Fungal Diversity

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BRCAS
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Lecture objective

- Fungal diversity – a description
- Their impact on ecology
- How do we study them? Some case studies.

Recommended text

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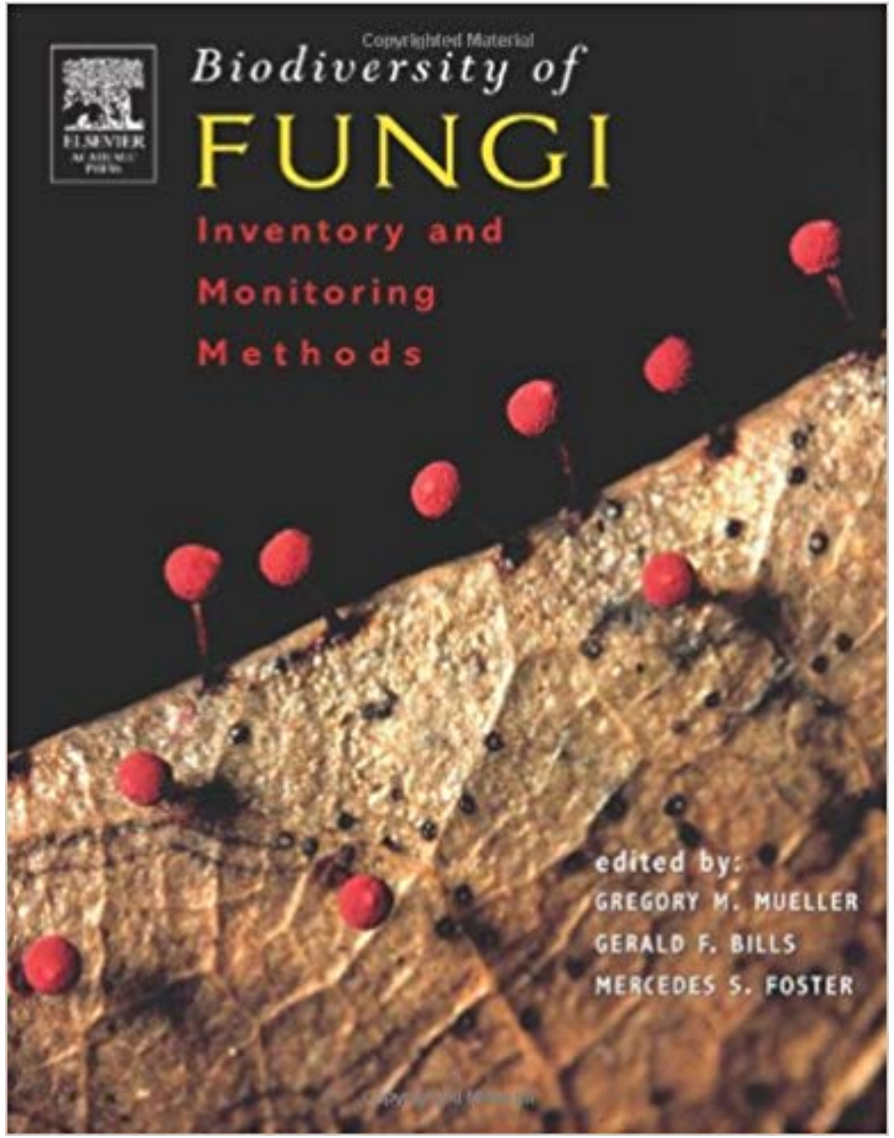
Royal Botanic Gardens

Kew

State of the World's Fungi

2018

https://www.kew.org/state-of-the-worlds-fungi



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Biodiversity of

FUNGI

Inventory and Monitoring Methods

edited by:

GREGORY M. MUELLER

GERALD F. BILLS

MERCEDES S. FOSTER

Video references

National Geographic - Kingdom Of The Forest - Fungi
https://www.youtube.com/watch?v=zb4y40kFhL4

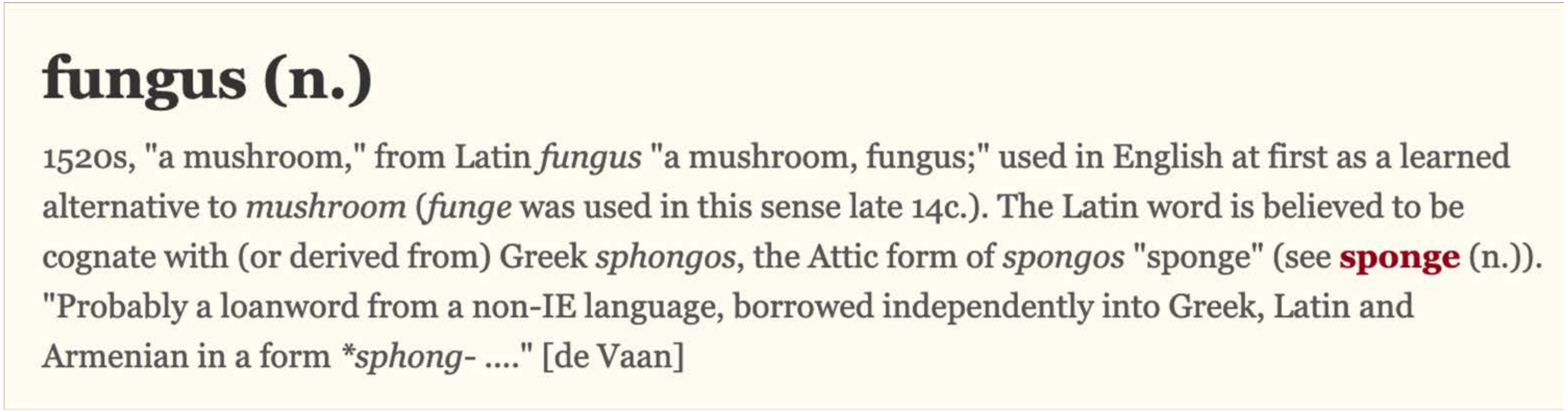
Fungi matter
https://youtu.be/H9KLf-URS1g

The Wonderful Wolrd Of Fungi Documentary 2018
https://www.youtube.comv=H9KLf-URS1g

Lecture outline

General descriptions of fungi
The ”good”
The “bad”
Methods of studying fungi
Fungal genomics
Case studies

General descriptions of fungi



fungus (n.)

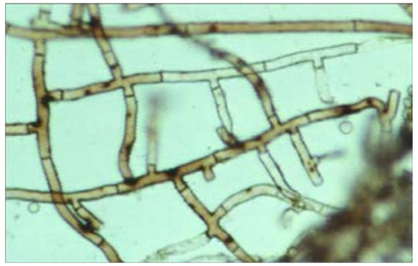
1520s, "a mushroom," from Latin *fungus* "a mushroom, fungus;" used in English at first as a learned alternative to *mushroom* (*funge* was used in this sense late 14c.). The Latin word is believed to be cognate with (or derived from) Greek *sphongos*, the Attic form of *spongos* "sponge" (see **sponge** (n.)). "Probably a loanword from a non-IE language, borrowed independently into Greek, Latin and Armenian in a form **sphong-* ...." [de Vaan]

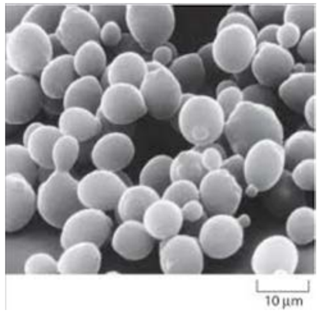
“The concept of a ‘‘fungus’’ has developed over many years, and the historic definition of fungi as nonphotosynthetic plants has been shown to be both too simplistic and phylogenetically inaccurate"

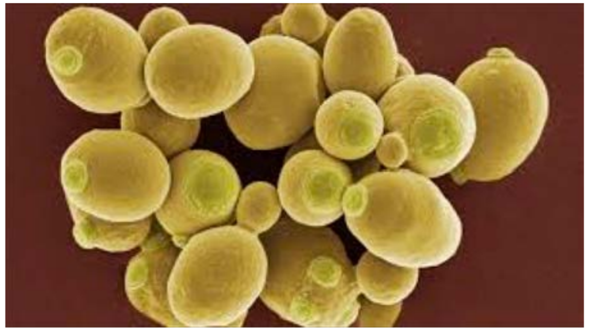
Bridge *et al* (2005) Advances in Botanical Research

https://www.etymonline.com/word/fungus

Fungi are eukaryotes







General Characteristics of Fungi

- Cell wall present, composed of cellulose and/or chitin.
- Food storage - generally in the form of lipids and glycogen.
- Eukaryotes - true nucleus and other organelles present.
- Most fungi require water and oxygen (no obligate anaerobes).
- Fungi grow in almost every habitat imaginable, as long as there is some type of organic matter present and the environment is not too extreme.
- Diverse group, number of described species is **~70,000** (estimated 5.1 million species total).

Blackwell 2011

Fungal systematics – introduction

- Phyla within the fungi are defined primarily on the basis of life cycles, mode of reproduction, and cell wall and septum structure.

- One important feature of the fungi is that many have life cycles that consist of two or more stages. These are primarily differentiated by the mode of reproduction and may be asexual, where growth and reproduction is by mitosis, or sexual, where reproduction involves meiosis.

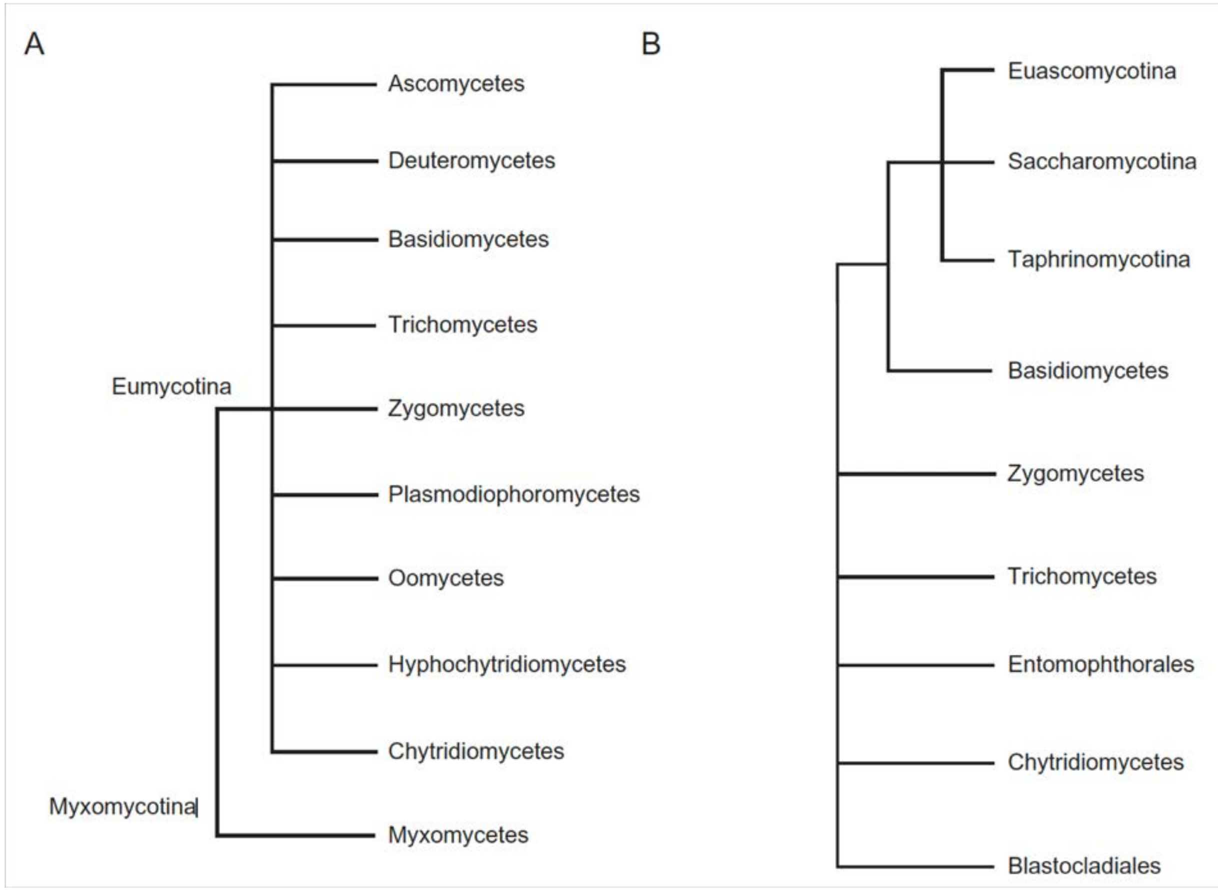
- A fungus either producing asexual diaspores or no spores at all is termed ***anamorphic*** or imperfect, and the sexual state when present is termed the ***teleomorph*** or the perfect state. The mode of **sexual reproduction** is a major characteristic for assigning individual fungi to phyla, and a fungus that is known only from its vegetative state cannot be easily placed in a phylum using traditional morphological analysis. Historically such fungi were placed in an additional phylum, the "**Deuteromycota**." This placement, however, suggests a phylogenetic relationship between vegetative fungi that has been demonstrated to be incorrect.

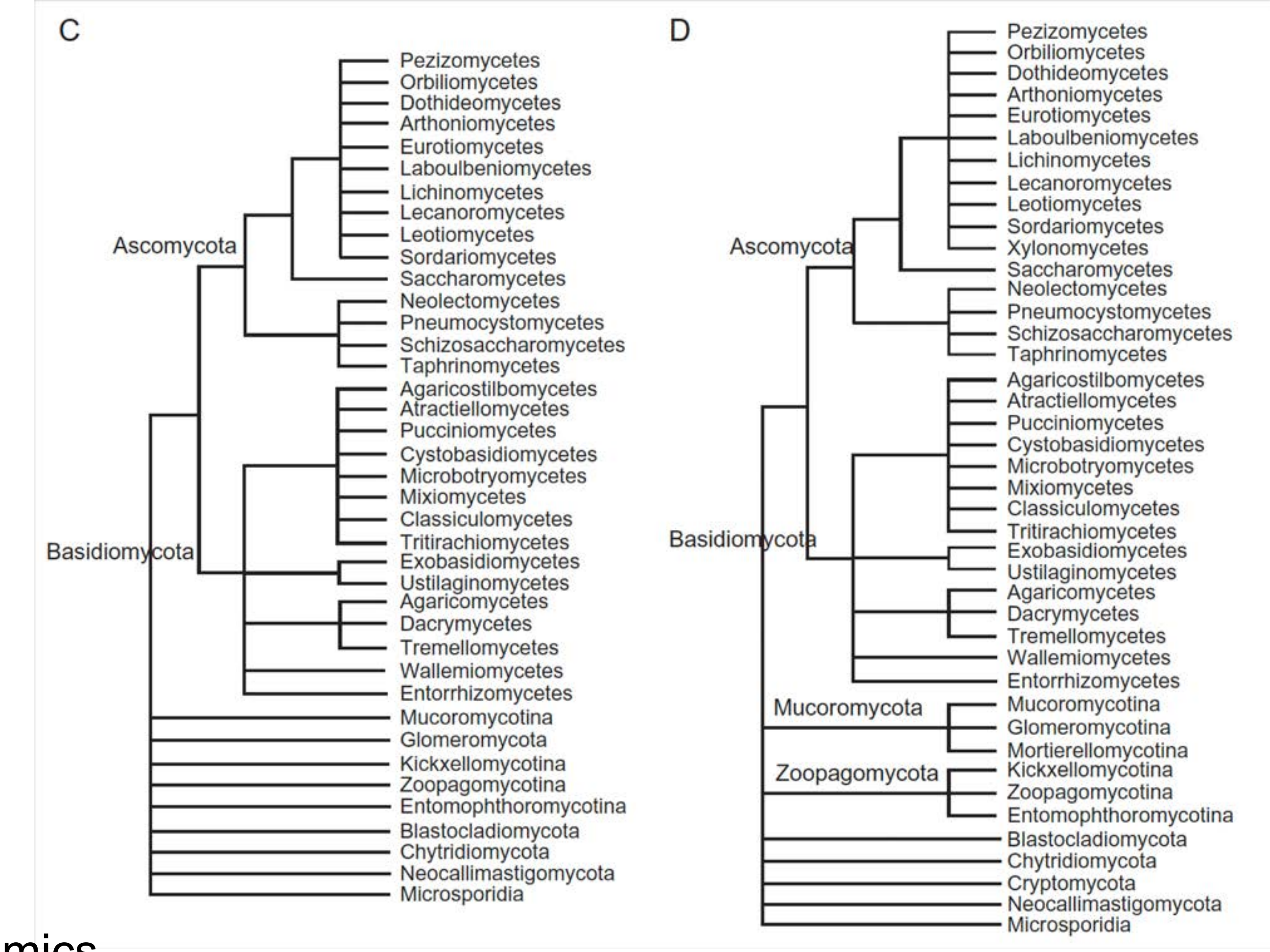
- When anamorph and teleomorph forms both exist and occur separately, **there are generally dual names**, with **one name being used for the anamorph and a different name being used for the teleomorph**. In some cases, the morphology of the anamorph can be very basic, and so apparently similar anamorphic forms may produce different and sometimes unrelated teleomorphs. This occurs commonly in the Ascomycetes, and examples of common anamorphic genera with more than one genus of teleomorph include *Phoma, Aspergillus*, and *Paecilomyces*.

Bridge *et al* (2005) Advances in Botanical Research

Fungal systematics – a history

- Traditional Fungal Systematics Relying on Morphological or Other Phenotypic Characters (1729–1864)
- Fungal Systematics Using Physiological and Biochemical Characters (1865–1989)
- Fungal Phylogeny Based on One or a Few Genes (1990–2005)
- **Fungal Phylogenomic Analysis (2006–Present)**



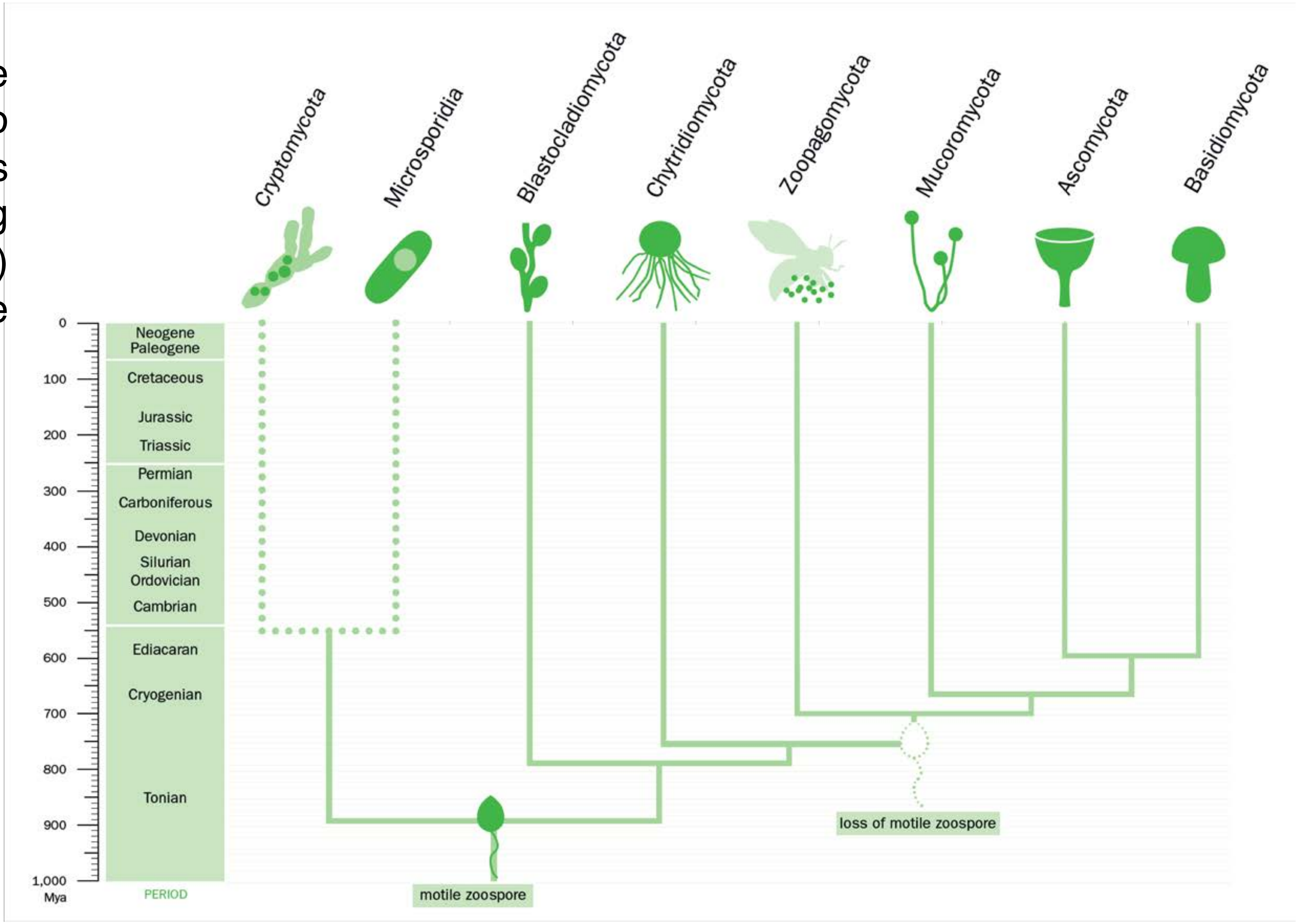


Zhang *et al* (2017) Fungal Phylogenetics and Phylogenomics

Fungi phylogeny

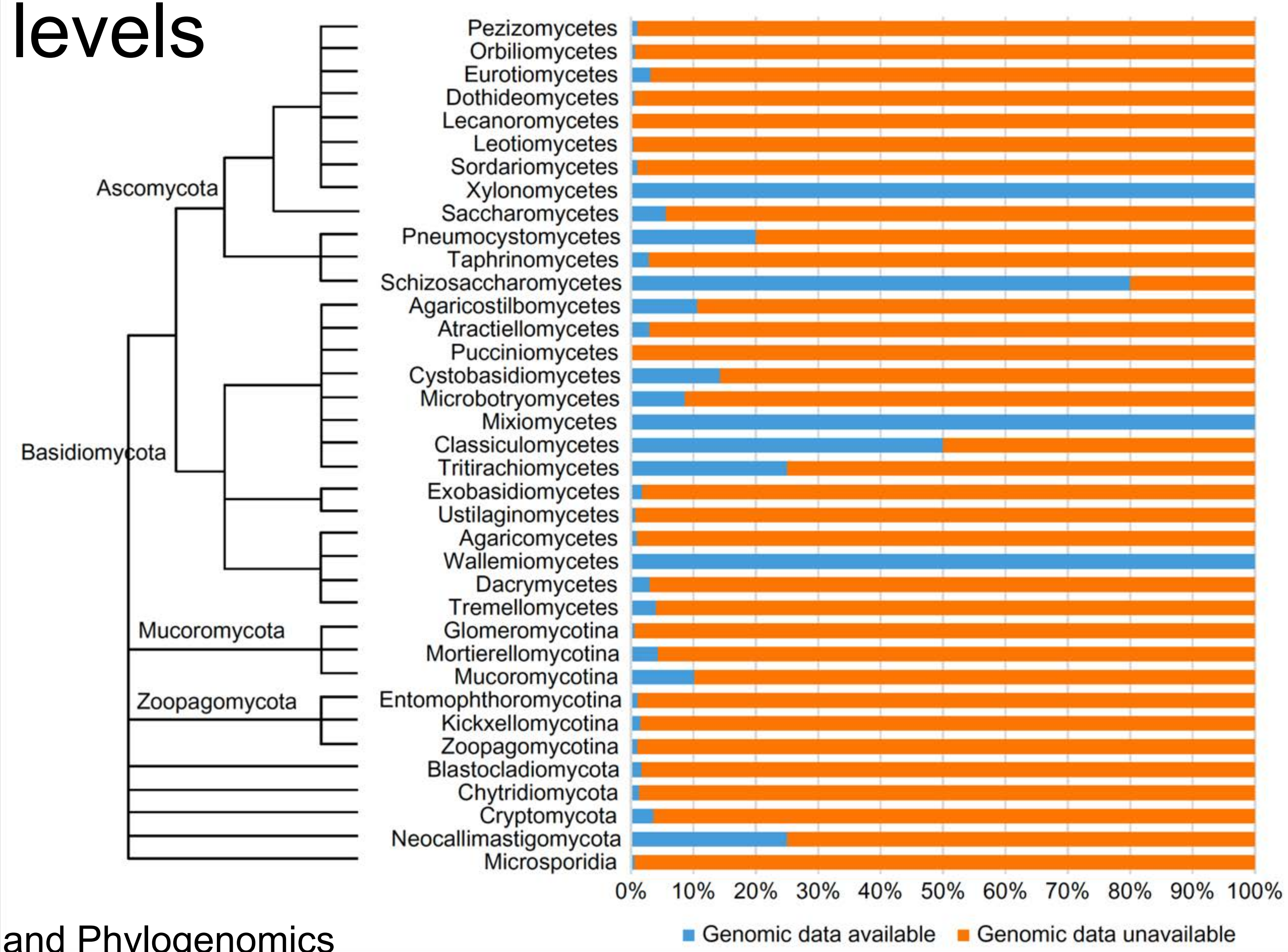
The earliest fungi are thought to have evolved around **1 billion years ago** and to have been simple, single-celled organisms living in water and reproducing using motile asexual spores (zoospores) propelled by a posterior whip-like structure called the flagellum

The evolution of the two fungal groups that contain species capable of forming highly complex spore-bearing structures (i.e. Ascomycota and Basidiomycota) is considered to have occurred around 600–700 Mya. Together they contain the vast majority of known fungal species diversity – **c. 90,000 species in Ascomycota and c. 50,000 species in Basidiomycota**



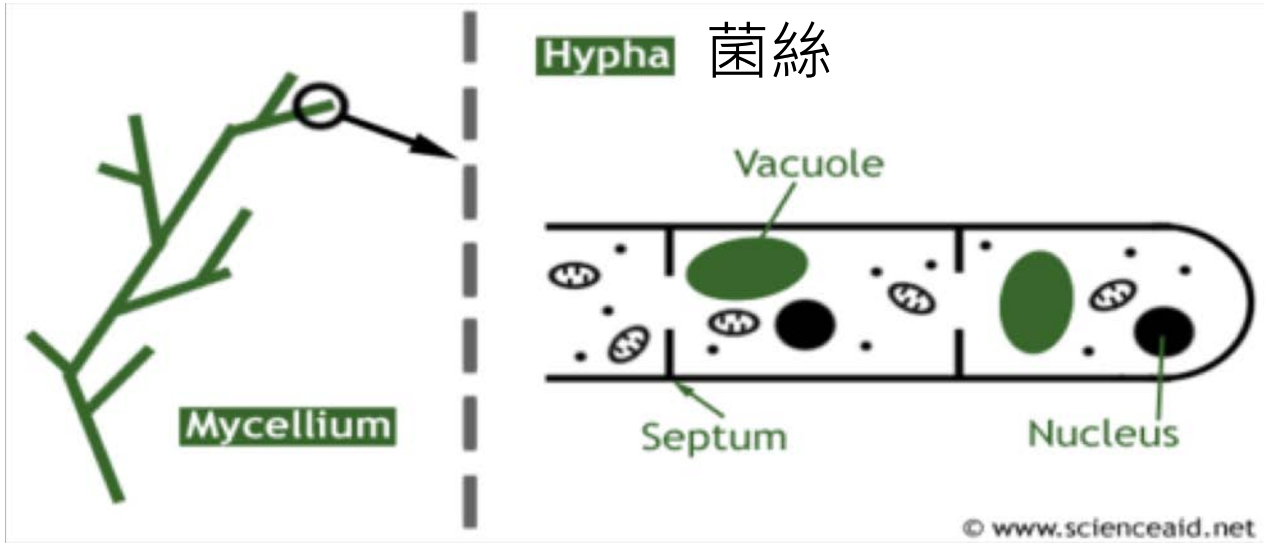
Relative proportion of fungal taxa with released genomes among published taxa at the class or higher levels

- Despite advances in phylogenomics, many fungal groups are still woefully undersampled
- A final note of caution needs to be made about horizontal gene transfer (HGT), the bane of multigene phylogenetics



Zhang *et al* (2017) Fungal Phylogenetics and Phylogenomics

Fungi structure

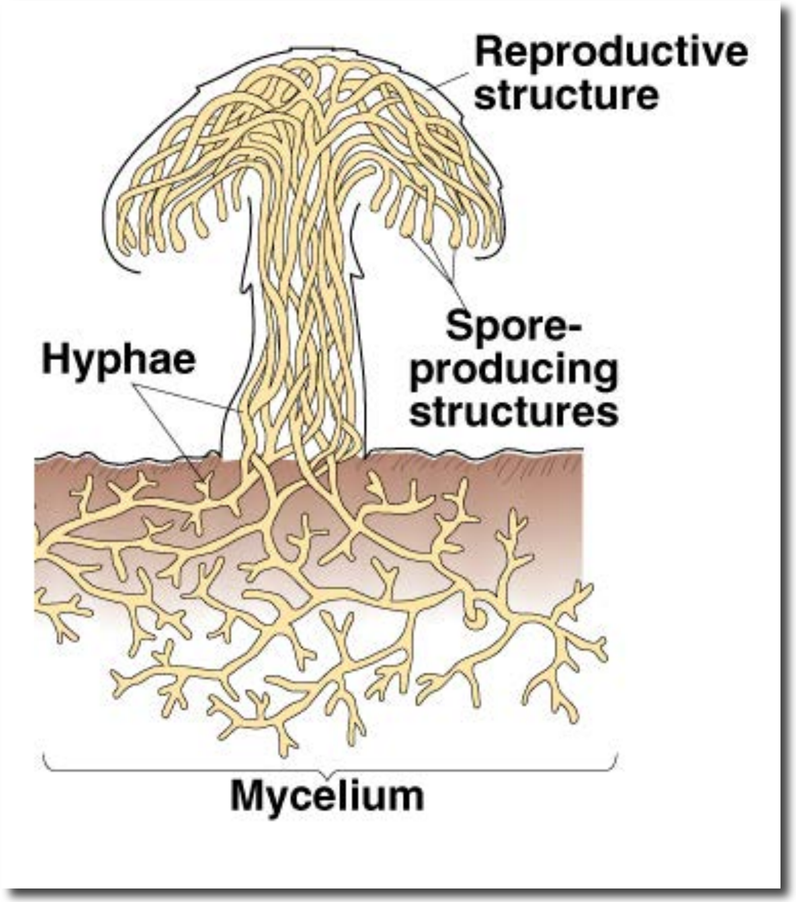


sclerotium = hardened mass of mycelium that generally serves as an overwintering stage.
multicellular, such as mycelial cords, rhizomorphs, and fruit bodies (mushrooms)

Body form

unicellular filamentous (tube-like strands called hypha (singular) or **hyphae** (plural)

mycelium = aggregate of hyphae



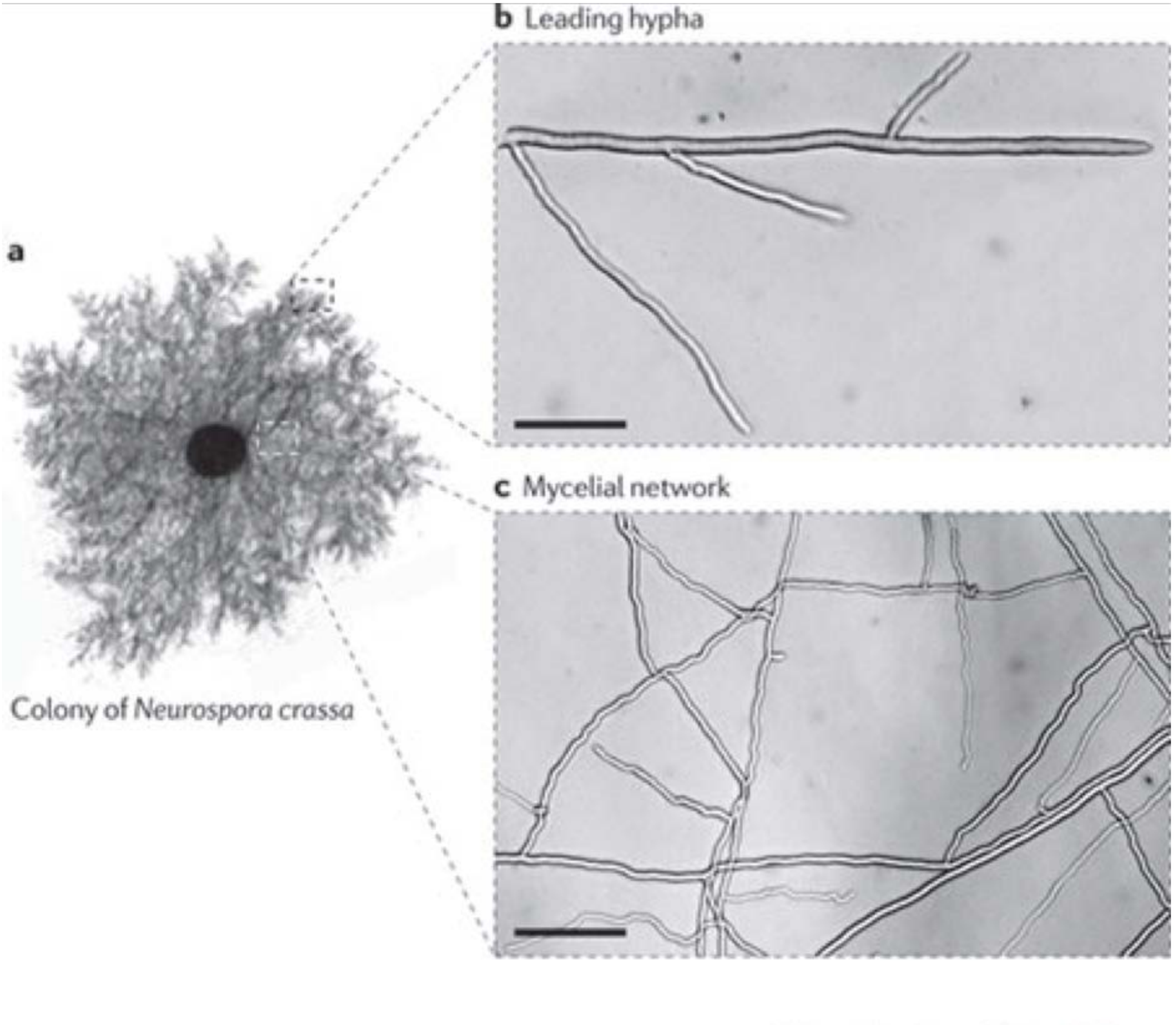
Fungi are heterotrophs (‘other food’)

- i.e., acquire nutrients by absorption

Credit: UWA 2005

- Three main types:
  - **Saprophytes** or saprobes - absorb nutrients from dead organic material
  - **Parasitic** fungi - absorb nutrients from cells of living hosts; some are pathogenic
  - **Mutualistic** fungi - absorb nutrients from a host, but reciprocate to benefit the host

Hyphal growth



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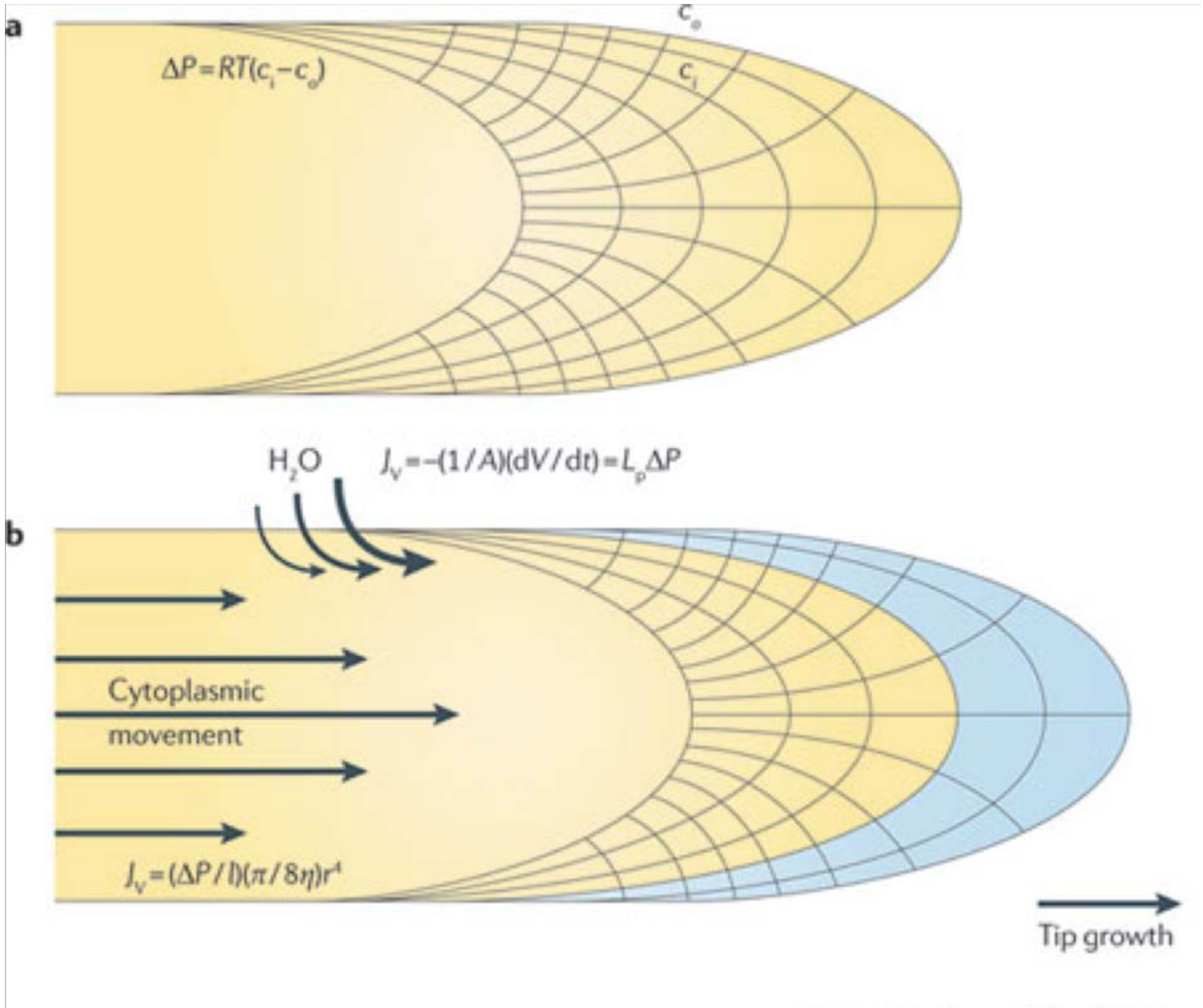

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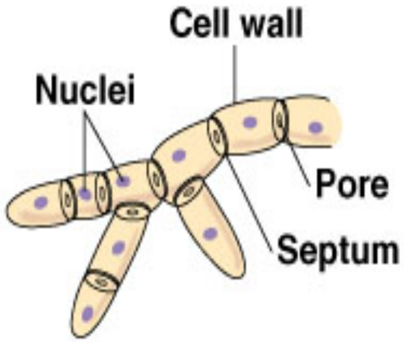
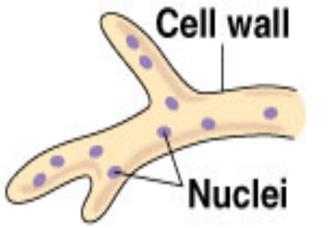
is of the order of 5–10 μ m in diameter, and their immediate effect on the environment is restricted to a few micrometers on each side of these hyphae

Lew et al., (2011)

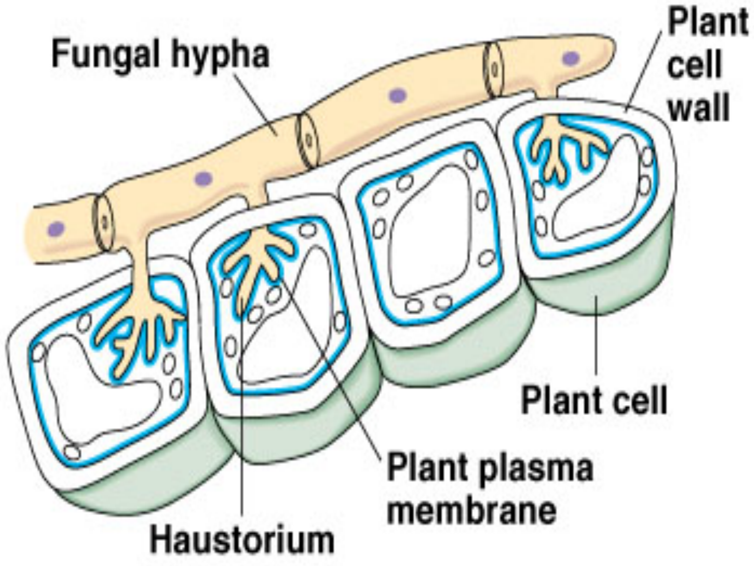
Hyphae modifications



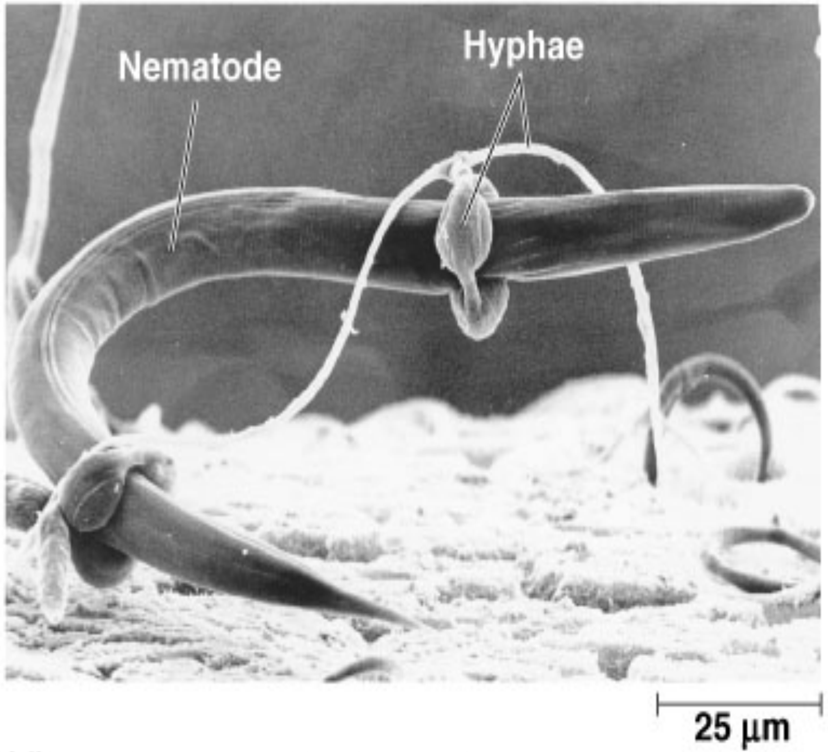
(a) Septate hypha



(b) Coenocytic hypha



(c) Haustoria

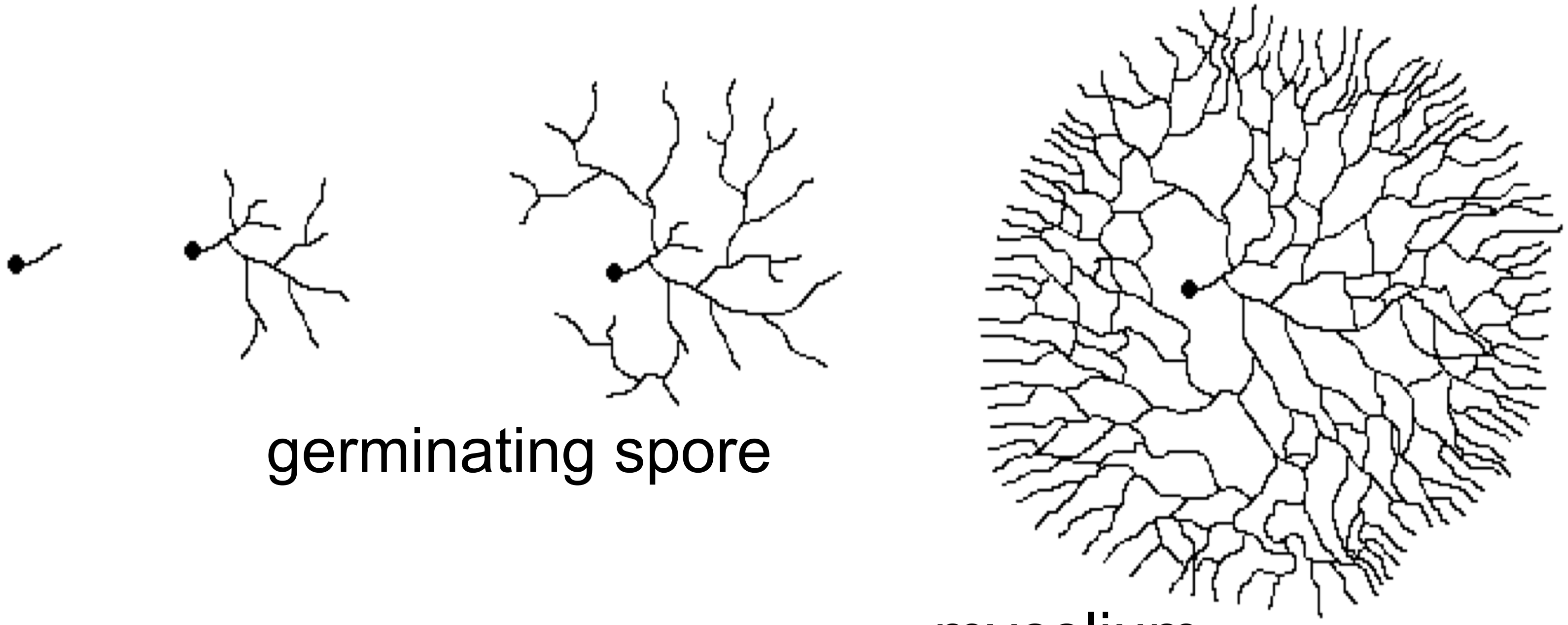


(d) Hyphae adapted for trapping and killing prey

Spores 胞子

- Spores can arise both from sex (harsh condition?) or asexual (favourable condition?) phases
- Purpose of Spores
  - Allows the fungus to move to new food source.
  - Resistant stage - allows fungus to survive periods of adversity.
  - Means of introducing new genetic combinations into a population
- Formed:
  - Directly on hyphae
  - Inside sporangia
  - Fruiting bodies

Hyphal growth from spore



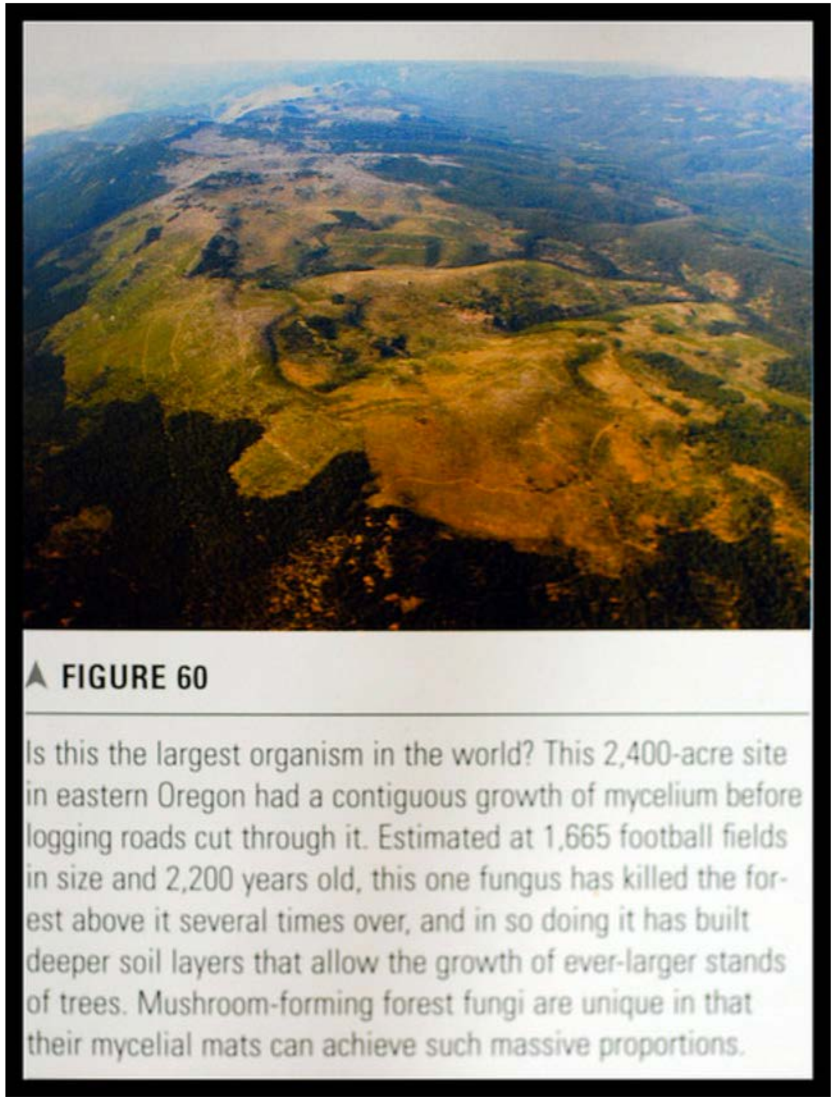
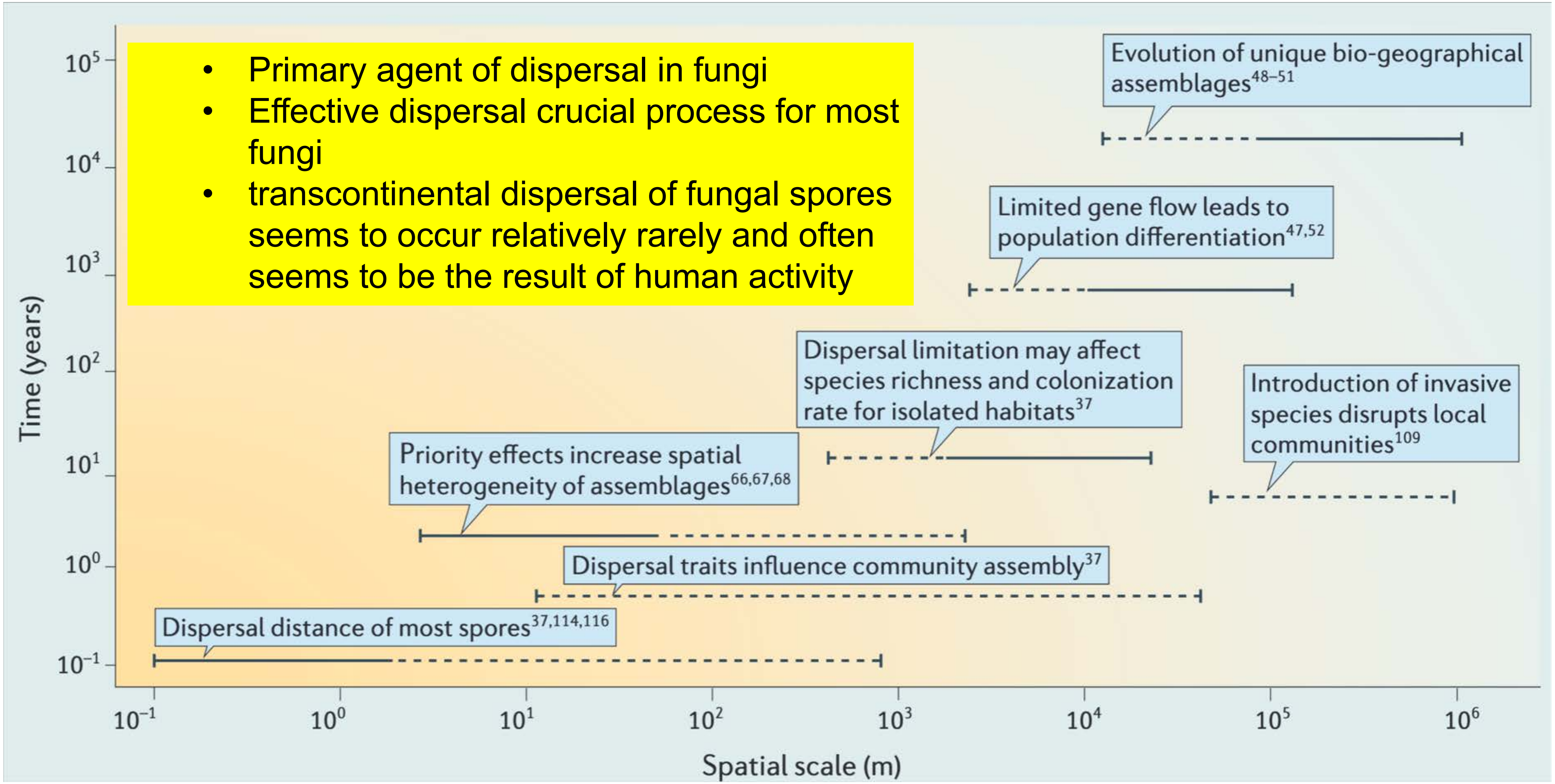


FIGURE 60

Is this the largest organism in the world? This 2,400-acre site in eastern Oregon had a contiguous growth of mycelium before logging roads cut through it. Estimated at 1,665 football fields in size and 2,200 years old, this one fungus has killed the forest above it several times over, and in so doing it has built deeper soil layers that allow the growth of ever-larger stands of trees. Mushroom-forming forest fungi are unique in that their mycelial mats can achieve such massive proportions.

Spore dispersal

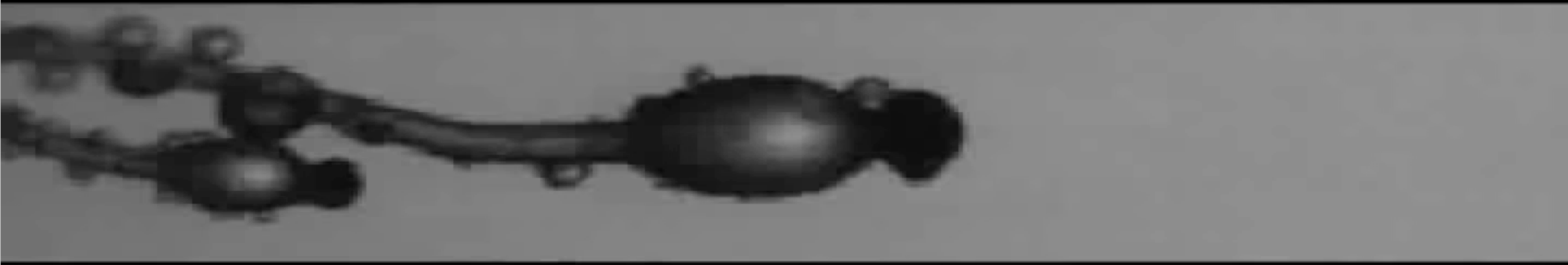
- Primary agent of dispersal in fungi
- Effective dispersal crucial process for most fungi
- transcontinental dispersal of fungal spores seems to occur relatively rarely and often seems to be the result of human activity



Peay *et al* (2016) Nature Reviews Microbiology

Fungi are everywhere

Photo credit: 張道弘



Rifle acceleration = 9,395G

Shotgun acceleration = 9,313G

Pilobolus acceleration = 20000G!!!!!

Division Ascomycota 子囊菌门
: sac fungi produce sexual spores in saclike asci

Sexual Reproduction – asci (sing. = ascus)

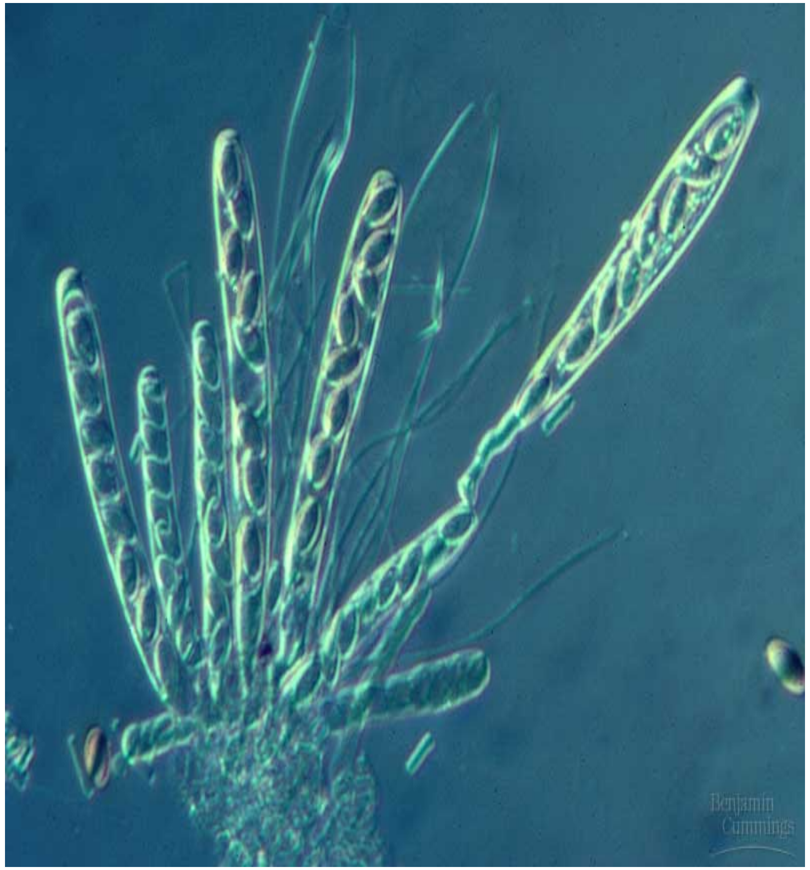
Asexual reproduction is common

Cup fungi, morels, truffles

Important plant parasites & saprobes

Yeast - *Saccharomyces*

Decomposers, pathogens, and found in most lichens



A cluster of asci with spores inside

Basidiomycota – "club fungi"

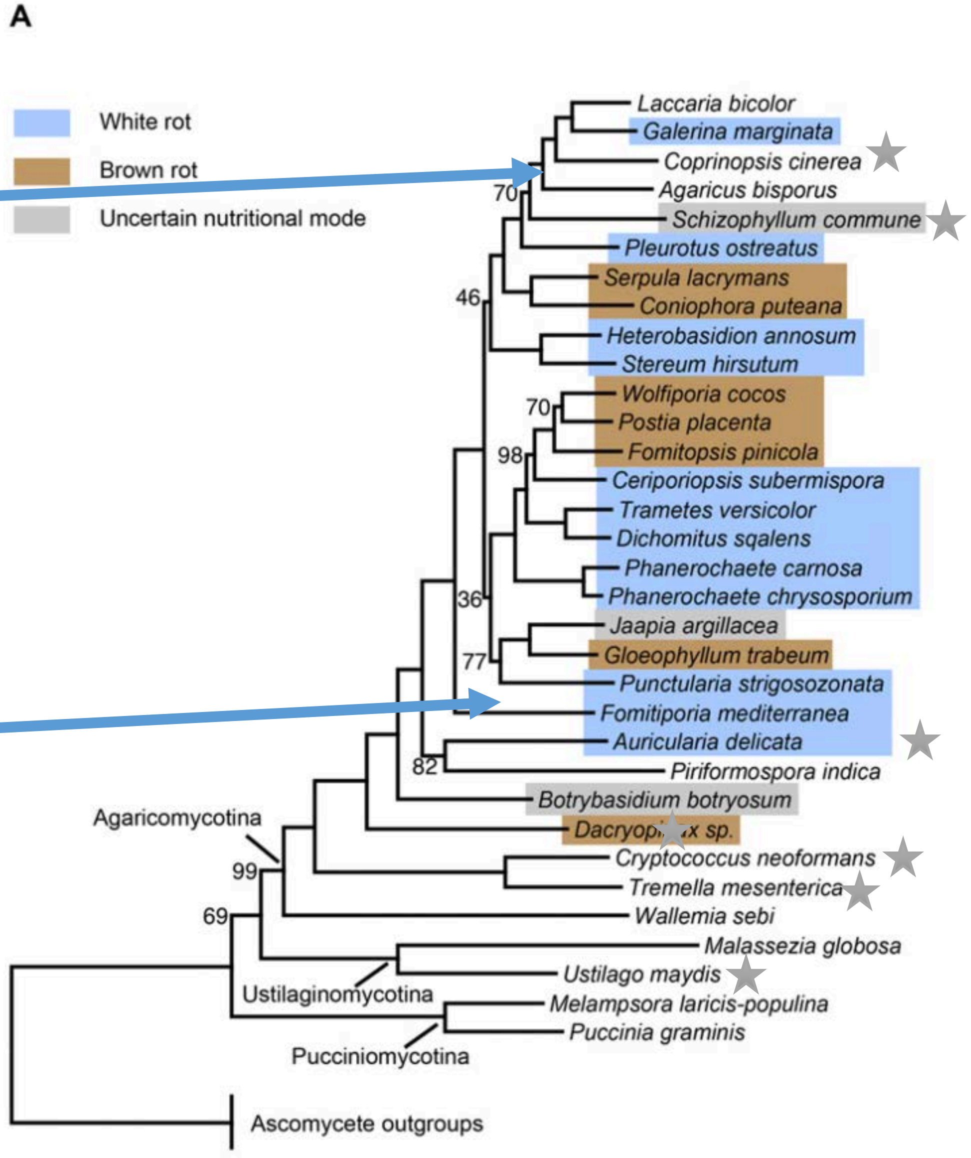
- Named after transient diploid stage: basidium
- Important decomposers of wood / plant material
- Include:
  - Mycorrhiza-forming mutualists
  - Mushroom-forming fungi
  - Plant parasites e.g. rusts and smuts
- Characterised by dikaryotic mycelium that reproduces sexually via basidiocarps

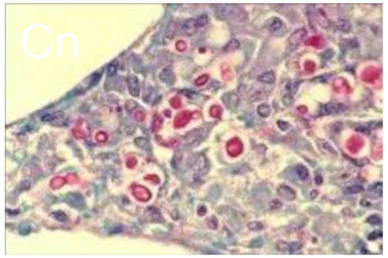
- Sexual Reproduction – basidia
- Asexual reprod – not so common
- Long-lived **dikaryotic** mycelia
- Rusts & smuts –plant parasites
- Mushrooms, polypores, puffballs, boletes, bird's nest fungi
- Enzymes decompose wood, leaves, and other organic materials
- Decomposers, pathogens, and some form mycorrhizal associations with plants

Phylogeny of basidiomycetes 擔子菌綱

Mycena

Phellinus noxius

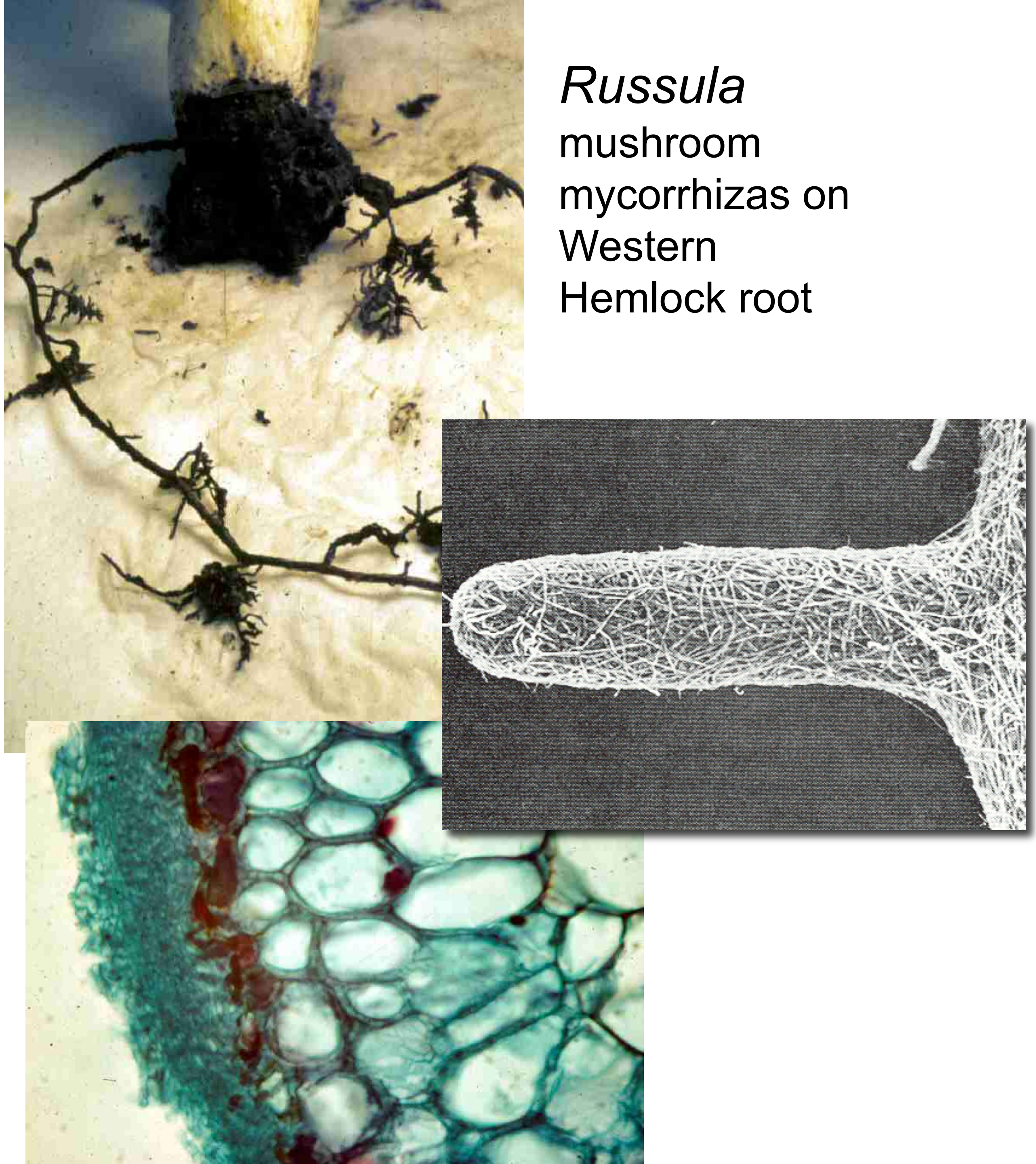




Riley et al., PNAS (2014)

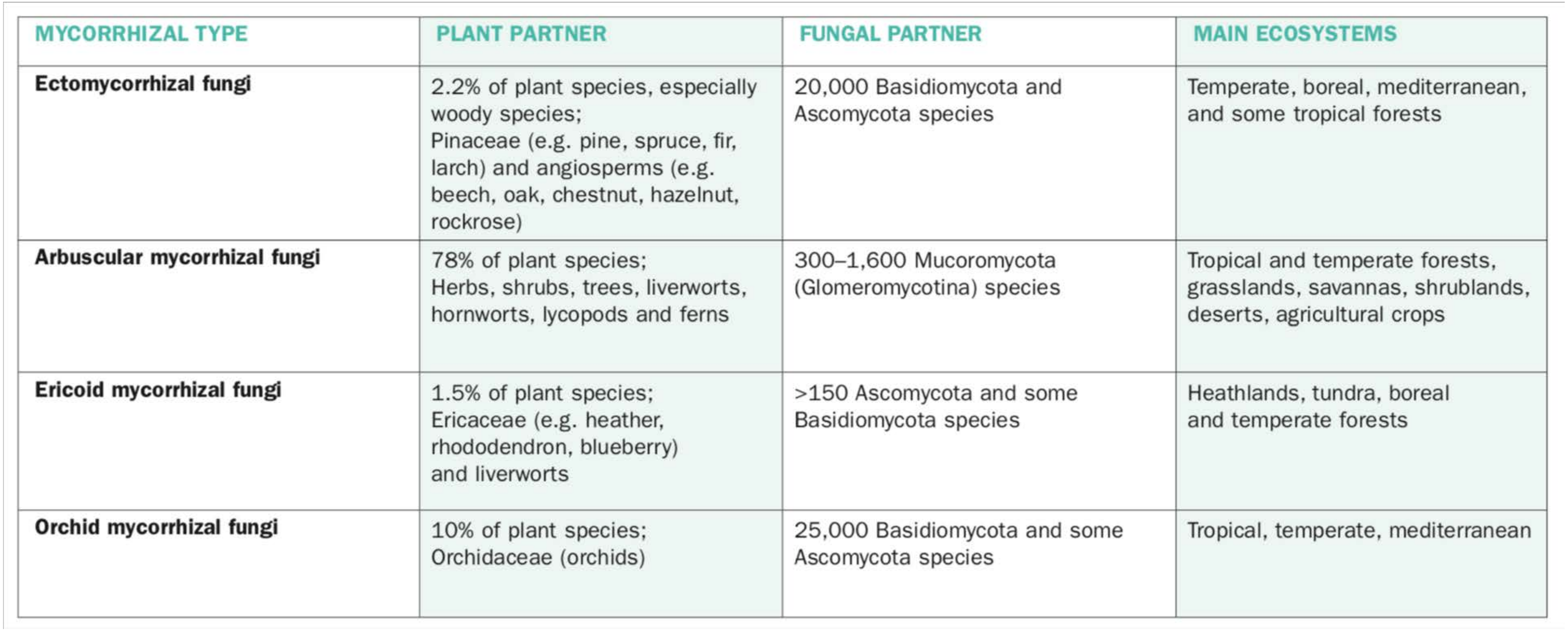
Mycorrhizae 菌根

- “Fungus roots”
- Mutualism between:
  - Fungus (nutrient & water uptake for plant)
  - Plant (carbohydrate for fungus)
- Several kinds
  - Zygomycota – hyphae invade root cells
  - Ascomycota & Basidiomycota – hyphae invade root but don’t penetrate cells
- **Extremely** important ecological role of fungi!



Russula mushroom mycorrhizas on Western Hemlock root

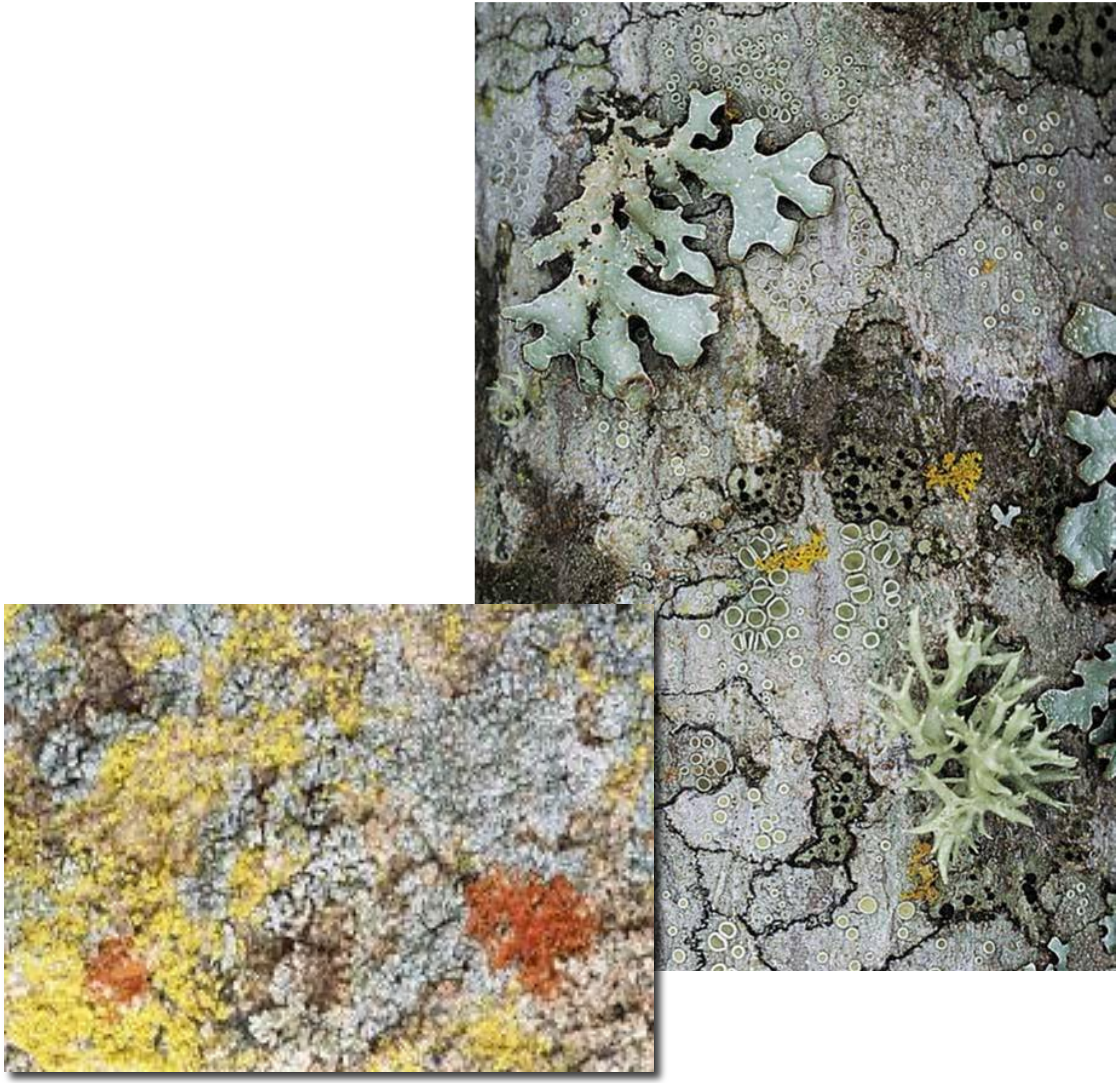
Main types of Mycorrhizae and their plant partners



MYCORRHIZAL TYPE	PLANT PARTNER	FUNGAL PARTNER	MAIN ECOSYSTEMS
Ectomycorrhizal fungi	2.2% of plant species, especially woody species; Pinaceae (e.g. pine, spruce, fir, larch) and angiosperms (e.g. beech, oak, chestnut, hazelnut, rockrose)	20,000 Basidiomycota and Ascomycota species	Temperate, boreal, mediterranean, and some tropical forests
Arbuscular mycorrhizal fungi	78% of plant species; Herbs, shrubs, trees, liverworts, hornworts, lycopods and ferns	300–1,600 Mucoromycota (Glomeromycotina) species	Tropical and temperate forests, grasslands, savannas, shrublands, deserts, agricultural crops
Ericoid mycorrhizal fungi	1.5% of plant species; Ericaceae (e.g. heather, rhododendron, blueberry) and liverworts	>150 Ascomycota and some Basidiomycota species	Heathlands, tundra, boreal and temperate forests
Orchid mycorrhizal fungi	10% of plant species; Orchidaceae (orchids)	25,000 Basidiomycota and some Ascomycota species	Tropical, temperate, mediterranean

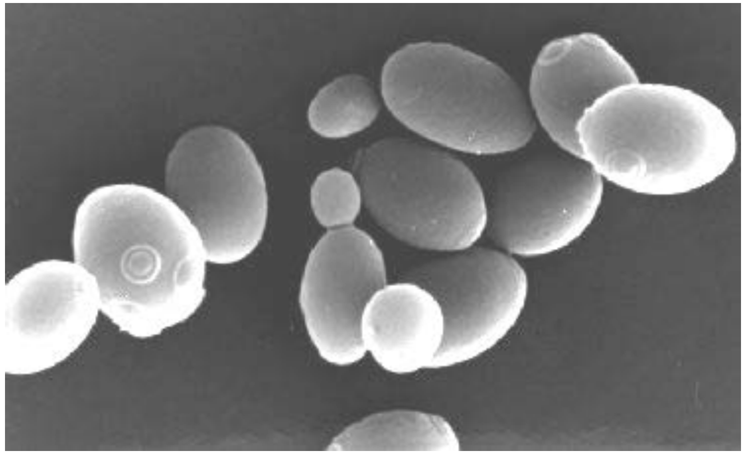
Lichens 地衣

- “Mutualism” between
  - Fungus – structure
  - Alga or cyanobacterium – provides food
- Three main types of lichens:
  - **Crustose lichens** form flat crusty plates.
  - **Foliose lichens** are leafy in appearance, although lobed or branched structures are not true leaves.
  - **Fruticose lichens** are even more finely branched and may hang down like beards from branches or grow up from the ground like tiny shrubs.

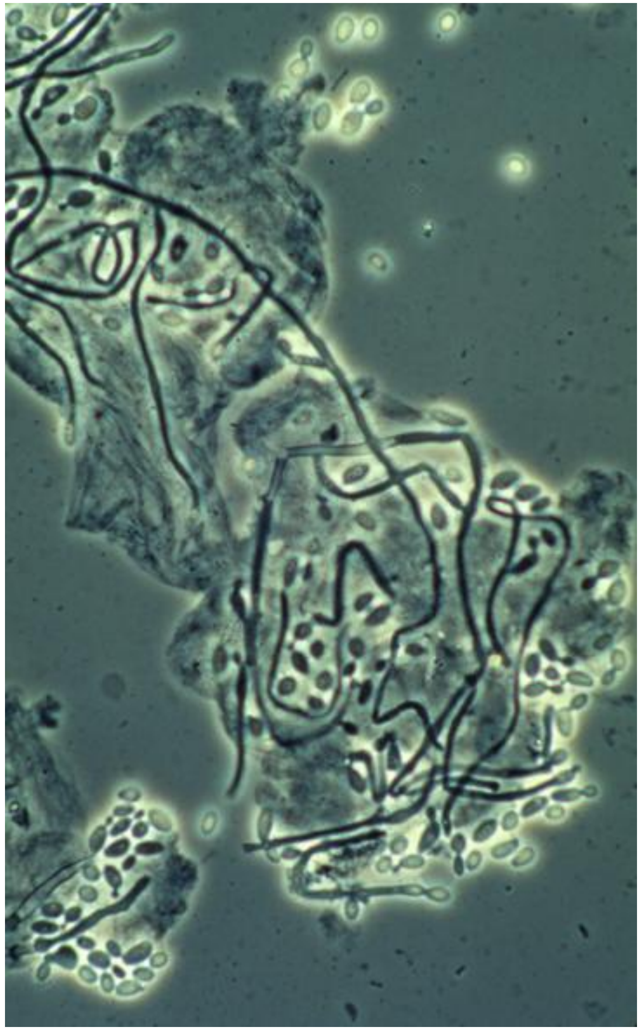


Yeasts 酵母菌

- Single celled fungi
- Adapted to liquids
    - Plant saps
    - Water films
    - Moist animal tissues



Saccharomyces

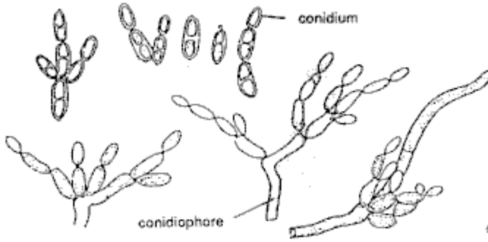


Candida

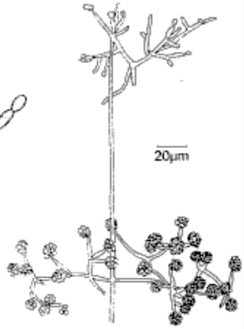
Molds黴菌

- Rapidly growth ; mostly asexual spores
- May develop into a sexual fungus, producing zygosporangia, ascocarps or basidiocarps
- Many human importances
  - Food spoilage
  - Food products (cheese flavour)
  - Antibiotics (*Penicillium*) etc.

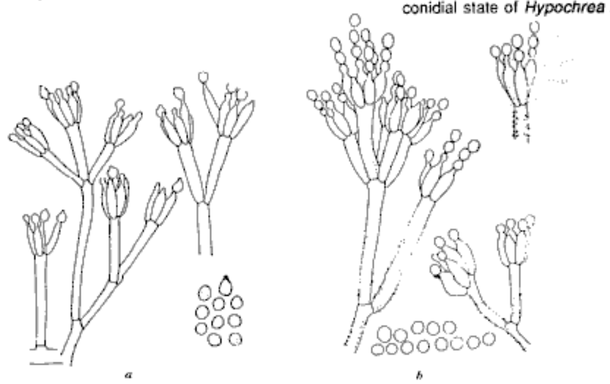
Noble Rot - *Botrytis*



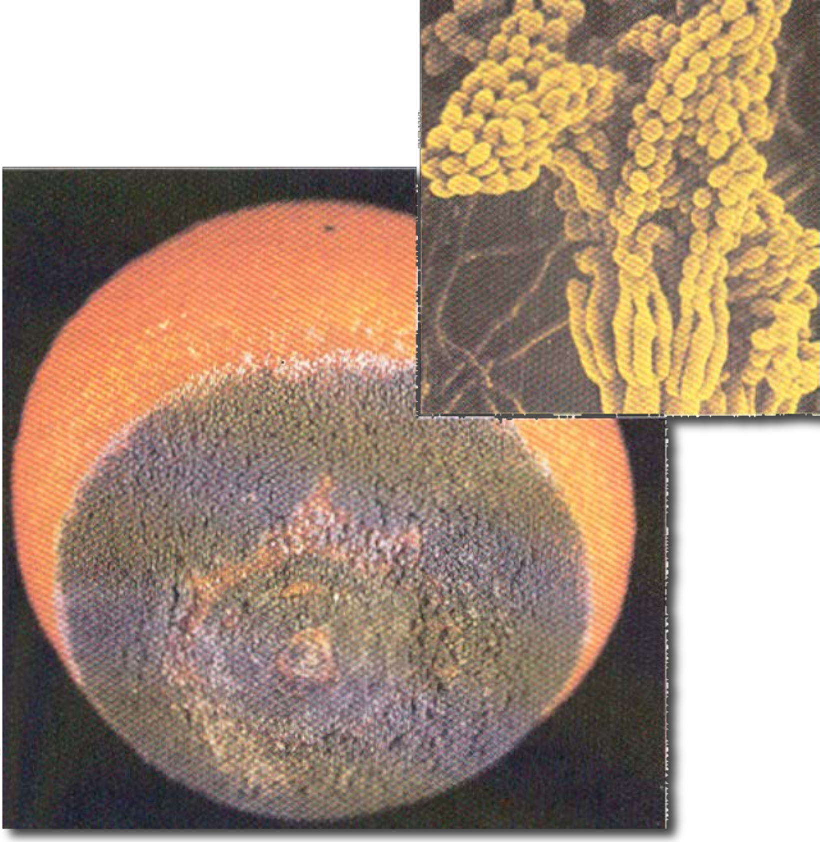
Cladosporium herbarum



Trichoderma viride
conidial state of *Hypochrea rufa*

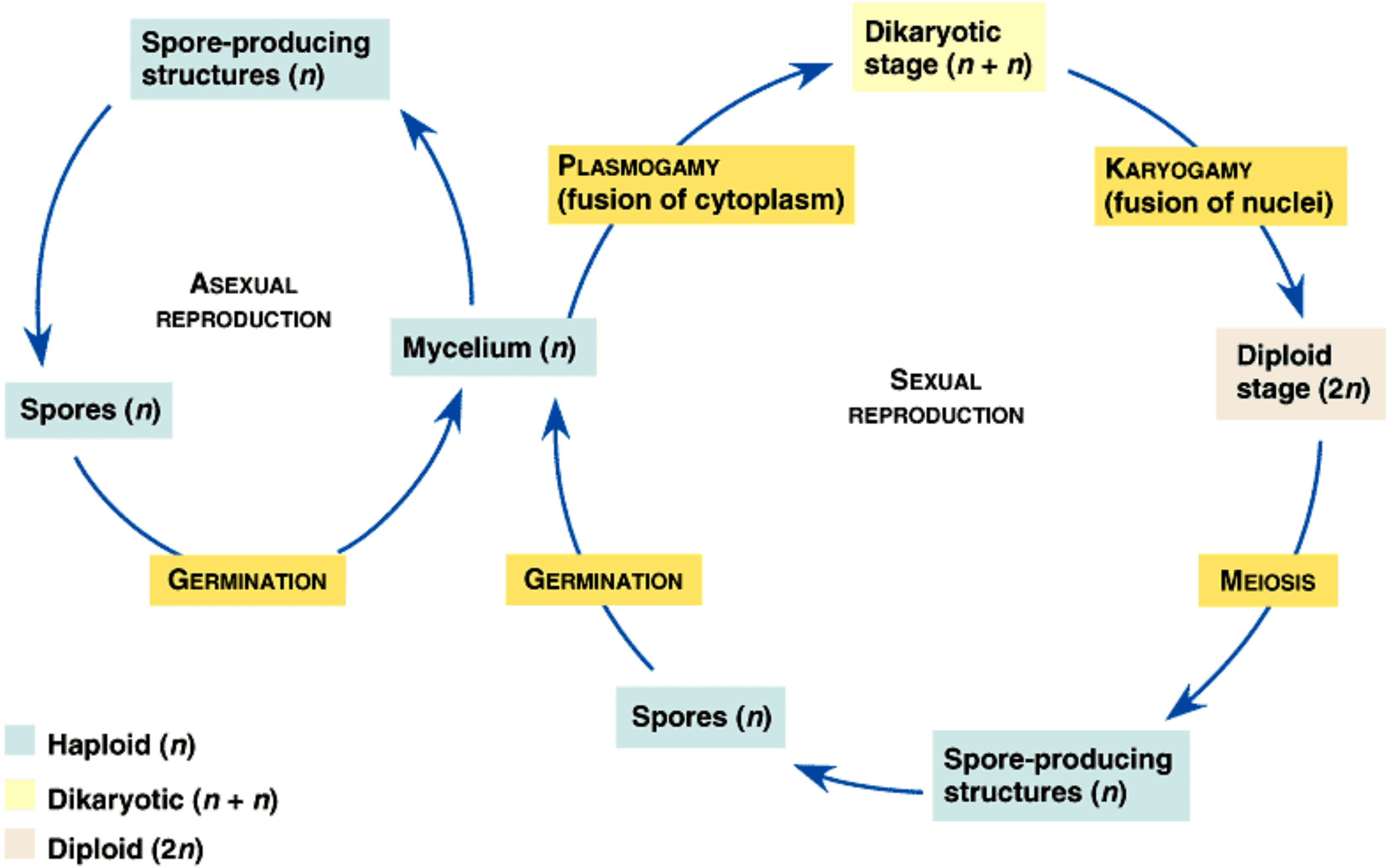


Penicillium janthinellum Conidiophores with phialospores (1000 : 1)
(a) strain with smooth-walled conidiophores; (b) strain with verrucose conidiophores with dense branching



Fungal life cycle

Generalized Life Cycle of a Fungus



Spore-producing structures (n)

Spores (n)

GERMINATION

Mycelium (n)

ASEXUAL REPRODUCTION

PLASMOGAMY (fusion of cytoplasm)

Dikaryotic stage ($n + n$)

KARYOGAMY (fusion of nuclei)

Diploid stage ($2n$)

MEIOSIS

Spore-producing structures (n)

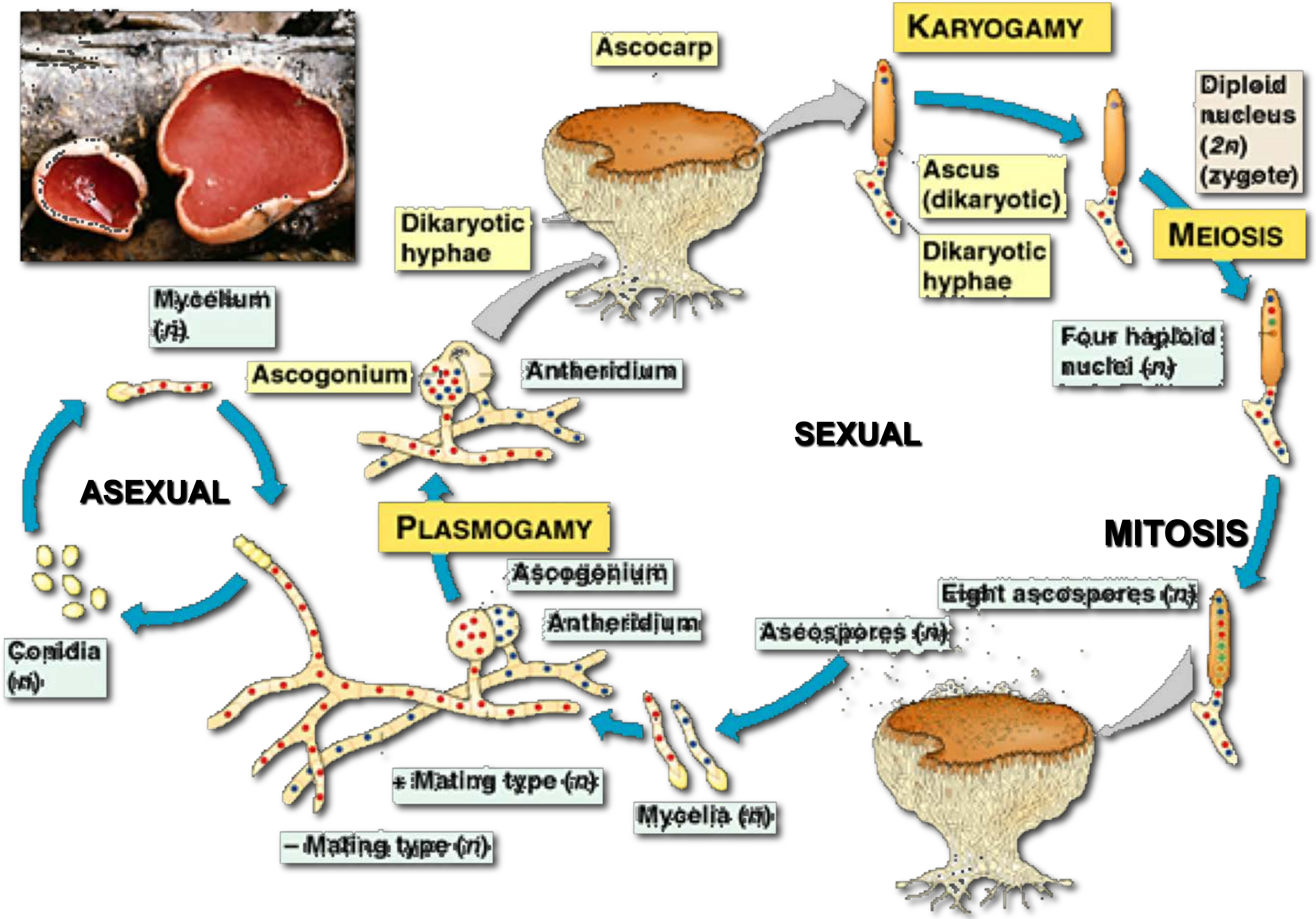
Spores (n)

GERMINATION

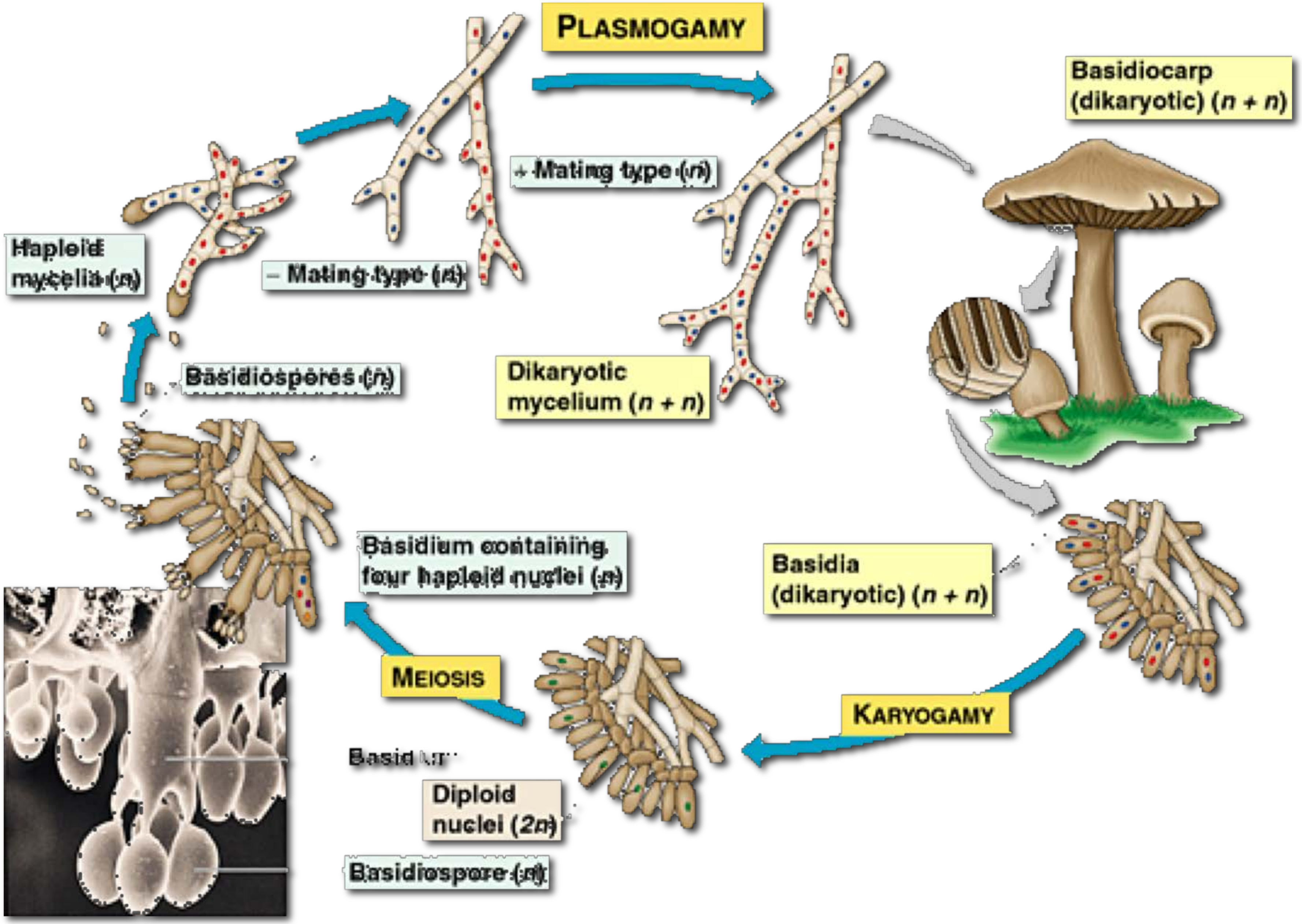
SEXUAL REPRODUCTION

🟦 Haploid (n)
🟨 Dikaryotic ($n + n$)
🟫 Diploid ($2n$)

Life cycle of an ascomycete



Life cycle of a mushroom-forming basidiomycete



Life cycle of a mushroom-forming basidiomycete

Haploid basidiospores grow into short-lived haploid mycelia: under certain conditions, plasmogamy occurs

Resulting dikaryotic mycelium grows forming mycorrhiza or mushrooms (basidiocarps)

Mushroom cap supports and protects gills: karyogamy in the terminal, dikaryotic cells lining the gills produces diploid basidia

Resulting basidium immediately undergoes meiosis producing four haploid basidiospores

Asexual reproduction less common than in ascomycetes

Fungal life style

Fungi as Symbionts (Mutualism)

CrossMark
click for updates

PNAS

Small genome of the fungus *Escovopsis weberi*, a specialized disease agent of ant agriculture

Tom J. B. de Man[a], Jason E. Stajich[b], Christian P. Kubicek[c], Clotilde Teiling[d], Komal Chenthamara[c], Lea Atanasova[c], Irina S. Druzhinina[c], Natasha Levenkova[d], Stephanie S. L. Birnbaum[a], Seth M. Barribeau[a,e], Brooke A. Bozick[a], Garret Suen[f], Cameron R. Currie[f], and Nicole M. Gerardo[a,1]

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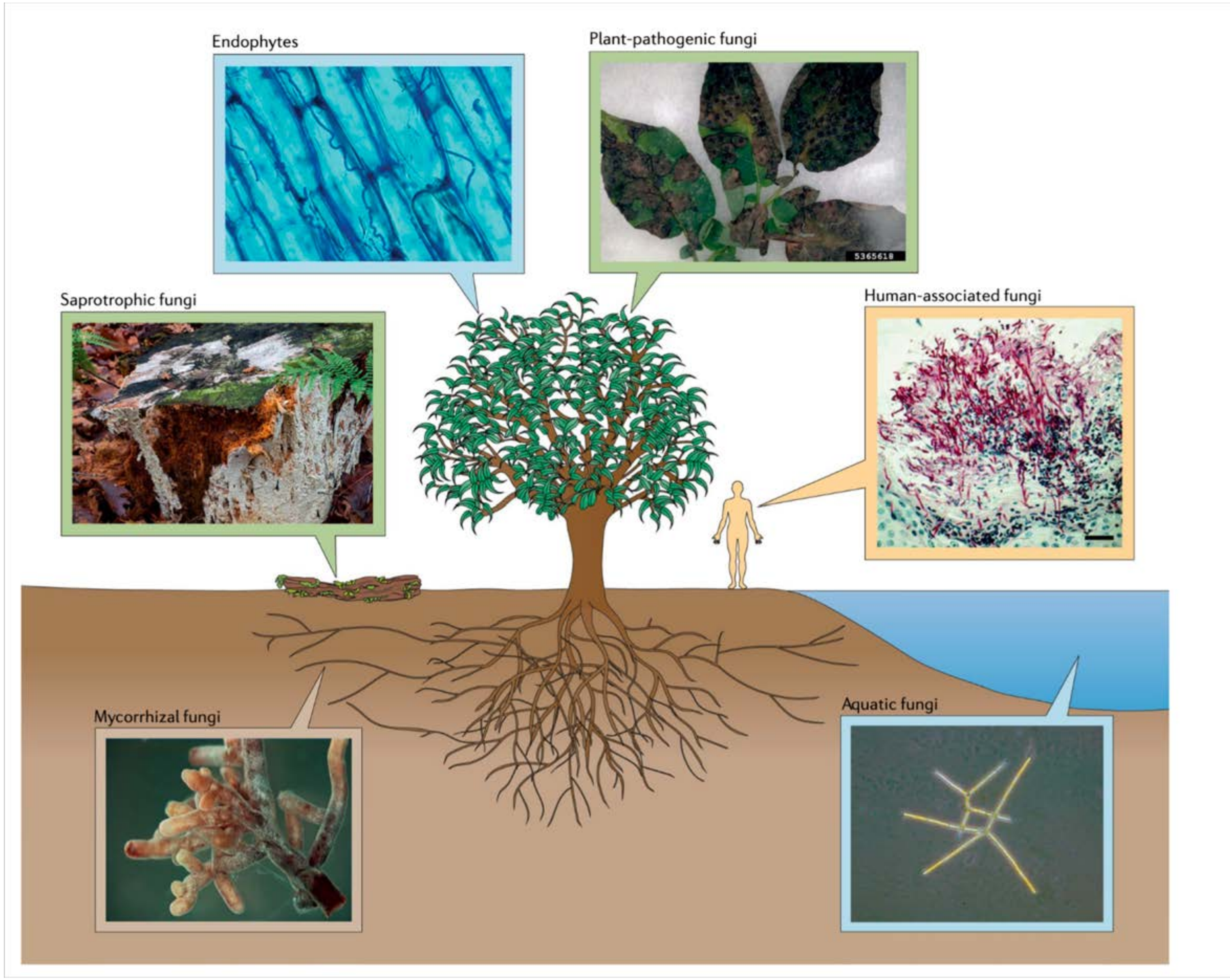
Edited by Nancy A. Moran, University of Texas, Austin, TX, and approved February 9, 2016 (received for review September 23, 2015)

Fungi as Parasites & Pathogens

Photo by V. Jedlicka

Fungal diversity in different environments



Nilsson *et al* (2018) Nature Reviews Microbiology

Ecological impacts of fungi

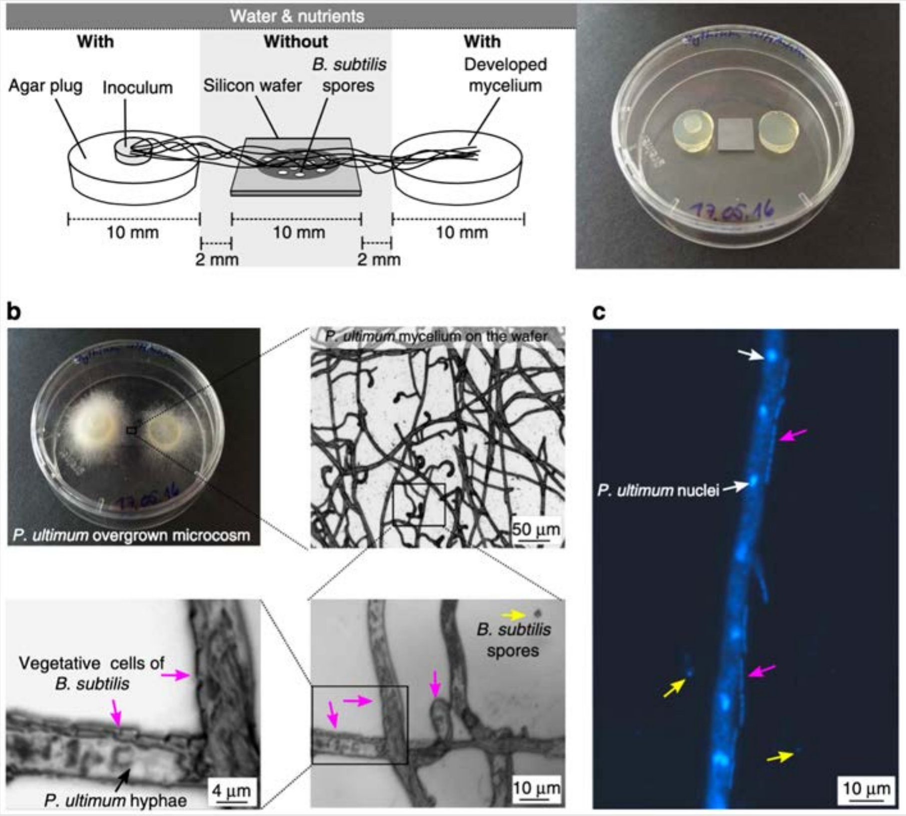
- **Beneficial Effects of Fungi**
  - Many organisms depend on/utilise fungi
  - Decomposition - nutrient and carbon recycling.
  - Biosynthetic factories. Can be used to produce drugs, antibiotics, alcohol, acids, food (e.g., fermented products, mushrooms).
  - Traffic network for microorganisms and host
  - Model organisms for biochemical and genetic studies.

- **(Host) Harmful Effects of Fungi**
  - Destruction of food, lumber, paper, and cloth.
  - Animal and human diseases, including allergies.
  - Toxins produced by poisonous mushrooms and within food (e.g., grain, cheese, etc.).
  - Plant diseases.

Received 3 Nov 2016 | Accepted 29 Mar 2017 | Published 7 Jun 2017
DOI: 10.1038/ncomms15472 OPEN

Mycelium-mediated transfer of water and nutrients stimulates bacterial activity in dry and oligotrophic environments

Anja Worrich[1,2,†], Hryhoriy Stryhanyuk[3], Niculina Musat[3], Sara König[2,4], Thomas Banitz[4], Florian Centler[2], Karin Frank[4,5,6], Martin Thullner[2], Hauke Harms[2,5], Hans-Hermann Richnow[3], Anja Miltner[1], Matthias Kästner[1,*] & Lukas Y. Wick[2,*]



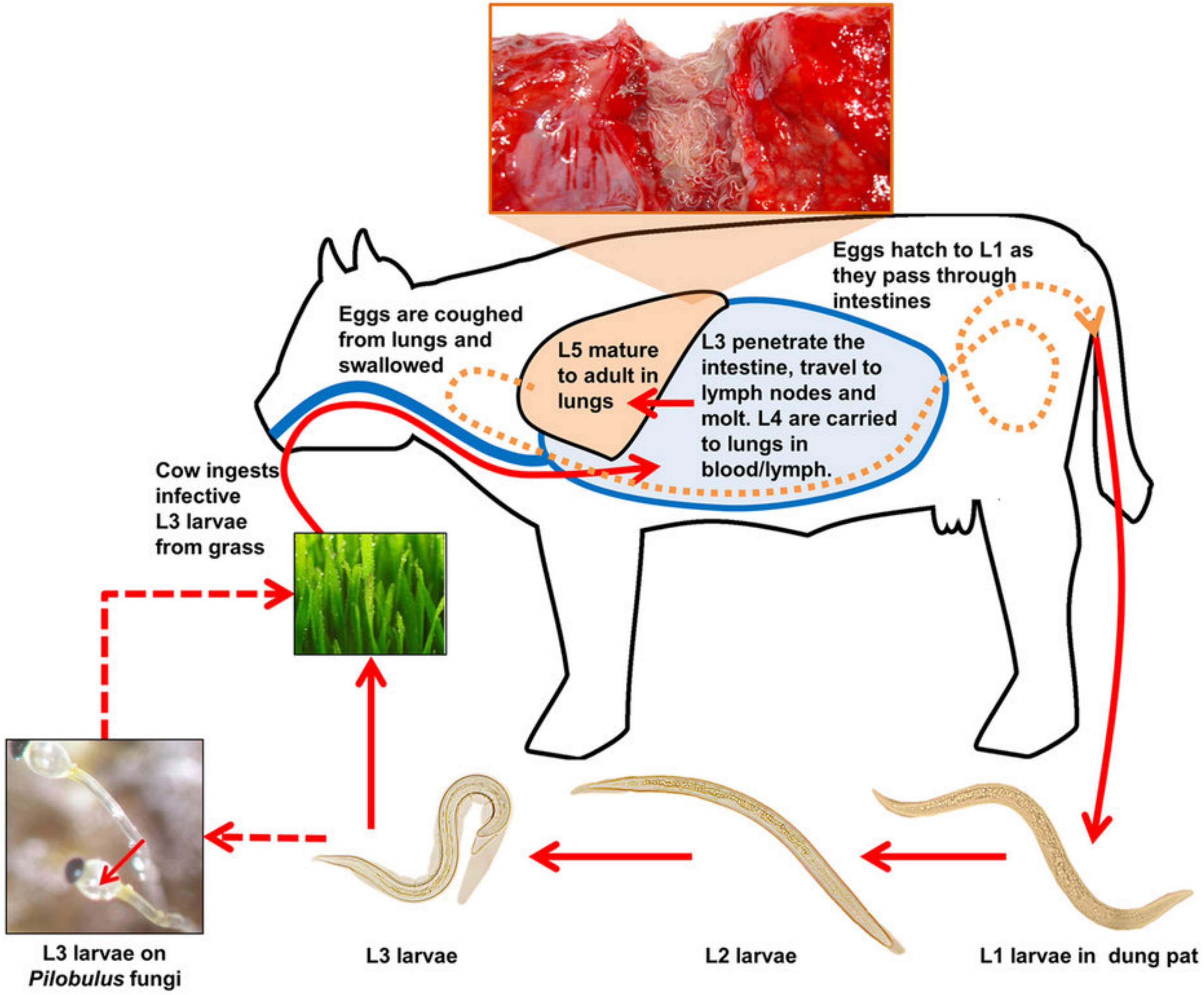
https://www.youtube.com/watch?v=AnsYh6511Ic

Figure 1 | Synthetic microbial ecosystem reveals spore germination in presence of mycelia in dry and oligotrophic environments. (**a**) Scheme and photographs of the setup employed to carry out the germination, growth and labelling experiments. The synthetic ecosystem is comprised of two agar plugs serving as water and nutrient sources ('with') for the fungi or the oomycete inoculated on top of one of the agar plugs. A silicon wafer free of water and nutrients ('without') placed in the middle between the two 'with' zones served as carrier for spores of *B. subtilis*. An air gap between the 'with' and 'without' zone prevented the diffusion of water or substrates to the spore region. (**b**) Gradual enlargement of bright-field micrographs of the silicon wafer overgrown by mycelium of *P. ultimum*. In close vicinity to the hyphae (black arrow) rod-shaped, vegetative bacterial cells (magenta arrows) were found, whereas smaller, round-shaped spores (yellow arrows) were located more distantly. (**c**) Fluorescence micrograph of the 4′,6-diamidine-2-phenylindol (DAPI)-stained wafer showing *P. ultimum* hyphae containing nuclei (white arrows) and vegetative cells as well as spores of *B. subtilis*.

Cattle lungworm *Dictyocaulus viviparus*

#Pilobolus and Lungworm Larvae
https://www.youtube.com/watch?v=4LrWjnYyc28

Actively utilize *Pilobulus* to disperse



Eggs hatch to L1 as they pass through intestines

Eggs are coughed from lungs and swallowed

L5 mature to adult in lungs

L3 penetrate the intestine, travel to lymph nodes and molt. L4 are carried to lungs in blood/lymph.

Cow ingests infective L3 larvae from grass

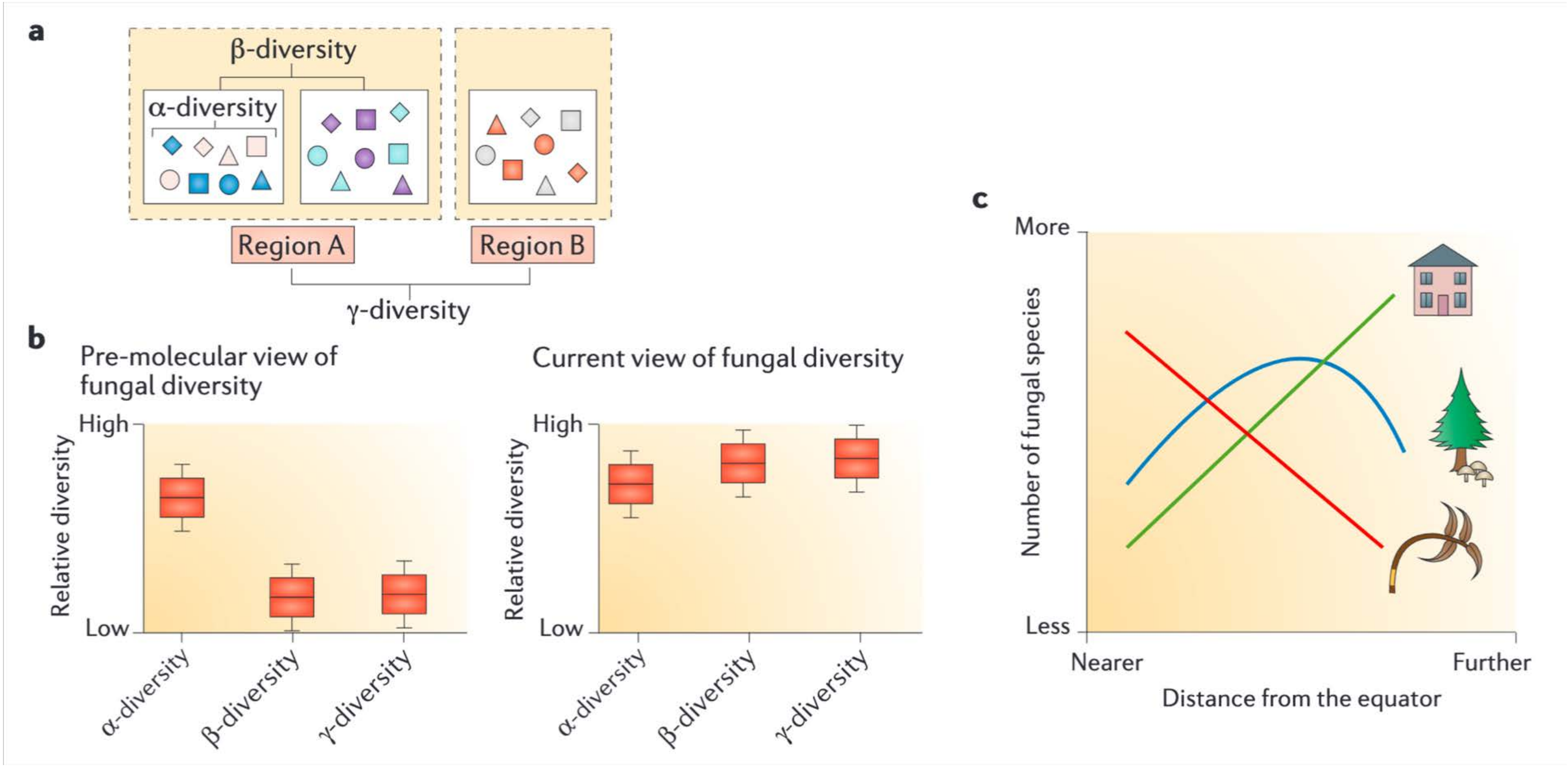
L3 larvae on *Pilobulus* fungi

L3 larvae

L2 larvae

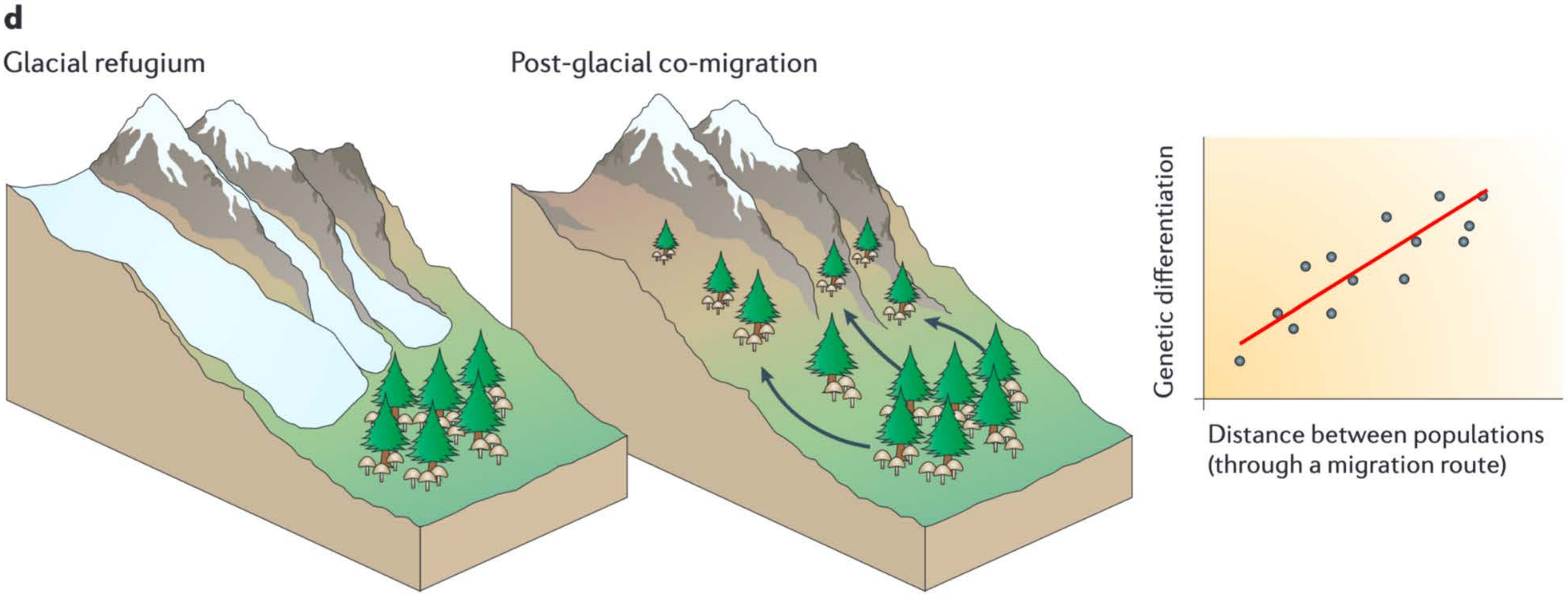
L1 larvae in dung pat

Biogeography and emerging views of fungal diversity



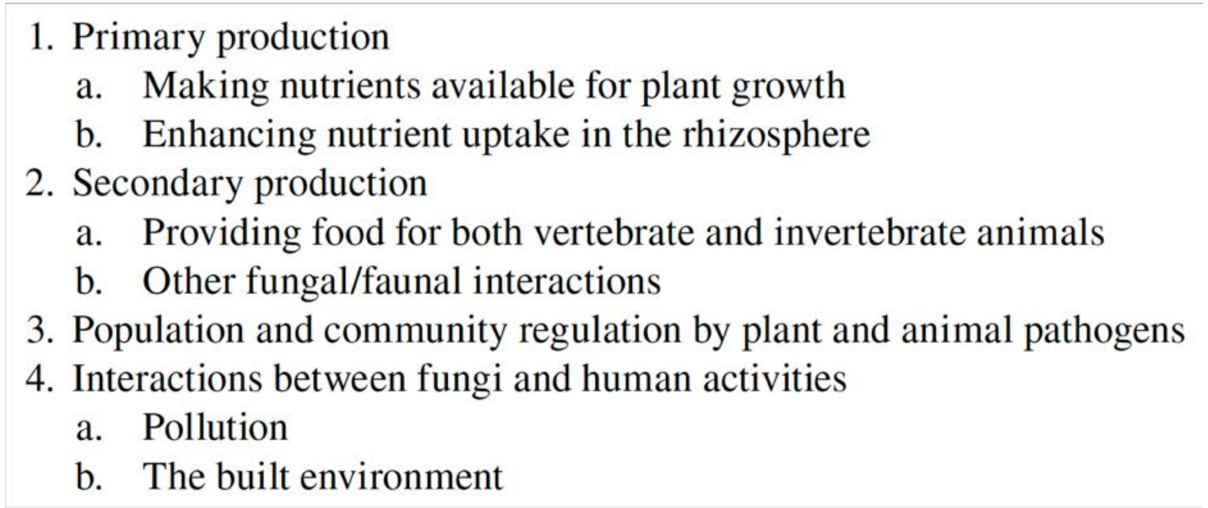
Peay *et al* (2016) Nature Reviews Microbiology

The evolution of new species or genetic diversity in fungi is often associated with dispersal or migration into new habitats

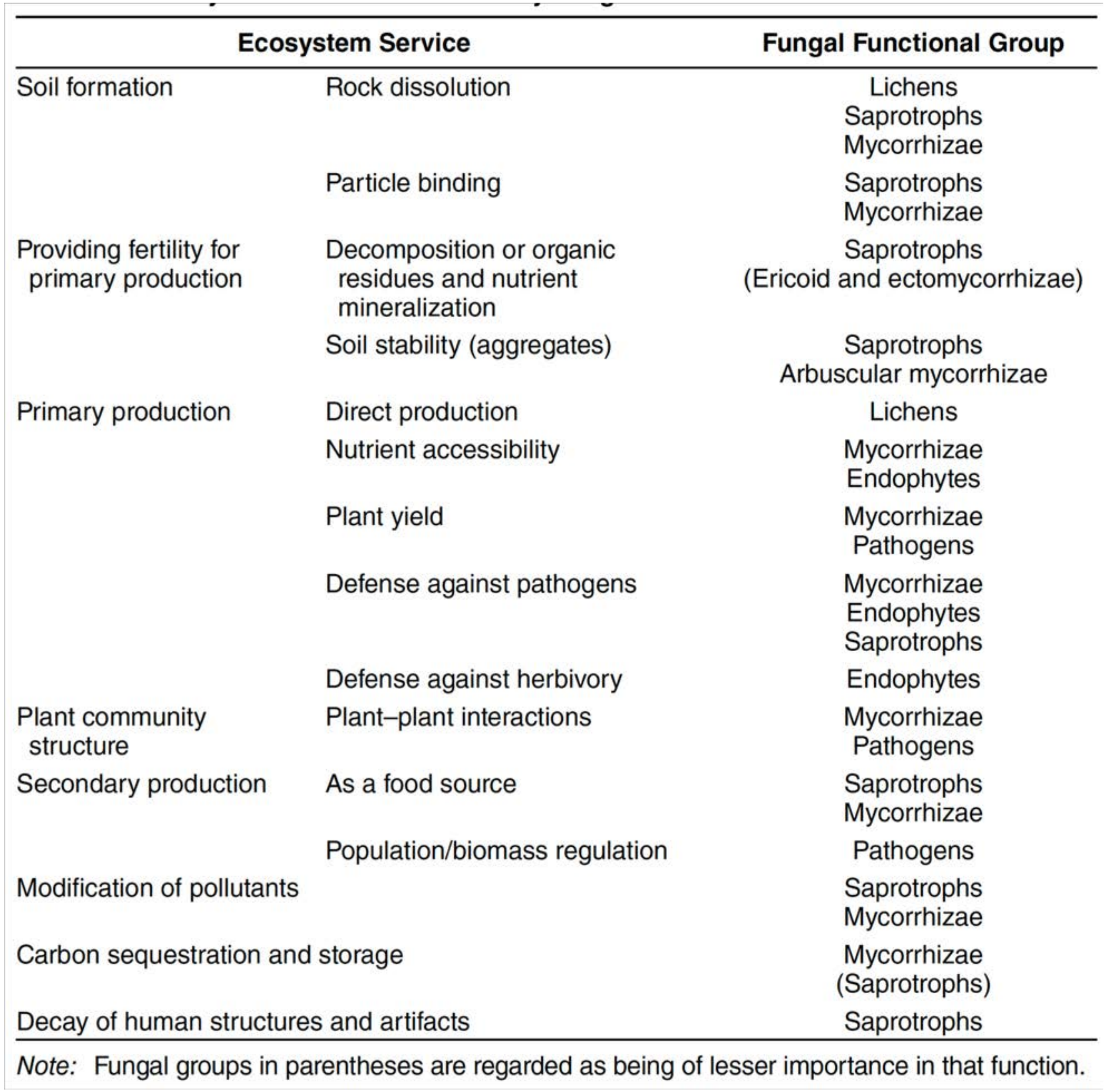


Peay *et al* (2016) Nature Reviews Microbiology

How fungi are engaged in ecosystem processes



1. Primary production
    a. Making nutrients available for plant growth
    b. Enhancing nutrient uptake in the rhizosphere
2. Secondary production
    a. Providing food for both vertebrate and invertebrate animals
    b. Other fungal/faunal interactions
3. Population and community regulation by plant and animal pathogens
4. Interactions between fungi and human activities
    a. Pollution
    b. The built environment



Ecosystem Service		Fungal Functional Group
Soil formation	Rock dissolution	Lichens Saprotrophs Mycorrhizae
	Particle binding	Saprotrophs Mycorrhizae
Providing fertility for primary production	Decomposition or organic residues and nutrient mineralization	Saprotrophs (Ericoid and ectomycorrhizae)
	Soil stability (aggregates)	Saprotrophs Arbuscular mycorrhizae
Primary production	Direct production	Lichens
	Nutrient accessibility	Mycorrhizae Endophytes
	Plant yield	Mycorrhizae Pathogens
	Defense against pathogens	Mycorrhizae Endophytes Saprotrophs
	Defense against herbivory	Endophytes
Plant community structure	Plant–plant interactions	Mycorrhizae Pathogens
Secondary production	As a food source	Saprotrophs Mycorrhizae
	Population/biomass regulation	Pathogens
Modification of pollutants		Saprotrophs Mycorrhizae
Carbon sequestration and storage		Mycorrhizae (Saprotrophs)
Decay of human structures and artifacts		Saprotrophs

Note: Fungal groups in parentheses are regarded as being of lesser importance in that function.

Fungi in Ecosystem Processes (2nd Edition) CRC Press

The good

350

At least 350 species
are consumed as foods

15%

15% of all vaccines
and therapeutic proteins
are made in yeast

Fungi are being used
to turn crop waste
into bioethanol

216

216 species of fungi
are thought to
be hallucinogenic

$C_5H_6O_4$

Itaconic acid from
fungi is used to
make Lego®

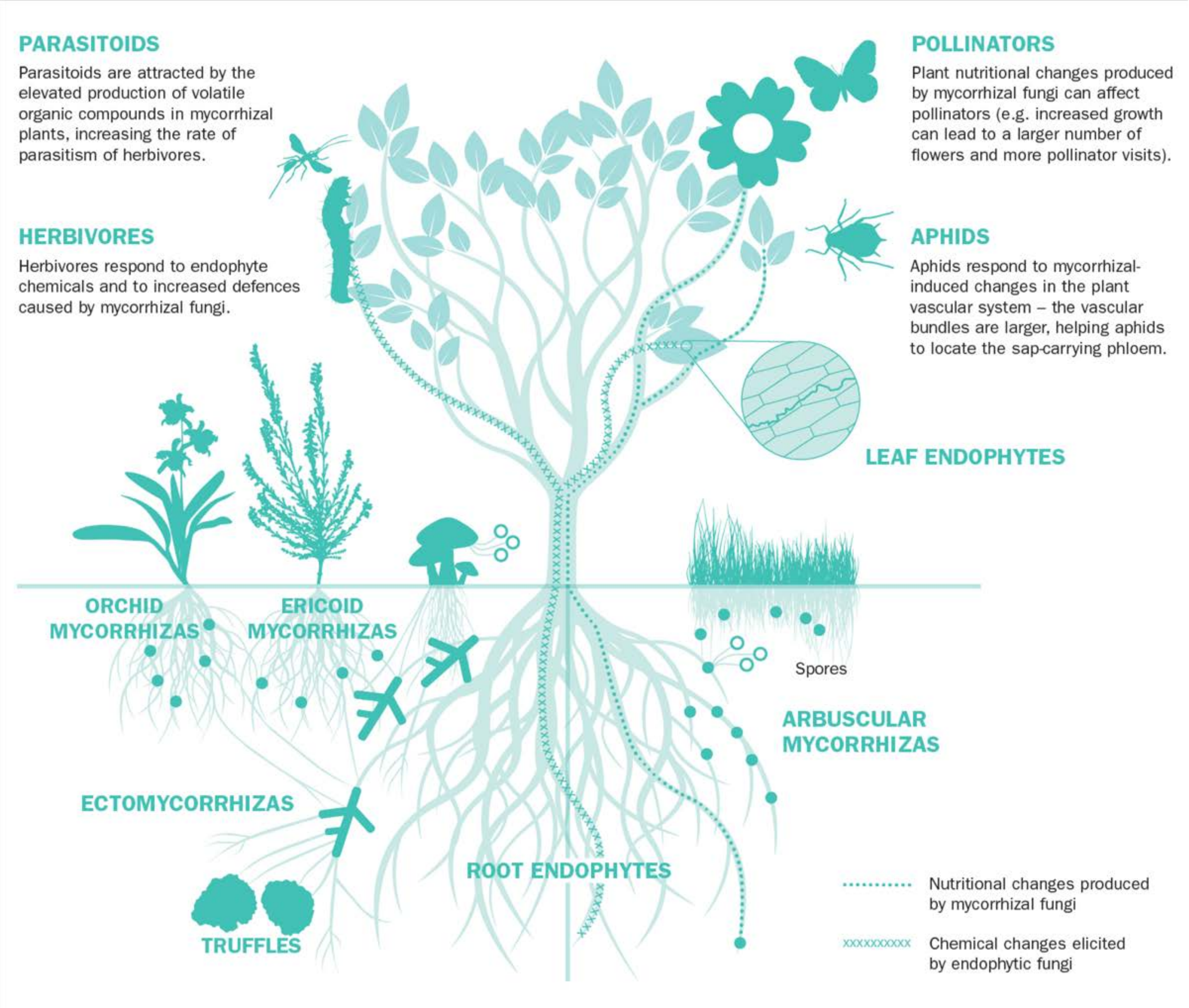
AGRICULTURE	Species of *Trichoderma* are used to enhance the growth of crops and as a source of enzymes added to improve animal feeds[49,50]. Fungi are also the source of an important class of agricultural fungicides called strobilurins[51]. *Aspergillus flavus* is used as a biocontrol agent on peanut crops to out-compete aflatoxin-producing fungi[52].
BEVERAGES	Yeasts underpin alcoholic drink production from beer to wine to spirits. Soft drinks contain citric acid that is produced from the fermentation of *Aspergillus niger*[53]. Glucoamylase from species of *Aspergillus* is used to convert starch to high-fructose corn syrup, which is used as a sweetener in soft drinks[54].
BIOFUELS	Second-generation bioethanol makes use of species of *Trichoderma* to break down agricultural waste such as maize straw into sugars that can be fermented using yeast to produce ethanol[42].
BIOREMEDIATION	White rot fungi, including *Pleurotus ostreatus* and *Trametes versicolor*, can degrade toxic polychlorinated biphenyl (PCB) chemicals in soil and polluted wastewaters[55,56].
COTTON PROCESSING	Catalase enzymes from species of *Aspergillus* are used to break down excess bleach in the wastewater from cotton processing[57]. *Trichoderma* cellulases are used to remove fine cotton threads, which prevents the fibre aggregating into pills[57].
FOOD	At least 350 edible mushroom species are known to be collected for food[2]. The meat substitute Quorn™ is manufactured using a fungus (*Fusarium venenatum*)[5]. Moulds such as *Penicillium camemberti* and *P. roqueforti* are integral to the ripening process in many types of cheese[6]. Live yeast and fungal enzymes are used in breadmaking[58]. The food colourings lycopene and beta-carotene are now produced from the fungus *Blakeslea trispora*[59]. Soy sauce is produced using koji (*Aspergillus oryzae*) and the Asian snack tempeh makes use of *Rhizopus microsporus*[60,61].
HALLUCINOGENS	Worldwide, 216 species of fungi are believed to be hallucinogenic – of these, 116 species belong to the genus *Psilocybe*[62].
LEATHER PROCESSING	Leather hides are degreased with lipase enzymes from *Aspergillus oryzae*[63,64].

MEDICINES	Many drugs come from fungi. Penicillin from *Penicillium rubens* revolutionised the treatment of bacterial infections and cyclosporine from *Tolypocladium inflatum* made organ transplantation possible[11–13]. Gestodene is an active ingredient in third-generation contraceptive pills; a key step in its synthesis is achieved using fungal fermentation with *Penicillium raistrickii*[65].
PAPER MANUFACTURING	Cellulase enzymes produced by species of *Trichoderma* and *Humicola* are used to speed up the pulping process thereby reducing water usage[37,38].
PLASTICS AND BIOMATERIALS	Plastic car parts, synthetic rubber and Lego™ are made using itaconic acid derived from species of *Aspergillus*[66,67]. Additionally, fungal mycelium-based products are now being used as replacements for polystyrene foam, leather and building materials[68–70].
RESEARCH	Since 2010, more than a quarter of Nobel prizes for physiology or medicine were awarded for work based on yeast[71].
VITAMINS	The vitamin B2 used for vitamin supplements is produced by fermentation of the fungus *Eremothecium gossypii*[72].
WASHING DETERGENTS	Cellulase enzymes produced by the thermophilic fungus *Humicola insolens* are added to washing powders and liquids. They trim the fine cotton threads on the surface of cotton fabric to produce a smoother, newer feel[41,73]. Lipase enzymes from the same species are also added to break down fat stains[40,41].

PLANT–FUNGAL MUTUALISMS

1. Endophytes
can be beneficial to plant growth, especially in harsh environments

2. Mycorrhizas.
key benefits to terrestrial ecosystems, including: (i) enhanced nutrient uptake, (ii) soil structure; and (iii) carbon sequestration,



PARASITOIDS
Parasitoids are attracted by the elevated production of volatile organic compounds in mycorrhizal plants, increasing the rate of parasitism of herbivores.

HERBIVORES
Herbivores respond to endophyte chemicals and to increased defences caused by mycorrhizal fungi.

POLLINATORS
Plant nutritional changes produced by mycorrhizal fungi can affect pollinators (e.g. increased growth can lead to a larger number of flowers and more pollinator visits).

APHIDS
Aphids respond to mycorrhizal-induced changes in the plant vascular system – the vascular bundles are larger, helping aphids to locate the sap-carrying phloem.

·········· Nutritional changes produced by mycorrhizal fungi
xxxxxxxxxx Chemical changes elicited by endophytic fungi

The bad

Ophiocordyceps unilateralis

Andersen *et al.,* Am Nat (2009)

BOX 1: FROM FUNGAL IMMUNOSUPPRESSANT TO BILLION-DOLLAR DRUG

The entomopathogenic fungus *Isaria sinclairii* infects cicada larvae; it grows inside its host, initially without killing it but instead replacing the host tissue with fungal mycelium. Eventually its spore-bearing structures emerge from the dead larvae. *Isaria sinclairii* produces an immunosuppressant chemical compound called myriocin. Extensive chemical redesign of myriocin resulted in the immunosuppressive multiple sclerosis treatment fingolimod. Fingolimod is a blockbuster drug with sales of US$2.48 billion in 2018[83].

Fungi can even consume nematodes (線蟲)

https://vimeo.com/125211921

REVIEW

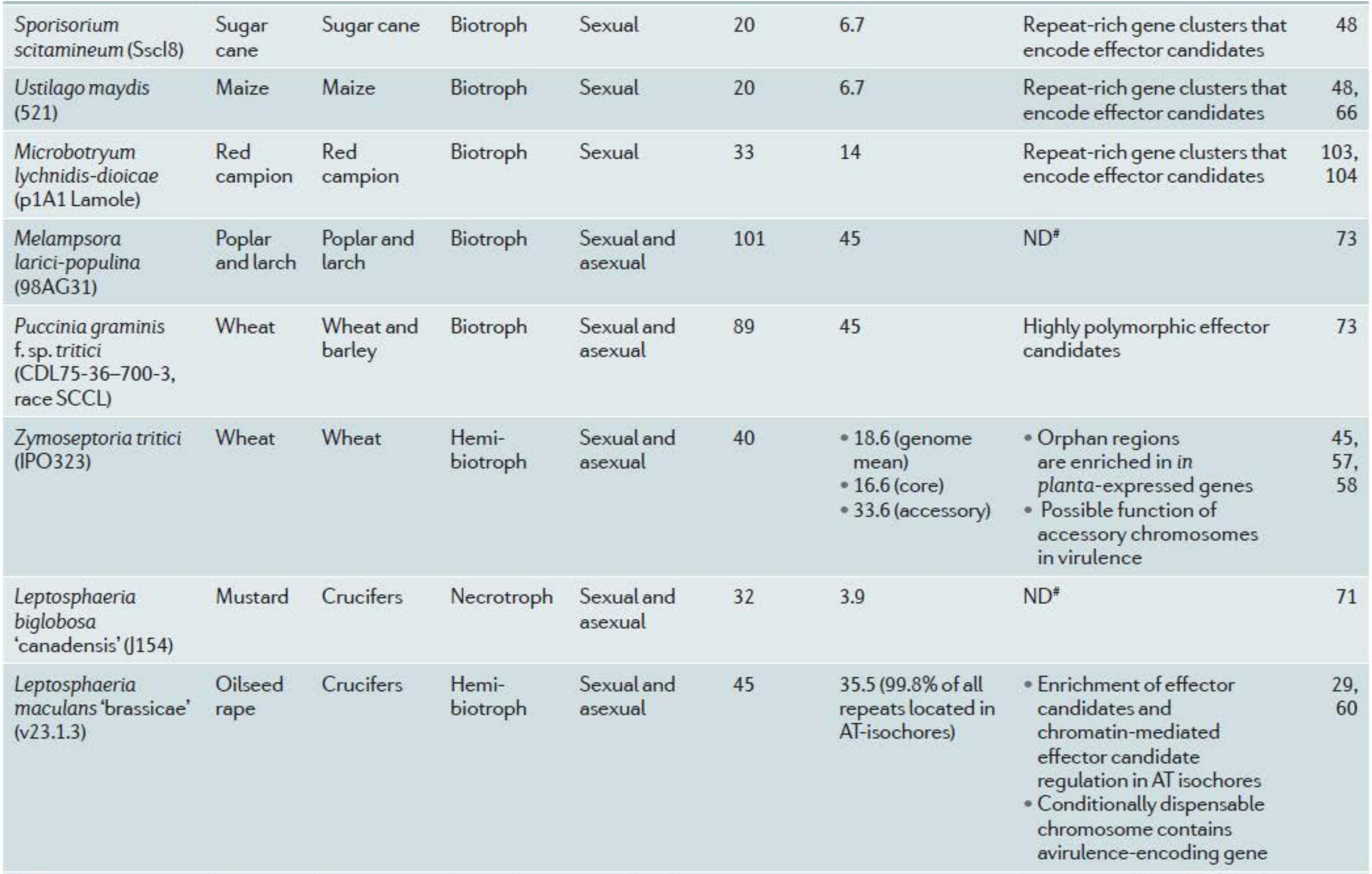
doi:10.1038/nature10947

Emerging fungal threats to animal, plant and ecosystem health

Matthew C. Fisher[1], Daniel. A. Henk[1], Cheryl J. Briggs[2], John S. Brownstein[3], Lawrence C. Madoff[4], Sarah L. McCraw[5]
& Sarah J. Gurr[5]

Fisher *et al* (2013) Nature

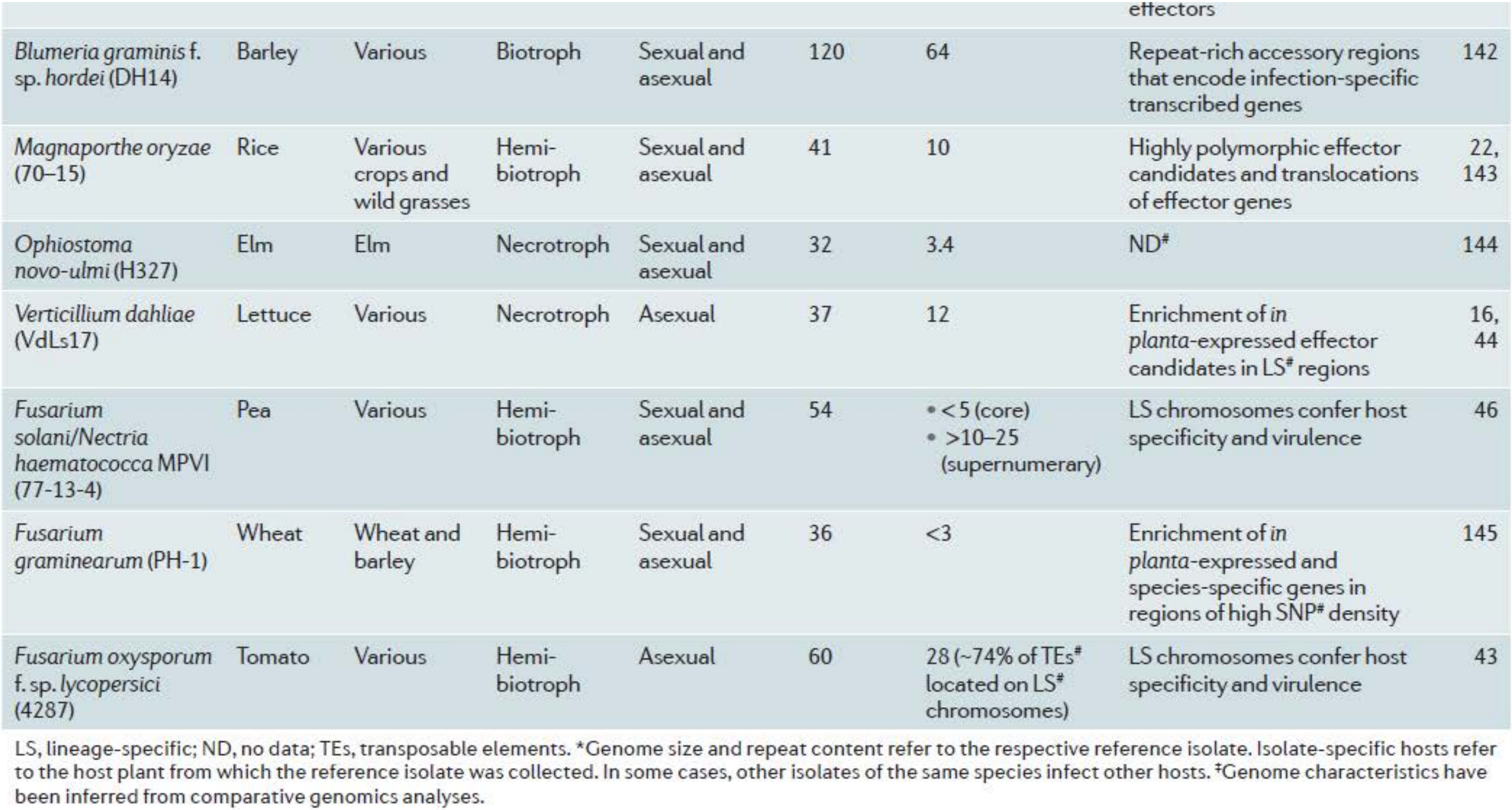
Plant pathogens



Sporisorium scitamineum (Sscl8)	Sugar cane	Sugar cane	Biotroph	Sexual	20	6.7	Repeat-rich gene clusters that encode effector candidates	48
Ustilago maydis (521)	Maize	Maize	Biotroph	Sexual	20	6.7	Repeat-rich gene clusters that encode effector candidates	48, 66
Microbotryum lychnidis-dioicae (p1A1 Lamole)	Red campion	Red campion	Biotroph	Sexual	33	14	Repeat-rich gene clusters that encode effector candidates	103, 104
Melampsora larici-populina (98AG31)	Poplar and larch	Poplar and larch	Biotroph	Sexual and asexual	101	45	ND#	73
Puccinia graminis f. sp. *tritici* (CDL75-36–700-3, race SCCL)	Wheat	Wheat and barley	Biotroph	Sexual and asexual	89	45	Highly polymorphic effector candidates	73
Zymoseptoria tritici (IPO323)	Wheat	Wheat	Hemi-biotroph	Sexual and asexual	40	• 18.6 (genome mean) • 16.6 (core) • 33.6 (accessory)	• Orphan regions are enriched in *in planta*-expressed genes • Possible function of accessory chromosomes in virulence	45, 57, 58
Leptosphaeria biglobosa ‘canadensis’ (J154)	Mustard	Crucifers	Necrotroph	Sexual and asexual	32	3.9	ND#	71
Leptosphaeria maculans ‘brassicae’ (v23.1.3)	Oilseed rape	Crucifers	Hemi-biotroph	Sexual and asexual	45	35.5 (99.8% of all repeats located in AT-isochores)	• Enrichment of effector candidates and chromatin-mediated effector candidate regulation in AT isochores • Conditionally dispensable chromosome contains avirulence-encoding gene	29, 60

Mareike Möller & Eva H. Stukenbrock (2017) Nature Microbiology Review

Plant pathogens



							effectors	
Blumeria graminis f. sp. *hordei* (DH14)	Barley	Various	Biotroph	Sexual and asexual	120	64	Repeat-rich accessory regions that encode infection-specific transcribed genes	142
Magnaporthe oryzae (70–15)	Rice	Various crops and wild grasses	Hemi-biotroph	Sexual and asexual	41	10	Highly polymorphic effector candidates and translocations of effector genes	22, 143
Ophiostoma novo-ulmi (H327)	Elm	Elm	Necrotroph	Sexual and asexual	32	3.4	ND#	144
Verticillium dahliae (VdLs17)	Lettuce	Various	Necrotroph	Asexual	37	12	Enrichment of *in planta*-expressed effector candidates in LS# regions	16, 44
Fusarium solani/Nectria haematococca MPVI (77-13-4)	Pea	Various	Hemi-biotroph	Sexual and asexual	54	• <5 (core) • >10–25 (supernumerary)	LS chromosomes confer host specificity and virulence	46
Fusarium graminearum (PH-1)	Wheat	Wheat and barley	Hemi-biotroph	Sexual and asexual	36	<3	Enrichment of *in planta*-expressed and species-specific genes in regions of high SNP# density	145
Fusarium oxysporum f. sp. *lycopersici* (4287)	Tomato	Various	Hemi-biotroph	Asexual	60	28 (~74% of TEs# located on LS# chromosomes)	LS chromosomes confer host specificity and virulence	43

LS, lineage-specific; ND, no data; TEs, transposable elements. *Genome size and repeat content refer to the respective reference isolate. Isolate-specific hosts refer to the host plant from which the reference isolate was collected. In some cases, other isolates of the same species infect other hosts. ‡Genome characteristics have been inferred from comparative genomics analyses.

Mareike Möller & Eva H. Stukenbrock (2017) Nature Microbiology Review

Corn smut *Ustilago*

Photo by David Cohen/flickr/CC BY 2.0

Zizania latifolia infected by *Ustilago esculenta*

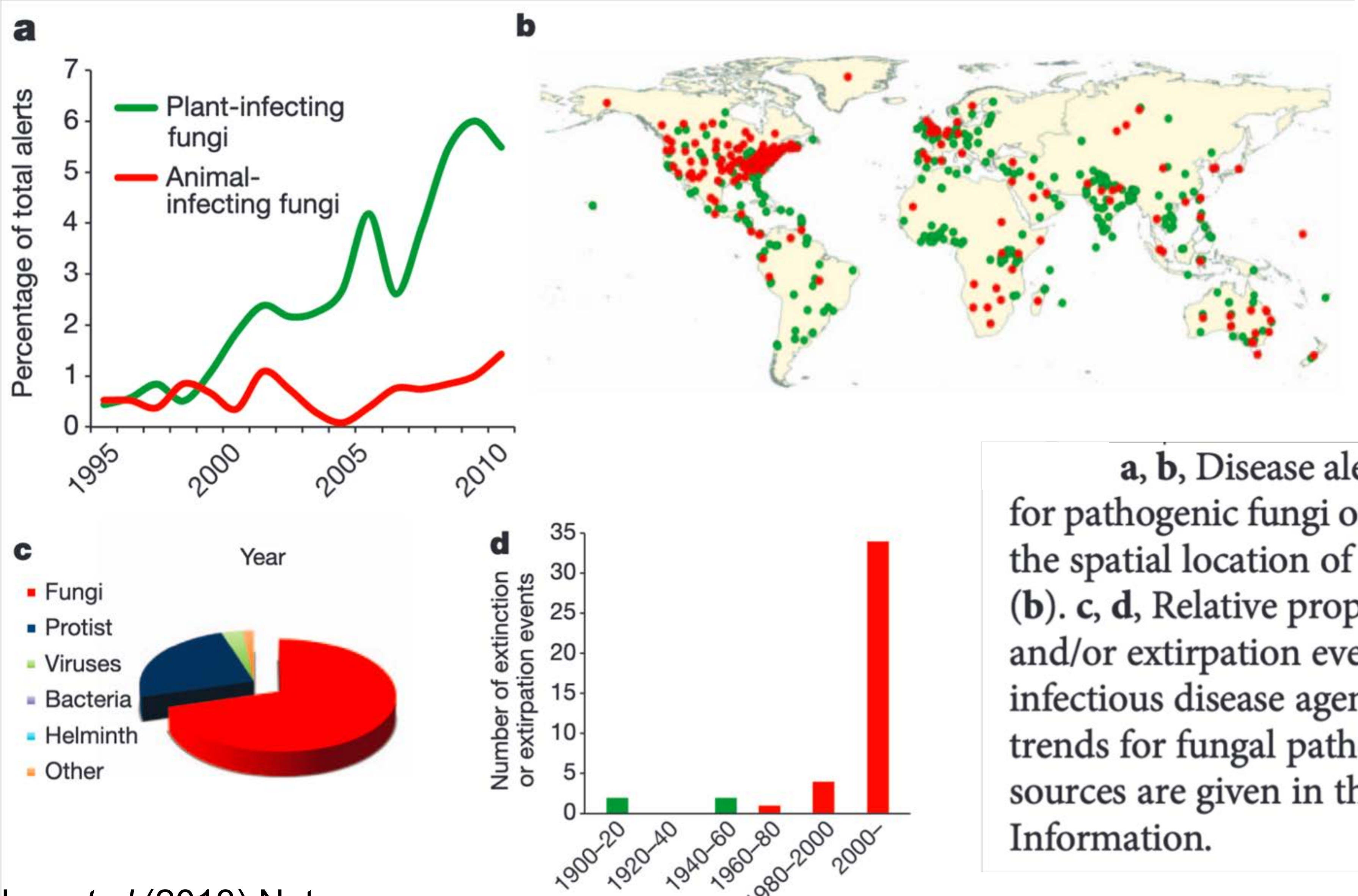
Nutritional Requirements of the Edible Gall-producing Fungus *Ustilago esculenta*
黑胡桃網路閣 https://blackwalnut.npust.edu.tw/archives/325221

Animal pathogens

	Host	Pathogen (Phylum)	Disease dynamics leading to mass mortality in animal and plant hosts
	Amphibian species (for example, the common midwife toad, *Alytes obstetricans*)	*Batrachochytrium dendrobatidis* (Chytridiomycota)	Worldwide dispersal of a hypervirulent lineage by trade[64]. Ultra-generalist pathogen manifesting spillover between tolerant/susceptible species. Extent of chytridiomycosis is dependent on biotic and abiotic context[15,82] .
	Coral species (for example, the sea fan, *Gorgonia ventalina*)	*Aspergillus sydowii* (Ascomycota)	Sea-fan aspergillosis caused by a common terrestrial soil fungus[21,86]. Epizootics are associated with warm-temperature anomalies. Coral immunosuppression is probably a factor causing decline.
	Bee species (for example, the hive of the domestic honeybee (*Apis mellifera*) suffering colony collapse disorder)	*Nosema* species (Microsporidia)	Microsporidian fungal infections are associated with colony collapse disorder and declining populations. Pathogen prevalence is probably a part of a multifactorial phenomenon that includes environmental stressors and polyparasitism[87,88].

Fisher *et al* (2013) Nature

Worldwide reporting trends in fungal Emerging Infectious Diseases (EIDs)



a, **b**, Disease alerts in the ProMED database for pathogenic fungi of animals and plants (**a**), and the spatial location of the associated reports (**b**). **c**, **d**, Relative proportions of species extinction and/or extirpation events for major classes of infectious disease agents (**c**) and their temporal trends for fungal pathogens (**d**). Primary data sources are given in the Supplementary Information.

Fisher *et al* (2013) Nature

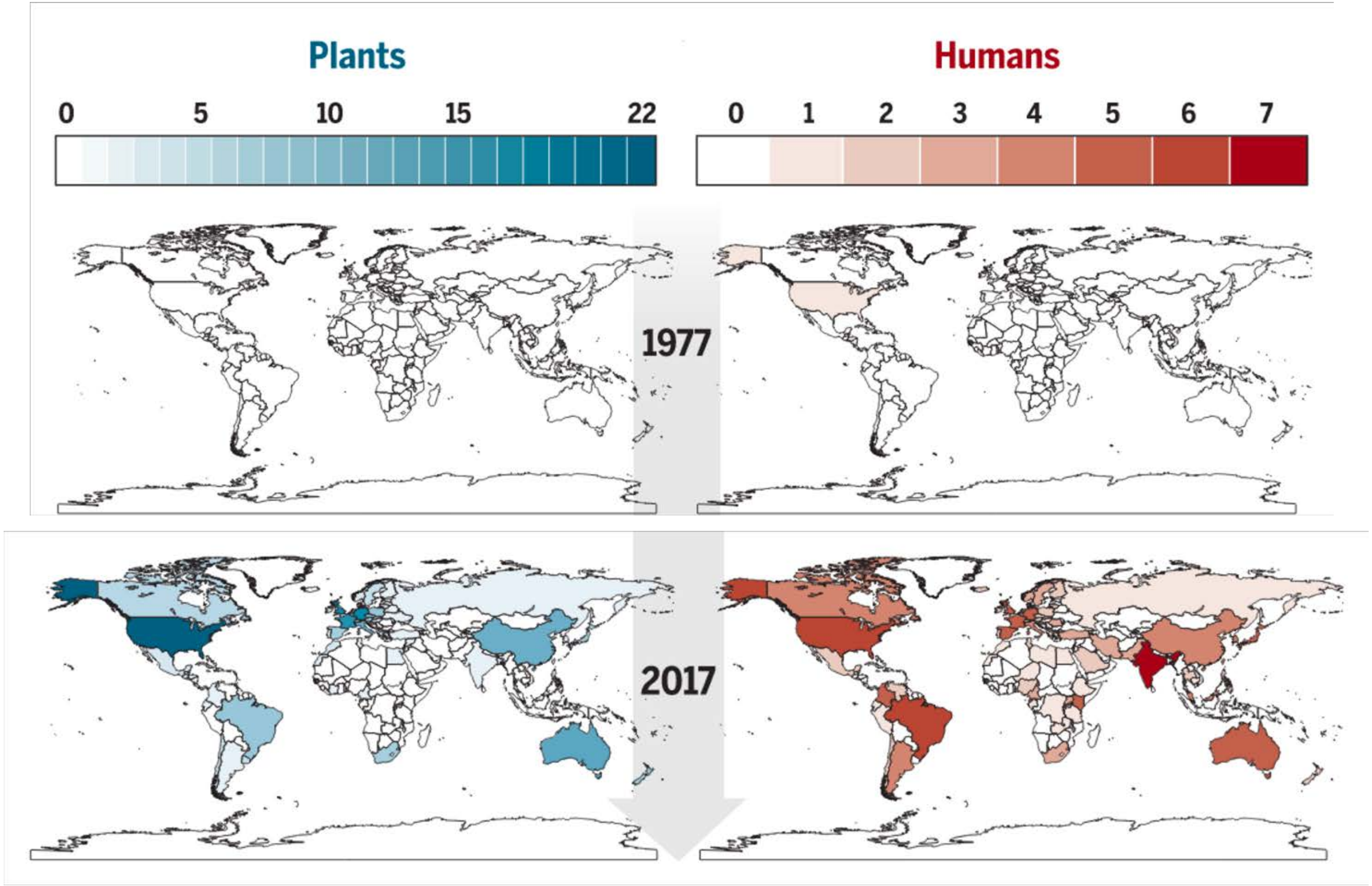
Worldwide emergence of resistance to antifungal drugs challenges human health and food security

Matthew C. Fisher,[1*] Nichola J. Hawkins,[2] Dominique Sanglard,[3] Sarah J. Gurr[4,5*]

The recent rate of emergence of pathogenic fungi that are resistant to the limited number of commonly used antifungal agents is unprecedented. The azoles, for example, are used not only for human and animal health care and crop protection but also in antifouling coatings and timber preservation. The ubiquity and multiple uses of azoles have hastened the independent evolution of resistance in many environments. One consequence is an increasing risk in human health care from naturally occurring opportunistic fungal pathogens that have acquired resistance to this broad class of chemicals. To avoid a global collapse in our ability to control fungal infections and to avoid critical failures in medicine and food security, we must improve our stewardship of extant chemicals, promote new antifungal discovery, and leverage emerging technologies for alternative solutions.

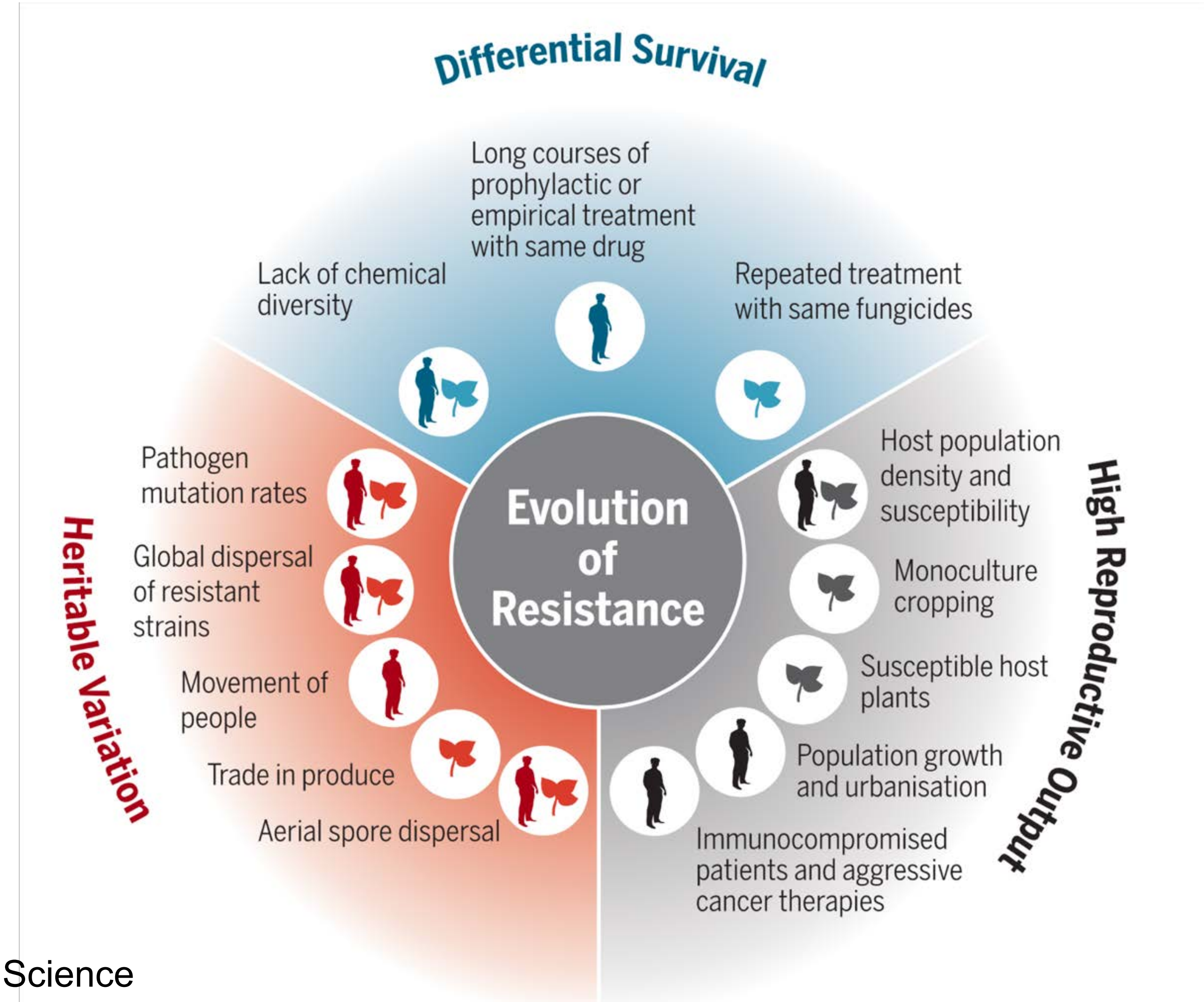
Fisher *et al* (2018) Science

Fungal species with reported antifungal resistance, by country



Fisher *et al* (2018) Science

Evolutionary drivers of antifungal resistance



Differential Survival

Long courses of prophylactic or empirical treatment with same drug

Lack of chemical diversity

Repeated treatment with same fungicides

Heritable Variation

Pathogen mutation rates

Global dispersal of resistant strains

Movement of people

Trade in produce

Aerial spore dispersal

Evolution of Resistance

High Reproductive Output

Host population density and susceptibility

Monoculture cropping

Susceptible host plants

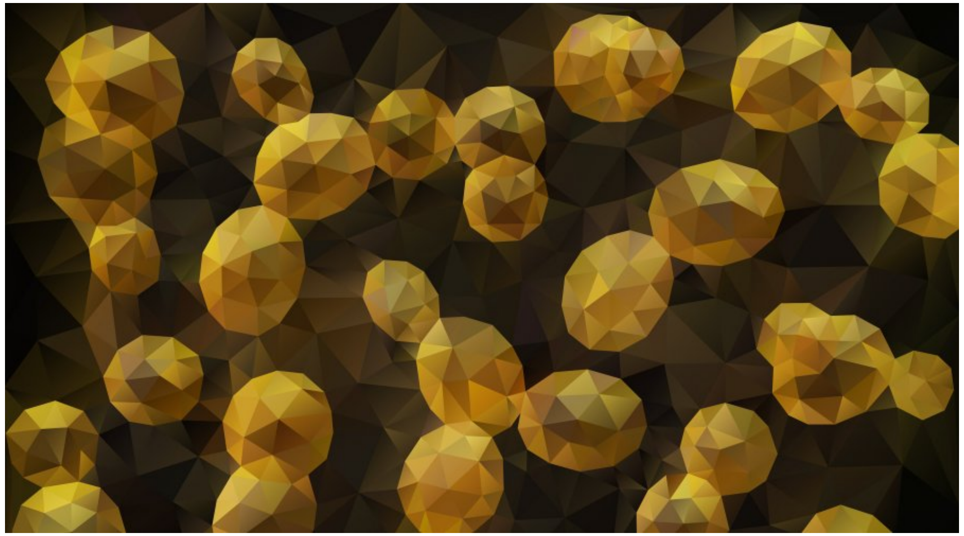
Population growth and urbanisation

Immunocompromised patients and aggressive cancer therapies

Fisher *et al* (2018) Science

How do we study all these?

Model organisms



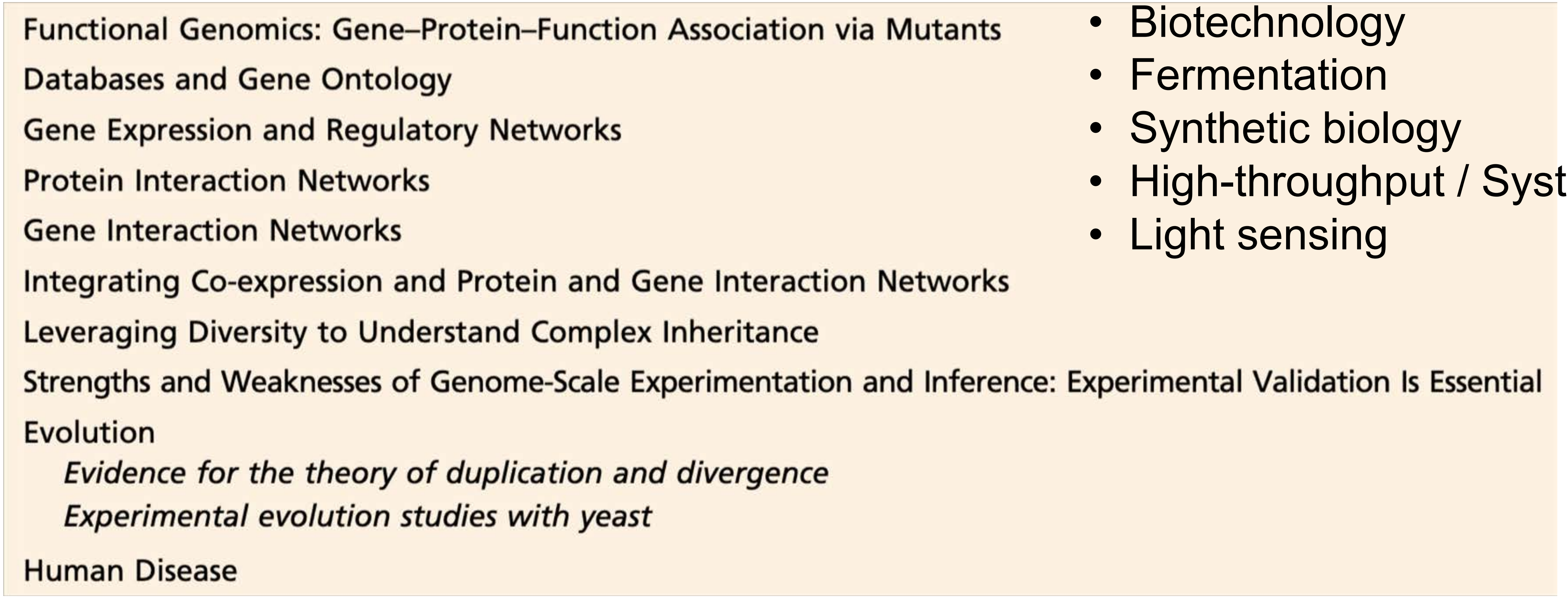
- Easy to maintain and breed in a laboratory setting.
- Many model organisms can breed in large numbers.
- Some have a very short generation time, which is the time between being born and being able to reproduce, so several generations can be followed at once
- Mutants allow scientists to study certain characteristics or diseases.
- Easy and cheap genetic manipulation
- Some model organisms have orthologs to humans.
- Model organisms can be used to create highly detailed genetic maps.
- Or they may occupy a pivotal position in the evolutionary tree

https://www.yourgenome.org/facts/what-are-model-organisms

Research in model yeast *Saccharomyces cerevisiae*

Yeast: An Experimental Organism for 21st Century Biology

David Botstein*,[1] and Gerald R. Fink†
*Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, New Jersey 08544, and †Whitehead Institute for Biomedical Research and Massachusetts Institute of Technology, Cambridge, Massachusetts 02139



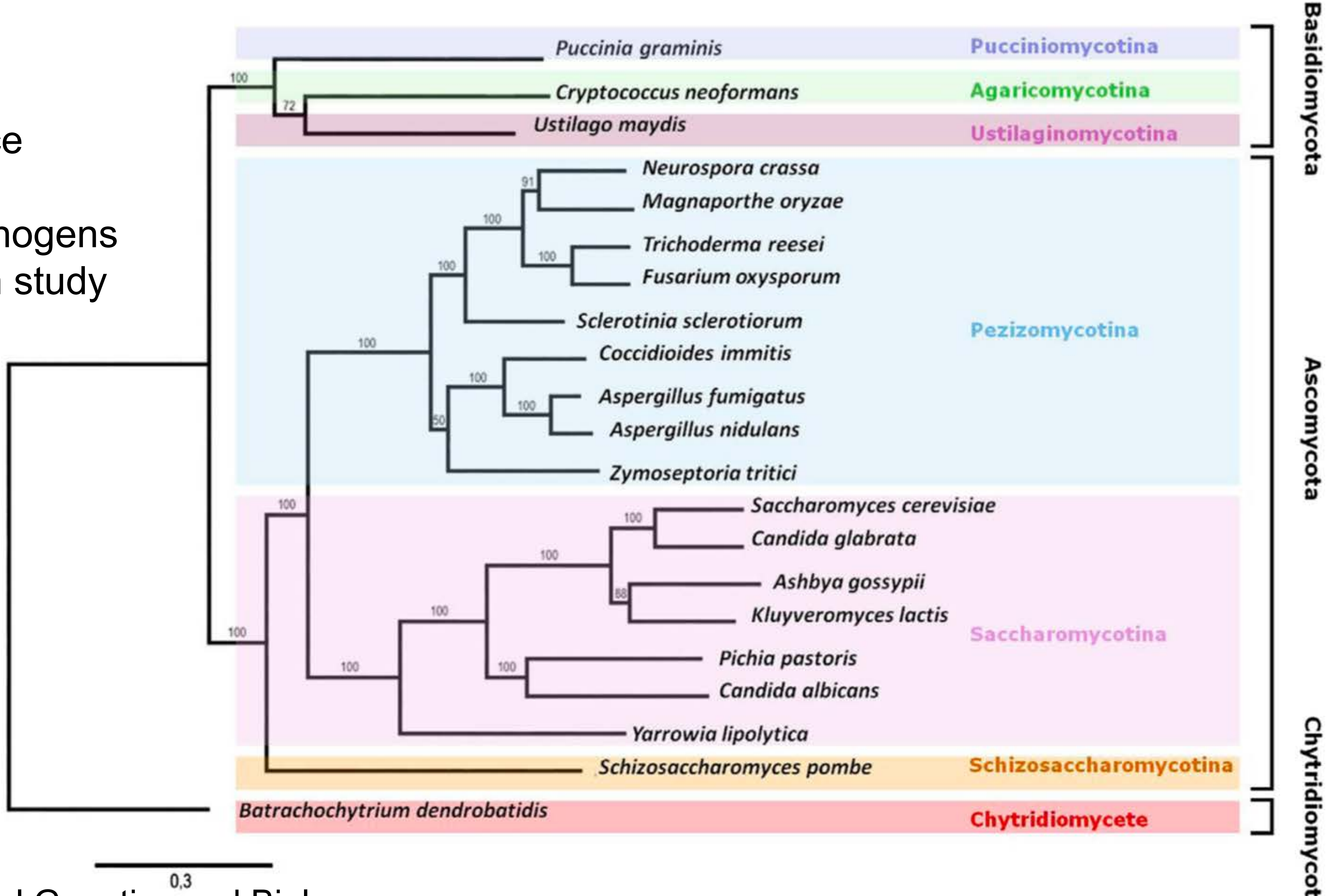
Functional Genomics: Gene–Protein–Function Association via Mutants
Databases and Gene Ontology
Gene Expression and Regulatory Networks
Protein Interaction Networks
Gene Interaction Networks
Integrating Co-expression and Protein and Gene Interaction Networks
Leveraging Diversity to Understand Complex Inheritance
Strengths and Weaknesses of Genome-Scale Experimentation and Inference: Experimental Validation Is Essential
Evolution
    Evidence for the theory of duplication and divergence
    Experimental evolution studies with yeast
Human Disease

- Biotechnology
- Fermentation
- Synthetic biology
- High-throughput / Systematic
- Light sensing

https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3213361/pdf/695.pdf

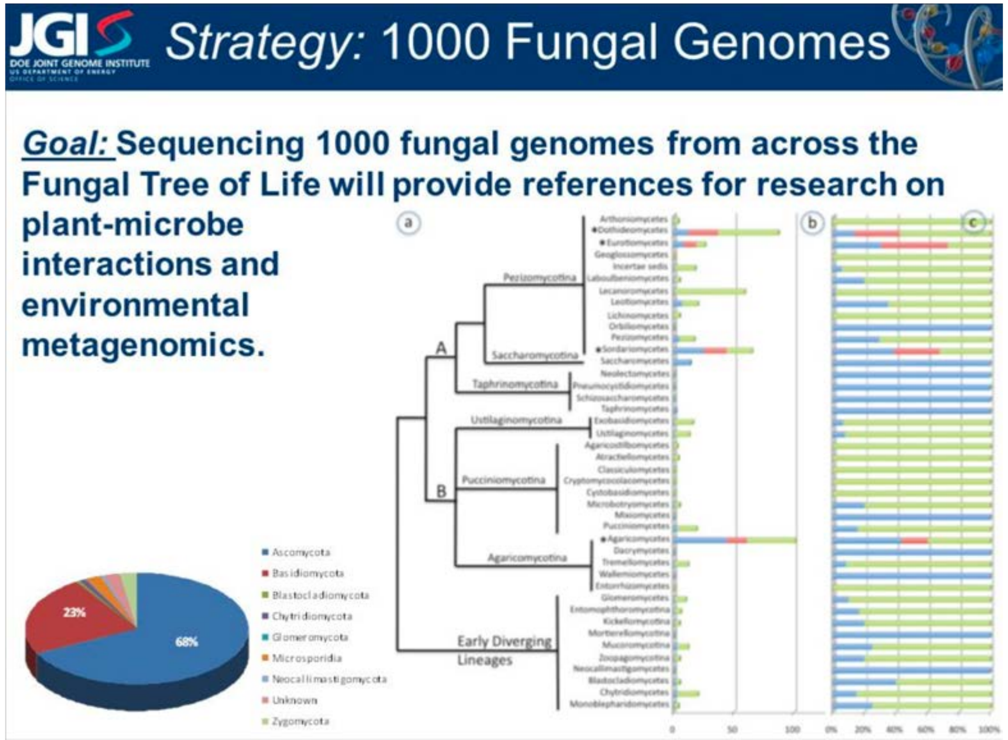
Research in other model fungi

- All have genome sequence available
- Most are animal/plant pathogens
- So much emphasis put on study of virulence



Perez-Nadales *et al* (2014) Fungal Genetics and Biology

Fungal genomes



JGI DOE JOINT GENOME INSTITUTE US DEPARTMENT OF ENERGY OFFICE OF SCIENCE *Strategy:* 1000 Fungal Genomes

Goal: **Sequencing 1000 fungal genomes from across the Fungal Tree of Life will provide references for research on plant-microbe interactions and environmental metagenomics.**

SCIENTIFIC REPORTS

OPEN

The Genome Sequences of 90 Mushrooms

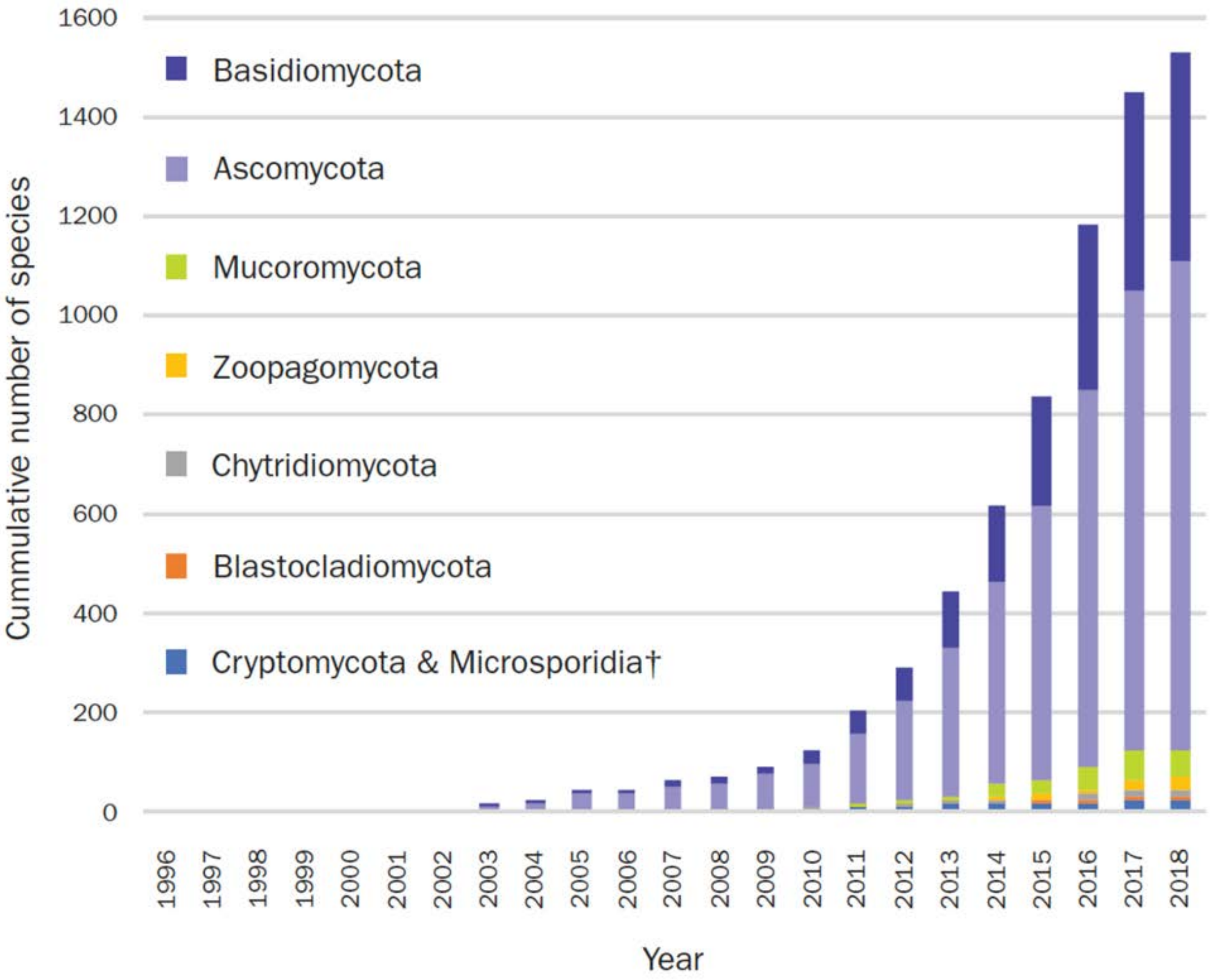
Huiying Li[1], Surui Wu[3], Xiao Ma[4,5], Wei Chen[2,4], Jing Zhang[6], Shengchang Duan[6], Yun Gao[6], Ling Kui[7,8], Wenli Huang[12], Peng Wu[4], Ruoyu Shi[4,5], Yifan Li[5], Yuanzhong Wang[9], Jieqing Li[9], Xiang Guo[3], Xiaoli Luo[3], Qiang Li[12], Chuan Xiong[12], Honggao Liu[9], Mingying Gui[3], Jun Sheng[4,5] & Yang Dong[2,10,11]

d: 4 December 2017

d: 6 June 2018

FIGURE 1: CUMULATIVE NUMBER OF FUNGAL SPECIES WITH WHOLE-GENOME SEQUENCES

[Data collated from online genome databases including NCBI Genome database (ncbi.nlm.nih.gov/genome), JGI Genome Portal: MycoCosm (genome.jgi.doe.gov/fungi), and EnsembleFungi (fungi.ensembl.org)]

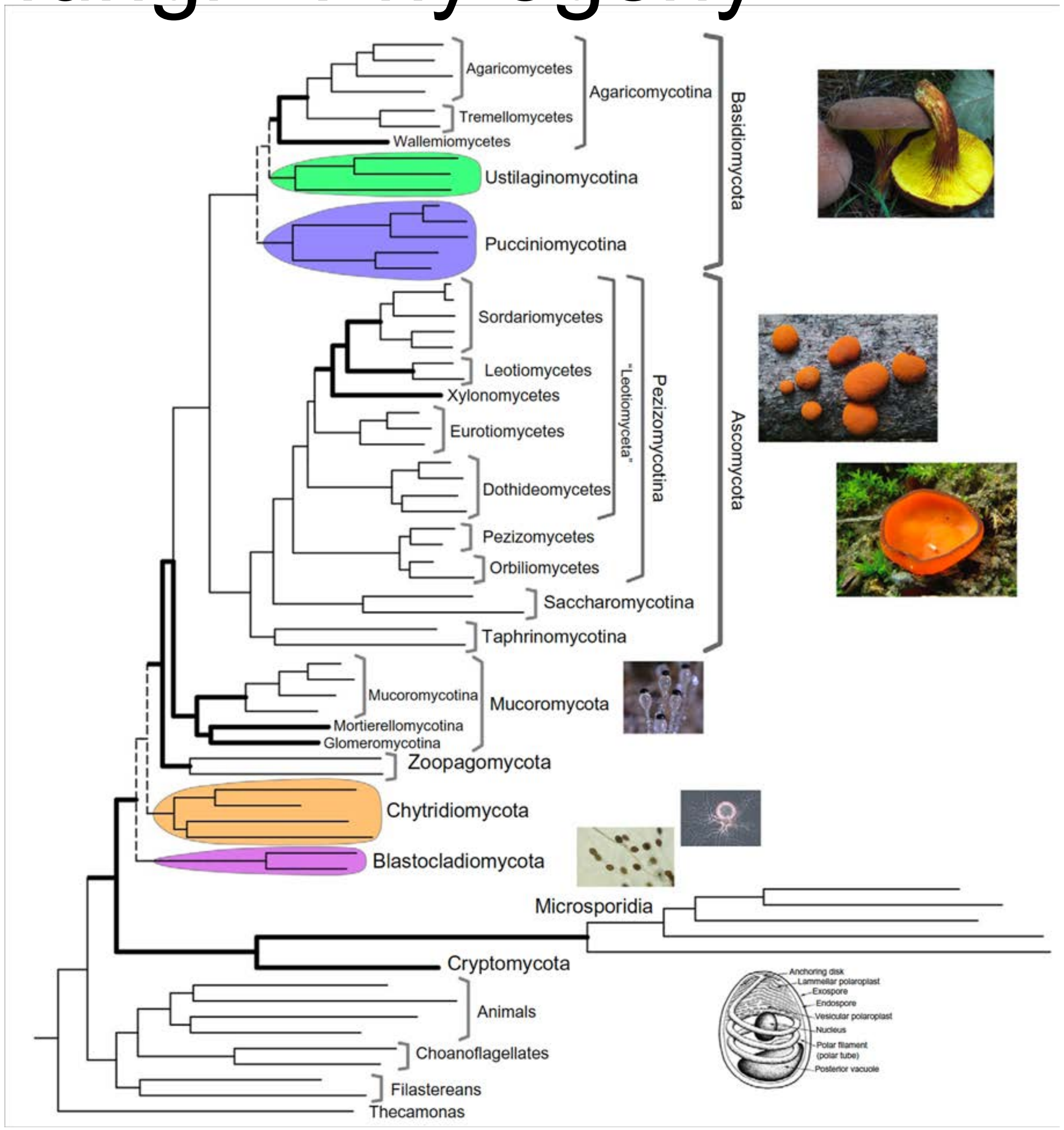


Importance of genomics in fungi - Phylogeny

The accelerating pace of fungal genome sequencing by a number of large-scale sequencing projects paved the way for assembling larger and taxon-specific datasets that clarified some of the puzzling fungal relationships.

- sister relationship between the Leotiomycetes and Sordariomycetes
- resolved the position of the Xylonomycetes, a small class of leaf endophytes,as a sister group to the Lecanoromycetes and Eurotiomycetes.

Resolving ancient divergences poses significant challenges even for phylogenomic datasets. For example, the definition of the fungal kingdom and the placement of the Microsporidia as fungi or nonfungal eukaryotes have been debated. (to be discussed in the next lecture)



Nagy and Szollosi (2017) Fungal Phylogenetics and Phylogenomics

Importance of genomics in fungi - Comparative

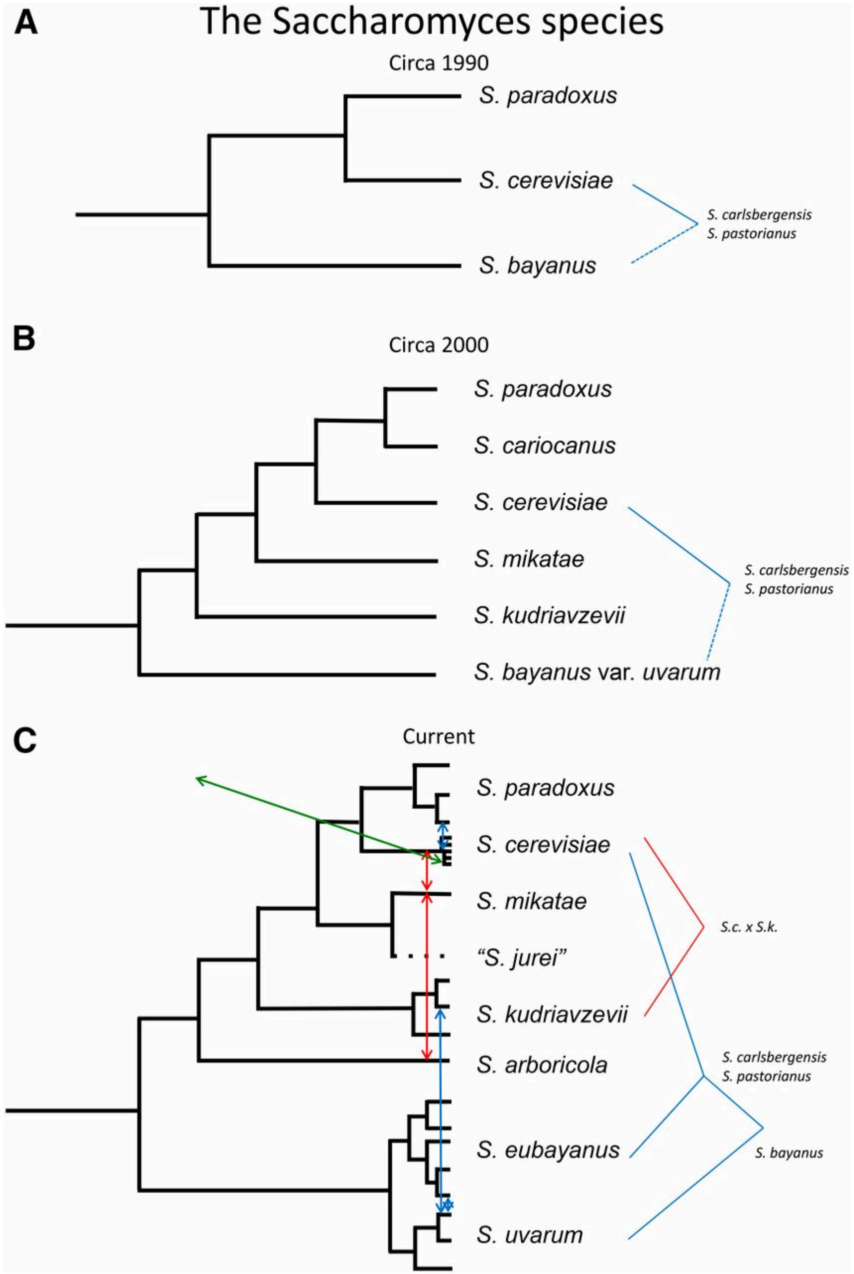
- Comparative genomics analysis of *S. cerevisiae* and closely related species has contributed to our understanding of **how new species emerge and has shed light on the various mechanisms that contribute to reproductive isolation.**

- Genomic analysis of *Saccharomyces* yeasts has provided a better understanding of the mechanisms underlying large-scale genomic changes, such as polyploidy, and their consequences for genome evolution and cell physiology.

- Genomic approaches are increasingly contributing to our understanding of how budding yeasts adapt to natural environments by identifying the genes that are involved in adaptation within natural substrates.

Dujon and Louis (2017) Genetics

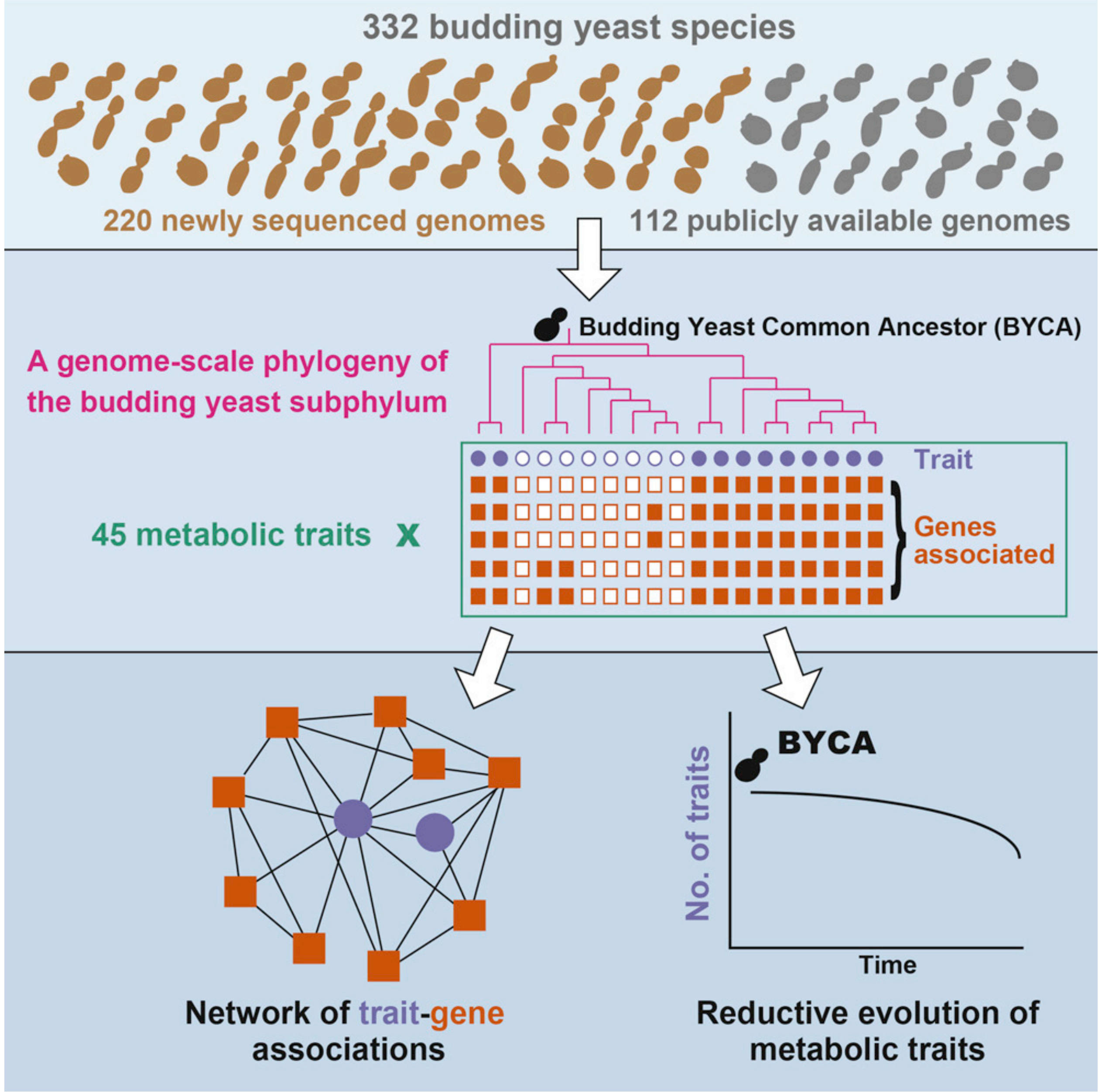
Marsit *et al* (2017) Nature Genetics Review



Importance of genomics in fungi - Comparative (example)

Highlights

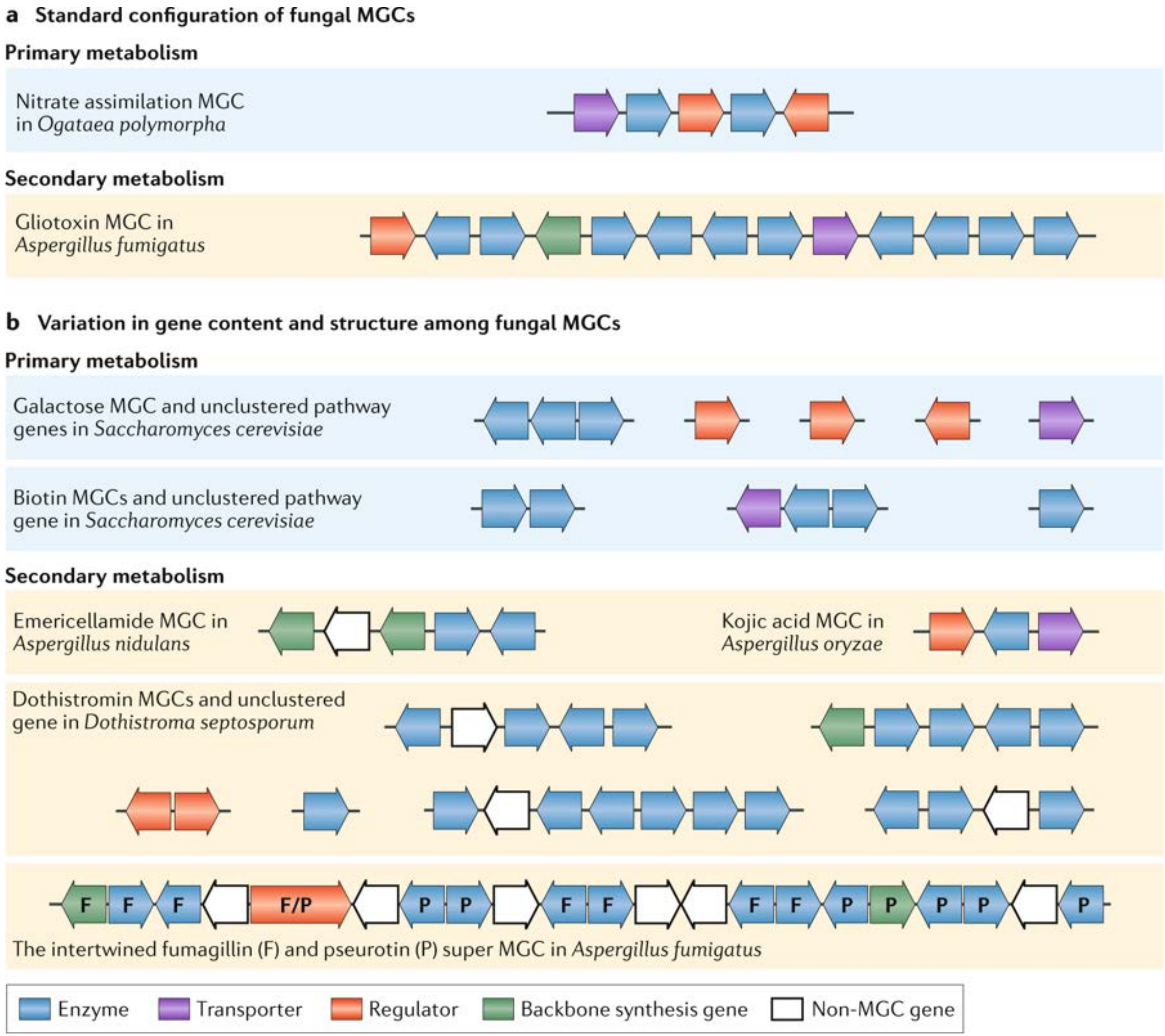
- 332 genomes, including 220 newly sequenced, covering ~1/3 of known budding yeasts
- Genome-scale inference of robust phylogeny and time tree of budding yeast subphylum
- Reconstruction of 45 metabolic traits infers complex budding yeast common ancestor
- Reductive evolution of traits and genes is a major mode of evolutionary diversification



Shen *et al* (2018) Cell

Importance of genomics in fungi - Comparative (example2)

- Fungi contain a remarkable diversity of both primary and secondary metabolic pathways involved in ecologically specialized or accessory functions.
- Genes in these pathways are frequently physically linked on fungal chromosomes, forming metabolic gene clusters (MGCs).
- Improved knowledge of the evolutionary life cycle of MGCs will advance our understanding of the ecology of specialized metabolism and of the interplay between the lifestyle of an organism and genome architecture.



Rokas *et al* (2018) Nature Reviews Microbiology

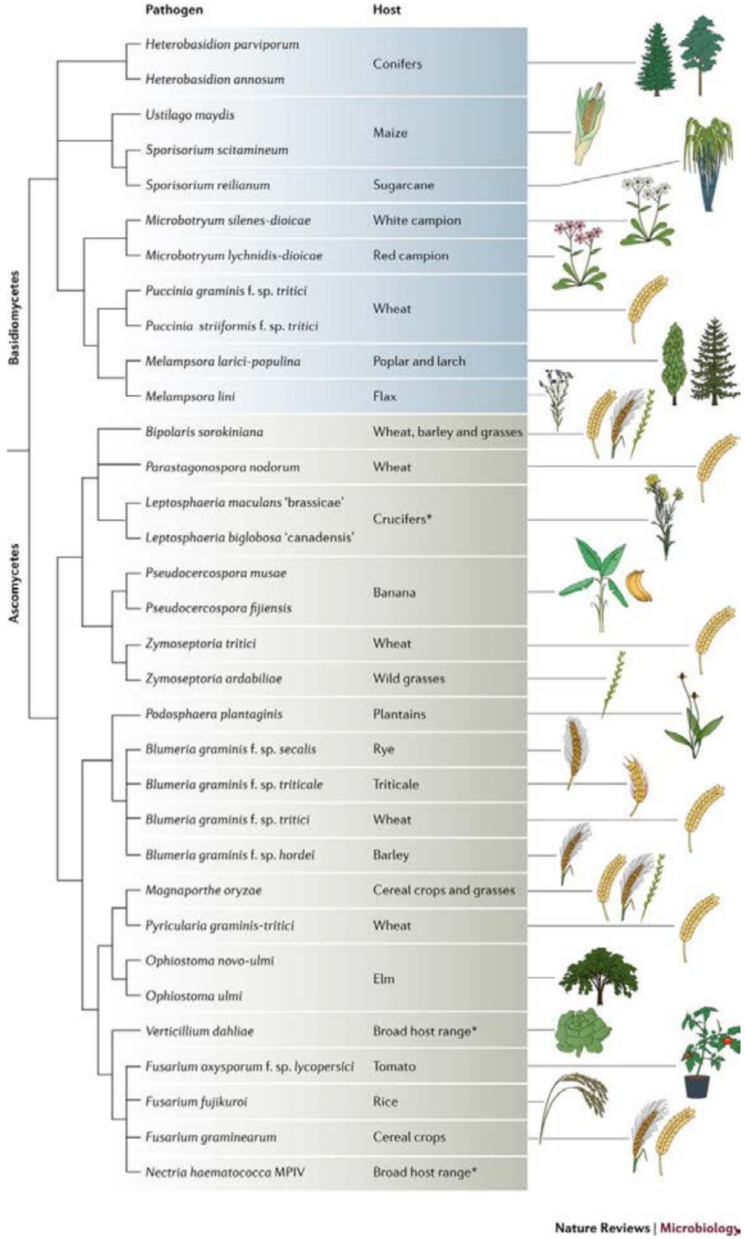
Importance of genomics in fungi – plant pathogens

- The genomes of fungal plant pathogens can vary in size and composition, even between closely related species. Differences in the content of transposable elements cause variation in genome architecture.

- Variation in genome architecture results from differences in population genetic factors, including effective population size and the strength of genetic drift.

- During periods of low effective population size, non-adaptive mutations, such as transposable elements, can invade genomes and shape their architecture.

- Transposable elements contribute to the establishment and maintenance of rapidly evolving genome compartments that can comprise virulence genes. High mutation rates in these compartments support the evolution of new virulence phenotypes.



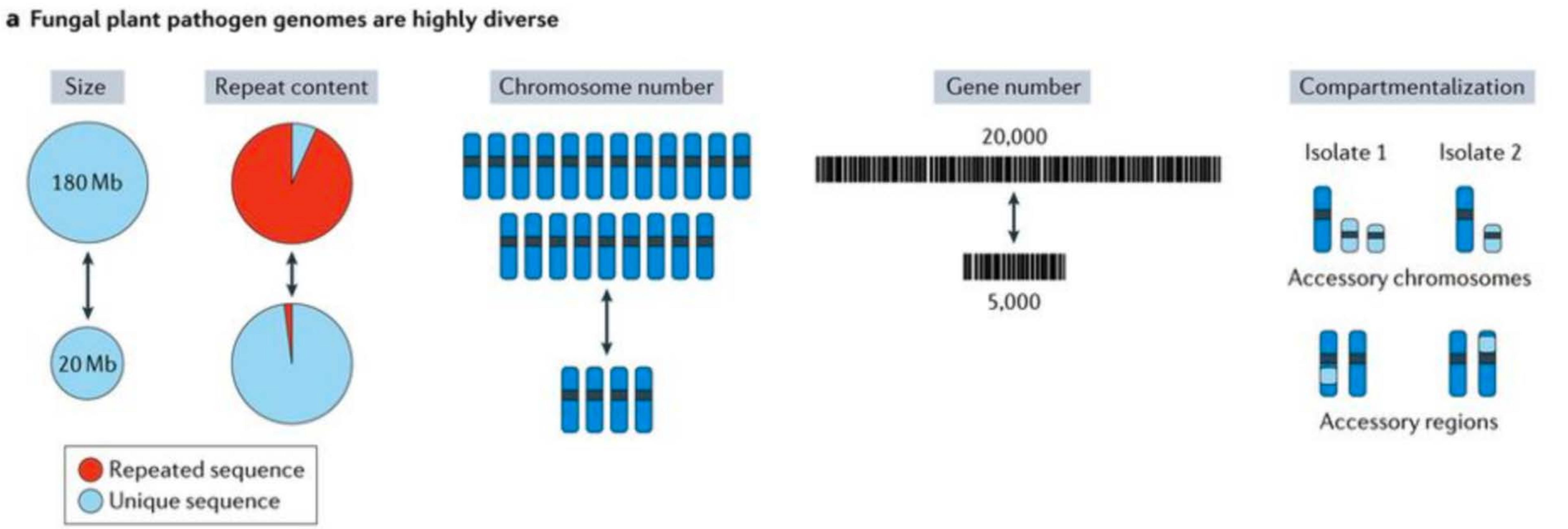
Pathogen	Host
Heterobasidion parviporum	Conifers
Heterobasidion annosum	
Ustilago maydis	Maize
Sporisorium scitamineum	
Sporisorium reilianum	Sugarcane
Microbotryum silenes-dioicae	White campion
Microbotryum lychnidis-dioicae	Red campion
Puccinia graminis f. sp. *tritici*	Wheat
Puccinia striiformis f. sp. *tritici*	
Melampsora larici-populina	Poplar and larch
Melampsora lini	Flax
Bipolaris sorokiniana	Wheat, barley and grasses
Parastagonospora nodorum	Wheat
Leptosphaeria maculans 'brassicae'	Crucifers*
Leptosphaeria biglobosa 'canadensis'	
Pseudocercospora musae	Banana
Pseudocercospora fijiensis	
Zymoseptoria tritici	Wheat
Zymoseptoria ardabiliae	Wild grasses
Podosphaera plantaginis	Plantains
Blumeria graminis f. sp. *secalis*	Rye
Blumeria graminis f. sp. *triticale*	Triticale
Blumeria graminis f. sp. *tritici*	Wheat
Blumeria graminis f. sp. *hordei*	Barley
Magnaporthe oryzae	Cereal crops and grasses
Pyricularia graminis-tritici	Wheat
Ophiostoma novo-ulmi	Elm
Ophiostoma ulmi	
Verticillium dahliae	Broad host range*
Fusarium oxysporum f. sp. *lycopersici*	Tomato
Fusarium fujikuroi	Rice
Fusarium graminearum	Cereal crops
Nectria haematococca MPIV	Broad host range*

Nature Reviews | Microbiology

Mareike Möller & Eva H. Stukenbrock (2017) Nature Microbiology Review

Importance of genomics in fungi – plant pathogens

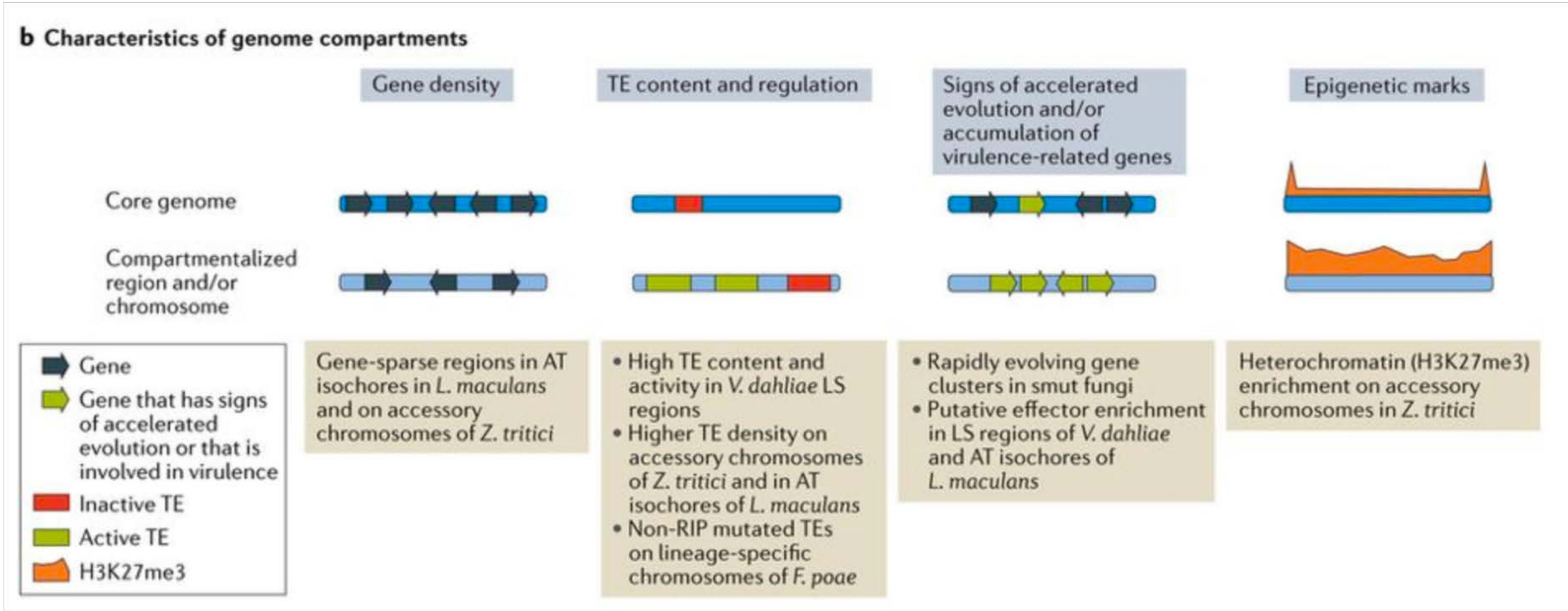
- The genomes of fungal plant pathogens can vary in size and composition, even between closely related species. Differences in the content of transposable elements cause variation in genome architecture..



Mareike Möller & Eva H. Stukenbrock (2017) Nature Microbiology Review

Importance of genomics in fungi – plant pathogens

- The genomes of fungal plant pathogens can vary in size and composition, even between closely related species. Differences in the content of transposable elements cause variation in genome architecture..



b Characteristics of genome compartments

Gene-sparse regions in AT isochores in *L. maculans* and on accessory chromosomes of *Z. tritici*

- High TE content and activity in *V. dahliae* LS regions
- Higher TE density on accessory chromosomes of *Z. tritici* and in AT isochores of *L. maculans*
- Non-RIP mutated TEs on lineage-specific chromosomes of *F. poae*

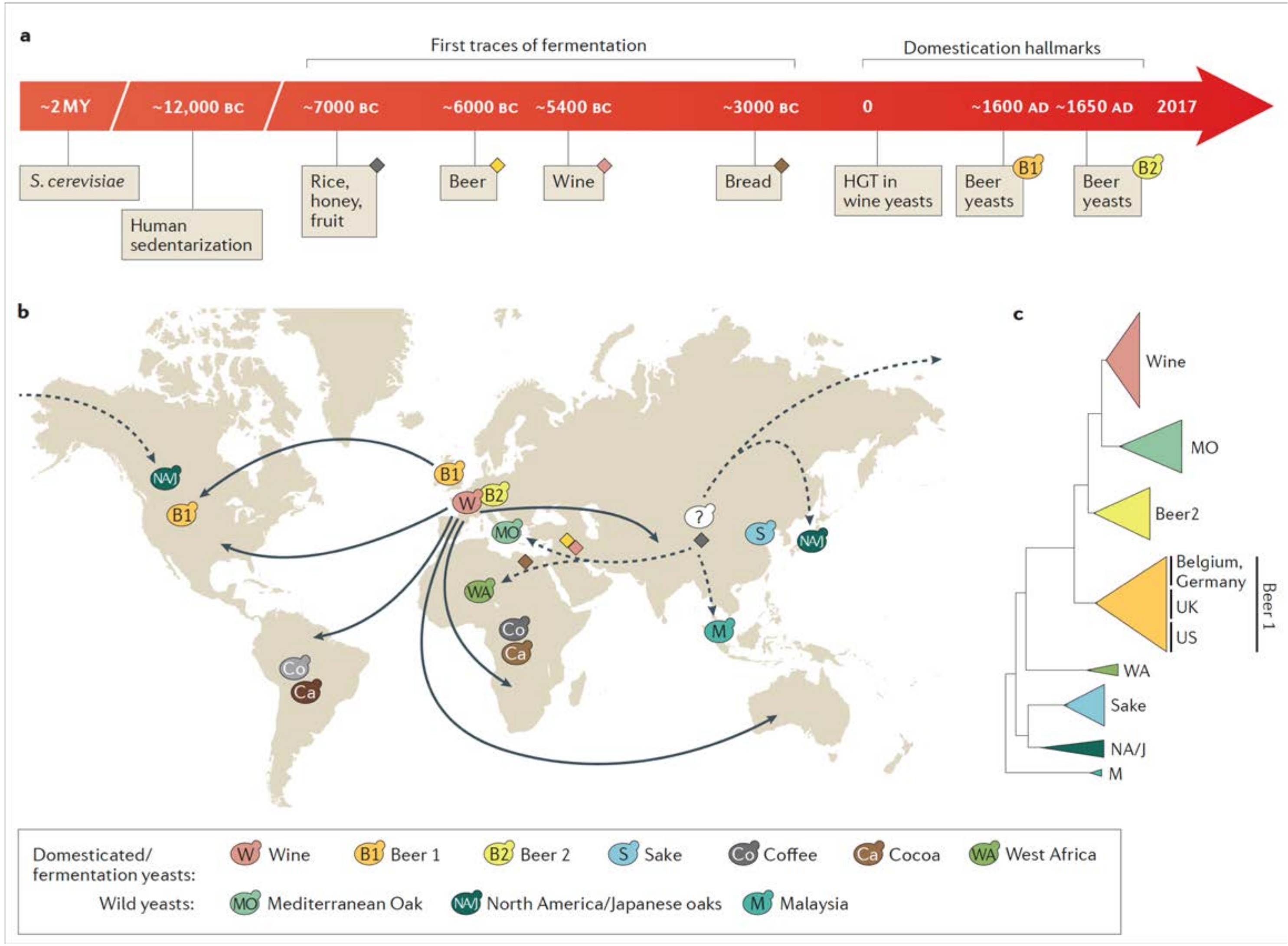
- Rapidly evolving gene clusters in smut fungi
- Putative effector enrichment in LS regions of *V. dahliae* and AT isochores of *L. maculans*

Heterochromatin (H3K27me3) enrichment on accessory chromosomes in *Z. tritici*

Mareike Möller & Eva H. Stukenbrock (2017) Nature Microbiology Review

Importance of genomics in fungi - Population

- Population genomics and comparative genomics of *Saccharomyces* yeasts have revealed that hybridization occurred frequently throughout, and has had substantial effects on, yeast evolution. Hybridization could itself be a mechanism of adaptation and speciation.
- Genomic analysis of yeast strains associated with humans has revealed the history of yeast domestication and the mechanisms that have contributed to its adaptation to anthropogenic environments.



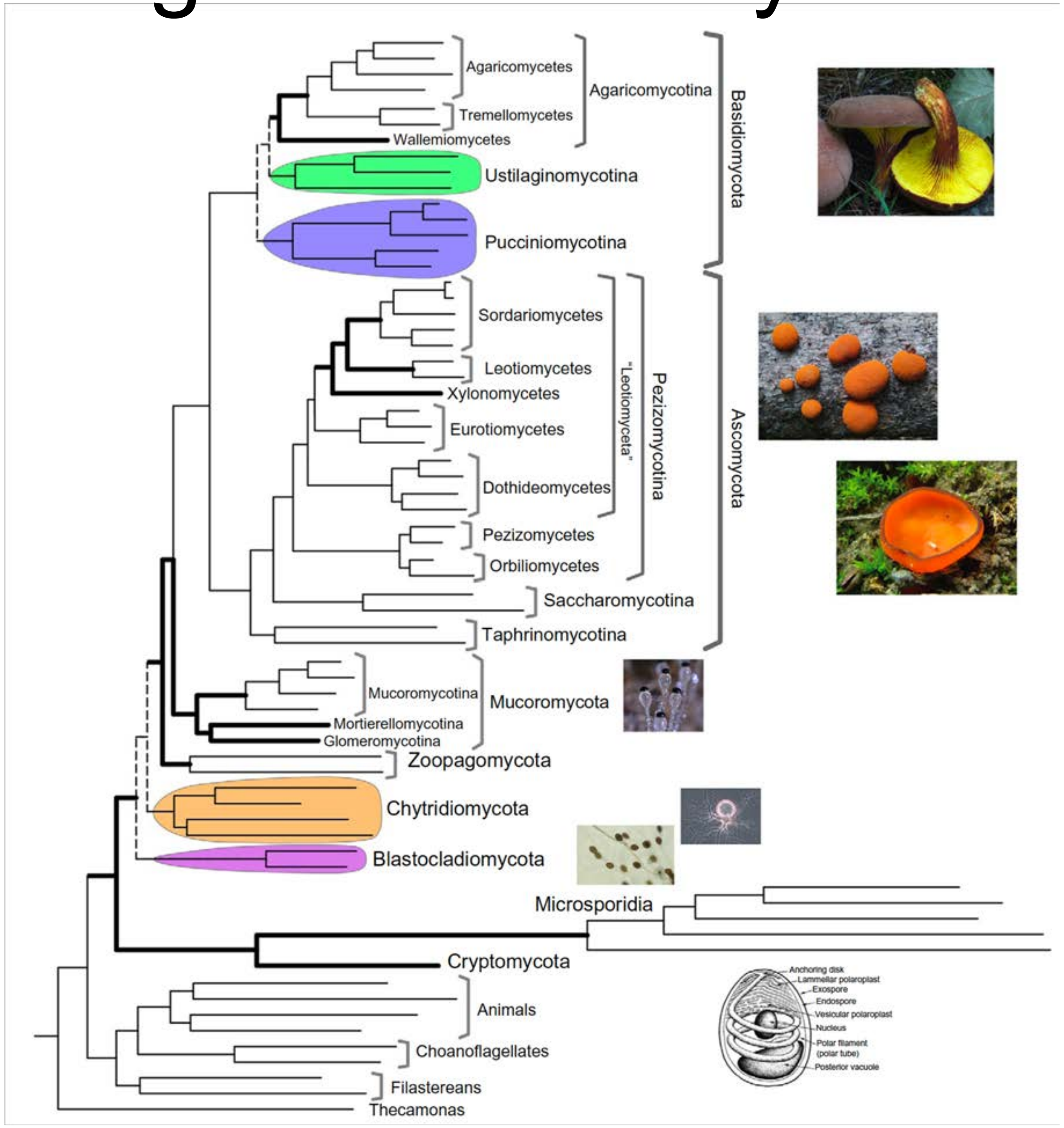
Marsit *et al* (2017) Nature Genetics Review

Importance of genomics in fungi - Community

The accelerating pace of fungal genome sequencing by a number of large-scale sequencing projects paved the way for assembling larger and taxon-specific datasets that clarified some of the puzzling fungal relationships.

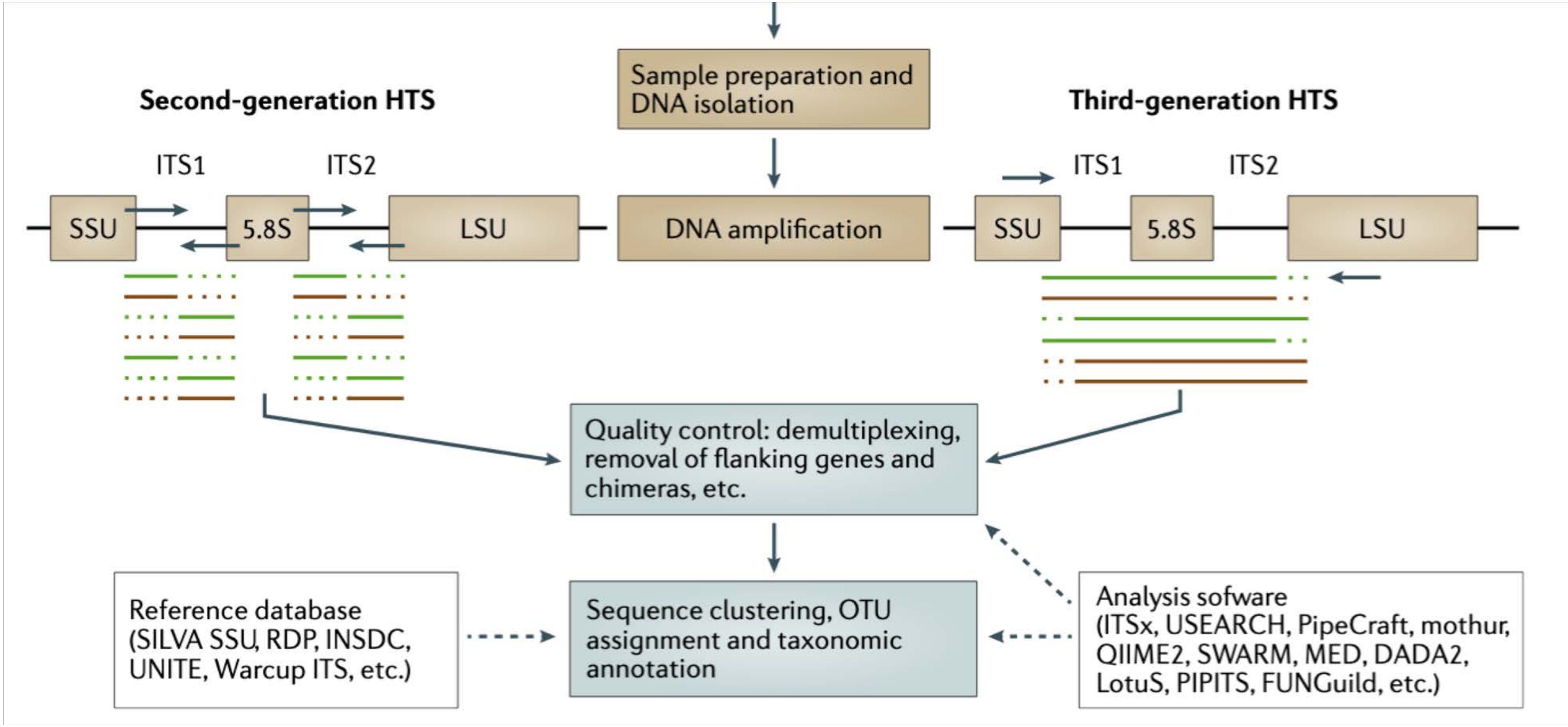
- sister relationship between the Leotiomycetes and Sordariomycetes
- resolved the position of the Xylonomycetes, a small class of leaf endophytes,as a sister group to the Lecanoromycetes and Eurotiomycetes.

Resolving ancient divergences poses significant challenges even for phylogenomic datasets. For example, the definition of the fungal kingdom and the placement of the Microsporidia as fungi or nonfungal eukaryotes have been debated. (to be discussed in the next lecture)



Marsit *et al* (2017) Nature Genetics Review

Main steps in a fungal metabarcoding project



Sample preparation and DNA isolation

DNA amplification

Quality control: demultiplexing, removal of flanking genes and chimeras, etc.

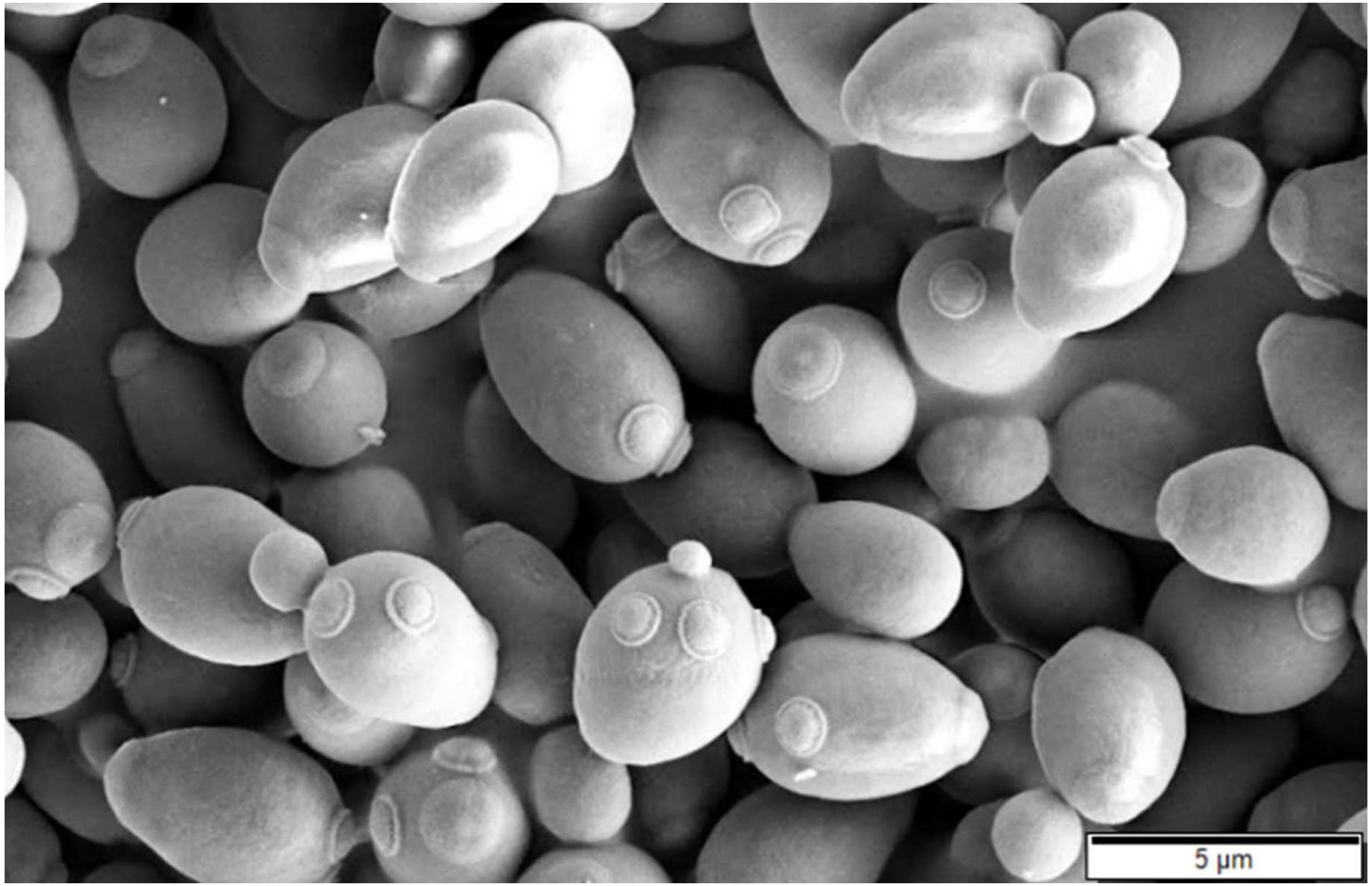
Sequence clustering, OTU assignment and taxonomic annotation

Reference database (SILVA SSU, RDP, INSDC, UNITE, Warcup ITS, etc.)

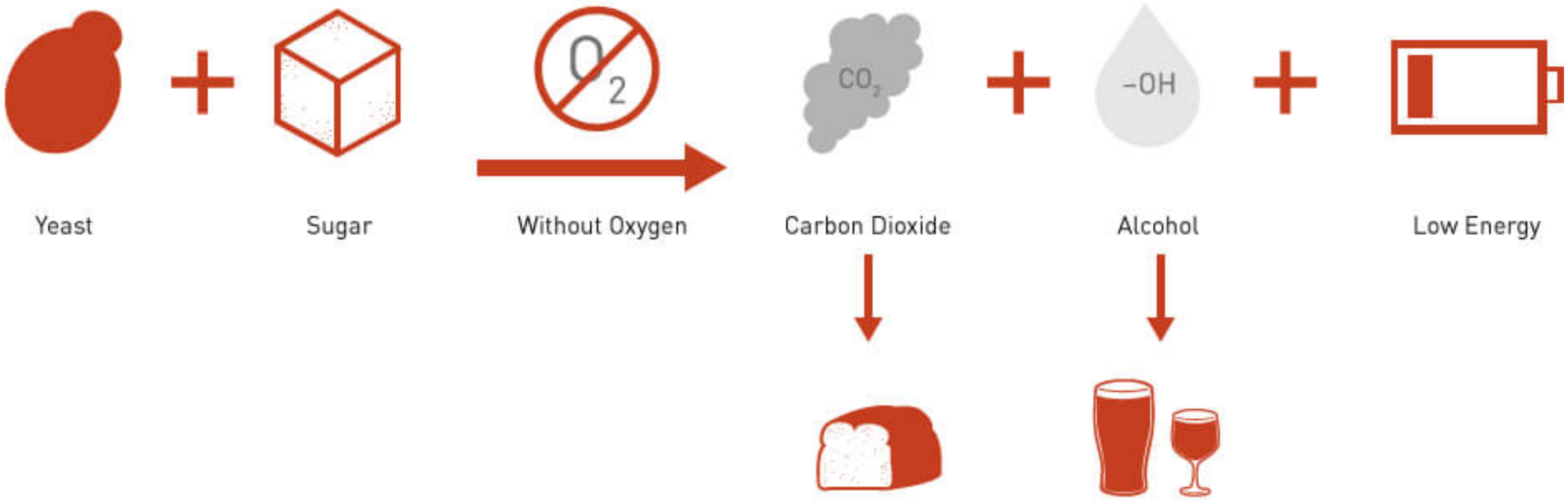
Analysis sofware (ITSx, USEARCH, PipeCraft, mothur, QIIME2, SWARM, MED, DADA2, LotuS, PIPITS, FUNGuild, etc.)

Nilsson *et al* (2018) Nature Reviews Microbiology

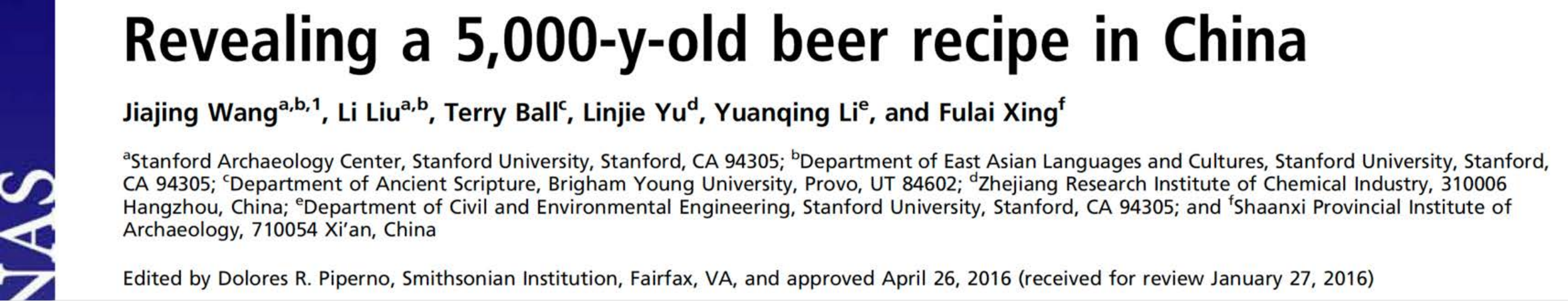
Case studies: Origin of *Saccharomyces cerevisiae*



S. cerevisiae arguably one of the most domesticated species for its fermentation product



https://www.singerinstruments.com/resource/what-is-yeast/



Revealing a 5,000-y-old beer recipe in China

Jiajing Wang[a,b,1], Li Liu[a,b], Terry Ball[c], Linjie Yu[d], Yuanqing Li[e], and Fulai Xing[f]

[a]Stanford Archaeology Center, Stanford University, Stanford, CA 94305; [b]Department of East Asian Languages and Cultures, Stanford University, Stanford, CA 94305; [c]Department of Ancient Scripture, Brigham Young University, Provo, UT 84602; [d]Zhejiang Research Institute of Chemical Industry, 310006 Hangzhou, China; [e]Department of Civil and Environmental Engineering, Stanford University, Stanford, CA 94305; and [f]Shaanxi Provincial Institute of Archaeology, 710054 Xi'an, China

Edited by Dolores R. Piperno, Smithsonian Institution, Fairfax, VA, and approved April 26, 2016 (received for review January 27, 2016)

https://www.youtube.com/watch?time_continue=2&v=ypenv68qt5s

'World's oldest brewery' found in cave in Israel, say researchers

FEMS Yeast Research, 15, 2015, fov009

doi: 10.1093/femsyr/fov009
Advance Access Publication Date: 27 February 2015
Commentary

COMMENTARY

Saccharomyces cerevisiae: a nomadic yeast with no niche?

Matthew R. Goddard[1,2,*] and Duncan Greig[3,4]

Role of social wasps in *Saccharomyces cerevisiae* ecology and evolution

Irene Stefanini[a,1], Leonardo Dapporto[b,c,1], Jean-Luc Legras[d,e,f], Antonio Calabretta[a,b], Monica Di Paola[g], Carlotta De Filippo[h], Roberto Viola[h], Paolo Capretti[c], Mario Polsinelli[b], Stefano Turillazzi[b,i], and Duccio Cavalieri[a,h,2]

[a]Dipartimento di Farmacologia, University of Florence, 50139, Florence, Italy; [b]Dipartimento di Biologia Evoluzionistica, University of Florence, 50125, Florence, Italy; [c]Dipartimento di Biotecnologie Agrarie, University of Florence, 50144, Florence, Italy; [d]INRA (Institut National de la Recherche Agronomique), UMR1083 (Unité Mixte de Recherche Sciences pour l'Oenologie), F-34060 Montpellier, France; [e]Montpellier SupAgro, UMR1083 (Unité Mixte de Recherche Sciences pour l'Oenologie), F-34060 Montpellier, France; [f]Université Montpellier I, UMR1083 (Unité Mixte de Recherche Sciences pour l'Oenologie), F-34060 Montpellier, France; [g]Dipartimento di Scienze per la Salute della Donna e del Bambino, Ospedale Pediatrico Meyer, University of Florence, 50139, Florence, Italy; [h]Centre for Research and Innovation, Fondazione Edmund Mach, Via E. Mach 1, 38010 San Michele all'Adige, Trento, Italy; and [i]Centro di Servizi di Spettromeria di Massa, University of Florence, Florence, Italy

Edited by Nancy A. Moran, Yale University, West Haven, CT, and approved July 5, 2012 (received for review May 18, 2012)

ARTICLE

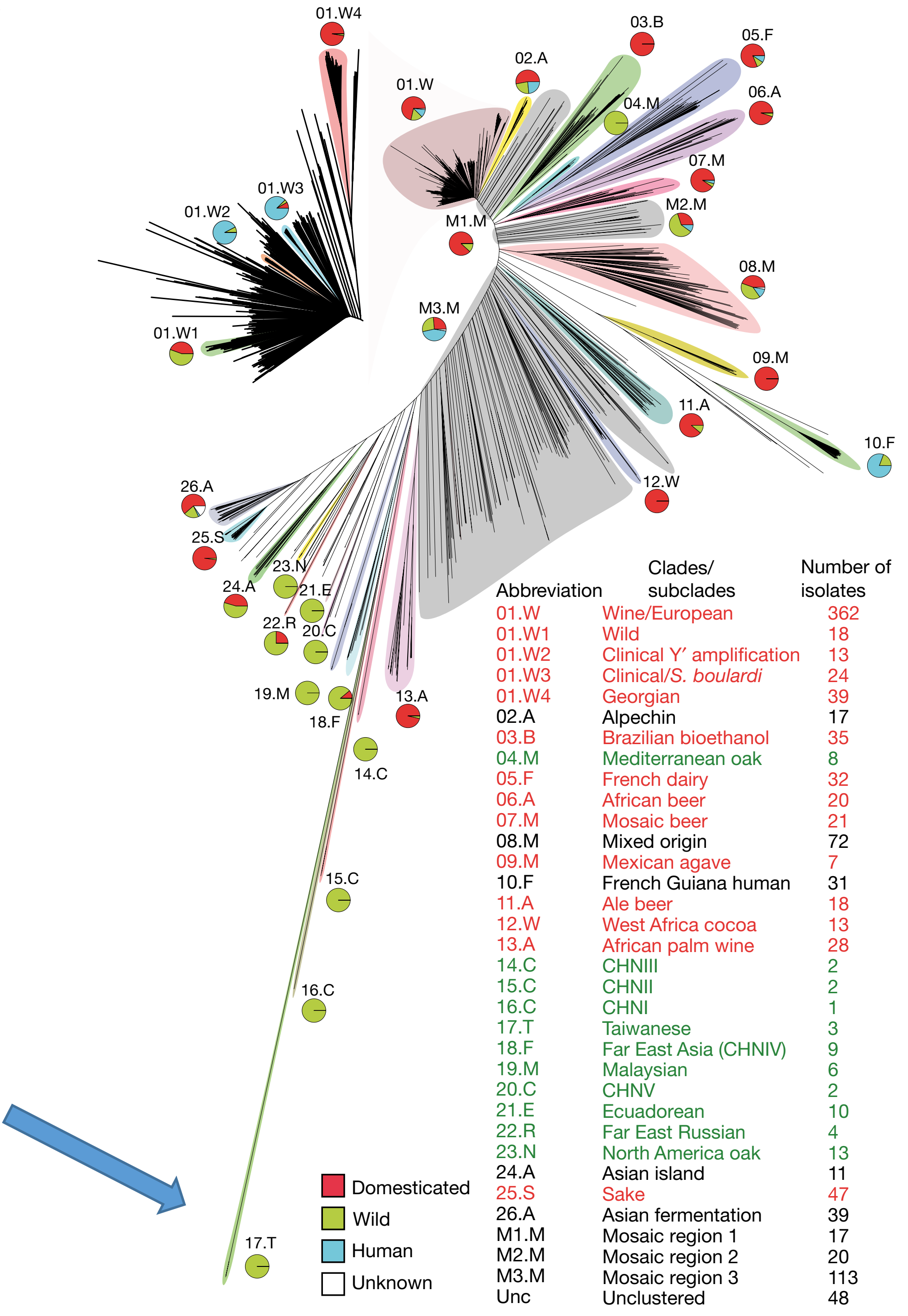
OPEN

https://doi.org/10.1038/s41586-018-0030-5

Genome evolution across 1,011 *Saccharomyces cerevisiae* isolates

Jackson Peter[1,6], Matteo De Chiara[2,6], Anne Friedrich[1], Jia-Xing Yue[2], David Pflieger[1], Anders Bergström[2], Anastasie Sigwalt[1], Benjamin Barre[2], Kelle Freel[1], Agnès Llored[2], Corinne Cruaud[3], Karine Labadie[3], Jean-Marc Aury[3], Benjamin Istace[3], Kevin Lebrigand[4], Pascal Barbry[4], Stefan Engelen[3], Arnaud Lemainque[3], Patrick Wincker[3,5,7], Gianni Liti[2,7]* & Joseph Schacherer[1,7]*

“The Taiwanese wild lineage represents the most divergent population that has yet been described (average of 1.1% sequence divergence to non-Taiwanese strains).”



🟥 Domesticated
🟩 Wild
🟦 Human
☐ Unknown

Abbreviation	Clades/ subclades	Number of isolates
01.W	Wine/European	362
01.W1	Wild	18
01.W2	Clinical Y′ amplification	13
01.W3	Clinical/*S. boulardi*	24
01.W4	Georgian	39
02.A	Alpechin	17
03.B	Brazilian bioethanol	35
04.M	Mediterranean oak	8
05.F	French dairy	32
06.A	African beer	20
07.M	Mosaic beer	21
08.M	Mixed origin	72
09.M	Mexican agave	7
10.F	French Guiana human	31
11.A	Ale beer	18
12.W	West Africa cocoa	13
13.A	African palm wine	28
14.C	CHNIII	2
15.C	CHNII	2
16.C	CHNI	1
17.T	Taiwanese	3
18.F	Far East Asia (CHNIV)	9
19.M	Malaysian	6
20.C	CHNV	2
21.E	Ecuadorean	10
22.R	Far East Russian	4
23.N	North America oak	13
24.A	Asian island	11
25.S	Sake	47
26.A	Asian fermentation	39
M1.M	Mosaic region 1	17
M2.M	Mosaic region 2	20
M3.M	Mosaic region 3	113
Unc	Unclustered	48

ARTICLE

DOI: 10.1038/s41467-018-05106-7

OPEN

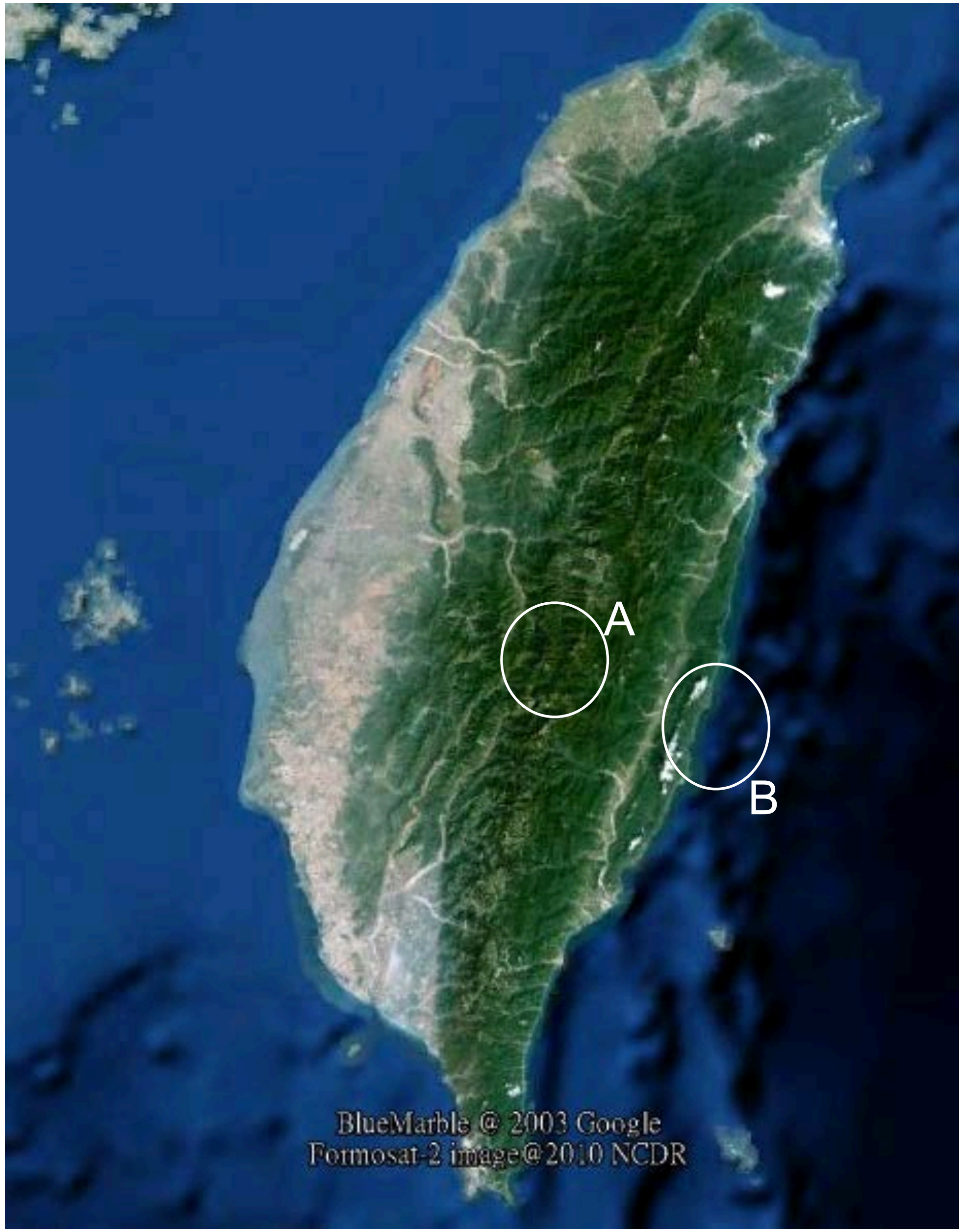
The origin and adaptive evolution of domesticated populations of yeast from Far East Asia

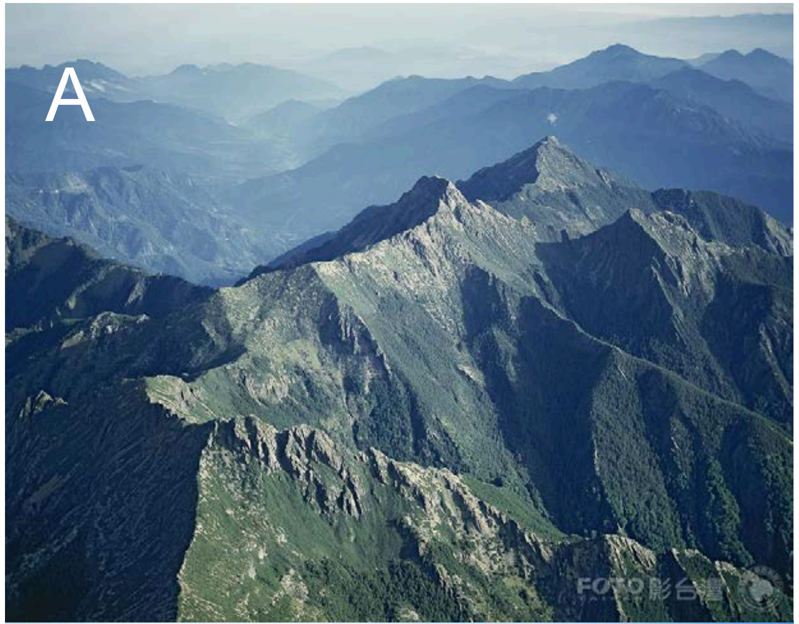
Shou-Fu Duan[1,2], Pei-Jie Han[1], Qi-Ming Wang[1], Wan-Qiu Liu[1], Jun-Yan Shi[1,2], Kuan Li[1], Xiao-Ling Zhang[1] & Feng-Yan Bai[1,2]

Case studies: fungi in Taiwan

Taiwan has 9% of world’s described fungal species

TaiBNET

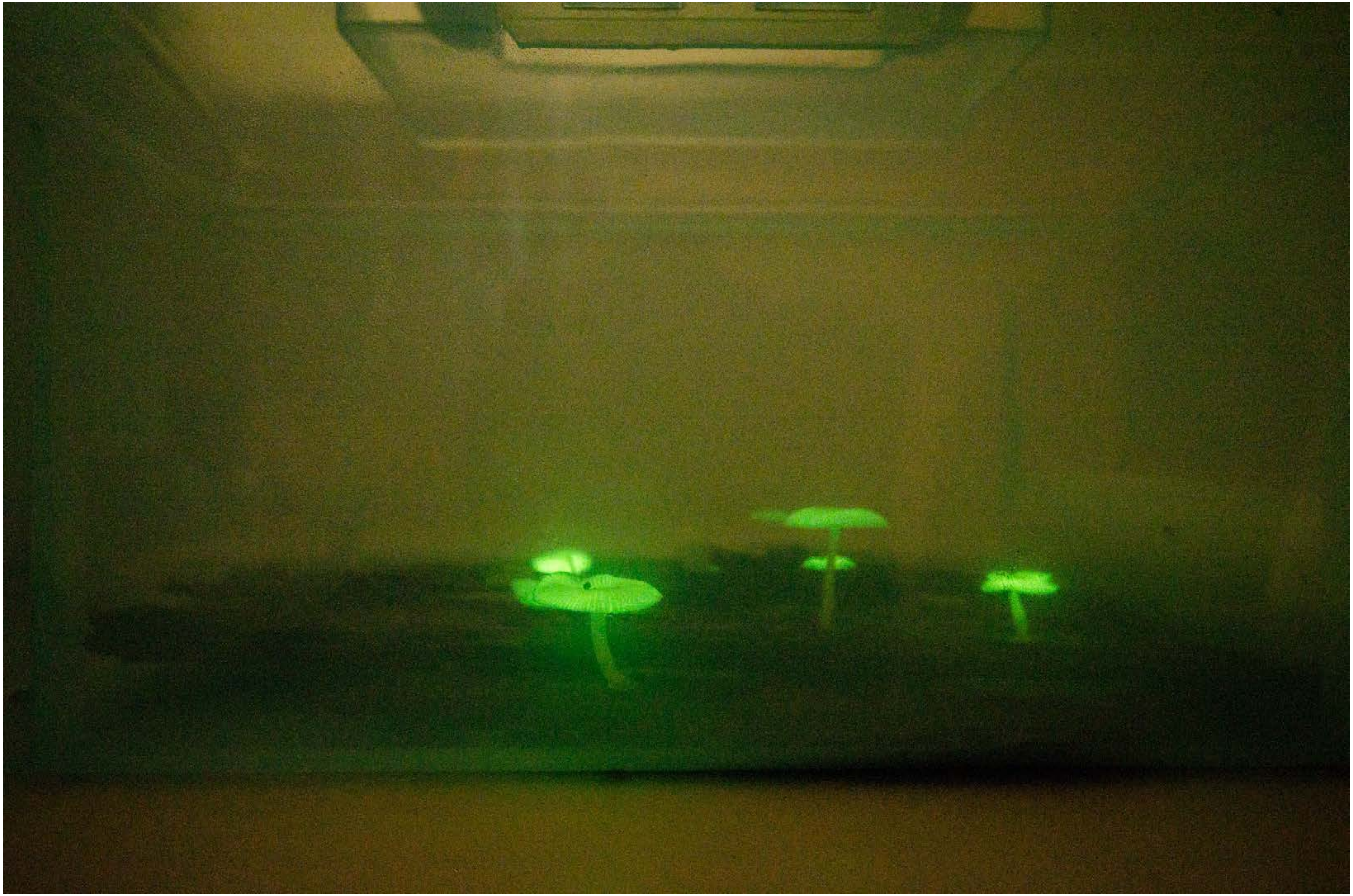

A
B
BlueMarble @ 2003 Google
Formosat-2 image@2010 NCDR


A


B

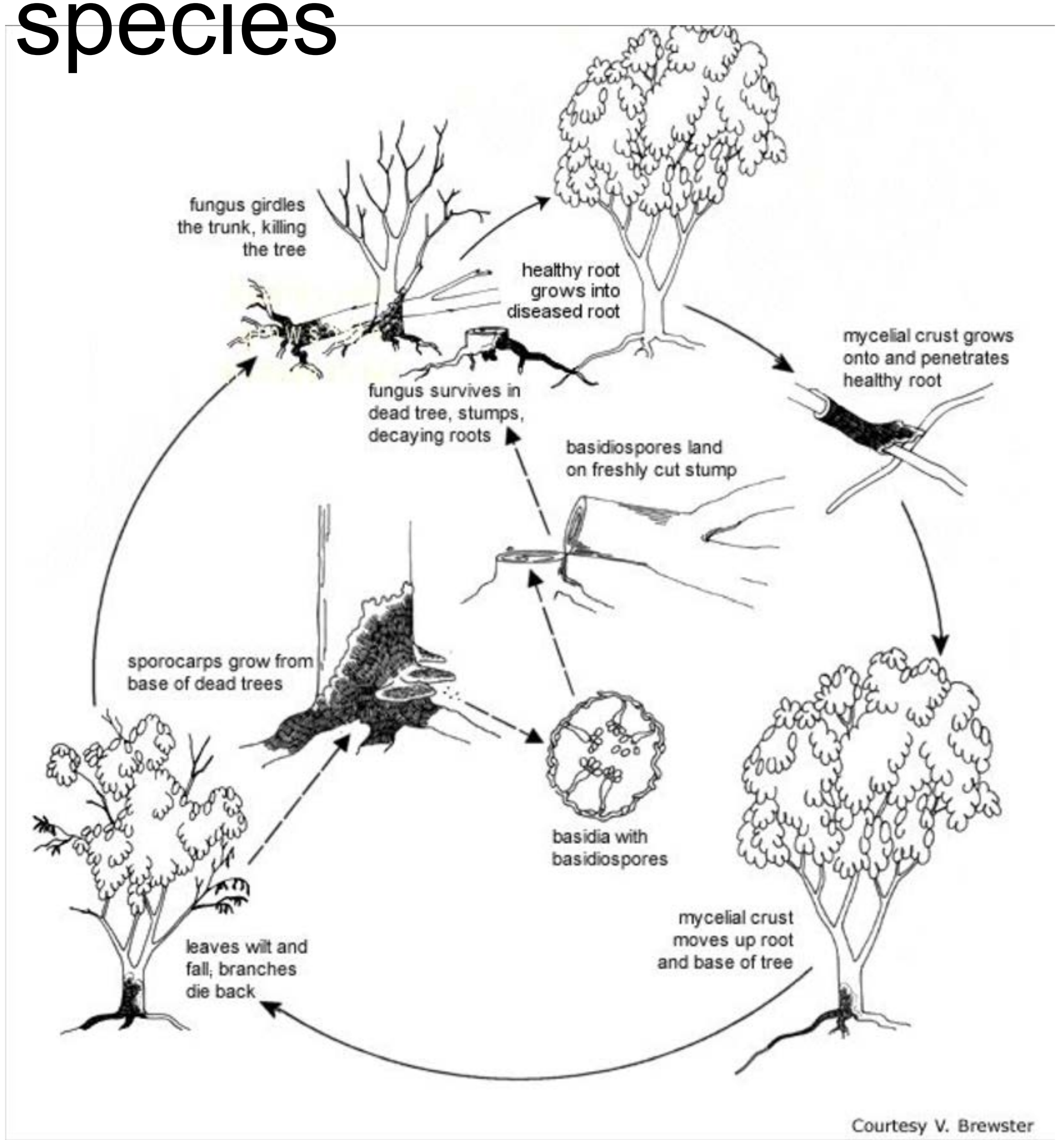
Expedition

Expedition



Case study : *Phellinus noxius*

Phellinus noxius causing brown root rot in 200 + tree species



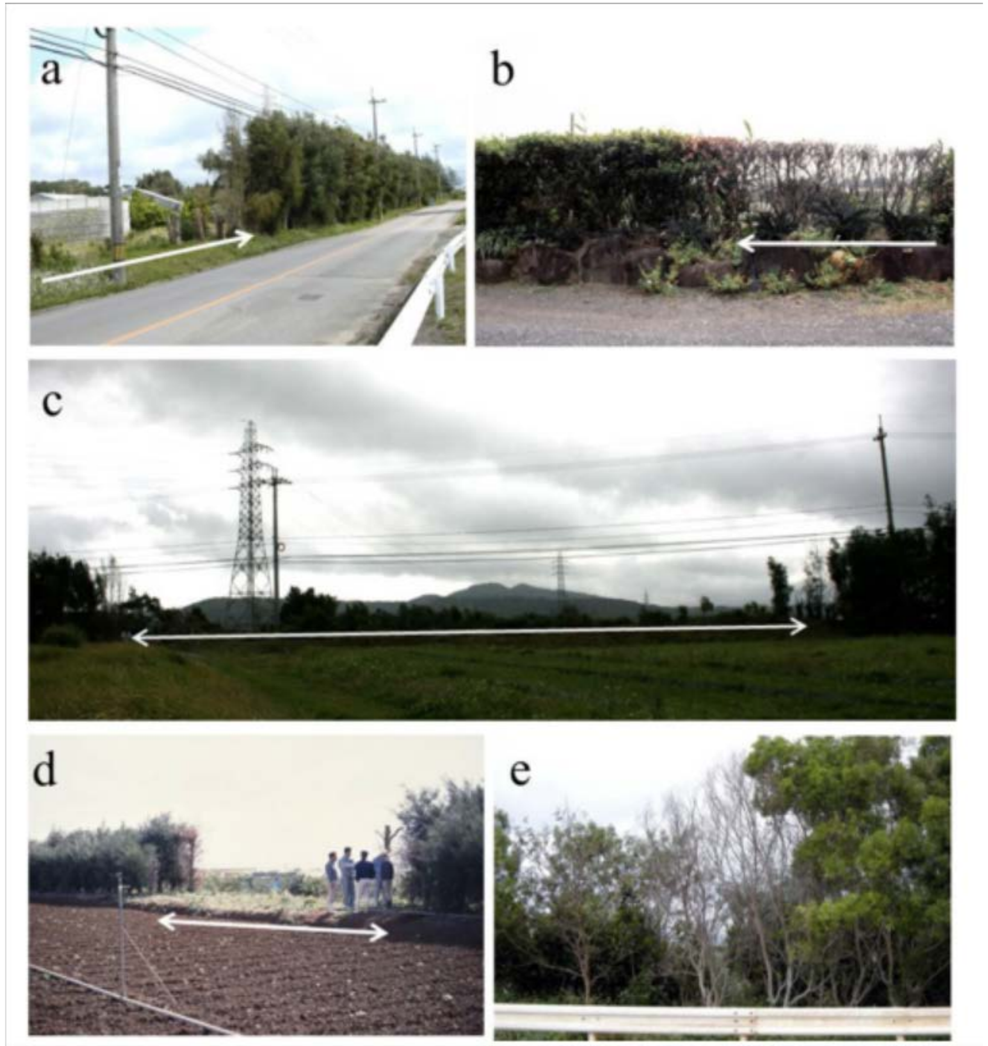
Courtesy V. Brewster

Ann et al., (2002

Phellinus noxius 褐根病 causing brown root rot in trees

Grows in optimum temperature of 28C – an emerging issue due to climate change

http

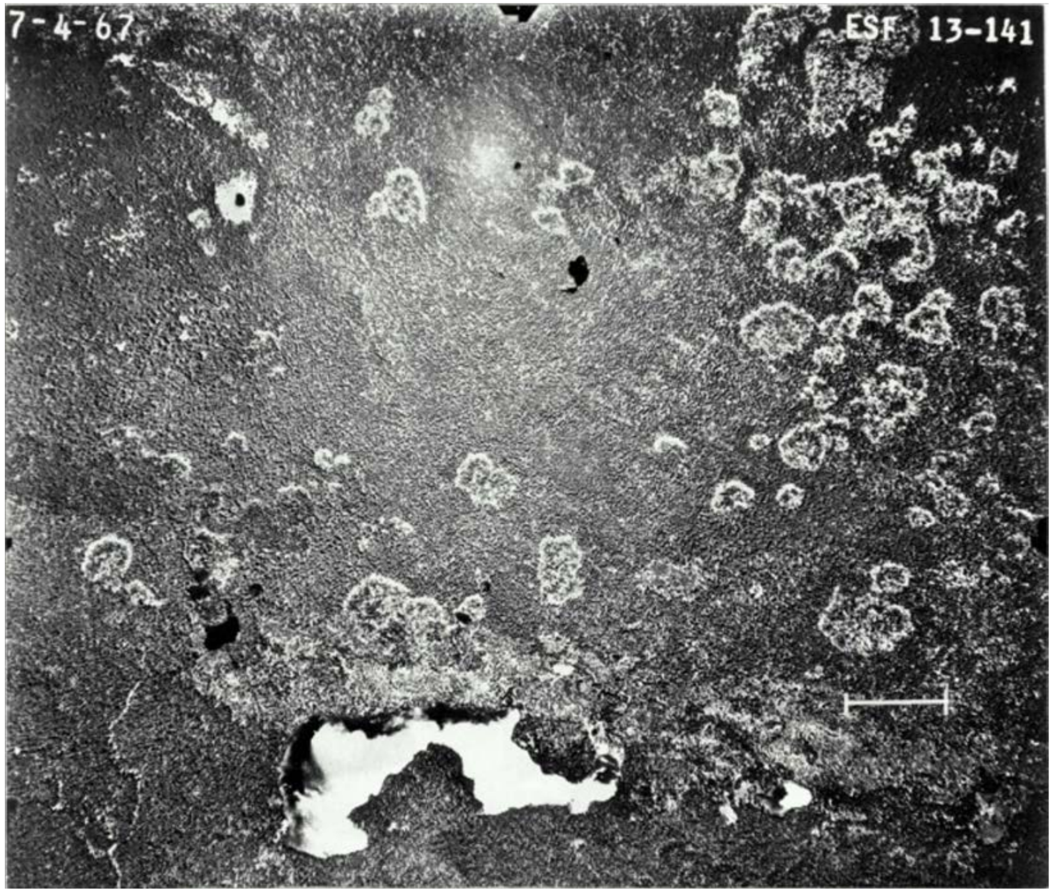


Norio *et al.*, (2014, 2015)

Disease foci in forests caused by *Phellinus*

Ogasawana island, Japan

Norio *et al.,* (2015)



Mortality centers in mountain hemlock forest at 1700 m elevation in the central Oregon Cascades.
Scale bar = 200m

Hansen 2000

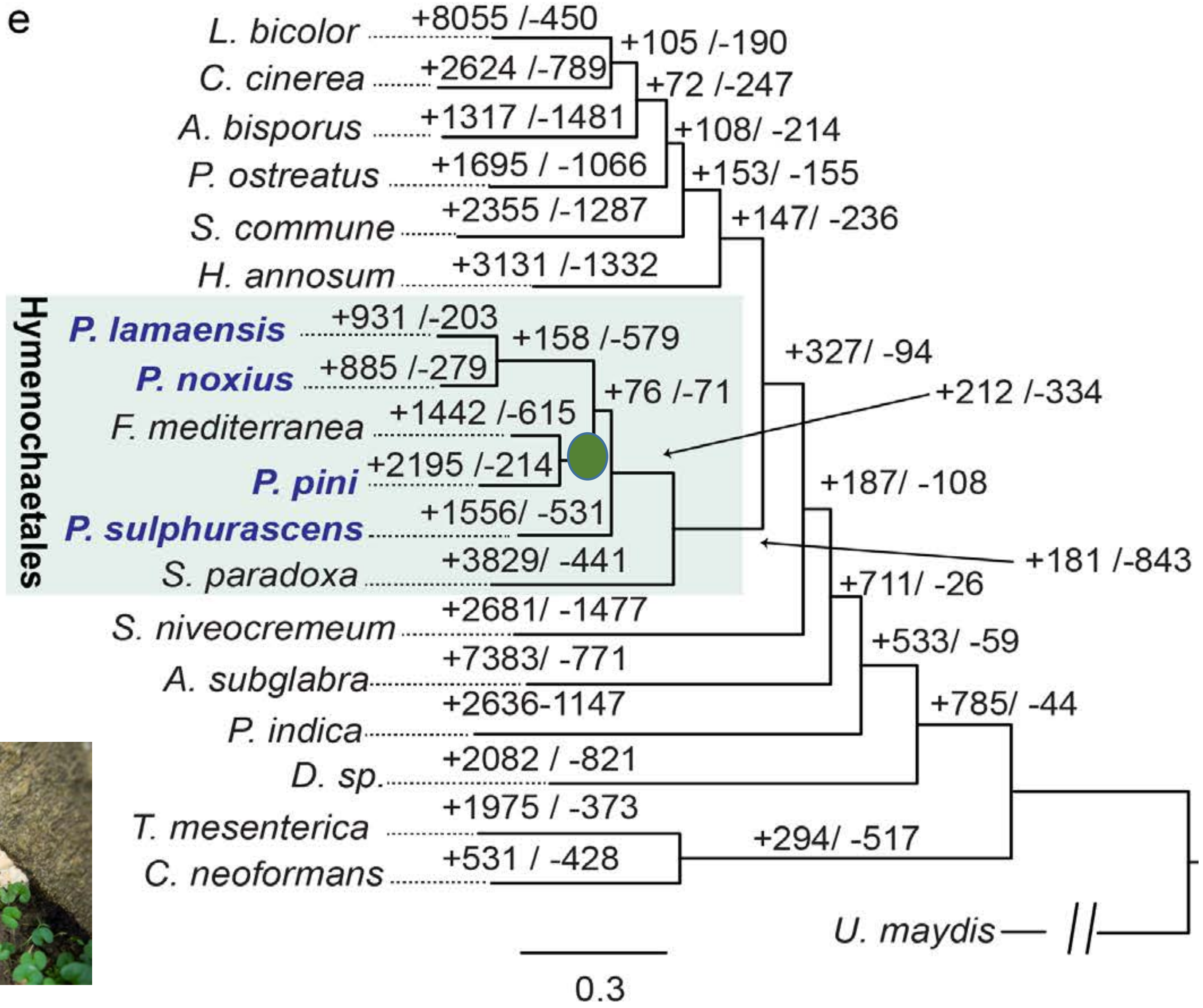
Phellinus noxius distribution in the world

Transition from wood decayer to root pathogen to trunk pathogen

Trunk pathogen ●

F. mediterranea

P. pini

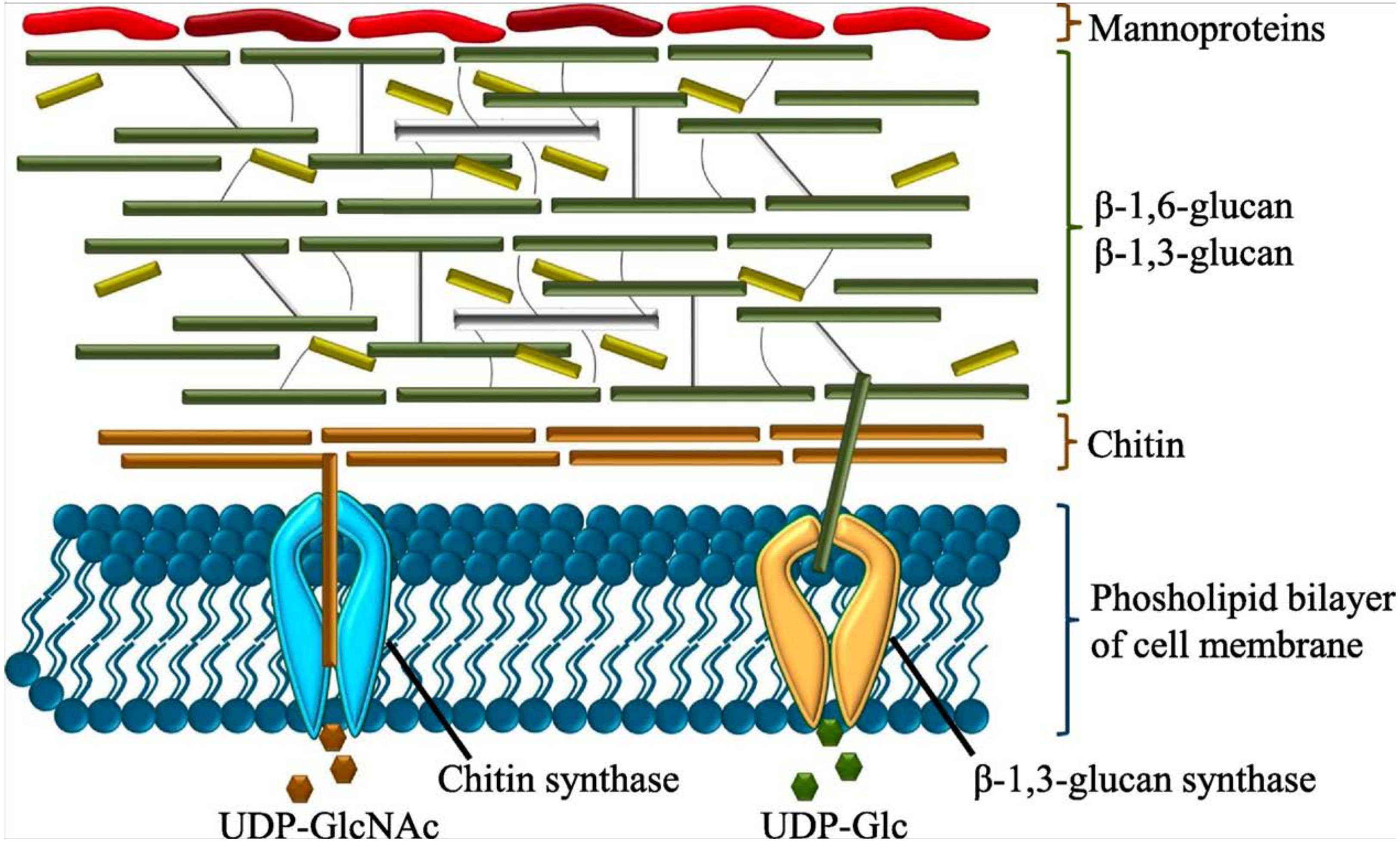


P. sulphrascens

S. paradoxa

P. noxius

1,3-beta-glucan synthase is highly expanded in *P. noxius*

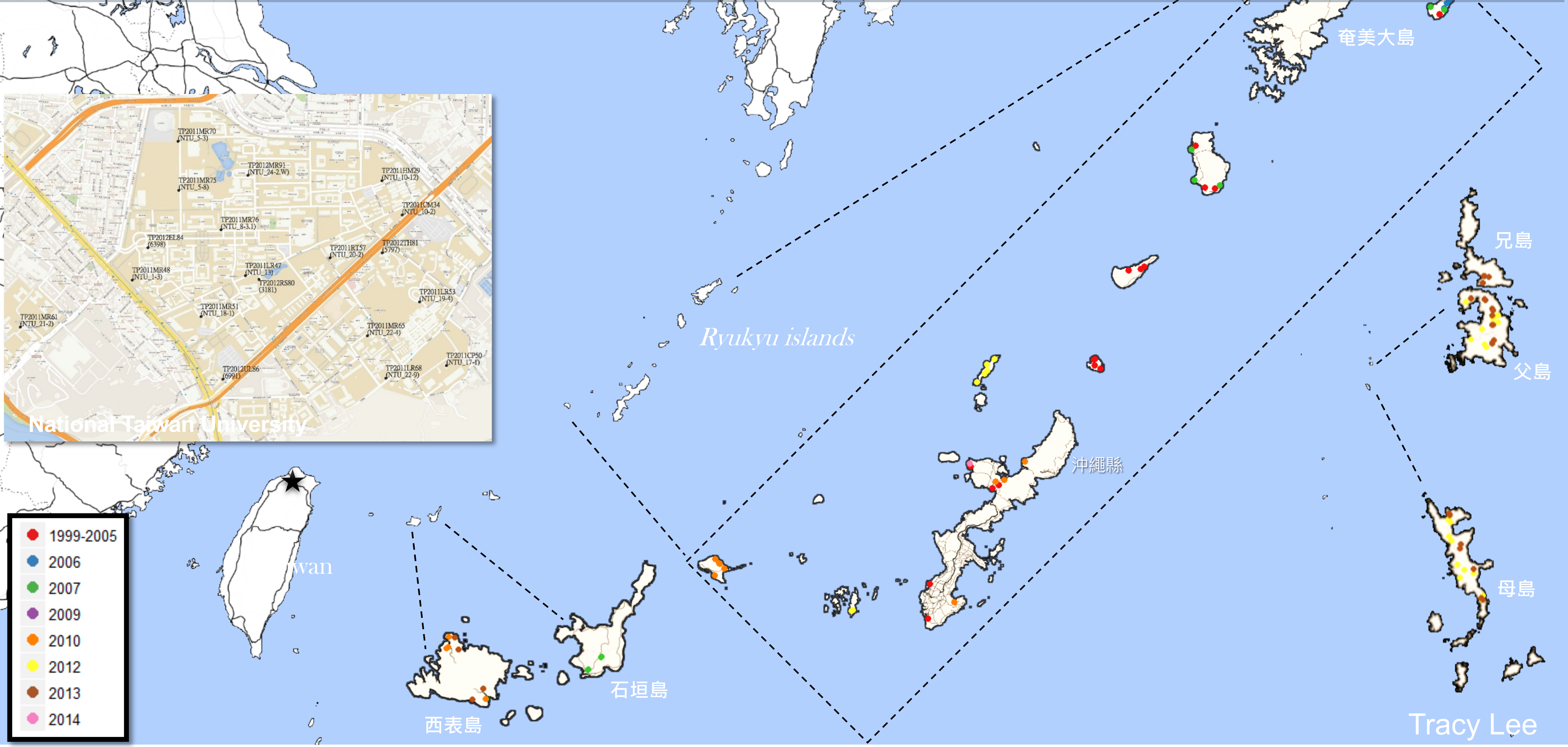


Schematic overview of fungal cell wall composition

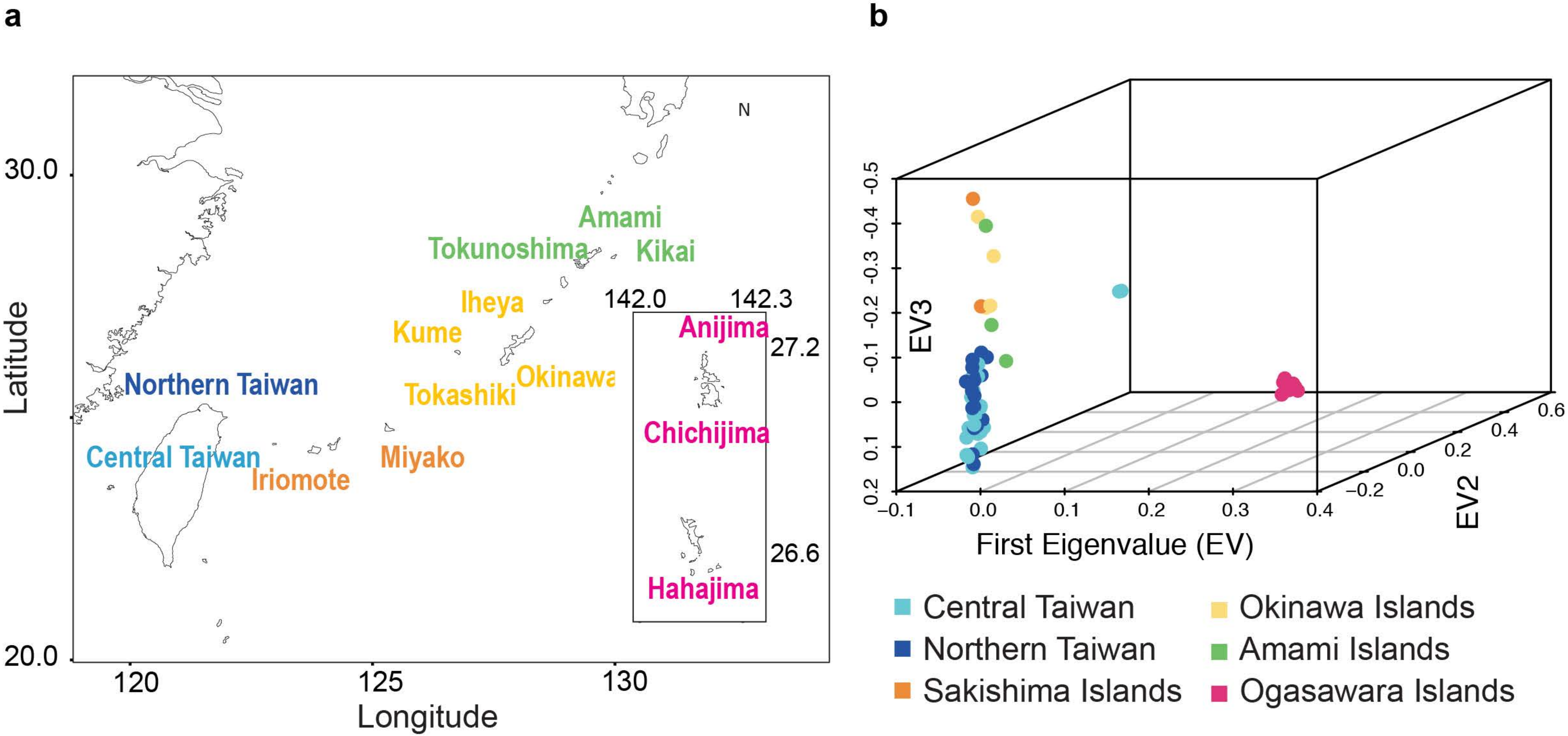
1,3-beta-glucan synthase is responsible for the formation of beta-glucan components in fungal cell wall

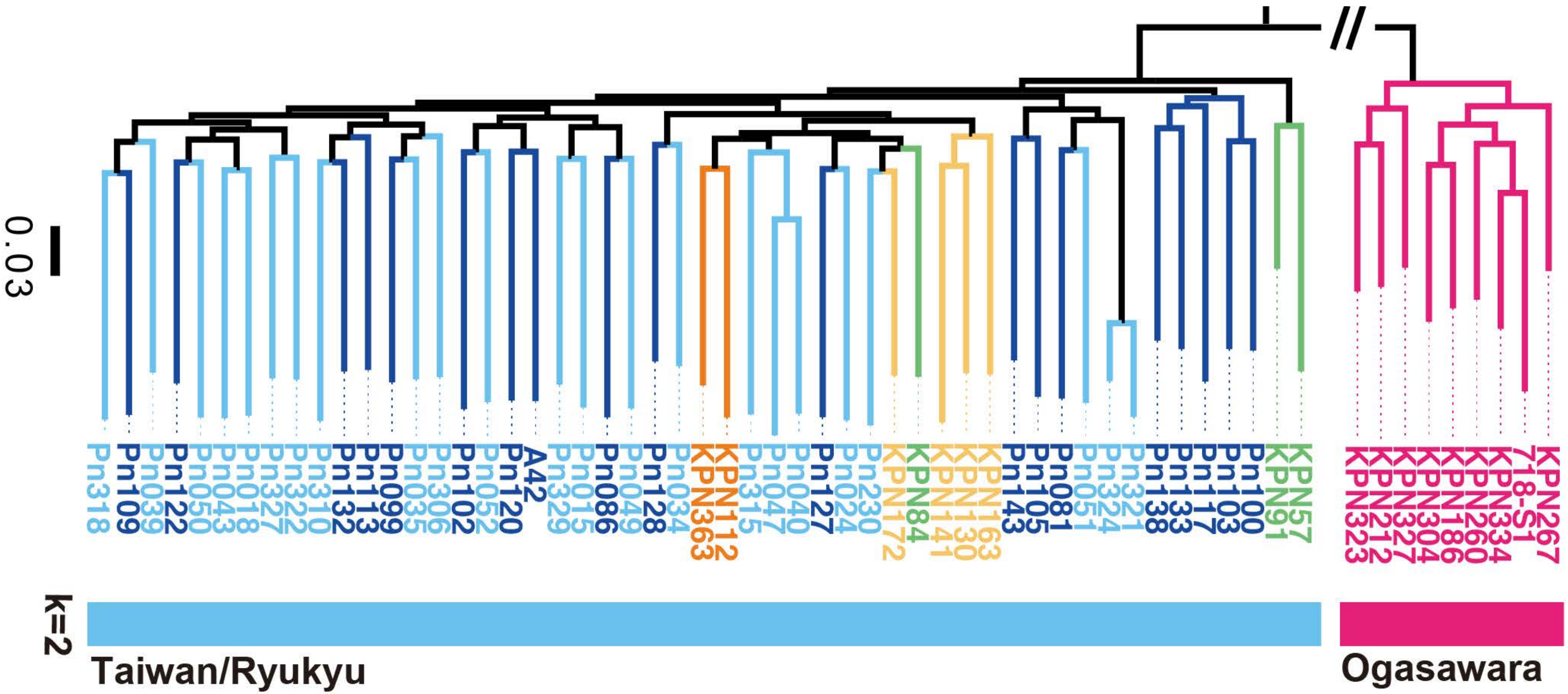
***P. noxius* has 14** copies, compared to an average of 1.8 copies across fungi

First phase: sequencing of 40+ isolates around Japan and Taiwan collected during 1999-2014

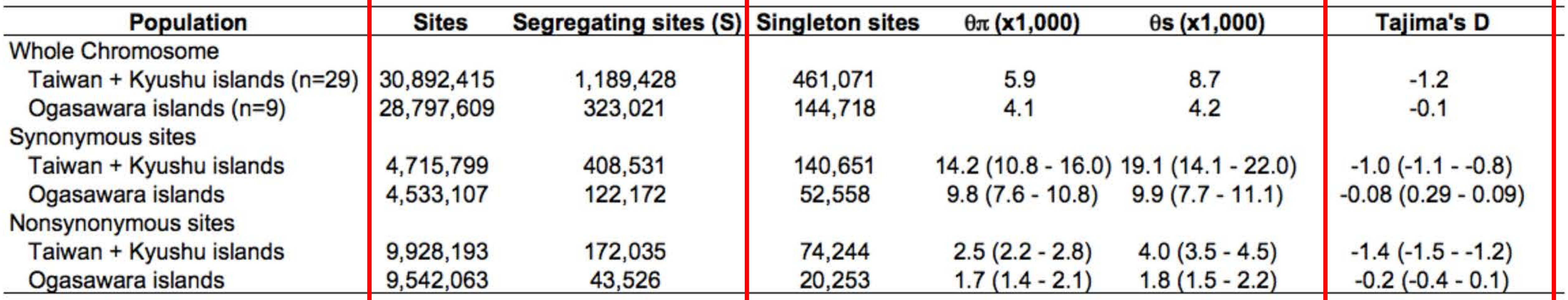


Tracy Lee


a
30.0
20.0
Latitude
120
125
130
Longitude
N
Amami
Tokunoshima
Kikai
Iheya
Kume
Okinawa
Tokashiki
Northern Taiwan
Central Taiwan
Iriomote
Miyako
142.0
142.3
27.2
26.6
Anijima
Chichijima
Hahajima
b
EV3
-0.5
-0.4
-0.3
-0.2
-0.1
0
0.1
0.2
−0.1
0.0
0.1
0.2
0.3
0.4
First Eigenvalue (EV)
−0.2
0.0
0.2
0.4
0.6
EV2
Central Taiwan
Northern Taiwan
Sakishima Islands
Okinawa Islands
Amami Islands
Ogasawara Islands


0.03
Pn318
Pn109
Pn039
Pn122
Pn050
Pn043
Pn018
Pn327
Pn322
Pn310
Pn132
Pn113
Pn099
Pn035
Pn306
Pn102
Pn052
Pn120
A42
Pn329
Pn015
Pn086
Pn049
Pn128
Pn034
KPN363
KPN112
Pn315
Pn047
Pn040
Pn127
Pn024
Pn230
KPN172
KPN84
KPN141
KPN130
KPN163
Pn143
Pn105
Pn081
Pn051
Pn324
Pn321
Pn138
Pn133
Pn117
Pn103
Pn100
KPN91
KPN57
KPN323
KPN212
KPN327
KPN304
KPN186
KPN260
KPN334
718-S1
KPN267
k=2
Taiwan/Ryukyu
Ogasawara

High diversity in *P. noxius*



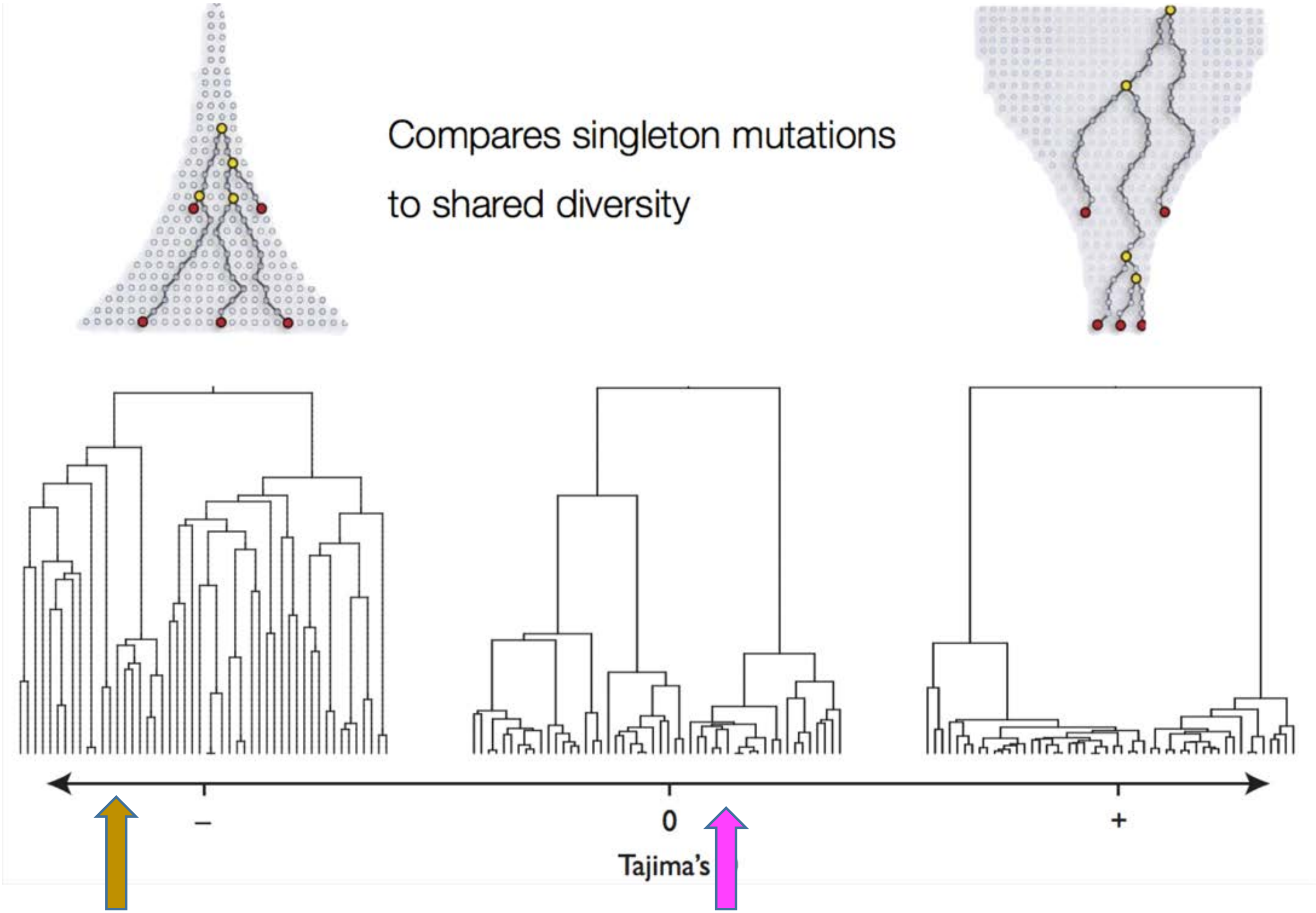
Population	Sites	Segregating sites (S)	Singleton sites	$\theta\pi$ (x1,000)	θs (x1,000)	Tajima's D
Whole Chromosome						
Taiwan + Kyushu islands (n=29)	30,892,415	1,189,428	461,071	5.9	8.7	-1.2
Ogasawara islands (n=9)	28,797,609	323,021	144,718	4.1	4.2	-0.1
Synonymous sites						
Taiwan + Kyushu islands	4,715,799	408,531	140,651	14.2 (10.8 - 16.0)	19.1 (14.1 - 22.0)	-1.0 (-1.1 - -0.8)
Ogasawara islands	4,533,107	122,172	52,558	9.8 (7.6 - 10.8)	9.9 (7.7 - 11.1)	-0.08 (0.29 - 0.09)
Nonsynonymous sites						
Taiwan + Kyushu islands	9,928,193	172,035	74,244	2.5 (2.2 - 2.8)	4.0 (3.5 - 4.5)	-1.4 (-1.5 - -1.2)
Ogasawara islands	9,542,063	43,526	20,253	1.7 (1.4 - 2.1)	1.8 (1.5 - 2.2)	-0.2 (-0.4 - 0.1)

Human: 1 SNP every 1.3kb
Yeast: 1 SNP every 0.6-1.2kb
Drosophila: 1 SNP every 0.5kb
***Phellinus*: 1 SNP every 26-95bp**

Tajima's D test if DNA is evolved under a neutral scenario (mean = 0)

A negative Tajima's D signifies an **excess of low frequency polymorphisms relative to expectation**, indicating **population size expansion** (e.g., after a bottleneck or a selective sweep) and/or purifying selection

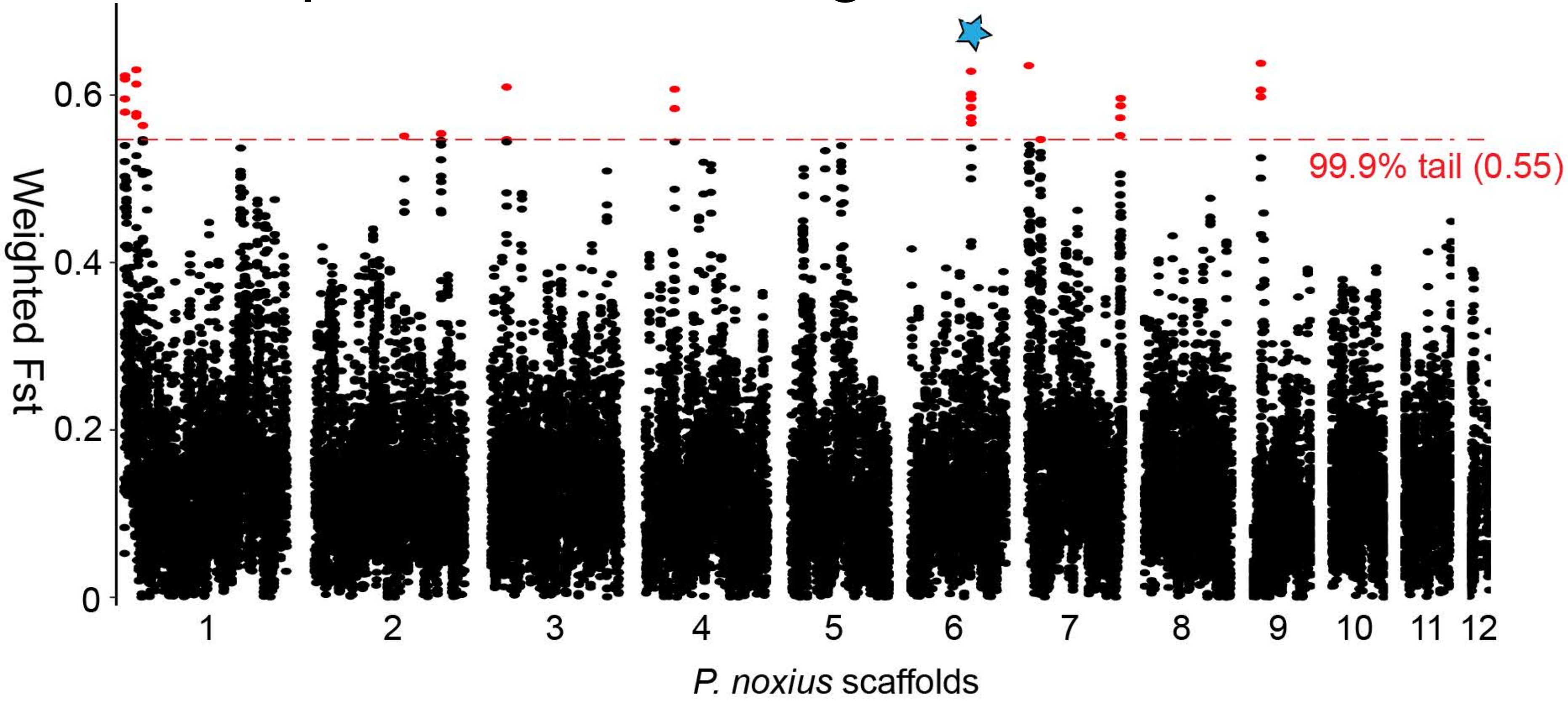
Tajima's D statistics reveals Taiwan/Ryukyu population undergoing expansion



Taiwan / Ryukyu

Ogasawara

Population differentiated loci involved in fungal cell wall organization and plant cell wall degradation



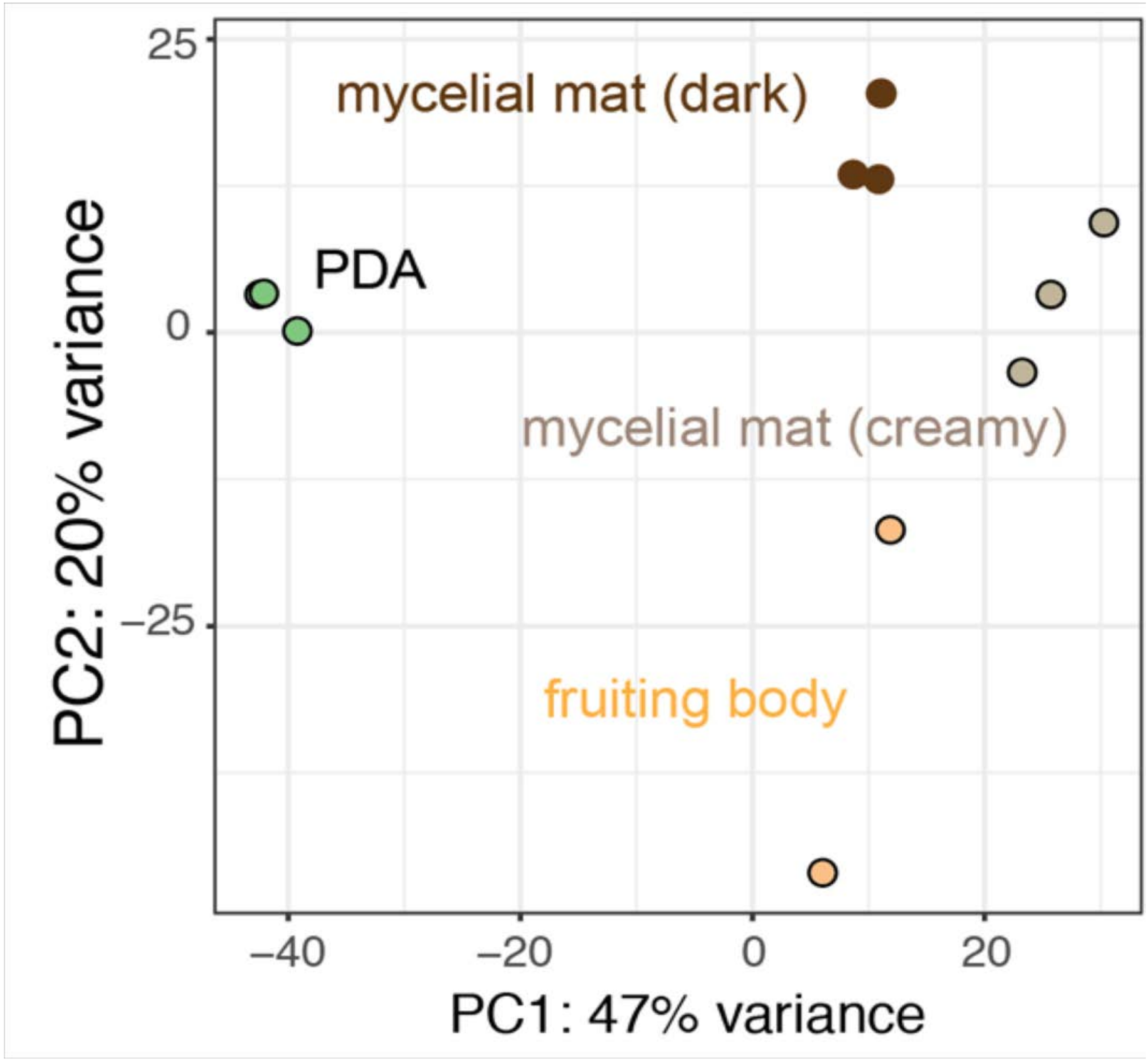
★

Gene ID	Product Description	Reference of homologs
PNOK_0653900	glycosylphosphatidylinositol-anchored	Szeto *et al.,* 2007
PNOK_0654000	BEACH-domain-containing protein	Steffens *et al.,* 2015
PNOK_0654100	endo-1,4-beta xylanase	Bray and Clark (1994)
PNOK_0654200	hypothetical protein	N/A

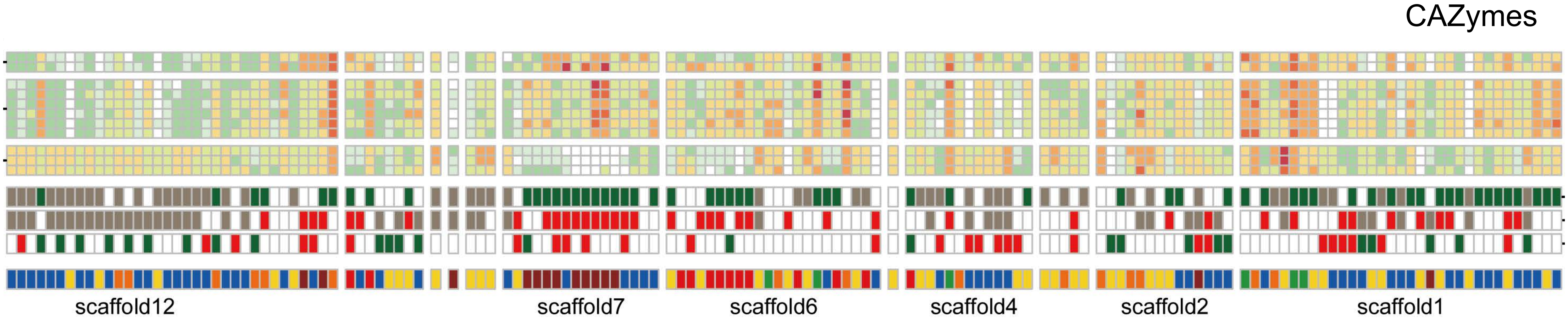
Test: RNA between different parts of infection

Tree 1 ▲

Tree 2 ●



RNAseq of *in planta* samples during *P. noxius* infection



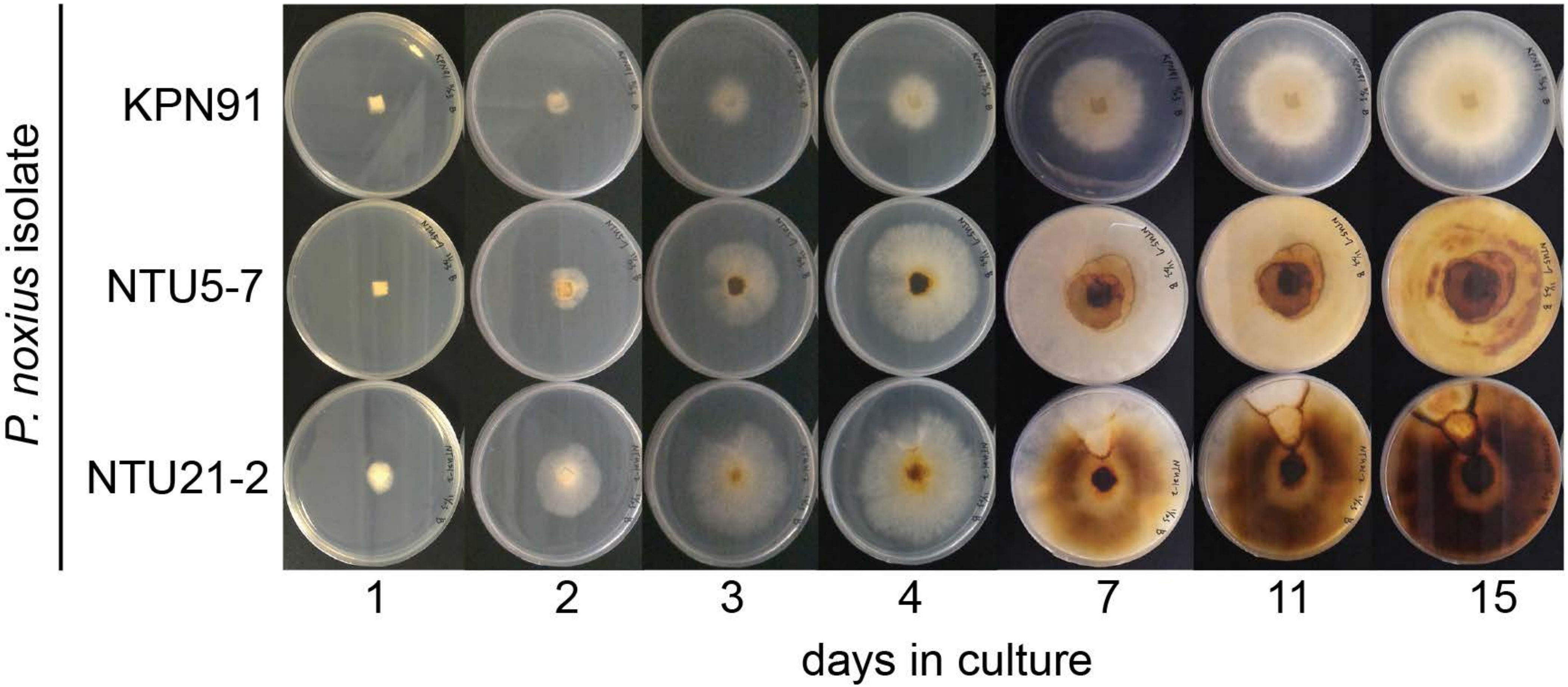
RNA between different parts of infection

Highly expressed:
Tyrosinase – key enzyme in production of melanin
Many **Hydrolases** – plant cell wall degrading enzyme
Dehydrogenase

Highly expressed in bothstages:
Glycan synthetase: fungal cell wall production

Highly expressed:
Ligninase – catalyze the breakdown of lignin, a biopolymer commonly found in the cell walls of plants
P450– xenobiotic detoxification released from plant defense
Aspartic protease: important in the formation and germination of spores, in pathogenesis and in post-translational regulation

Brownness (melanin) associated with pathogenicity is different amongst isolates



Case study: Collect *Mycena* in Taiwan


Mycena interrupta

Mycena adonis


Mycena adonis


Mycena luceptipes


Mycena leaiana

Huei mien Ke

Of the 43 species that display bioluminescence, 9 are present in Taiwan

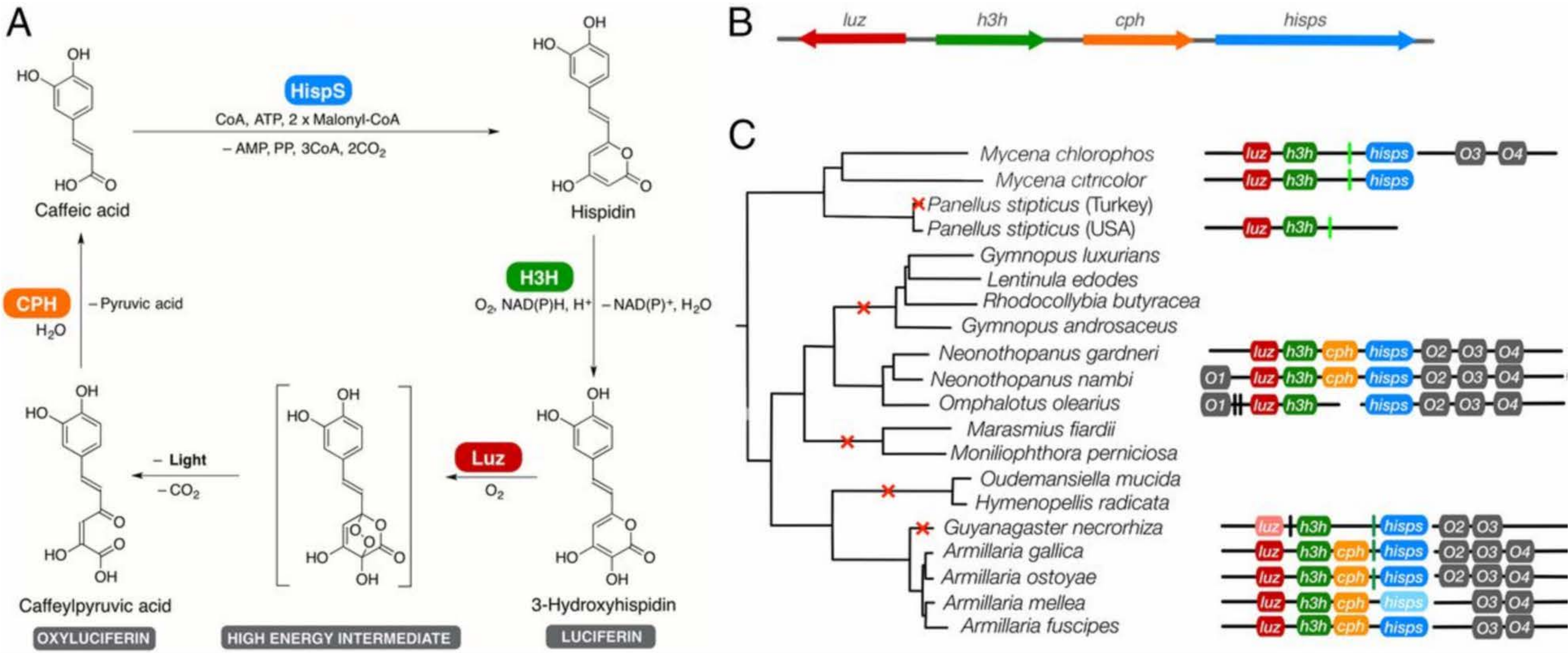

Mycena chlorophos


Mycena luxaeterna


Mycena kentingensis

#A glowing underground network of fungi - Attenborough's Life That Glows: Preview - BBC Two
https://www.youtube.com/watch?v=33-3UCTRZWM

Four genes cluster constitute the Luciferin biosynthesis pathway involved in fungal bioluminescence

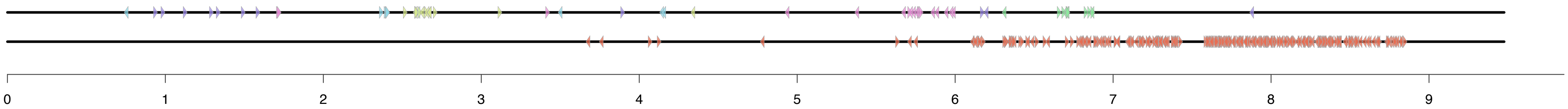


Kotlobay *et al* (2018) PNAS

Two mode of evolution across *Mycena* genomes

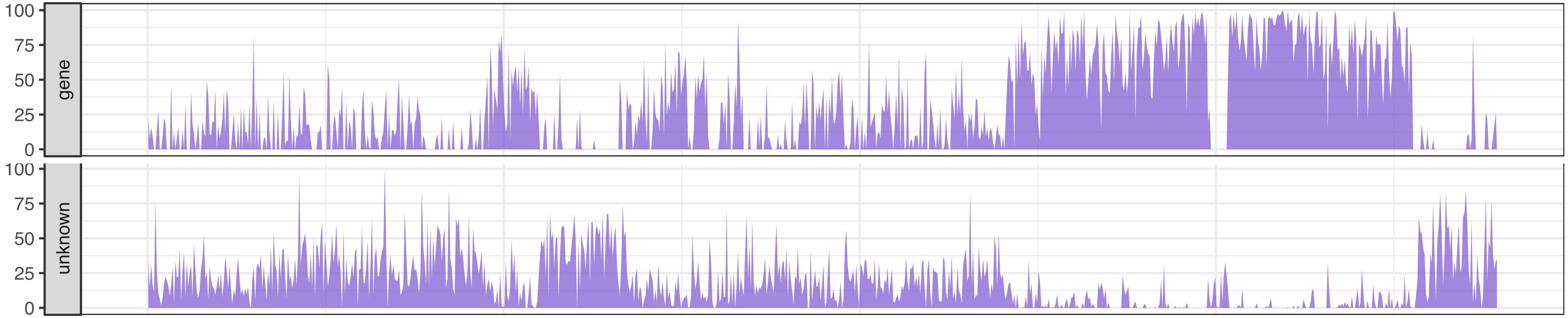
Tandem duplication of different gene families

Conserved, in synteny across all species



Gene sparse

Gene dense



9Mb

Repeat dense

Repeat sparse

- Various types of unknown repeat contribute to the expansion of genome
- Gene sparse region contain tandem duplication of various gene families
- Suggesting accumulation of repeats seems to break the synteny (regulatory) of genome allow gene families to expand

Yuching Liu

Questions and knowledge gaps

KEY UNRESOLVED QUESTIONS:

What is the relative importance of fungal adaptation, migration and acclimatisation?

How does climate change affect the yield of fungal spore-bearing structures?

How does climate change affect fungal growth and activity?

How do fungi mediate ecosystem responses to climate change?

How do changes in the phenology of spore-bearing structure production reflect changes in activity, abundance, biomass and distribution?

Can fungi track climate space shifts?

KEY INFORMATION GAPS:

Long-term data

Large-scale data

Data from tropical, subtropical and warm temperate ecosystems

Experimental data from fungi associated with trees, rather than seedlings

Fungal response and effect traits

Data from multiple simultaneous drivers of change (nitrogen deposition, carbon dioxide, ozone, UV, temperature, drought, fire)

More references

#Some nice papers
https://www.nature.com/subjects/fungi

 # Fungal Phylogenetics and Phylogenomics
https://www.sciencedirect.com/bookseries/advances-in-genetics/vol/100/suppl/C

 # The Impact of Molecular Data in Fungal Systematics
https://www.sciencedirect.com/science/article/pii/S0065229605420029

 # Genome Diversity and Evolution in the Budding Yeasts (Saccharomycotina)
http://www.genetics.org/content/206/2/717

 # Evolutionary biology through the lens of budding yeast comparative genomics
https://www.nature.com/articles/nrg.2017.49

 # Dimensions of biodiversity in the Earth mycobiome
https://www.nature.com/articles/nrmicro.2016.59

 # Evolution and genome architecture in fungal plant pathogens
https://www.nature.com/articles/nrmicro.2017.76