Importância dos Fungos em biotecnologia.

Mais de 66 % do genoma de fungos sequenciados correspondem ao filo Ascomycota.

•Importância:

•1. Decompositores e biossorventes em todos os ecossistemas terrestres;

•2. Associados de plantas vasculares tanto em relações mutualísticas como parasitárias;

•3. A maioria dos fitopatógenos e, como tal, têm um tremendo impacto económico e, portanto, representam a próxima onda de potenciais ameaças de bioterrorismo;

•4. Muitos fungos são patógenos humanos;

•5. Oferecer vários sistemas de modelos genéticos bem desenvolvidos para biólogos moleculares,

6. Possuem potencial significativo para biorremediação,

•7. São cruciais para as indústrias de fermentação e biotecnologia.

Baker et al. Fungal B iology Rev. 22 (2008) 1 – 5

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Research review paper

Biotechnology—a sustainable alternative for chemical industry

Maria Gavrilescu[a,*], Yusuf Chisti[b]

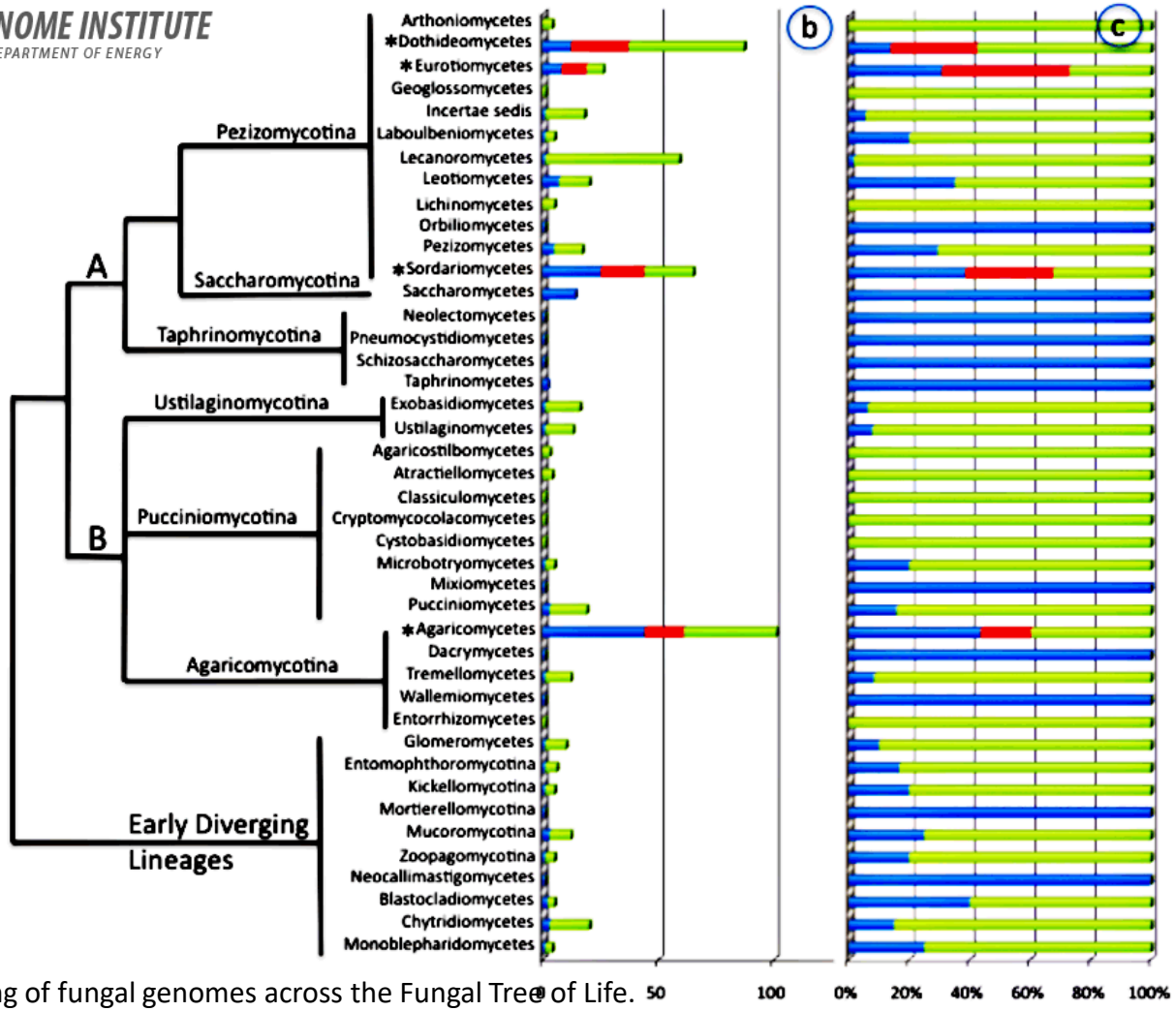
bioreactor technologies. Environmental and economic benefits that biotechnology can offer in manufacturing, monitoring and waste management are highlighted. These benefits include the following: greatly reduced dependence on nonrenewable fuels and other resources; reduced potential for pollution of industrial processes and products; ability to safely destroy accumulated pollutants for remediation of the environment; improved economics of production; and sustainable production of existing and novel products.

Table 1
Some well-established biotechnology products (by production volume)

Product	Annual production (tons)
Bioethanol	26,000,000
L-Glutamic acid (MSG)	1,000,000
Citric acid	1,000,000
L-Lysine	350,000
Lactic acid	250,000
Food-processing enzymes	100,000
Vitamin C	80,000
Gluconic acid	50,000
Antibiotics	35,000
Feed enzymes	20,000
Xanthan	30,000
L-Threonine	10,000
L-Hydroxyphenylalanine	10,000
6-Aminopoenicillanic acid	7000
Nicotinamide	3000
D-*p*-hydroxyphenylglycine	3000
Vitamin F	1000
7-Aminocephalosporinic acid	1000
Aspartame	600
L-Methionine	200
Dextran	200
Vitamin B12	12
Provitamin D2	5

Five-year project to sequence 1000 fungal genomes

JGI JOINT GENOME INSTITUTE
UNITED STATES DEPARTMENT OF ENERGY



Family level sampling of fungal genomes across the Fungal Tree of Life.
a) phylogenetic tree of current classification.
b) bar graphs of absolute number of families represented in genomic sampling by class or subphylum.
c) bar graphs of percentage of families represented in genomic sampling by class or subphylum.
Blue = completed or in progress, Red = proposed for Tier One sampling, Green = remaining unsampled families.
A=Ascomycota, B=Basidiomycota. *The four classes represent the most phylogenetically diverse classes of nonlichenized fungi will be Tier One targets for sequencing.

Meyer et al. Fungal Biol Biotechnol (2020) 7:5
https://doi.org/10.1186/s40694-020-00095-z

Fungal Biology and Biotechnology

REVIEW Open Access

Growing a circular economy with fungal biotechnology: a white paper

Abstract

Fungi have the ability to transform organic materials into a rich and diverse set of useful products and provide distinct opportunities for tackling the urgent challenges before all humans. Fungal biotechnology can advance the transition from our petroleum-based economy into a bio-based circular economy and has the ability to sustainably produce resilient sources of food, feed, chemicals, fuels, textiles, and materials for construction, automotive and transportation industries, for furniture and beyond. Fungal biotechnology offers solutions for securing, stabilizing and enhancing the food supply for a growing human population, while simultaneously lowering greenhouse gas emissions. Fungal biotechnology has, thus, the potential to make a significant contribution to climate change mitigation and meeting the United Nation's sustainable development goals through the rational improvement of new and established fungal cell factories. The White Paper presented here is the result of the 2nd Think Tank meeting held by the EUROFUNG consortium in Berlin in October 2019. This paper highlights discussions on current opportunities and research challenges in fungal biotechnology and aims to inform scientists, educators, the general public, industrial stakeholders and policy-makers about the current fungal biotech revolution.

.....tem como objectivo informar cientistas, educadores, público em geral, agentes industriais e gestores políticos sobre a actual revolução da biotecnológica com fungos

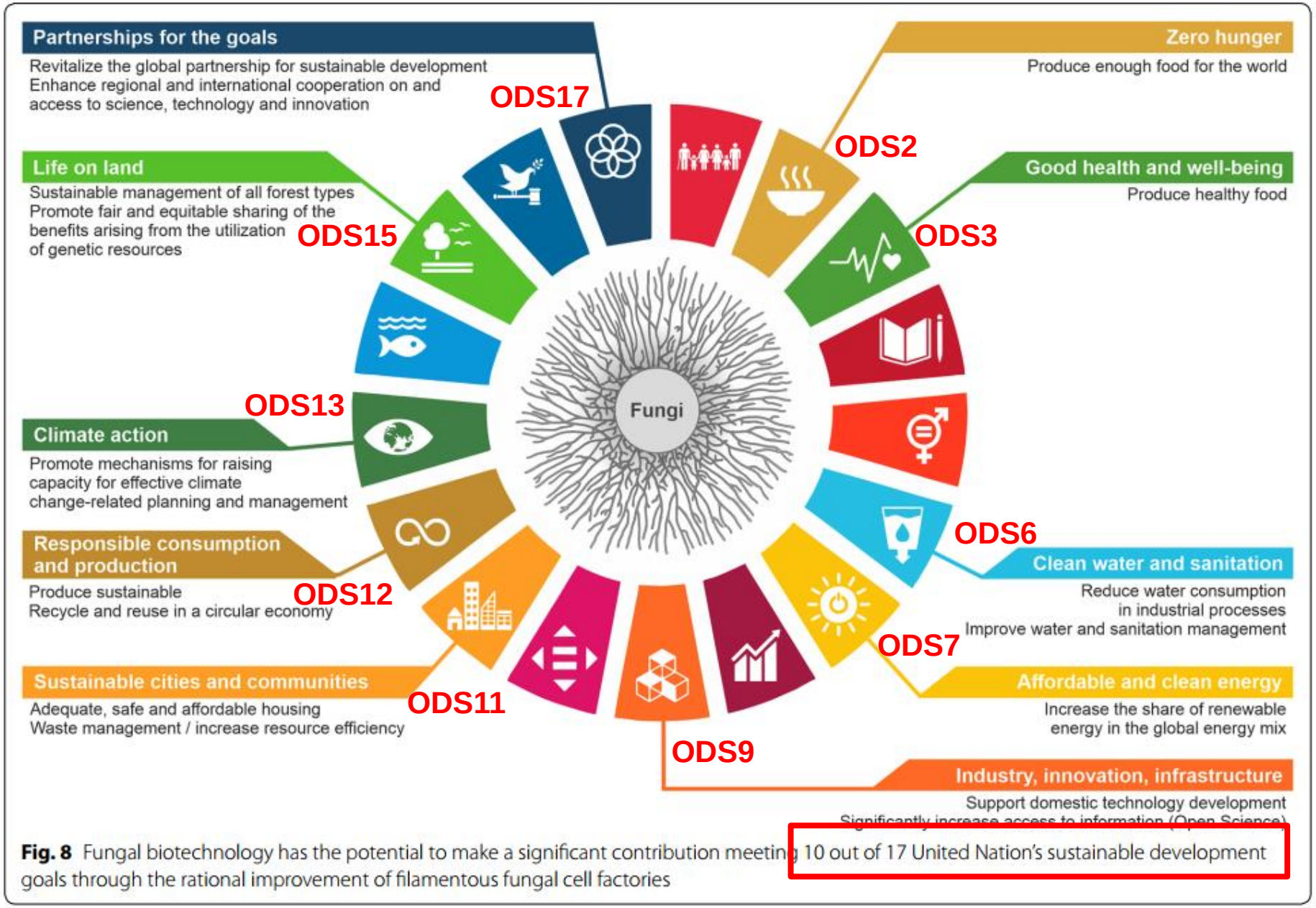


Fig. 8 Fungal biotechnology has the potential to make a significant contribution meeting 10 out of 17 United Nation's sustainable development goals through the rational improvement of filamentous fungal cell factories

(https://doi.org/10.1186/s40694-020-00095-z)

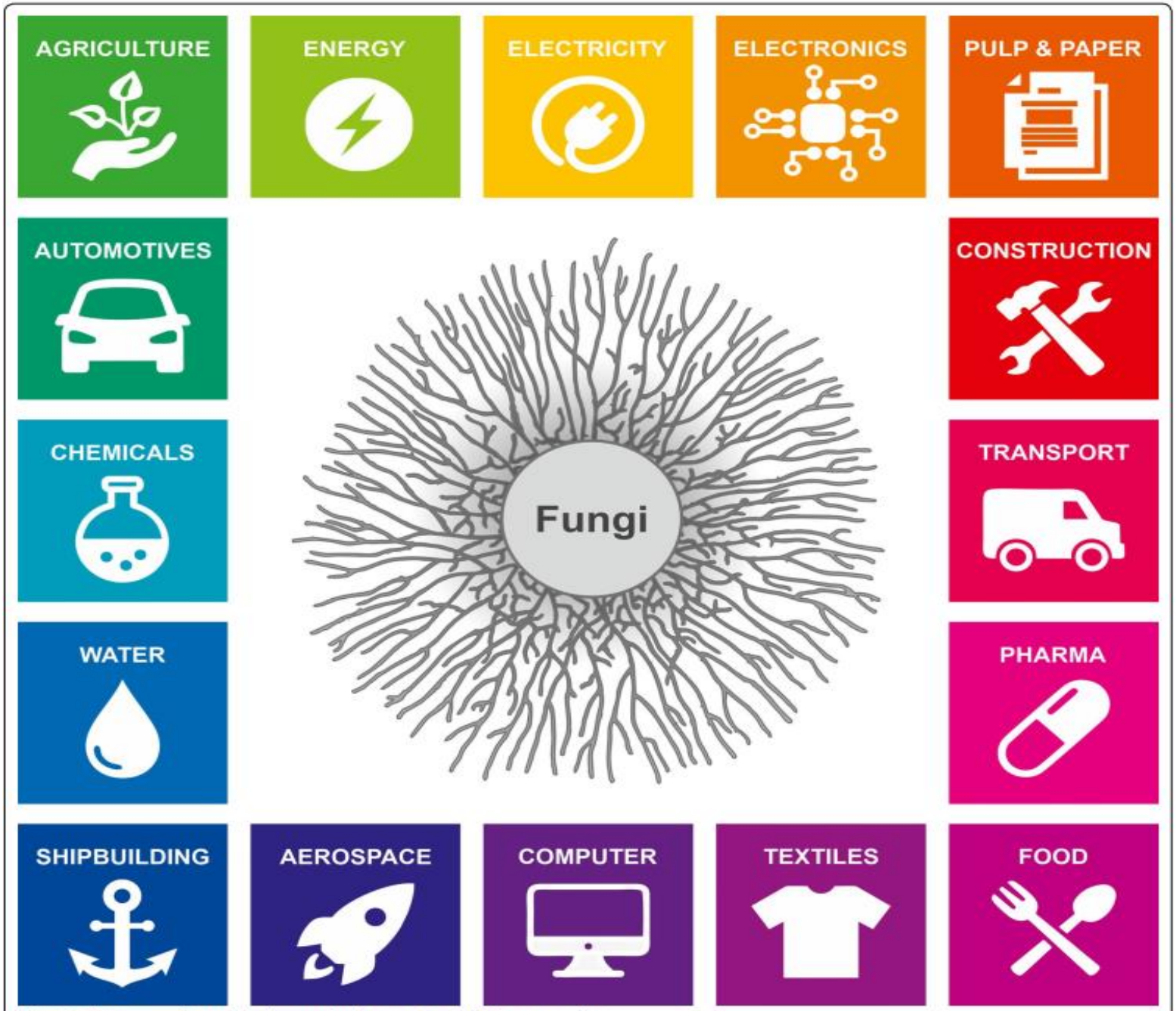


Fig. 2 Industries profiting from the metabolic capacities of filamentous fungi

Reviews, Critiques and New Technologies

Marine fungal biotechnology: an ecological perspective

Raghukumar, C.[1*]

[1]National Institute of Oceanography, Dona Paula, Goa 403 004, India

Raghukumar, C. (2008). Marine fungal biotechnology: an ecological perspective. Fungal Diversity 31: 19-35.

Table 1. Some examples of secondary metabolites produced in fermentation broth from marine endophytic fungi.

Host	Fungus	Secondary metabolite	Activity/application	Reference
Marine algae				
Red alga (*Actinotrichia fragilis*)	*Penicillium citrinum*	Alkaloid	Anti-cancer compound	Tsuda *et al*., 2004
Green alga (*Codium fragile*)	*Fusarium* sp	Cyclic tetrapeptide	Anti-cancer	Ebel, 2006
Red alga (*Polysiphonia violacea*)	*Apiospora montagnei*	Diterpene	Activity against human cancer cell lines	Klemke *et al*., 2004
Seagrasses				
Halodule wrightii	*Scytalidium* sp.	Hexa peptide	Inhibitor of Herpes simplex virus	Rowley *et al*., 2003
Mangrove plants				
Kandelia candel	Unidentified endophytic fungus	Lactones	Active against bollworm and parasitic copepods	Chen *et al*., 2003

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Organism Overview ; Genome Assembly and Annotation report [3] ; Organelle Annotation Report [1] ID: 429

Aspergillus niger

Filamentous fungus used in biotechnology

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Eurotiomycetes[54]; Eurotiomycetidae[43]; Eurotiales[26]; Aspergillaceae[22]; Aspergillus[11]; Aspergillus niger[1]

Used in industry to produce citric acid, pharmaceuticals, enzymes, and food products. The species shows great phenotypic diversity and is found globally, both as marine and terrestrial strains, producing both organic acids and hydrolytic enzymes in high amounts, and some isolates exhibit pathogenicity.The *Aspergillus niger* genome is approximately 34 Mb, organized in eight chromosomes.

Sequence data: genome assemblies: 3 (See Genome Assembly and Annotation report)

Publications

1. Genomic analysis of the aconidial and high-performance protein producer, industrially relevant Aspergillus niger SH2 strain. Yin C, et al. Gene 2014 May 15
2. Comparative genomics of citric-acid-producing Aspergillus niger ATCC 1015 versus enzyme-producing CBS 513.88. Andersen MR, et al. Genome Res 2011 Jun
3. Comparative analysis of the complete mitochondrial genomes of Aspergillus niger mtDNA type 1a and Aspergillus tubingensis mtDNA type 2b. Juhász A, et al. FEMS Microbiol Lett 2008 Apr

Organism Overview ; Genome Assembly and Annotation report [6] ; Organelle Annotation Report [2] ID: 526

Aspergillus oryzae

Filamentous fungus used in the production of fermented foods and beverages

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Eurotiomycetes[54]; Eurotiomycetidae[43]; Eurotiales[26]; Aspergillaceae[22]; Aspergillus[11]; Aspergillus oryzae[1]

The filamentous fungus *Aspergillus oryzae* has been widely used for centuries in the production of the traditional Japanese fermented foods such as sake (rice wine), shoyu (soy sauce), and miso (soybean paste). The *Aspergillus oryzae* genome is highly enriched for genes involved in metabolism; these comprise more than 6 Mb of the genome sequence. In addition to existing applications, this species has potential for use in biotechnology. In particular, it can be used for production of enzymes and other proteins of eukaryotic origin that cannot be produced with *E. coli*.The *Aspergillus oryzae* haploid genome is 37 Mb, organized into eight chromosomes. Less...

Sequence data: genome assemblies: 6; sequence reads: 1 (See Genome Assembly and Annotation report)

Publications

1. Draft Genome Sequence of Aspergillus oryzae 100-8, an Increased Acid Protease Production Strain. Zhao G, et al. Genome Announc 2014 Jun 5
2. Comparative proteome analysis of Aspergillus oryzae 3.042 and A. oryzae 100-8 strains: Towards the production of different soy sauce flavors. Zhao G, et al. J Proteomics 2012 Jul 16
3. Comparative genome analysis between Aspergillus oryzae strains reveals close relationship between sites of mutation localization and regions of highly divergent genes among Aspergillus species. Umemura M, et al. DNA Res 2012 Oct

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Organism Overview ; Genome Assembly and Annotation report [2] ID: 17

Aspergillus nidulans

Better known by its asexual name (Aspergillus nidulans) this model organism, unlike most aspergilli, possesses a well characterized sexual cycle.

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Eurotiomycetes[54]; Eurotiomycetidae[43]; Eurotiales[26]; Aspergillaceae[22]; Aspergillus[11]; Aspergillus nidulans[1]

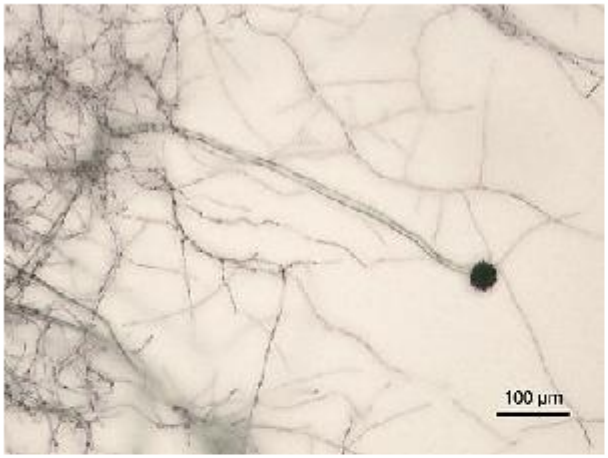
Aspergillus nidulans, also known as *Emericella nidulans*, is a filamentous Ascomycete that is normally haploid but can be induced to grow as a heterokaryon or a diploid. It produces both sexual and asexual spores. In contrast, most other *Aspergillus* fungi are asexual.The *Aspergillus nidulans* genome is approximately 31 Mb, organized in 8 chromosomes. It contains an estimated 11,000-12,000 genes.*Aspergillus nidulans* is one of the most extensively studied organisms in the fields of genetics and biochemistry. Spontaneous and induced mutations have been generated in hundreds of genes, which is of great value because mutation analysis helps to identify gene function and to characterize the biological roles of protein products. *Aspergillus nidulans* is an important model organism for studies in cell biology. This fungus has also been used to express mammalian genes.Aspergillosis, a clinical infection that can lead to an allergic response, a growth, or invasive disease, is caused by fungi of the genus *Aspergillus*, most commonly *Aspergillus fumigatus* and *Aspergillus flavus* but also *Aspergillus nidulans* and others. Due to the significance of *Aspergillus* fungi as human pathogens, the *Aspergillus nidulans* genome is important to study, as it will assist in understanding the biology, host interactions, and pathogenicity of these organisms, as well as aid in vaccine and drug development. Less...

Sequence data: genome assemblies: 2; sequence reads: 1 (See Genome Assembly and Annotation report)

Publications

1. The 2008 update of the Aspergillus nidulans genome annotation: a community effort. Wortman JR, et al. Fungal Genet Biol 2009 Mar

Aspergillus niger CBS 513.88



Micrograph of A. niger grown on Sabouraud agar

The genome sequence and gene prediction of *Aspergillus niger* CBS 513.88 were not determined by the JGI, but were downloaded from NCBI). Please note that this copy of the genome is not maintained by the author and is therefore not automatically updated.

DSM, The Netherlands and their collaborators sequenced the genome of *Aspergillus niger* strain CBS 513.88 at approximately 7.5X coverage using a BAC walking strategy. They produced an assembly consisting of 468 contigs arranged in 19 scaffolds. The genome underwent a combination of automatic and manual annotation. Used in industry to produce citric acid, pharmaceuticals, enzymes, and food products. The species shows great phenotypic diversity and is found globally, both as marine and terrestrial strains, producing both organic acids and hydrolytic enzymes in high amounts, and some isolates exhibit pathogenicity.The *Aspergillus niger* genome is approximately 34 Mb, organized in eight chromosomes.

citation: NCBI Genome publication: Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88.

Arnaud MB, Cerqueira GC, Inglis DO, Skrzypek MS, Binkley J, Chibucos MC, Crabtree J, Howarth C, Orvis J, Shah P, Wymore F, Binkley G, Miyasato SR, Simison M, Sherlock G, Wortman JR. The Aspergillus Genome Database (AspGD): recent developments in comprehensive multispecies curation, comparative genomics and community resources. Nucleic Acids Res. 2012 Jan;40(Database issue):D653-9. PMID: 22080559;

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Trichoderma reesei

Filamentous fungus (anamorph: Trichoderma reesei; teleomorph: Hypocrea jecorina) important to industry for its cellulase production

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Sordariomycetes[89]; Hypocreomycetidae[63]; Hypocreales[50]; Hypocreaceae[6]; Trichoderma[6]; Trichoderma reesei[1]

RefSeq genome sequence from ex-type culture. *Trichoderma reesei*, also known as *Hypocrea jecorina*, is a filamentous fungus that is widely used in industry for cellulase production. The *Trichoderma reesei* haploid genome is estimated at 33 Mb, organized in 7 chromosomes.

Sequence data: genome assemblies: 2 (See Genome Assembly and Annotation report)

Publications

1. Genome sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea jecorina). Martinez D, et al. Nat Biotechnol 2008 May
2. Elucidation of the metabolic fate of glucose in the filamentous fungus Trichoderma reesei using expressed sequence tag (EST) analysis and cDNA microarrays. Chambergo FS, et al. J Biol Chem 2002 Apr 19

Trichoderma reesei RUT C-30 v1.0

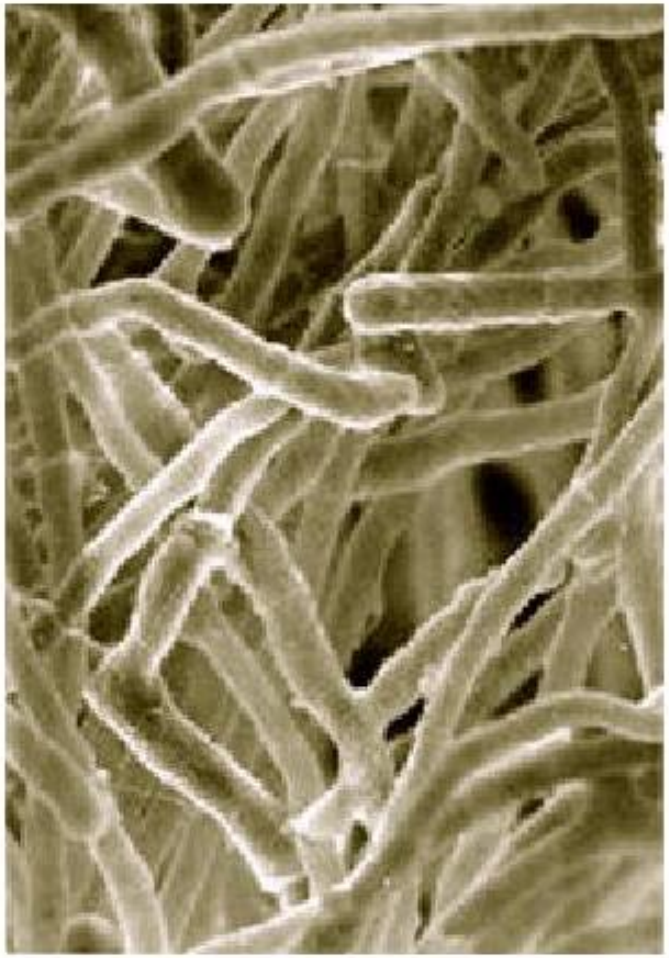


Photo credit: Irma Salovuori, VTT Biotechnology

Trichoderma reesei is an industrially important cellulolytic filamentous fungus. In light of of *T. reesei*'s capacity to secrete large amounts of cellulases and hemi cellulases, the DOE is funding research into developing *T. reesei* as a host to produce low cost enzymes for the conversion of plant biomass materials into industrially useful bioproducts such as sugars and bioethanol.

As a system for studying genomics, *T. reesei* with its genome size of 33Mb and seven chromosomes has many advantages: EST and cDNA collections, BAC libraries available to academic researchers from the Fungal Genomics Laboratory at NCSU, DNA mediated transformation is a routine procedure, gene knockout protocols have been developed and there is an active academic community of researchers world-wide.

Reference:

Koike H., Aerts A, LaButti K, Grigoriev IV, Baker SE (2013) Comparative genomics analysis of *Trichoderma reesei* strains. ***Ind. Biotech.*** 9(6):352-367.

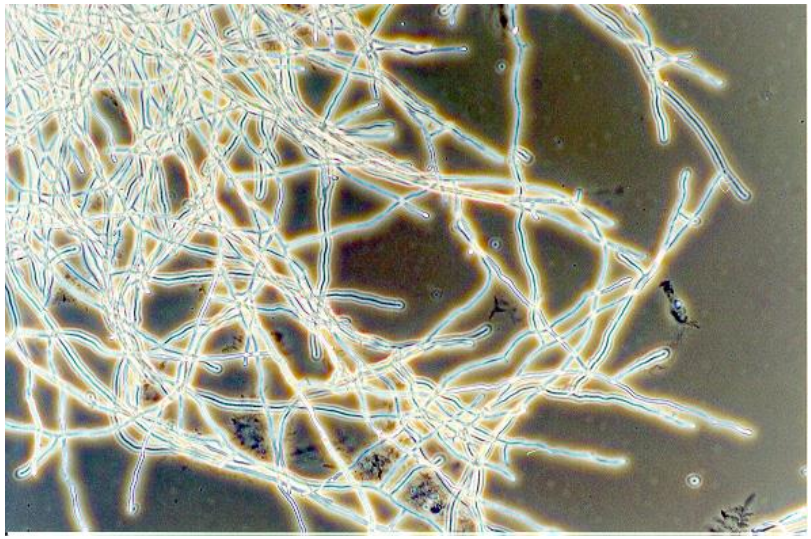
http://genome.jgi.doe.gov/

The biomass-degrading fungus *Trichoderma reesei* (syn. *Hypocrea jecorina*)

Trichoderma

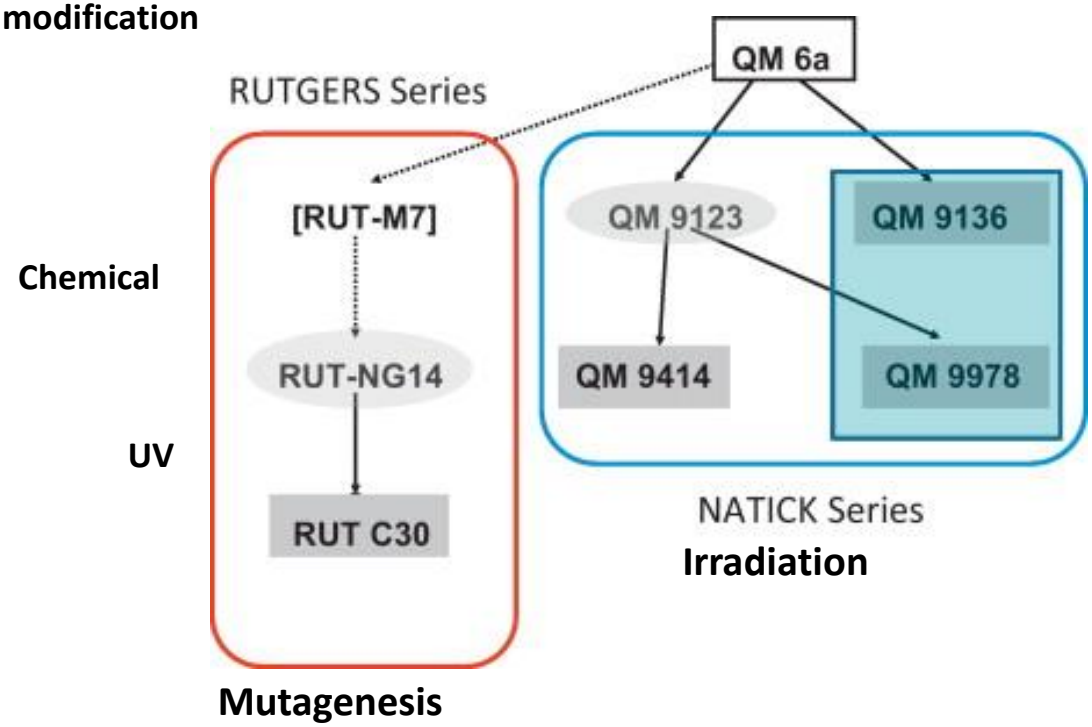
Diversity of ecological niches and competition for habitats.

- **Biotechnological industry**
- **Biological control**
- **Phytostimulating agents.**
- **Higher specific growth rate**
- **Post-translational modification**



Trichoderma

- **Single progenitor**
- **Complex mixtures of secreted enzymes high yield ~ 100 g/L.**
- **GRAS**



Kubicek CP. J Biotechnol. 2012.

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Organism Overview ; Genome Assembly and Annotation report [1] ; Plasmid Annotation Report [1] ; Organelle Annotation Report [1] ID: 2441

Trichoderma harzianum

An important model biocontrol agent of plant pathogens.

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Sordariomycetes[89]; Hypocreomycetidae[63]; Hypocreales[50]; Hypocreaceae[6]; Trichoderma[6]; Trichoderma harzianum[1]

Hypocrea lixii (asexual state: *Trichoderma harzianum*) has been successfully formulated and used commercially as a biocontrol agent, particularly isolate T39. This formulation is used to control *Botrytis cinerea* on grapes and other foliar pathogens. *H. lixii* also shows antagonistic activities towards soil-borne pathogens including various *Phythium* spp.

Publications

1. Complete DNA sequence and analysis of a mitochondrial plasmid in the mycoparasitic Trichoderma harzianum strain T95. Antal Z, et al. Plasmid 2002 Mar

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Organism Overview ; Genome Assembly and Annotation report [2] ; Organelle Annotation Report [1] ID: 10820

Penicillium chrysogenum

Filamentous fungus (aka Penicillium notatum) used in industrial penicillin production

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Eurotiomycetes[54]; Eurotiomycetidae[43]; Eurotiales[26]; Aspergillaceae[22]; Penicillium[10]; Penicillium chrysogenum complex[2]; Penicillium chrysogenum[1]

Penicillium chrysogenum, also known as *Penicillium notatum*, is a filamentous asexual fungus with a relatively small genome. It has been used for over 60 years for the industrial production of penicillin, an antibiotic commonly used to treat bacterial infections. It is currently the primary commercial source of penicillinV and penicillinG. Strain improvement has resulted in increased productivity over the original isolates, mainly due to the amplification of a large genomic fragment containing the penicillin biosynthesis gene cluster. The biosynthesis of penicillin and the genes involved have been characterized in detail. *P.chrysogenum* has a haploid genome size of 34.1 Mb and distributed over four chromosomes. Less...

Sequence data: genome assemblies: 2; sequence reads: 2 (See Genome Assembly and Annotation report)

Publications

1. Genome sequencing of high-penicillin producing industrial strain of Penicillium chrysogenum. Wang FQ, et al. BMC Genomics 2014
2. Complete Sequencing and Chromosome-Scale Genome Assembly of the Industrial Progenitor Strain P2niaD18 from the Penicillin Producer Penicillium chrysogenum. Specht T, et al. Genome Announc 2014 Jul 24

Appl Microbiol Biotechnol (2011) 92:45–53
DOI 10.1007/s00253-011-3476-z

MINI-REVIEW

Impact of the *Penicillium chrysogenum* genome on industrial production of metabolites

Marco Alexander van den Berg

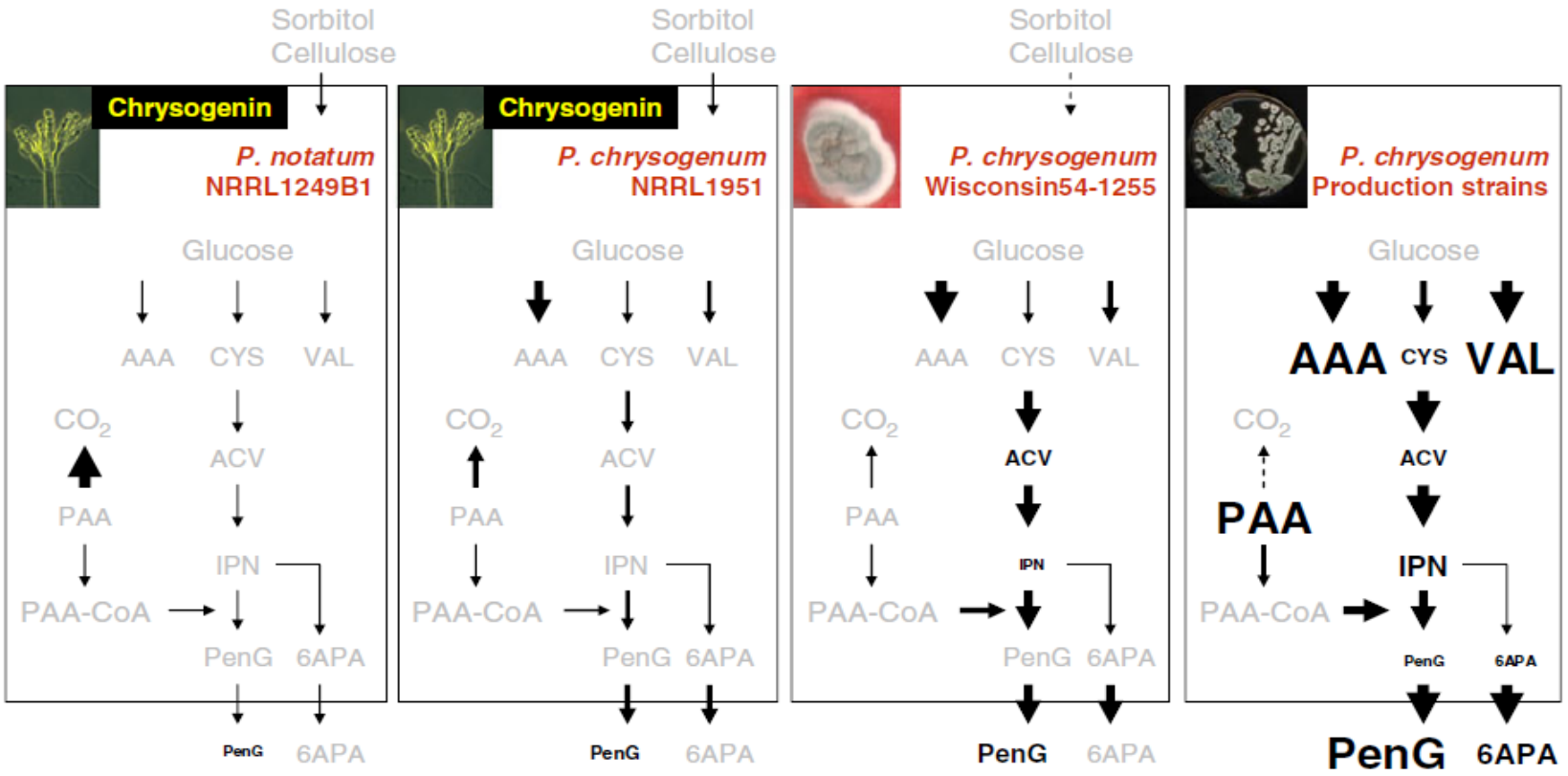

Fig. 2 Metabolic shift in *Penicillium chrysogenum* strains due to classical strain improvement. *Font sizes* of molecules in *black* correspond to concentration differences; concentrations of molecules in *grey* are not available. *Thickness of arrows* is indicative of the flux through that enzyme. Data was extracted from Lu et al. (1992), Theilgaard et al. (2001), Nasution et al. (2008), Jami et al. (2010a), Douma et al. (2010a), Nijland et al. (2010) and Cao et al. (2011)

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Phanerochaete chrysosporium

Most intensively studied white-rot fungus

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Basidiomycota[79]; Agaricomycotina[51]; Agaricomycetes[39]; Corticiales[3]; Corticiaceae[2]; Phanerochaete[2]; Phanerochaete chrysosporium[1]

The wood-decaying basidiomycete *Phanerochaete chrysosporium* does not produce mushrooms for reproduction; instead, it forms effuse, very flat fruiting bodies that appear as a crust on wood. *Phanerochaete chrysosporium* is the most intensively studied white-rot fungus. White-rot fungi degrade lignin, the brown polymer that surrounds and protects the cellulose microfibrils of plant cells. As part of their lignin-degrading enzyme system, these fungi produce unique peroxidases and oxidases that are also capable of degrading compounds related to lignin that are present in toxic wastes, pesticides, and explosive contaminated materials. These enzymes have great potential for environmental and biotechnological applications. Unlike some white-rot fungi, *Phanerochaete chrysosporium* leaves the white cellulose of wood nearly untouched. It also has a very high optimum temperature, which allows it to grow on wood chips in compost piles. These characteristics suggest several roles for *Phanerochaete chrysosporium* in biotechnology. The *Phanerochaete chrysosporium* genome is approximately 30 Mb, organized in 10 chromosomes. Less...

Publications

1. Genome sequence of the lignocellulose degrading fungus Phanerochaete chrysosporium strain RP78. Martinez D, et al. Nat Biotechnol 2004 Jun

Genome sequence of an omnipotent fungus

Tuula T Teeri

The draft sequence of a white-rot fungus offers new paths to sustainable sources of future fuels, chemicals and materials.

Fungi are ancient organisms that have long been harnessed for human benefit. Increased understanding of the role of fungal species in nutrient cycling and mycorrhizal associations promises improvements in agricultural practice. In the laboratory, fungi, such as the ascomycetes *Saccharomyces cerevisiae* and *Neurospora crassa*, have provided experimental systems on which much of our present understanding of cell biology and modern genetics is based. Other fungi have proven useful sources of natural products and enzymes (*e.g.*, antibiotics, ethanol and commercial enzymes) or as recombinant hosts for efficient heterologous expression and secretion of enzymes[1]. In this issue, Martinez *et al.*[2] describe the genome sequence of the white-rot basidiomycete *Phanerochaete chrysosporium* (see also http://www.jgi.doe.gov). Analysis of this basidiomycete sequence for new enzymes and other proteins promises to lead the way to a more detailed understanding and better exploitation of the biological degradation of plant biomass.

Plant biomass represents the key natural raw material for many current biotechnological processes and a sustainable source of future fuels, chemicals and materials. Lignocellulose, the major component of biomass, is composed of three main polymers: cellulose, hemicellulose and lignin. Cellulose microfib-

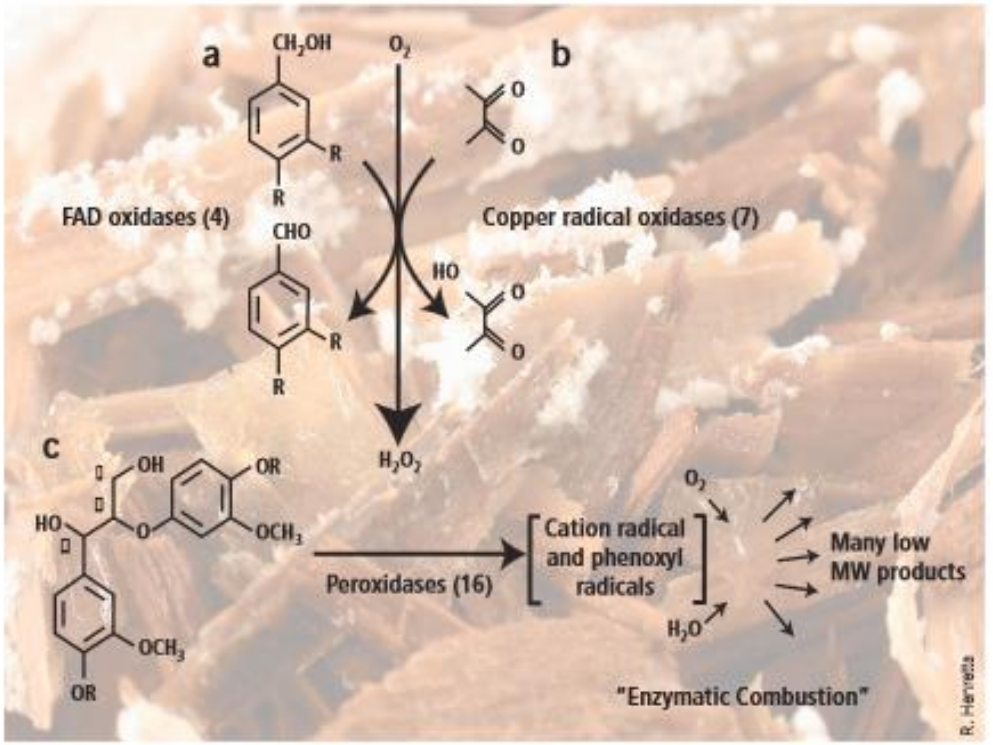
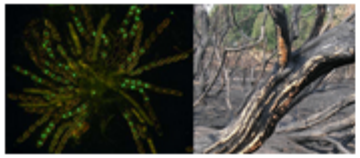


Figure 1 Schematic representation of major extracellular oxidative enzymes produced by lignin degrading fungi. Generation of H_2O_2 is physiologically coupled to peroxidases. (**a**) Benzyl alcohol derivatives are substrates for FAD-dependent oxidases, such as aryl alcohol oxidase (R = H or OCH_3). (**b**) Methyl glyoxal is a substrate for glyoxal oxidase and related copper radical oxidases. Peroxidase substrate C is a lignin model featuring the major β-*O*-4 linkage (R = H or ether linkage to additional monomeric units). Peroxidases extract one electron from aromatic substrates, which then undergo spontaneous degradation reactions or 'enzymatic combustion.' The resulting small molecular weight fragments are further metabolized intracellularly to CO_2 and H_2O. The background image shows *P. chrysosporium* colonizing wood chips. (Courtesy of Tom Volk, UW La Crosse, La Crosse, Wisconsin, TomVolkFungi.net.)

Organism Overview ; Genome Assembly and Annotation report [1] ; Plasmid Annotation Report [1] ID: 19



Neurospora crassa

A filamentous saprophyte that is one of the most intensively studied in genetic and biochemical research

Lineage: Eukaryota[1106]; Fungi[414]; Dikarya[361]; Ascomycota[282]; Pezizomycotina[210]; Sordariomycetes[89]; Sordariomycetidae[23]; Sordariales[12]; Sordariaceae[7]; Neurospora[6]; Neurospora crassa[1]

The *Neurospora crassa* genome is approximately 40 Mb, organized in 7 chromosomes and linkage group to chromosome assignments have been confirmed: I = 1; II = 6; III = 3; IV = 4; V = 2; VI = 5; VII = 7. Studies on this model organism led to the classical concept of "one gene, one enzyme". Beadle and Tatum received the Nobel Prize for Medicine/Physiology in 1958 for their landmark *Neurospora* work in 1941.*Neurospora crassa* is a haploid, heterothallic ascomycete and analysis of genetic recombination is facilitated by the ordered arrangement of the products of meiosis in the ascospores. *N. crassa* perceives light only in the blue/UV range and shows a pronounced circadian rhythm which makes it a preferred model organism for investigating light perception. It is also known for studies investigating epigenetics, gene silencing, cell polarity and cell fusion.*N. crassa* has a very effective mechanism of genome defense termed repeat-induced point mutation (RIP). The process detect gene duplications at the haploid dikaryotic phase of the sexual cycle and mutates both copies of a duplicated gene by causing numerous mutations from G-C to A-T pairs. Thereby eliminating intact mobile elements. Less...

Publications

1. The DNA sequence and genetic organization of a Neurospora mitochondrial plasmid suggest a relationship to introns and mobile elements.
Nargang FE, et al. Cell 1984 Sep

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Photochemical &
Photobiological Sciences

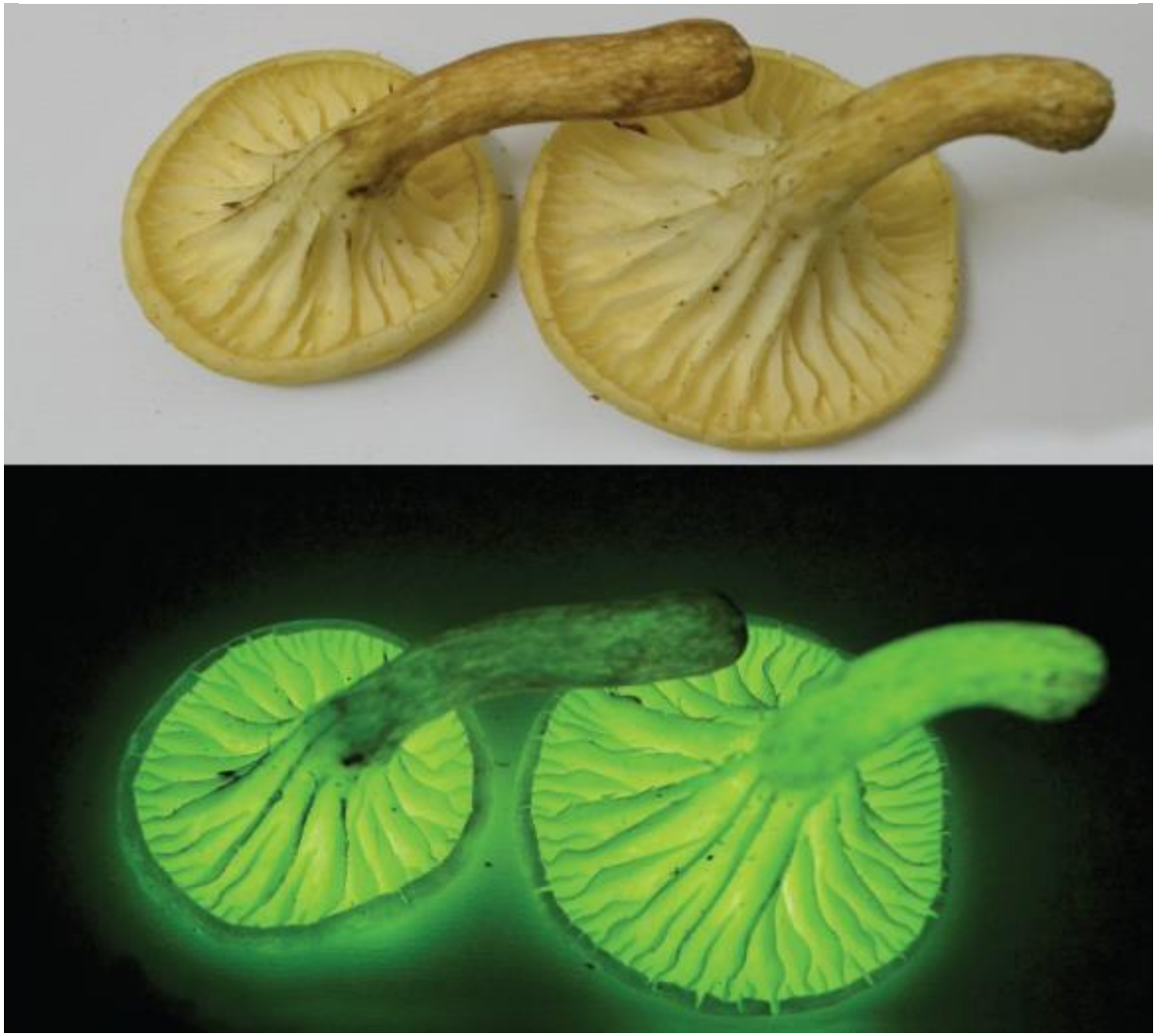
Cite this: *Photochem. Photobiol. Sci.*, 2012, **11**, 848

www.rsc.org/pps

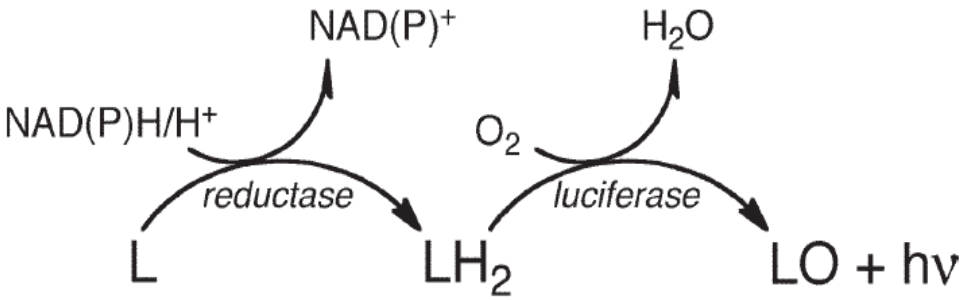
PAPER

Evidence that a single bioluminescent system is shared by all known bioluminescent fungal lineages†

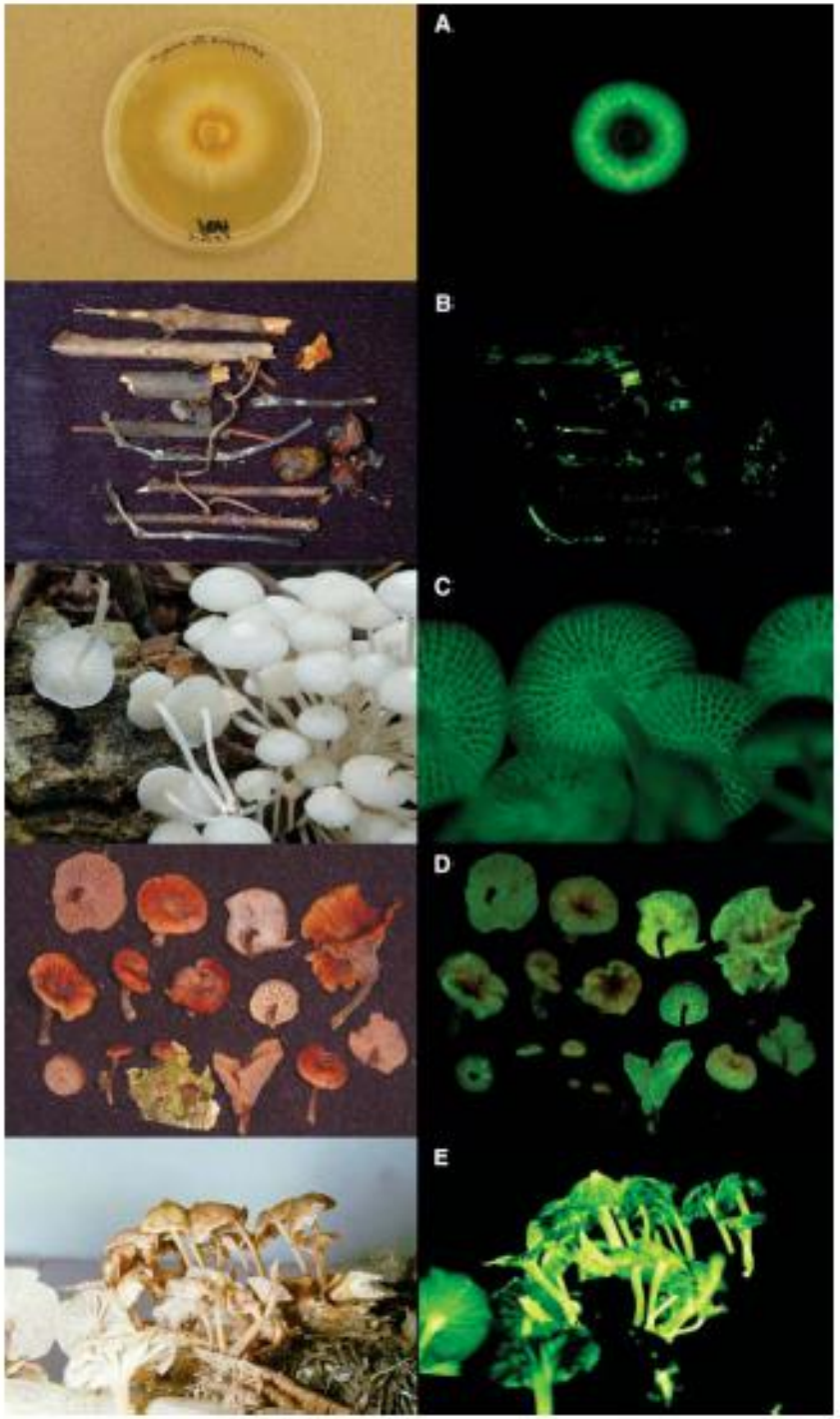
Anderson G. Oliveira,[a] Dennis E. Desjardin,[b] Brian A. Perry[c] and Cassius V. Stevani*[a,d]



Fungi bioluminescence revisited
Desjardin, Oliveira and Stevani
Photochem. Photobiol. Sci., 2008, 7, 170–182



L: luciferin, LH_2: reduced luciferin, LO: oxyluciferin



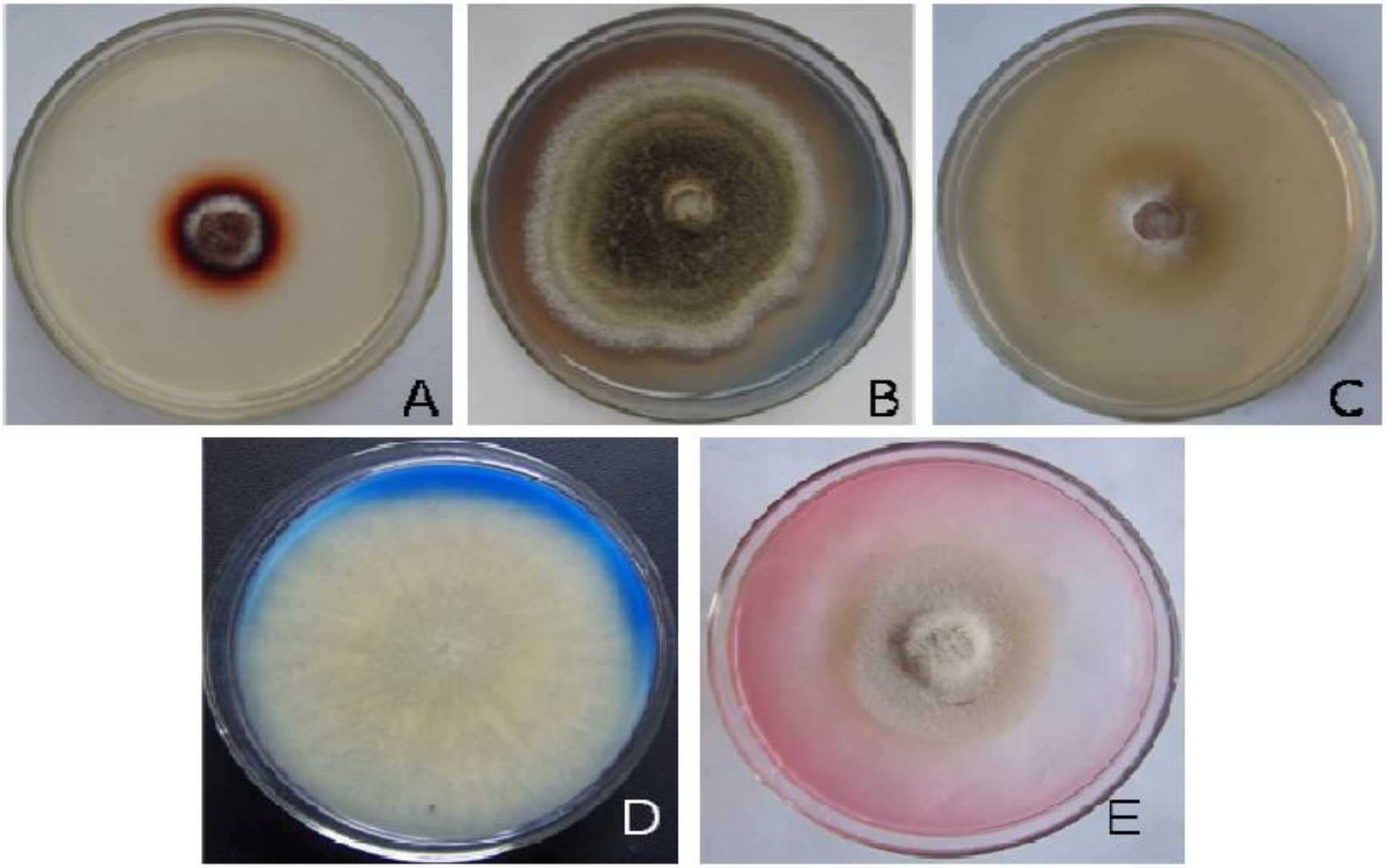
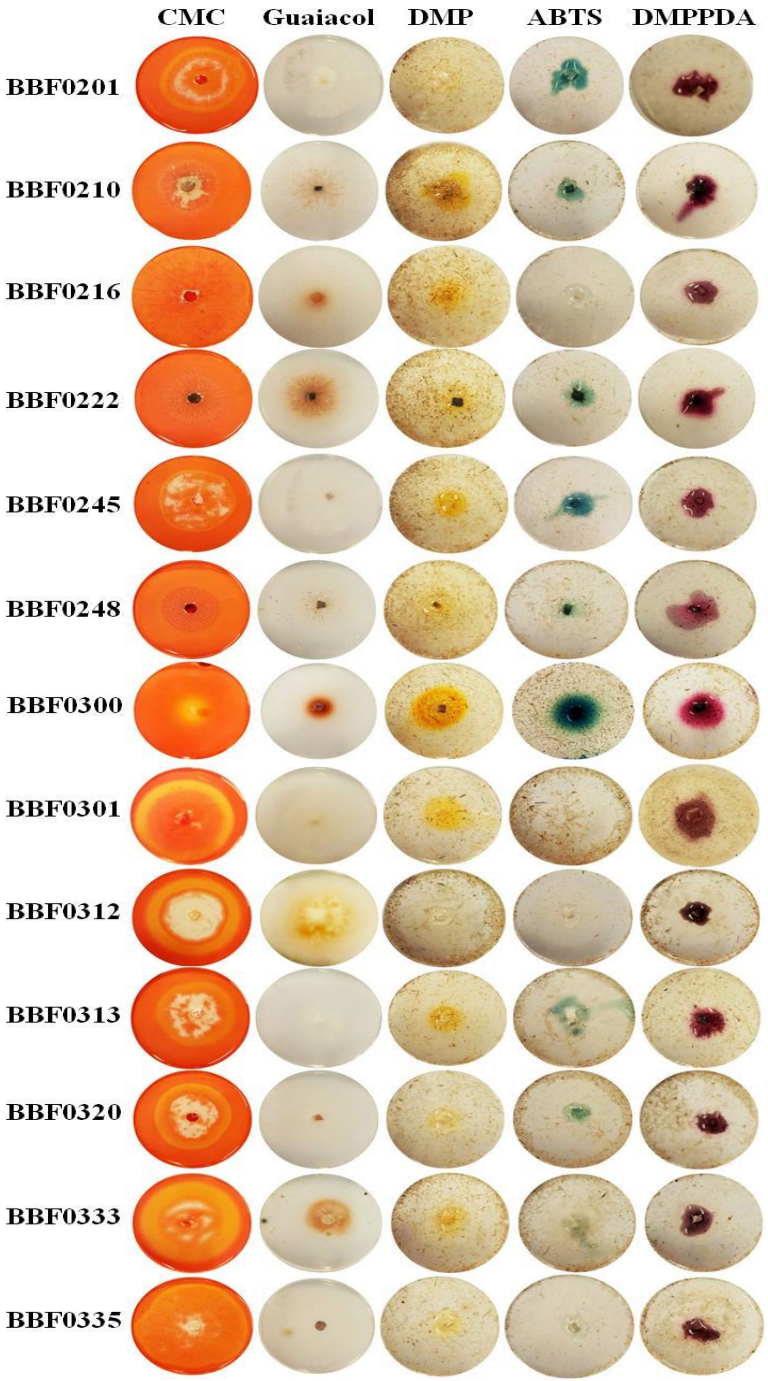


Figure 1. Reactions of GHJ-4 strain with different indicators on PDA plates. A, Reddish brown zones of guaiacol; B, decolourize of RBBR; C, yellow zones of tannic acid; D, decolourize of aniline blue; E, decolourize of phenol red.

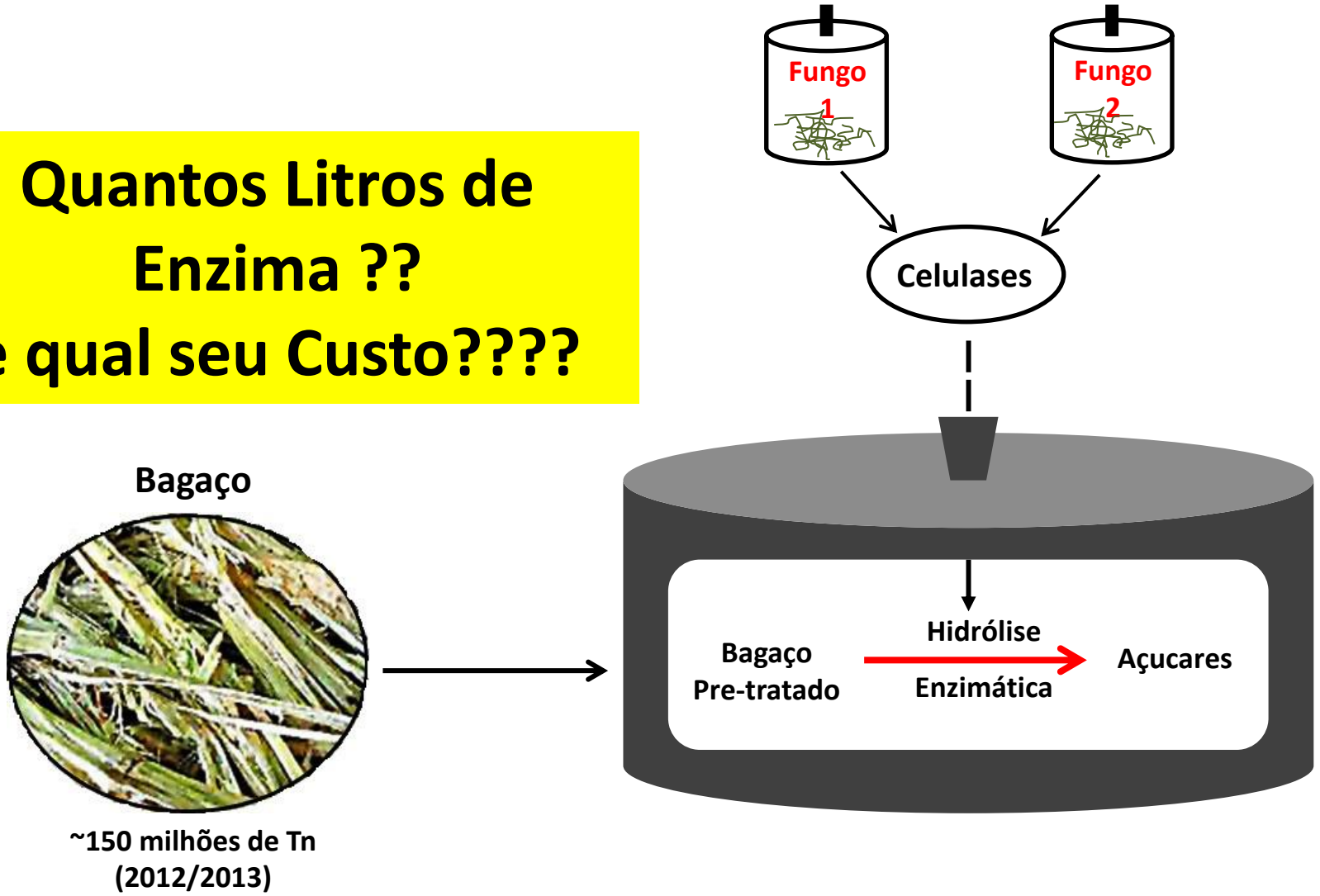
Gao et al., 2011

Ensaio de CMCase


CMC
Guaiacol
DMP
ABTS
DMPPDA
BBF0201
BBF0210
BBF0216
BBF0222
BBF0245
BBF0248
BBF0300
BBF0301
BBF0312
BBF0313
BBF0320
BBF0333
BBF0335

Fungos

Quantos Litros de Enzima ??
e qual seu Custo????



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MINI-REVIEW

Fungal biodiversity to biotechnology

Felipe S. Chambergo[1] · **Estela Y. Valencia**[2]

Abstract Fungal habitats include soil, water, and extreme environments. With around 100,000 fungus species already described, it is estimated that 5.1 million fungus species exist on our planet, making fungi one of the largest and most diverse kingdoms of eukaryotes. Fungi show remarkable metabolic features due to a sophisticated genomic network and are important for the production of biotechnological compounds that greatly impact our society in many ways. In this review, we present the current state of knowledge on fungal biodiversity, with special emphasis on filamentous fungi and the most recent discoveries in the field of identification and production of biotechnological compounds. More than 250 fungus species have been studied to produce these biotechnological compounds. This review focuses on three of the branches generally accepted in biotechnological applications, which have been identified by a color code: red, green, and white for pharmaceutical, agricultural, and industrial biotechnology, respectively. We also discuss future prospects for the use of filamentous fungi in biotechnology application.

Table S1. Selected fungi and (potential) application in Biotechnology.

Fungi	Products/Compounds/Enzyme/Metabolite/DNA	Activity/(Potential) Application	Reference
Aspergillus oryzae	Sake (rice wine), Shoyu (soy sauce), Miso (soybean paste)	Fermented Foods	Abe et al. 2006
Aspergillus sp	Phytase	Feed additive	Betancur et al. 2012
Fusarium sp	Bikaverin	Antibiotic properties against certain protozoa and fungi and antitumoral activity against different cancer cell lines.	Limon et al. 2010
Sporothrix schenkii, Alternaria alternata	Dihydroxynaphthalene–melanin	Ultraviolet sunscreens	Gao and Garcia-Pichel 2011
Aspergillus terreus	Lovastatin	HMG-CoA reductase inhibitors	Tobert 2003
Penicillium citrinum	Compactin		
Phoma sps	Equisetin and Phomasetin Fusidienol A Octahydronaphthol derivative MK8383 Phomadecalins A-D YM-202204; YM-215343 Herbarumins I,II,III Phomallenic acid (A–C)	Antiviral agent (against HIV) Antitumour Pesticide Antibacterial Antifungal Herbicide Antimicrobial	Rai et al. 2009
Aspergillus nidulans and Penicillium chrysogenum	Penicillin	β-lactam antibiotic	Van den Berg 2011
Cephalosporium acremonium	Cephalosporins	β-lactam antibiotic	Terfehr et al. 2014
Tolypocladium inflatum	Cyclosporin	Immunosuppressant	Bushley et al. 2013