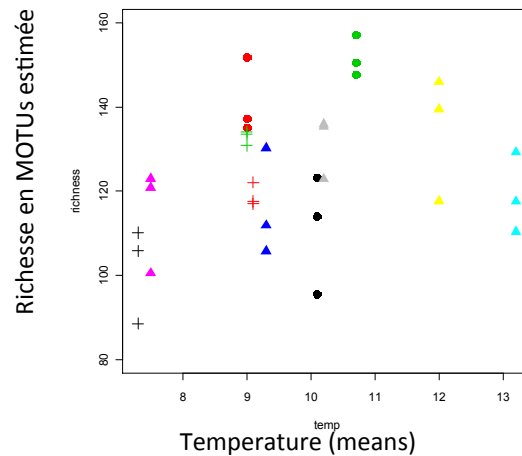
Axe 2 = mean temperatures in both studies



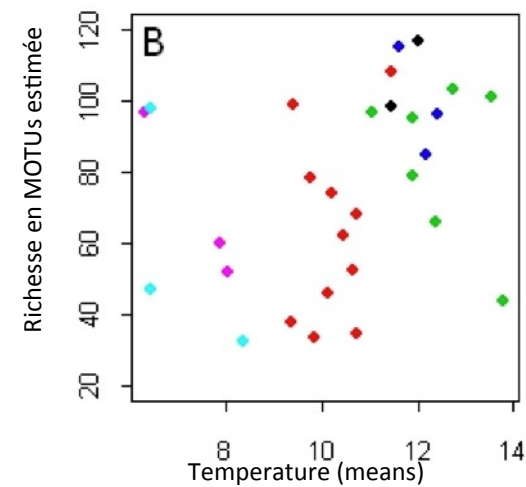
Richness estimation (proxy) in fungal communities along geographical gradients



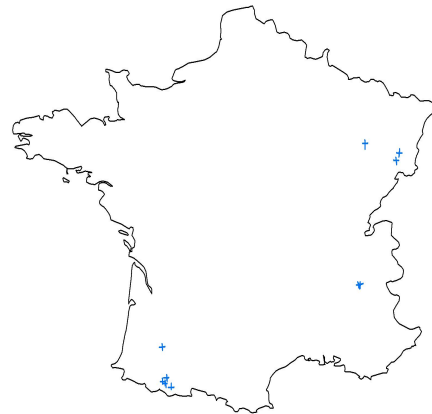
Elevation Diversity Gradient (EDG)
Mid Domain Effect model?



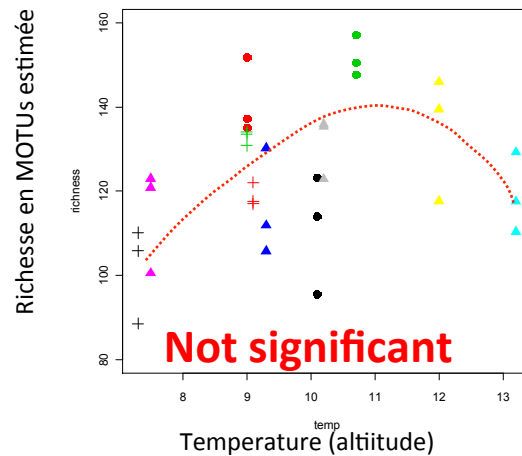
Latitudinal Diversity Gradient (LDG)
Monotonic relationship species /temperature ?



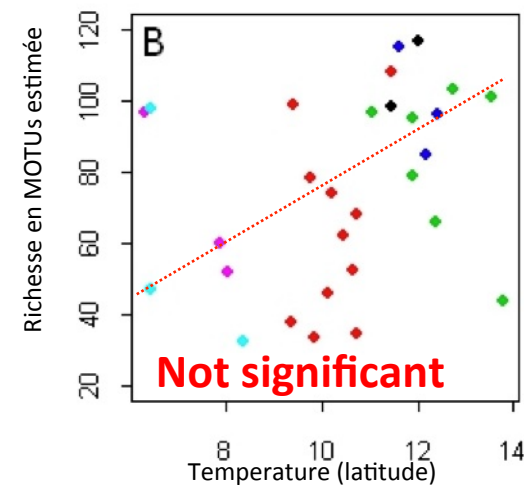
Richness estimation (proxy) in fungal communities along geographical gradients



Elevation Diversity Gradient (EDG)
Mid Domain Effect model? **No!**



Latitudinal Diversity Gradient (LDG)
Monotonic relationship species /temperature ? **No!**



Richness of fungi communities (altitudinal gradient) in *Pinus sylvestris* forests

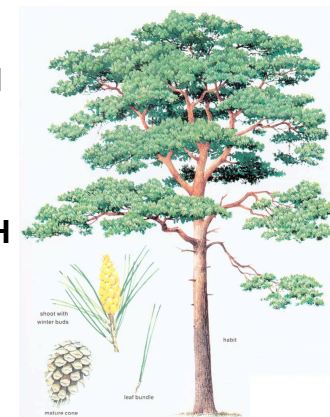


	ALL FUNGI [§]			MYCORRHIZAL FUNGI ^{††}						OTHERS ^Ω		
	BS			in RT			in BS			in BS		
	Estimate ± SE	F	p-value	Estimate ± SE	F	p-value	Estimate ± SE	F	p-value	Estimate ± SE	F	p-value
All MOTUs												
<i>Temperature</i>	-0.06 ± 0.02	0.2	ns	-0.02 ± 0.04	0.2	ns	-0.01 ± 0.04	0.0	ns	-0.04 ± 0.02	2.9	ns
<i>pH</i>	0.23 ± 0.06	13.4	0.002	0.02 ± 0.08	0.7	ns	0.08 ± 0.07	1.4	ns	0.26 ± 0.06	22.7	0.0003
<i>C/N</i>	-0.01 ± 0.00	1.4	ns	0.01 ± 0.00	0.2	ns	-0.01 ± 0.00	1.8	ns	0.003 ± 0.00	1.6	ns
<i>roots</i>	--	--	--	-0.61 ± 0.70	0.7	ns	--	--	--	--	--	--
<i>Precipitation</i>	0.001 ± 0.00	0.5	ns	0.01 ± 0.00	0.3	ns	-0.01 ± 0.00	6.0	0.027	0.000 ± 0.00	0.43	ns
<i>pH</i>	0.19 ± 0.05	9.6	0.007	0.01 ± 0.08	0.7	ns	0.06 ± 0.04	2.3	ns	0.222 ± 0.04	30.4	0.0001
<i>C/N</i>	-0.01 ± 0.00	2.3	ns	0.01 ± 0.00	0.2	ns	-0.05 ± 0.00	2.4	ns	0.002 ± 0.00	0.88	ns
<i>roots</i>	--	--	--	-0.50 ± 0.66	0.6	ns	--	--	--	--	--	--

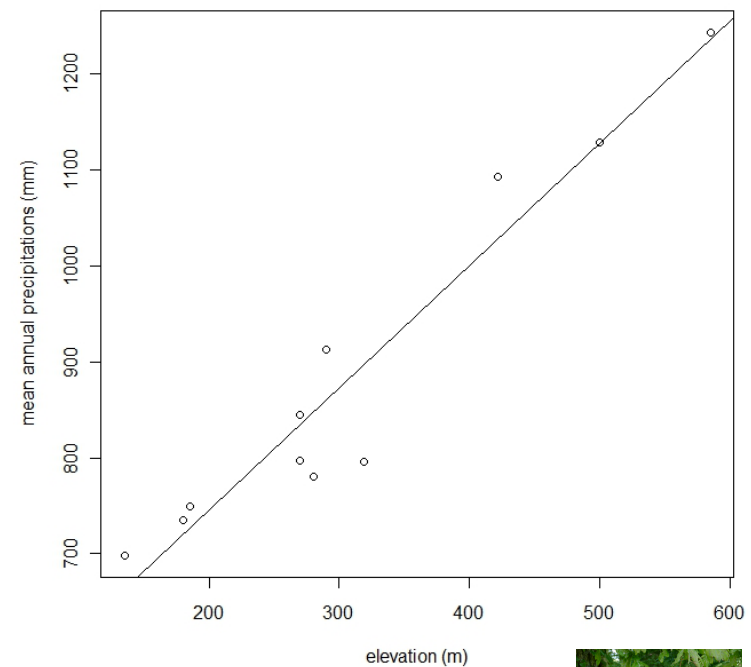
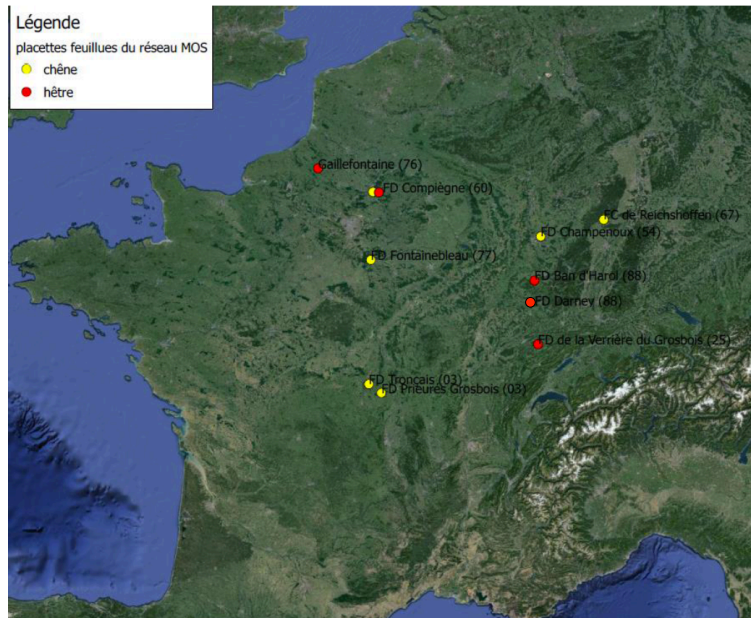
Generalized Linear Mixed Models testing the response of soil and mycorrhizal fungal communities to climatic (independent models for temperature and precipitation) and edaphic variables, considering the estimated richness as fixed effect.

Strong and significant positive correlation between fungal richness and soil pH (not for EcM fungi), but correlation between EcM fungi and annual precipitations (mm)

The host tree may modulate the impact of edaphic parameters on ECM fungal richness (?)



Fungal richness and climatic parameters: Do ectomycorrhizal and non-symbiotic fungi response differently to precipitations?

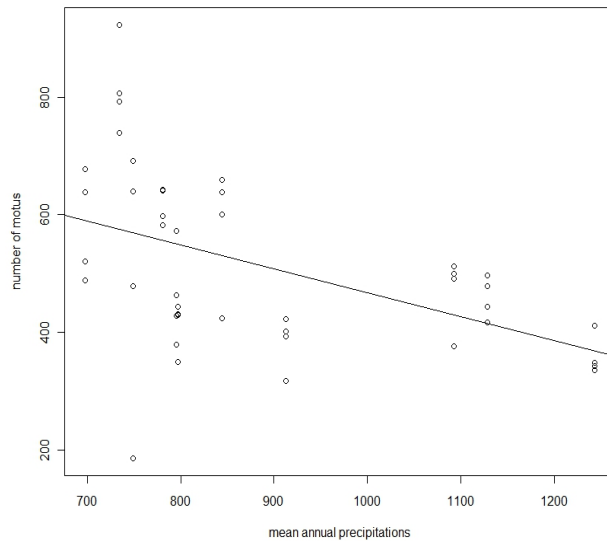


We focused especially on ECM fungi associated with Fagaceae *Fagus sylvatica* and *Quercus petraea*, which are particularly sensitive to climate changes using an East-West rainfall gradient in temperate French lowland forests (n=88 soil cores).

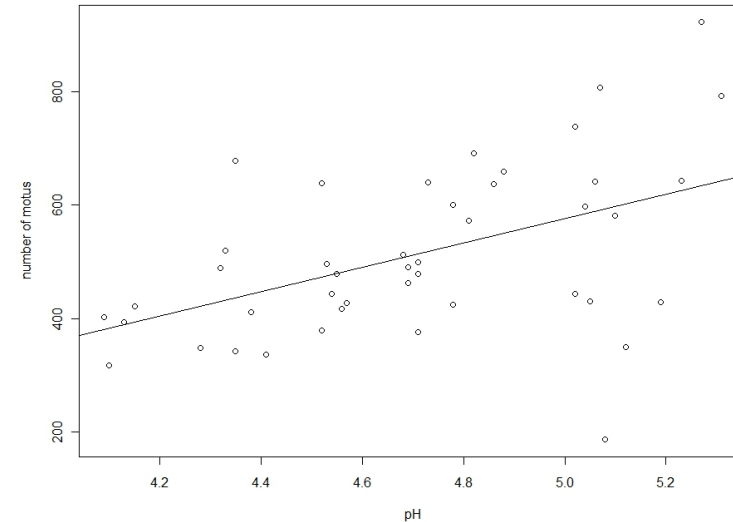


Akroume et al. (in preparation)

Fungal richness and climatic parameters:
Do ectomycorrhizal and non-symbiotic fungi response
differently to precipitations?



Linear regression between fungal **richness** and mean **annual precipitations** (mm)

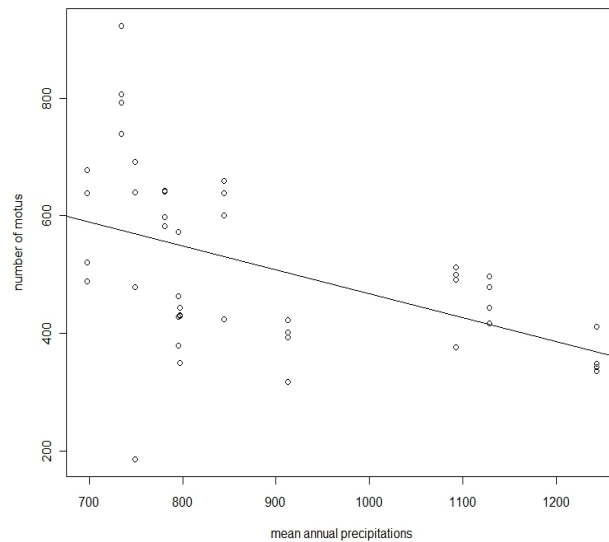


Linear regression between fungal **richness** and **soil pH**

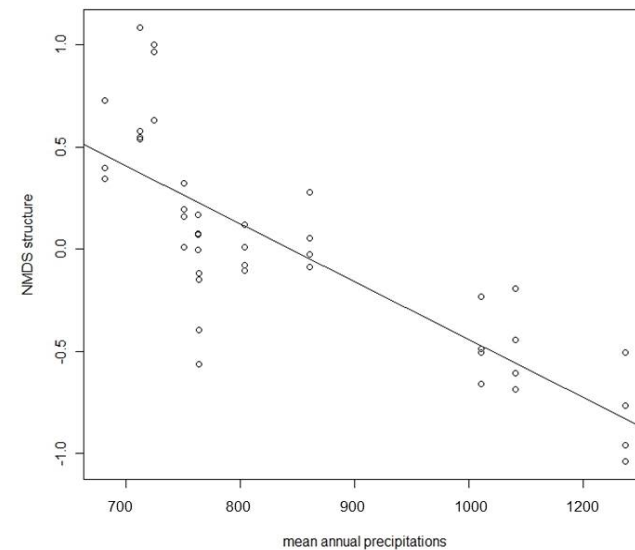
We confirm the relationship between the soil pH and fungal richness
+ significant link between fungal richness and precipitation (negative correlation).
By contrast, ECM richness is not linked with this climatic factor

For fungal communities: numerous controversies (Arnold and Ludzoni, 2007; Amend et al. 2010; Fierer et al. 2011; Bahram et al. 2012; Miyamoto et al. 2014; Tedersoo et al. 2014...)

Composition (species assemblage) of fungal communities in beech / oak forests



Linear regression between fungal **richness** and mean **annual precipitations** (mm)



Correlation between NMDS **structure** (axis1+axis2) and mean **annual precipitations** (mm)

Ectomycorrhizal fungi are more sensitive to mean annual precipitations and less structured by soil characteristics like pH or Ca concentrations than saprobes. The host tree modulates the impact of edaphic parameters on ECM fungal richness. In return EcM fungi may be more sensitive to climatic parameters, as their hosts...

Akroume et al. (in preparation)

In the “Omics era”, how fungal culture collections (and voucher individuals) can be a research tools in ecology?



Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for *Fungi*

Conrad L. Schoch^{a,1}, Keith A. Seifert^{b,1}, Sabine Huhndorf^c, Vincent Robert^d, John L. Spouge^a, C. André Levesque^b, Wen Chen^b, and Fungal Barcoding Consortium^{a,2}

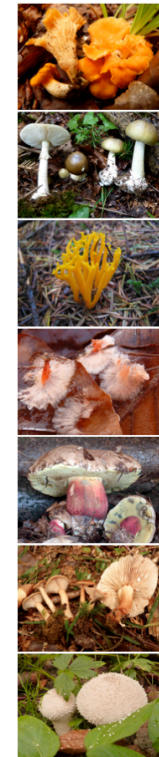
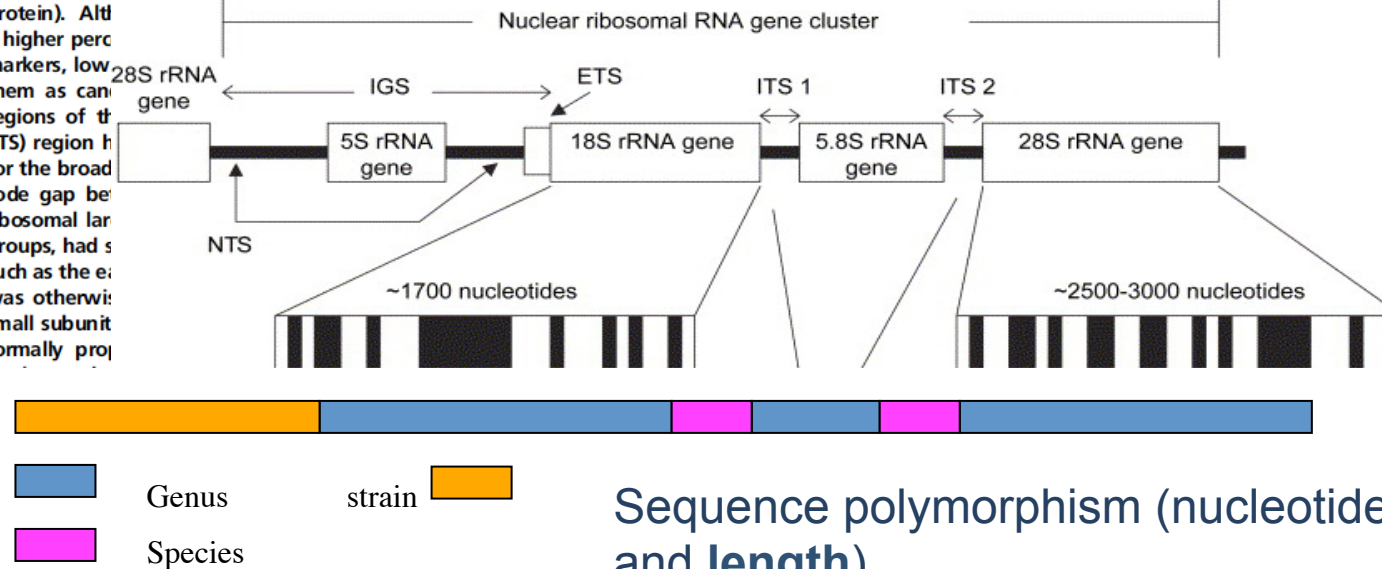
^aNational Center for Biotechnology Information, National Library of Medicine, National Institutes of Health and Microbiology), Agriculture and Agri-Food Canada, Ottawa, ON, Canada K1A 0C6; ^cDepartment of Botany, University of Guelph, Guelph, ON, Canada N1G 2W1; ^dCentraalbureau voor Schimmelcultures Fungal Biodiversity Centre (CBS-KNAW), 3508 AD, Utrecht, The Netherlands

Edited* by Daniel H. Janzen, University of Pennsylvania, Philadelphia, PA, and approved February 24, 2012

Six DNA regions were evaluated as potential DNA barcodes for *Fungi*, the second largest kingdom of eukaryotic life, by a multinational, multilaboratory consortium. The region of the mitochondrial cytochrome c oxidase subunit 1 used as the animal barcode was excluded as a potential marker, because it is difficult to amplify in fungi, often includes large introns, and can be insufficiently variable. Three subunits from the nuclear ribosomal RNA cistron were compared together with regions of three representative protein-coding genes (largest subunit of RNA polymerase II, second largest subunit of RNA polymerase II, and minichromosome maintenance protein). Although a higher percentage of markers, low variability in some regions of the ITS region hampers its use for the broadest code gap between ribosomal large subunit groups, had such as the eukaryotic small subunit formally proposed.

the intron of the *tmK* reconsidering *COI* as the

COI functions rease genera, such as *Penicillium* species resolution (67%) results in the few other consistent, and cloning primers applicable to the process, because amplification



Implementation of high quality Fungal Database (ITS regions) (annotated fruiting bodies, voucher specimens)



unite

A molecular database for the
identification of fungi

[Home](#) [Run Analysis](#) [Search Pages](#) [Notes and news](#) [Contributors](#) [Acknowledgements](#)

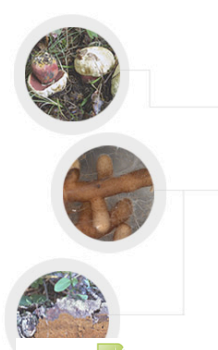
Number of UNITE barcoding sequences: **2705** ITS sequences of **1180** species from **180** genera.
Number of fungal ITS sequences in database (UNITE + INSd): **91688**
How to cite **UNITE** ?

UNITE is a rDNA sequence database focused on ectomycorrhizal asco- and basidiomycetes. The database initially holds only sequences from the ITS region. The sequences are generated from fruit bodies collected and identified by specialists and deposited in public herbaria; type specimens are used whenever possible. Selected species also have full descriptions and illustrations linked to the sequences.

The purpose of the database is to facilitate identification of environmental samples of fungal DNA. **UNITE** includes several tools that aid in the identification of unknown sequences. Since unequivocal identification is the main purpose behind **UNITE**, the implementation of tools that extend beyond simple similarity searches (as offered by BLAST and variations thereof) was an essential part of the database development. This requirement has been met by the development of galaxie, which allows web-based, basic phylogenetic analyses. Galaxie provides maximum parsimony heuristic and neighbour joining analyses under different evolutionary models. To date, two galaxie (galaxieBLAST, galaxieHMM) and one BLAST script have been implemented. We recommend galaxieBLAST as the most appropriate tool for the identification of unknown ITS sequence. Other identification methods will be considered for inclusion in the future. We stress again that the **UNITE** database is, in its present form, restricted to ITS sequences specific to ECM fungi and as such the input of query sequences from other fungi not covered by the database (i.e. saprotrophic or parasitic fungi) is not recommended for obvious reasons.

UNITE is a relational database built on a MySQL platform running on a Red Hat Linux Apache httpd server. It is accessed through a web interface system written in PHP, Perl, and Python scripting languages.

The development of **UNITE** is a Nordic-Baltic initiative and a collaboration between several



R-SYST

Réseau de Systématique Outil de caractérisation moléculaire et phénotypique d'organismes d'intérêts

[R-Syst A propos](#) [Bactéries](#) [Micro-Algues](#) [Plantes](#) [Champignons](#) [Insectes](#) [Ressources](#) [Outils](#) [Participants](#)

Home

Champignons

Submitted by francois dardet on Fri, 10/14/2011 - 13:27



Les champignons sont des micro-organismes présentant une grande diversité phylogénétique. Le nombre d'espèces est estimé à 1,5 millions dont peu de connues (environ 70000). La base R-Syst champignon, permettra de recueillir et de rassembler des informations pour l'identification moléculaire et phénotypique des espèces fongiques (et Oomycètes). Des données moléculaires (séquences ADN des marqueurs moléculaires), taxinomiques (ordre, famille, genre, espèce...), morphologiques, géographiques, épidémiologiques, éthologiques, autécologiques... seront rassemblées dans cette base de données interrogeable par la communauté scientifique et le grand public (interrogation sur mots clés ou soumission de séquences ADN).

Ressources Web :
Biogersyst: Le site de l'équipe R-SYST champignons de Versailles-Grignon
Mycor Web: La base de donnée l'équipe de Nancy
E-Phyto: site de diagnostic de santé des plantes

La majorité des champignons se distinguent par l'insuffisance de caractères morphologiques capables de discriminer efficacement les différentes espèces. Cette situation est bien illustrée par l'existence de nombreuses espèces fongiques cryptiques qui n'ont été mises en évidence qu'à l'aide d'outils moléculaires. Ainsi, une partie du projet R-Syst « champignons » se focalisera sur l'utilisation de marqueurs moléculaires (bar coding et gènes taxinomiquement fiables) pour réaliser une classification phylogénétique des espèces fongiques, en appui des approches morpho-taxinomiques classiques. C'est sur cette démarche que sera construite la base de donnée R-Syst.

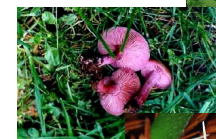
- Réseau R-Syst champignon : Structurer un réseau national distribué de compétences pour l'identification moléculaire et morphologique - phénotypique des espèces fongiques (liste de diffusion, forum).
- Validation de nouveaux marqueurs moléculaires (Bar Coding, phylogénie)
- Indexation des collections de champignons et mycothèques (herbiers, échantillons environnementaux, collections).
- Notion d'espèces, définitions de taxons, assignation
- Génomique comparative
- Méthodes de diagnostic moléculaire d'espèces fongiques

Language

[French](#)



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C. Réa



[Contact](#) [Connexion](#)

Les dernières nouvelles

1ère version du site R-SYST
Body:
Voici la toute première version du site R-SYST : vous pouvez dès maintenant consulter les 5 bases actuelles de R-SYST ainsi que

TreeBOL-Europe

Body:
TreeBOL est un consortium d'organismes impliqués dans le barcoding des arbres. Rendez-vous dans la Base Plantes pour plus d'informations...

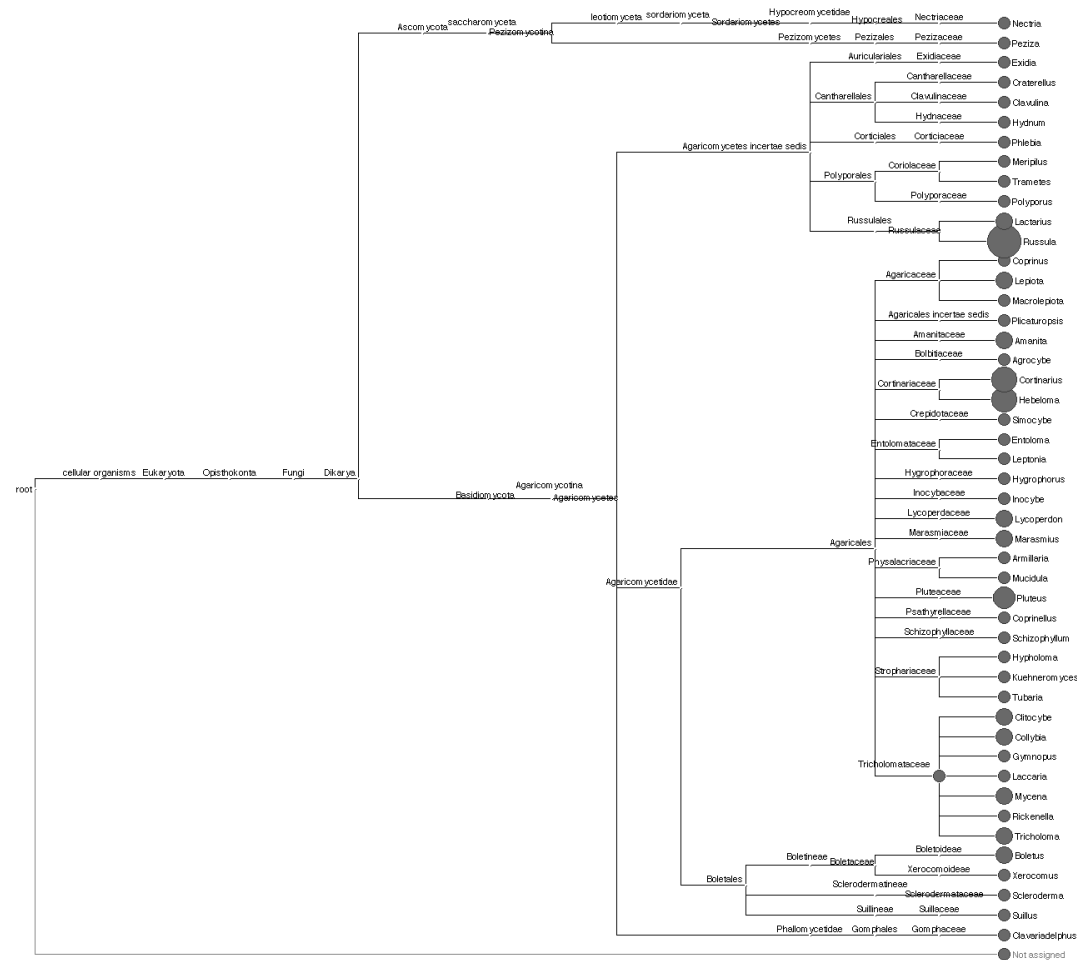
Barcoding chez les plantes

Body:
R-SYST et le barcoding chez les plantes.

>> Voir les archives ...



Production of Mock communities (positive controls in NGS process) (annotated fruiting bodies, voucher specimens, fungal culture collections)



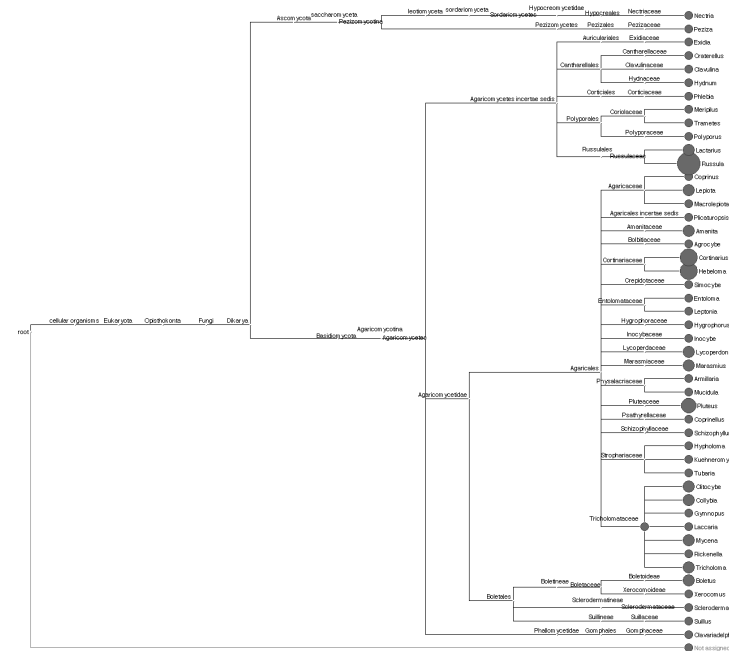
A mock community will also serve to inform the quality of the sequencing run (i.e. helps address run-to-run variation) and the processing steps necessary to retain the most data (i.e. addresses sequencing data quality).

This work was based on cultures from the INRA Nancy Culture Collection and dry voucher specimens (Mock community = 77 different species and 49 different genera)

Production of Mock communities (positive controls in NGS process) (annotated fruiting bodies, voucher specimens, fungal culture collections)



A mock community will also serve to inform the quality of the sequencing run (i.e. helps address run-to-run variation) and the processing steps necessary to retain the most data (i.e. addresses sequencing data quality).

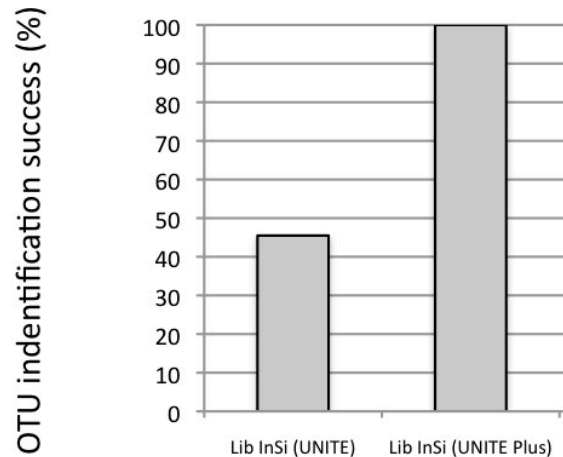


Lindahl et al. 2013

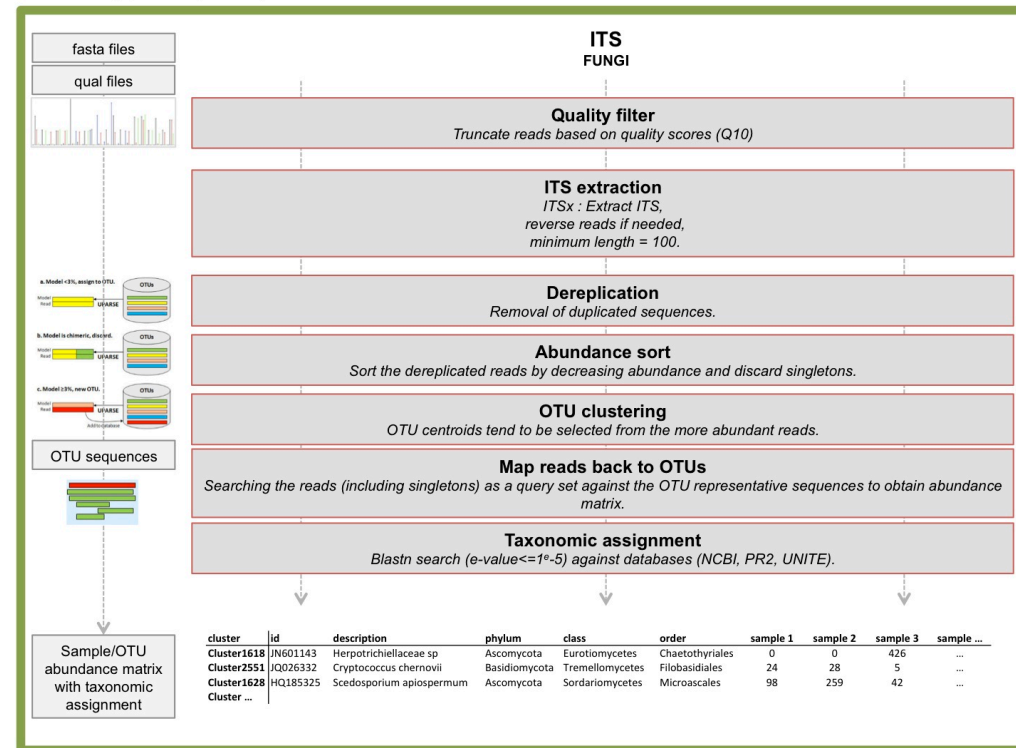
Overview of the steps involved in high-throughput sequencing of fungal communities.

Production of Mock communities

(annotated fruiting bodies, voucher specimens, fungal culture collections)



Bioinformatic pipeline v2 (UPARSE)



Bioinformatics analysis of a mock community from 77 fungal species using UPARSE (Edgar, 2013).

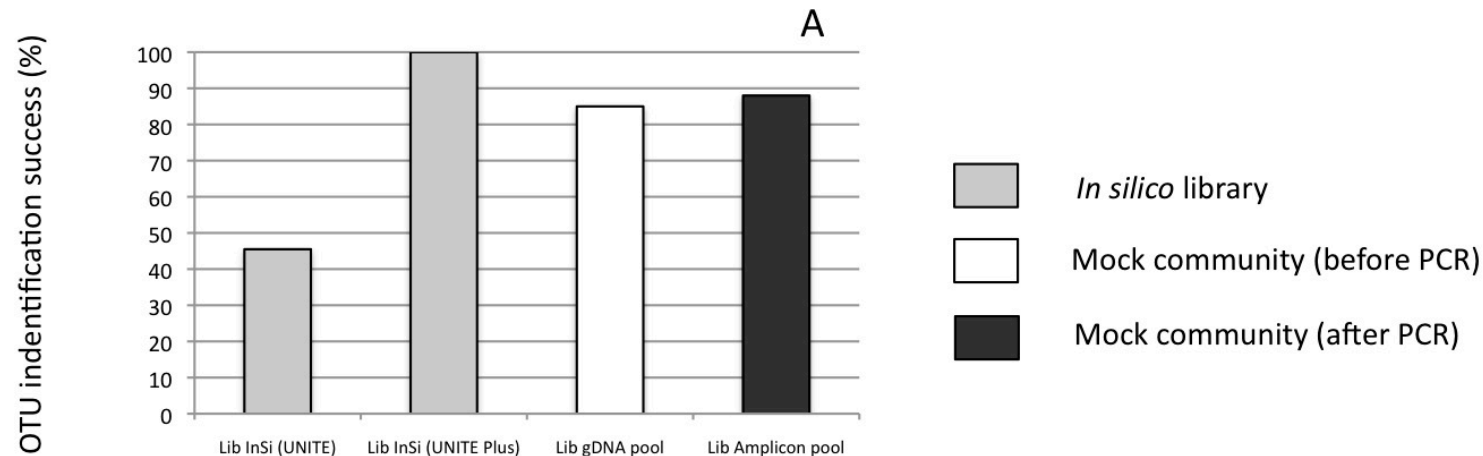
The rate of successful operational taxonomic unit (OTU) identification. Lib InSi corresponded to the in silico library of 77 Sanger sequences of ITS1 region.

Full "UNITE+INSD" dataset:

This FASTA file ("UNITE+INSDC") comprises "all" fungal ITS sequences of the UNITE and INSDC databases, updated and released some four times a year. Locked UNITE sequences and low quality (and overly short) INSDC sequences are however excluded. UNITE follows the [Index Fungorum](#) classification in nearly all regards.

Production of Mock communities

(annotated fruiting bodies, voucher specimens, fungal culture collections)

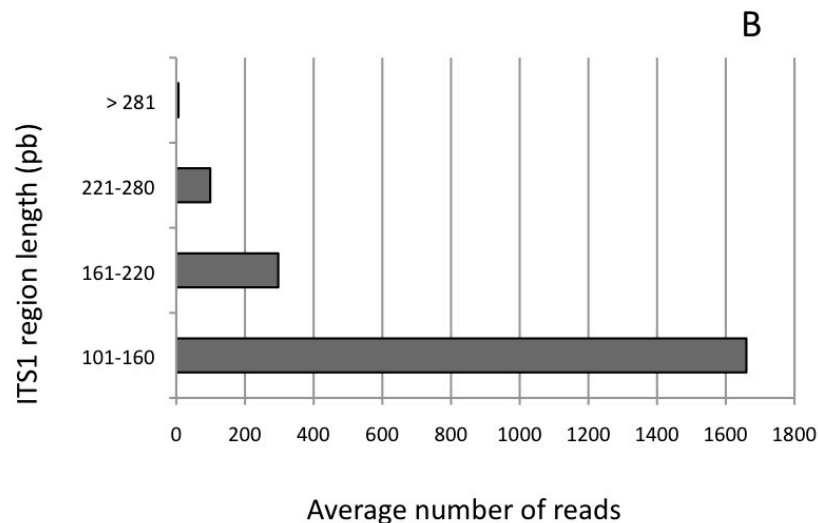
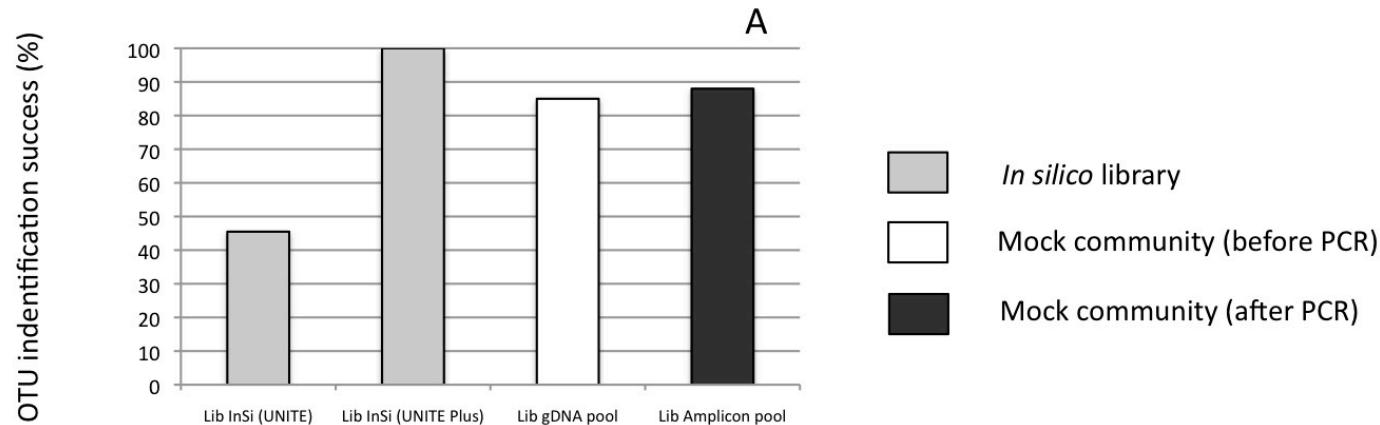


Bioinformatics analysis of a mock community from 77 fungal species using UPARSE (Edgar, 2013).

A. The rate of successful operational taxonomic unit (OTU) identification. Lib InSi corresponded to the in silico library of 77 Sanger sequences of ITS1 region. Lib gDNA pool was built by mixing equimolar amounts of genomic DNA from the 77 corresponding species, and Lib Amplicon pool by mixing equimolar amounts of independent PCR products from the same 77 species. “Lib gDNA” and “Lib Amplicon pool” were processed in the same way, and all the datasets were treated identically with the bioinformatics quality filtering and OTU clustering using UPARSE. The sequences were aligned using BLAST on “UNITE Plus” database (UNITE database [Kõljalg et al., 2013] together with the Sanger sequences of the mock community absent in the initial UNITE database). Only 45.5% of sequences of the mock community was present in the UNITE database.

Production of Mock communities

(annotated fruiting bodies, voucher specimens, fungal culture collections)



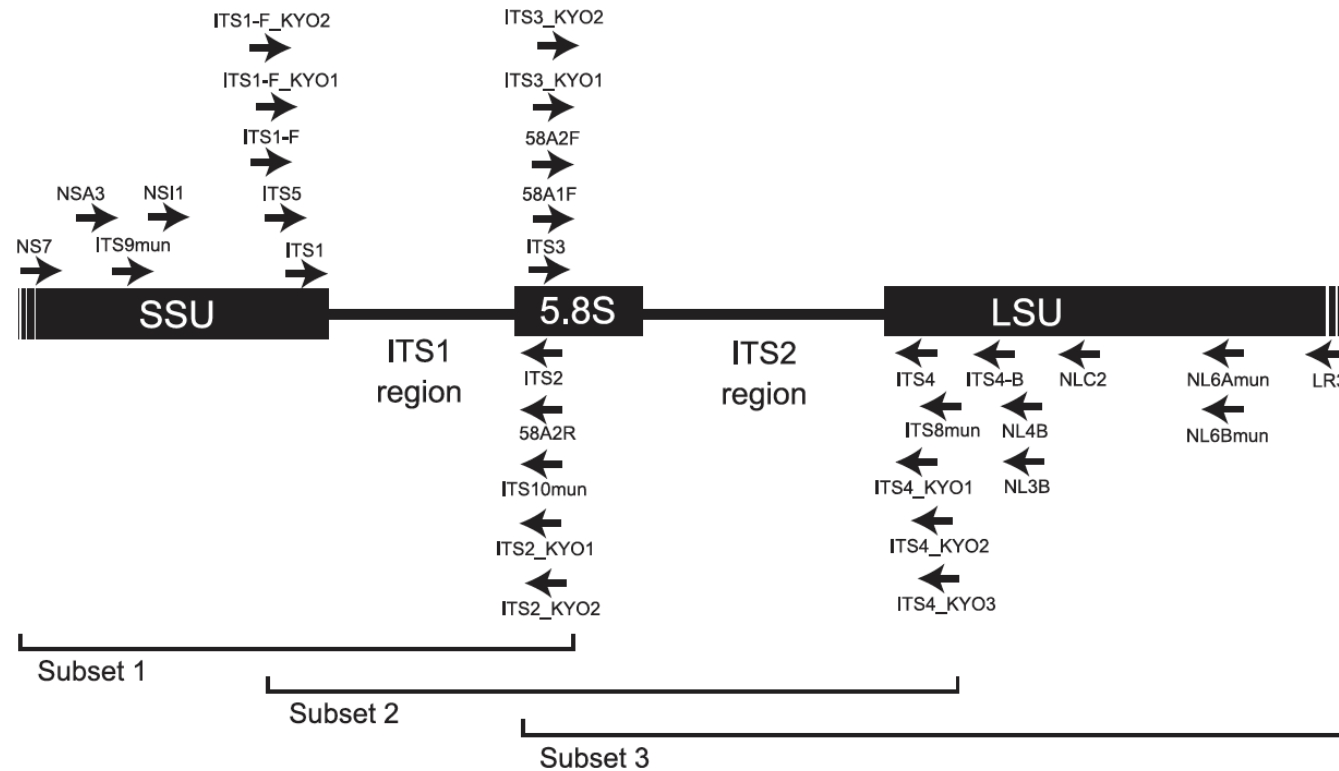
Bioinformatics analysis of a mock community from 77 fungal species using UPARSE (Edgar, 2013).

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B. Relationship between the number of reads generated by the Illumina MiSeq technology and the length of the fungal ITS1 fragment.

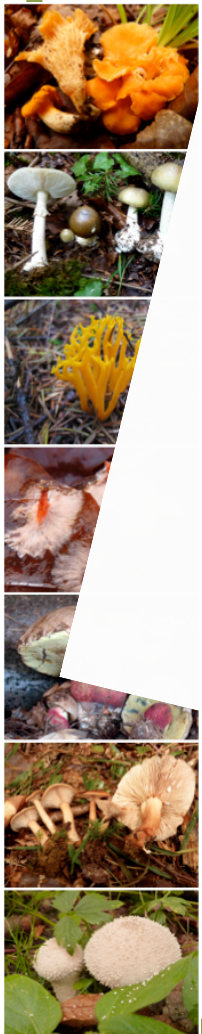
Buée et al. in preparation

Perspectives: validation of best primers and best regions (ITS2 vs ITS1 or SSU & LSU) for Miseq Illumina...



Map of nuclear ribosomal RNA genes and their ITS regions

*Perspectives: validation of best primers and best regions (**ITS2** vs ITS1 or SSU & LSU) for Miseq Illumina...*



ITS3_KYO2

MycoKeys 10: 1–43 (2015)
doi: 10.3897/mycokeys.10.4852
<http://mycokeys.pensoft.net>

RESEARCH ARTICLE



Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi

Leho Tedersoo¹, Sten Anslan², Mohammad Bahram^{2,3}, Sergei Põlme^{1,2}, Taavi Riit²,
Ingrid Liiv², Urmas Kõljalg³, Veljo Kisand⁴, R. Henrik Nilsson⁵, Falk Hildebrand⁶,
Peer Bork⁶, Kessy Abarenkov¹

Map of nuclear ribosomal

Metagenomics (or environmental genomics) is the study of genetic material recovered directly from environmental samples.

Who? Metabarcoding approach :
targeted genes (taxonomic barcodes or functional markers)

Fungal barcode marker sequencing to produce a profile of diversity from natural samples

Active organisms: Metatranscriptomics:
Living and active organisms and functional interactions: environmental RNA

Focus on RNA, in particular fungal transcripts (only on the expressed genes)



Metagenomics and NGS

Putative roles: DNA metagenomics ("shotgun")
"Shotgun" high-throughput sequencing (e.g. 454 pyrosequencing or Illumina) to get a maximum of genes from all organisms of the sampled communities



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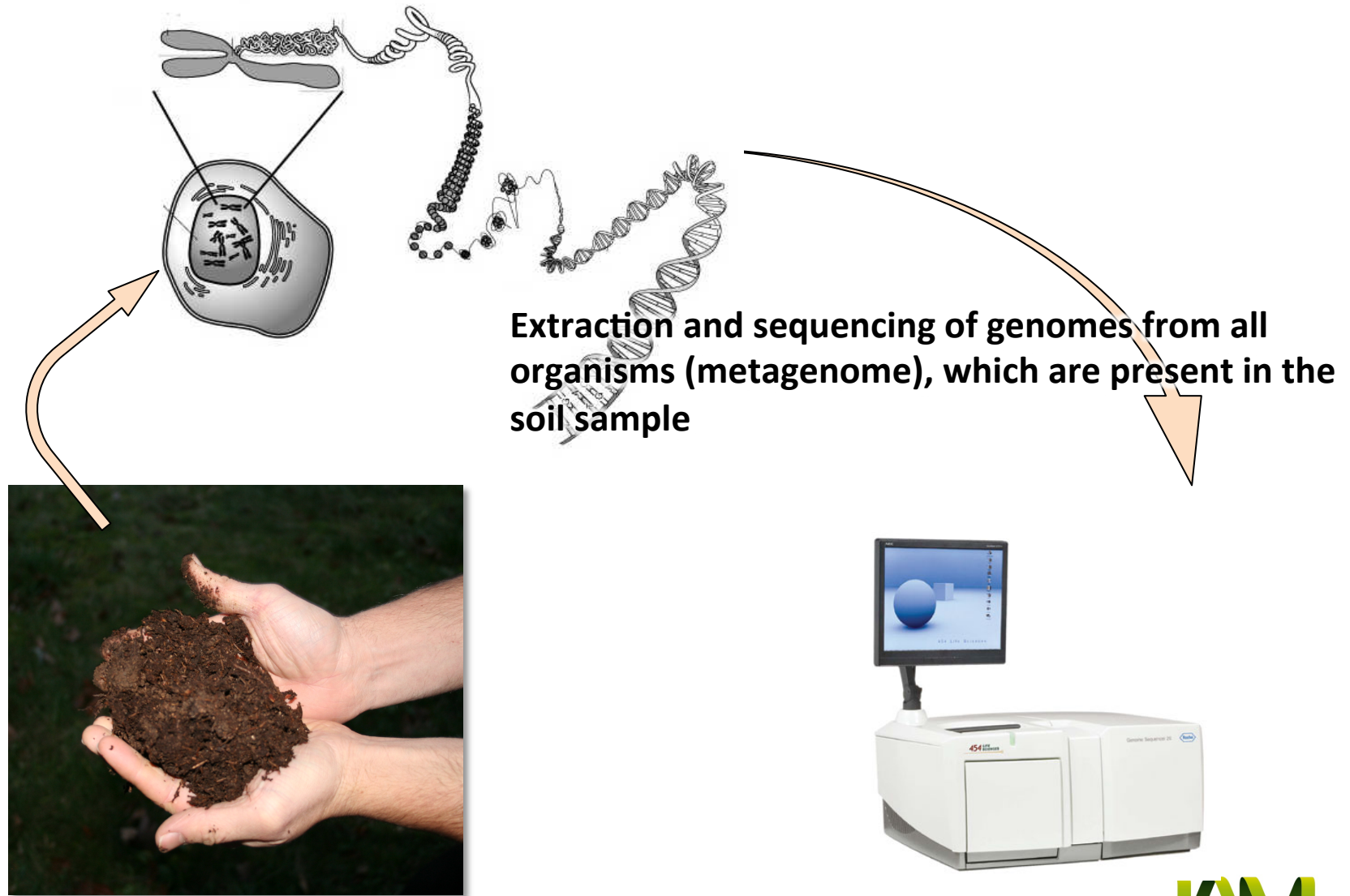
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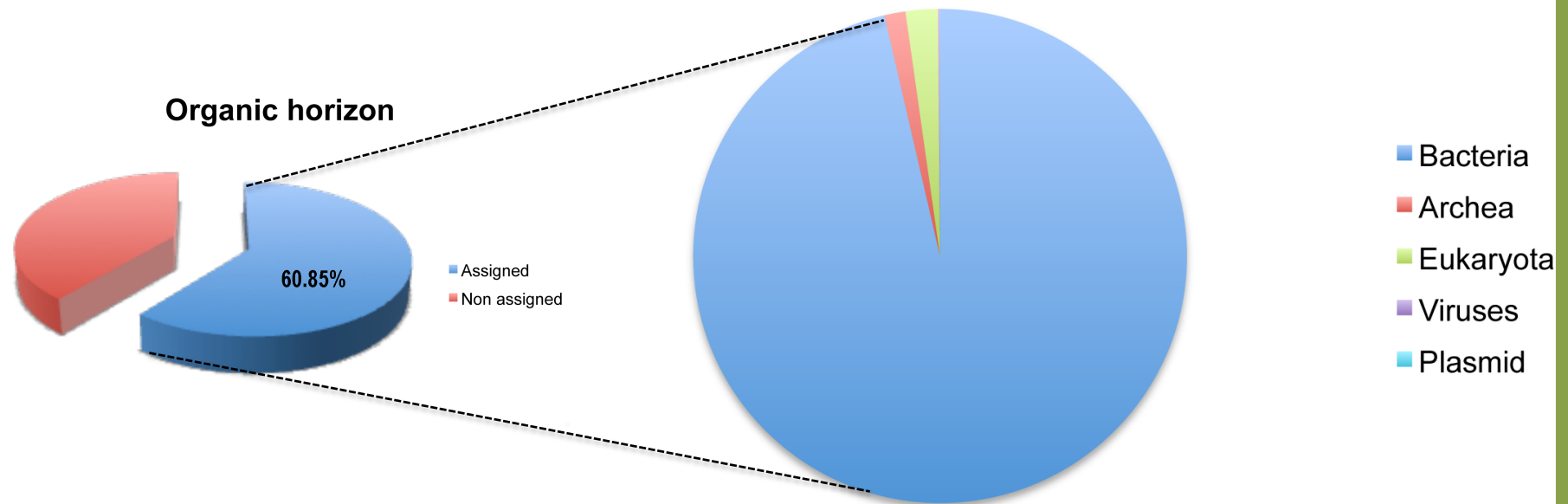


Forest soil metagenomics



Forest soil metagenomics

Shotgun Environmental 454 Sequencing



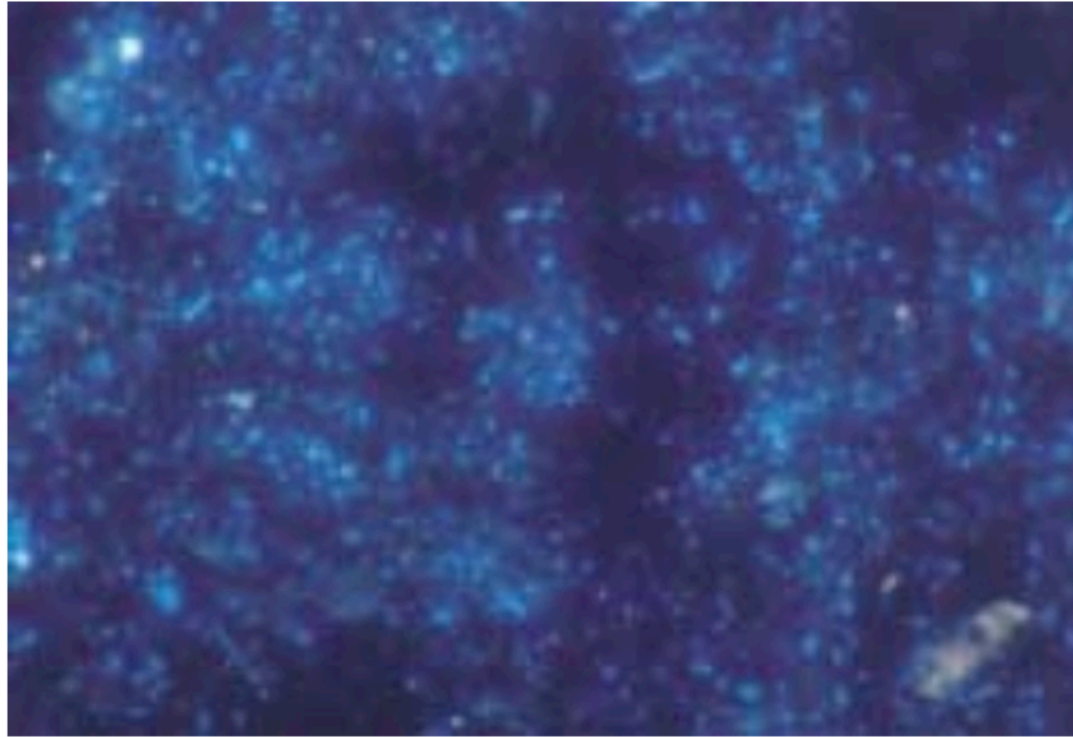
	Protein based		16s	
Archaea	1.23%	(4579)	0.00%	(0)
Bacteria	91.32%	(338916)	80.40%	(201)
Eukaryota	1.58%	(5851)	0.00%	(0)
Virus	0.00%	(0)	0.00%	(0)
Other	5.87%	(21783)	19.60%	(49)

→ Fungi :0,4% of total reads

Most of the reads assigned belong to bacteria [Bacteria/Fungi ratio confirmed by qPCR]

Large % of orphan sequences

The soil... A bacterial world! How study the fungal functions?



Current Opinion in Microbiology

Epifluorescence micrograph of soil microorganisms stained with 4',6-diamidino-2-phenylindole (DAPI). The total bacterial count was 4.2×10^{10} cells gram^{-1} soil (dry weight) by fluorescent microscopy, and 4.2×10^6 colony-forming units gram^{-1} soil (dry weight) by plating.

Vigdis Torsvik and Lise Øvreås
Current Opinion in Microbiology 2002, 5:240–245

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Metagenomics and NGS

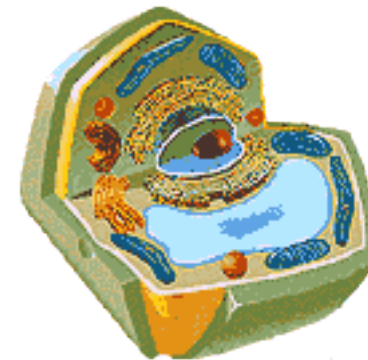
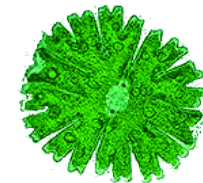
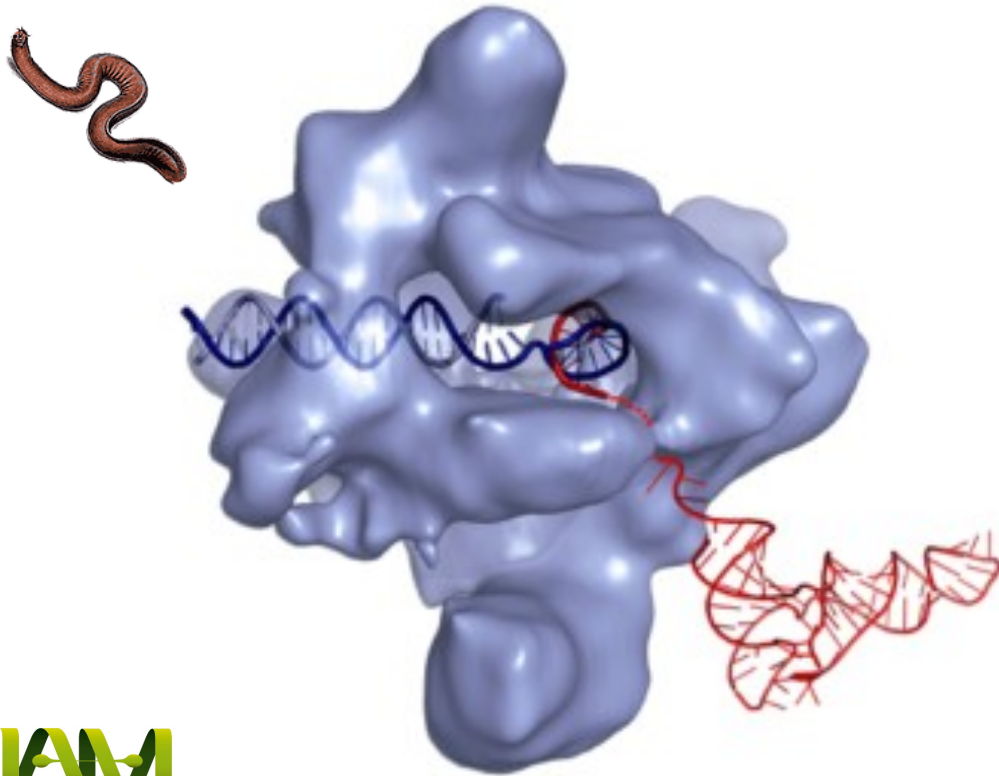


Putative roles: DNA metagenomics ("shotgun")
"Shotgun" high-throughput sequencing (e.g. 454
pyrosequencing or Illumina) to get a maximum of genes
from all organisms of the sampled communities



Eukaryotic and fungal metagenomic : focus on poly A+ transcripts = “Metatranscriptomic” approaches

Use only polyA+ transcripts and “concentrate” eukaryotic transcripts (only on the expressed genes).
Investigate the functioning of the ecosystem and the role of fungal species in soil forest



The poly A+ transcripts include
mRNA, microRNA and snoRNA
generated by RNA polymerase II



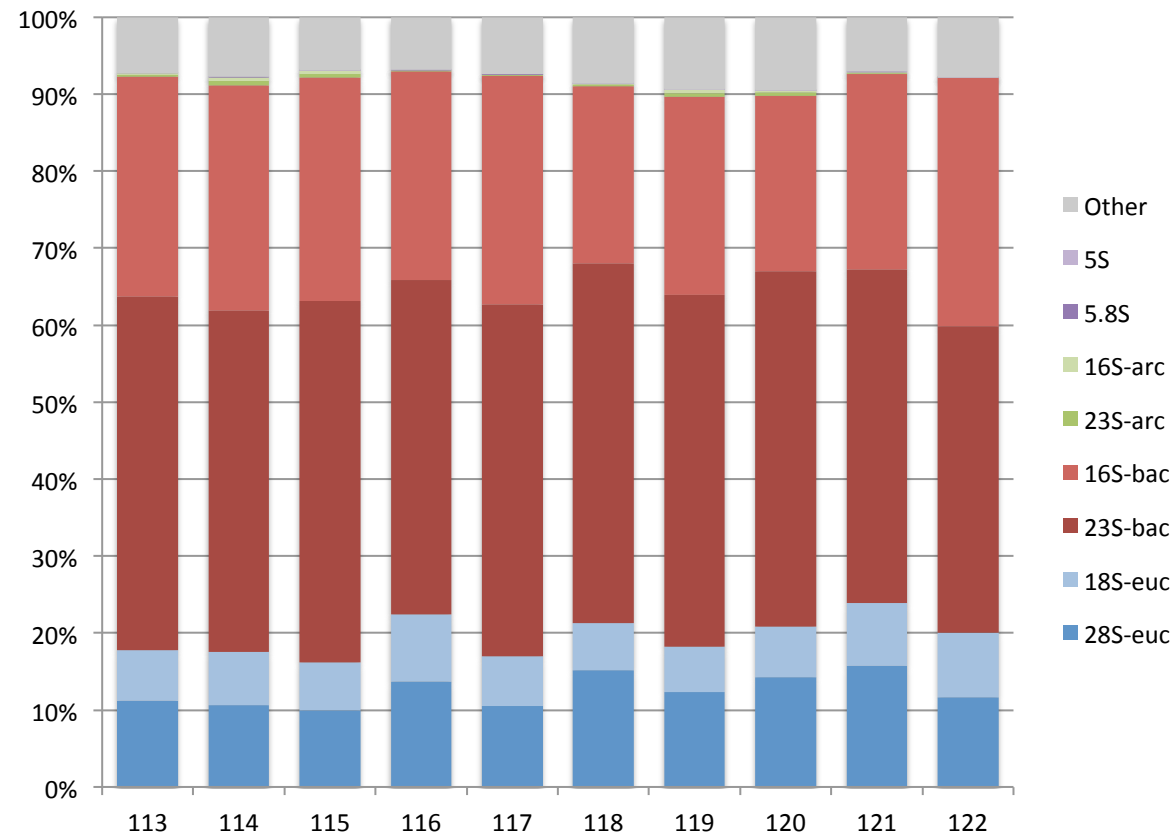
The Community Sequencing Program 2012

Metatranscriptomics of Forest Soil Ecosystems (coord. F. Martin)

Proposal ID: CSP # 570

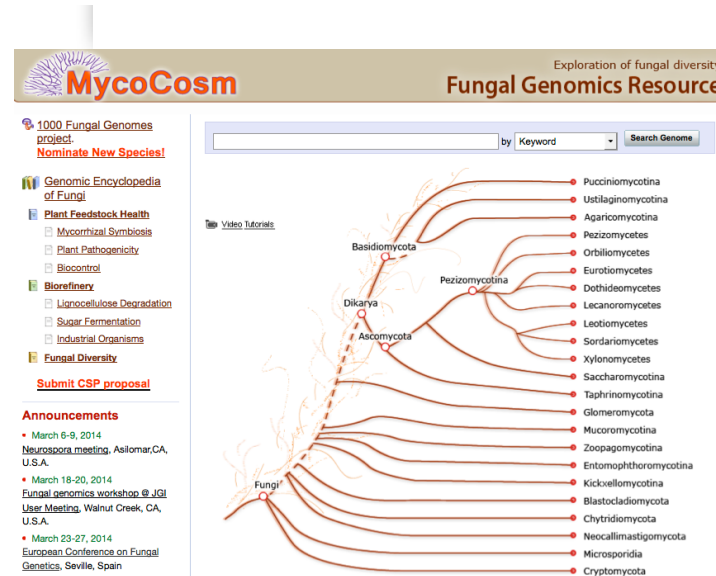
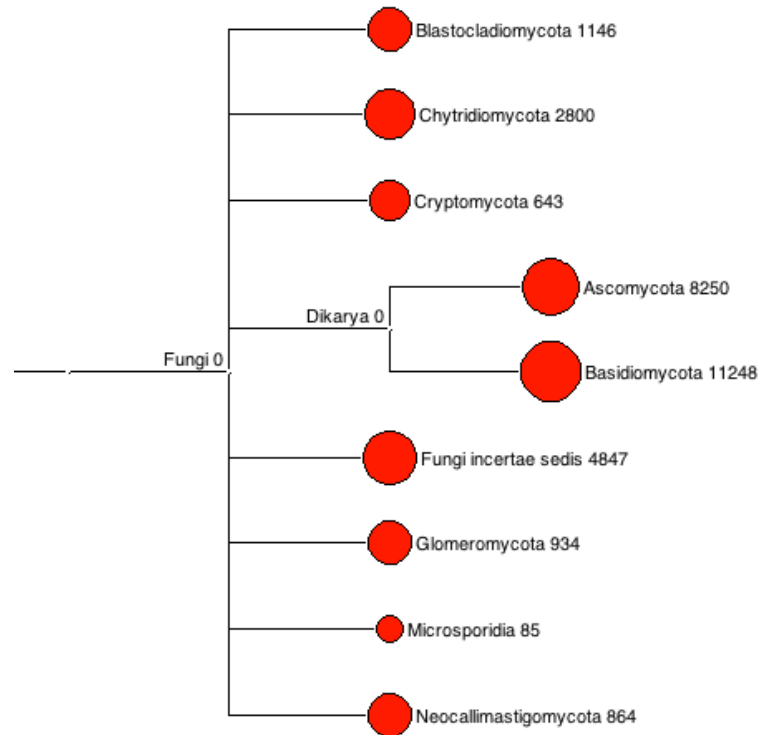
Eight laboratories in the world (11 sites)

**Analysis of rRNA reads (SortMeRNA) extracted from forest soils:
Beech and Spruce forests (spring and autumn) - Illumina sequencing –
(Pilot study: ANR Eumetasol)**



About 20% of sequences corresponded to active
EuK (only 1.6 % of genomic DNA)

Site Amance (54): Oak, Spring (Org) Illumina sequencing of soil mRNA (polyA)



Reads = sequenced EuK mRNA
Blast on Mycocosm (JGI)

Pilot analysis (Miseq):
14M reads were assembled into 72226 contigs,
median length - 238bp (**only on mRNA**)

31205 (43.2%) of contigs have hits to mycocosm
proteins by blastx at Evalue threshold 1e-05



In course: assignment of reads on fungal genomic database (JGI 1000fungalgеноmе project)



THE FUNGAL GENOMICS RESOURCE

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Please help us to improve the JGI Genome Portal. Your feedback is very important to us.
[Click here](#) to take the Annual JGI Genome Portal 2015 survey.

1000 Fungal Genomes project.
[Nominate New Species!](#)

Genomic Encyclopedia of Fungi

- Plant Feedstock Health**
 - [Mycorrhizal Symbiosis](#)
 - [Plant Pathogenicity](#)
 - [Biocontrol](#)
- Biorefinery**
 - [Lignocellulose Degradation](#)
 - [Sugar Fermentation](#)
 - [Industrial Organisms](#)
- Fungal Diversity**

[Submit CSP proposal](#)

Announcements

March 17-22, 2015
[Fungal Genetics Conference at Asilomar](#), Pacific Grove, CA, U.S.A.

March 23-26, 2015
[Fungal genomics workshop @ JGI User Meeting](#), Walnut Creek, CA, U.S.A.

August 1-5, 2015
[Americal Phytopathological Society annual meeting](#), Pasadena, CA, U.S.A.

Releases

- May 22, 2015
[Hydnum rufescens UP504 v2.0](#)
- May 22, 2015
[Thelephora ganbajun P2 v1.0](#)
- May 22, 2015
[Xerocomus badius 84.06 v1.0](#)
- May 18, 2015
[Hyalopezis blepharistoma ATCC 48560 v1.0](#)
- May 15, 2015
[Sympodiomyces attinorun NRRL Y-27639 v1.0](#)

[Video Tutorials](#)

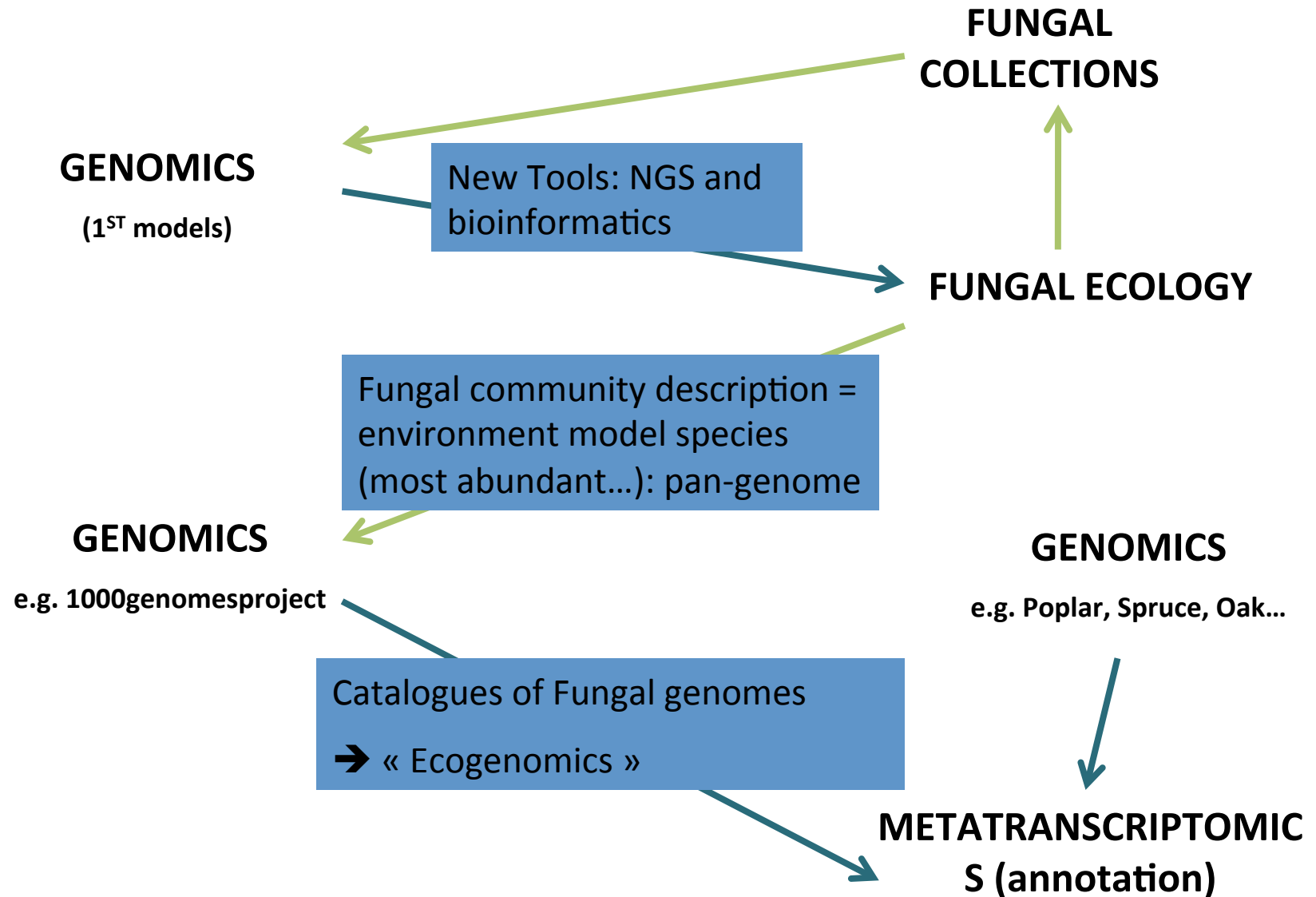
- Pucciniomycotina
- Ustilaginomycotina
- Agaricomycotina
- Pezizomycetes
- Orbiliomycetes
- Eurotiomycetes
- Dothideomycetes
- Lecanoromycetes
- Leotiomycetes
- Sordariomycetes
- Xylonomycetes
- Saccharomycotina
- Taphrinomycotina
- Glomeromycota
- Mucoromycotina
- Zoopagomycotina
- Entomophthoromycotina
- Kickxellomycotina
- Blastocladiomycota
- Chytridiomycota
- Neocallimastigomycota
- Microsporidia
- Cryptomycota

To use the tree navigation click a branch name and select an organism from the list.

For MycoCosm, please cite: Grigoriev IV, Nikitin R, Haridas S, Kuo A, Ohm R, Otilar R, Riley R, Salamov A, Zhao X, Korzeniewski F, Smirnova T, Nordberg H, Dubchak I, Shabalov I. (2014) [MycoCosm portal: gearing up for 1000 fungal genomes](#). Nucleic Acids Res. 42(1):D699-704.

For JGI Fungal Program, please cite: [Fueling the future with fungal genomics](#). Grigoriev IV, Cullen D, Goodwin SB, Hibbett D, Jeffries TW, Kubicek CP, Kuske C, Magnuson JK, Martin F, Spatafora JW, Tsang A, Baker SE. (2011) , Mycology. 2(3):192-209.

Analysis of Amance/Champenoux site (36 samples):
3.439.190.128 reads (Hiseq) from 36 samples, or 95.5 million reads on average per sample





UE BACCARA project

INRA, Nancy

**A. COINCE
B. MARCAIS
M. BUEE**

CSIC, Madrid

A. RINCON

Collection of soil samples

INRA, Bordeaux France

SLU, Uppsala Sweden

CEMAGREF, Grenoble France

UNITUS, Viterbo Italy

FRI, Raszyn Poland



INTERACTIONS
ARBRES-MICROORGANISMES



**UNIVERSITÉ
DE LORRAINE**

ANR Eumetasol project

INRA, Nancy

**M. BUEE
F. MARTIN
E. SENTOSA**

Univ Lyon

**P. Luis
R. Marmesse**

JGI CSP 2012

INRA, Nancy

**F. MARTIN
E. SENTOSA
A. KOHLER
M. BUEE**

JGI collaborators





THANK YOU FOR YOUR ATTENTION