



IVF · G06

中国农业科学院蔬菜花卉研究所

# 真菌分子系统发生学

## Molecular Phylogenetics of Fungi

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汇报时间：2017.12.13





# What is a Fungus?

Fungi are either macroscopic or microscopic (most)

cells



fruitbody



huge mushroom



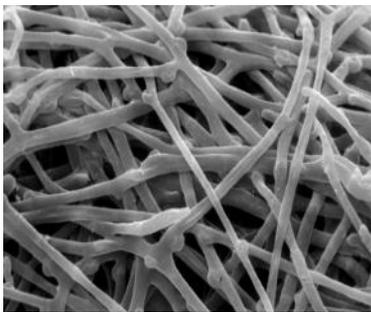
humungous fungus



*Armillaria ostoyae*

Mycelium over an area of more than 8.9 km<sup>2</sup> (3.4 square miles), it may be the largest organism on earth).

filamentous





# A Brief History of Fungi

## 1. 前期(1700年以前):

食用和药用的基础上对大型菌物进行描述。

543?	贾思勰	齐民要术	北魏
1250	陈仁玉	菌谱	宋
1277-1294		农桑辑要	元
1313	王桢	农书	元
1500	潘之恒	广菌谱	明
1578	李时珍	本草纲目	清
1703	吴林	吴菌谱	清
1675	Sterbeeck	描述了食菌和毒菌	比利时



### 2. 早期(1700-1900): 系统调查和分类时期。

- **van Leeuwenhoek** - invention of the microscope, 17th century (显微镜)



### 3. 近代(1900-1980):

菌物的细胞学、全型真菌、遗传学、生理学、医学菌物学和工业菌物学。





### 4. 现代(1980-2010):

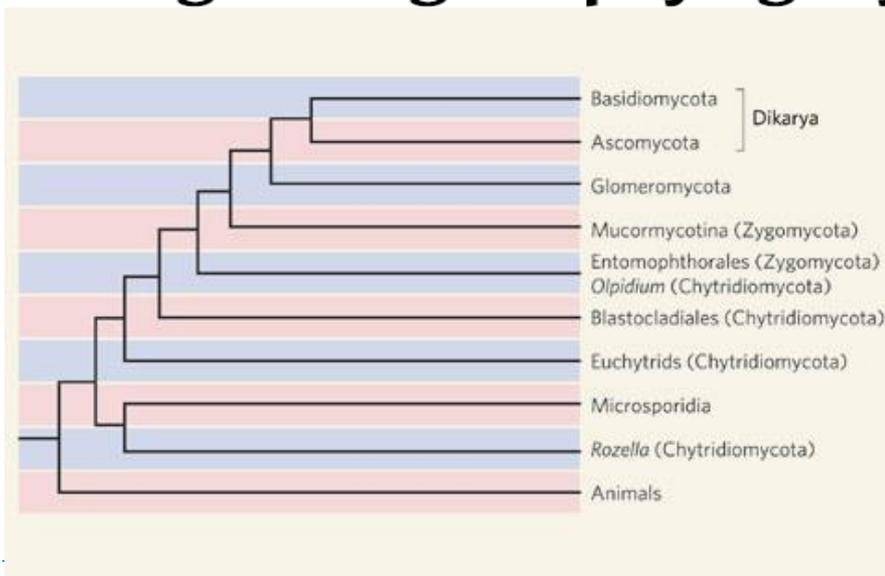
菌物质粒、菌物病毒、分子菌物学、菌物工艺学、分子系统学。

nature

Vol 443|19 October 2006|doi:10.1038/nature05110

## ARTICLES

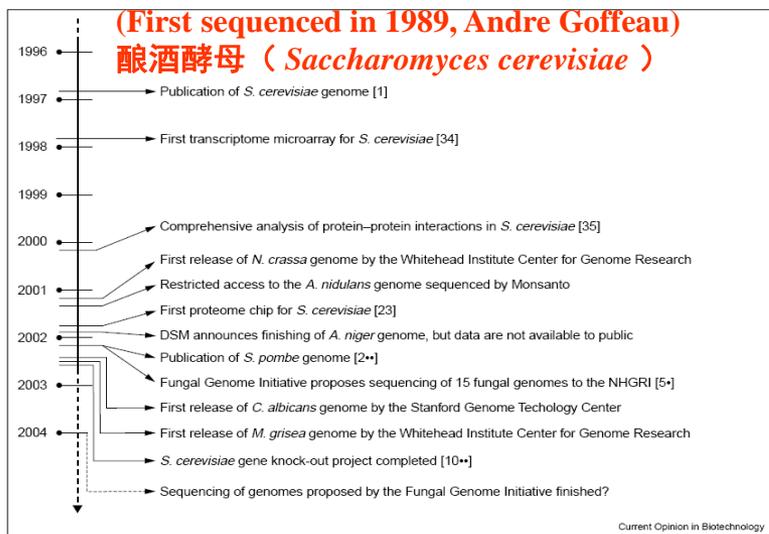
### Reconstructing the early evolution of Fungi using a six-gene phylogeny



Nature 443, 758-761

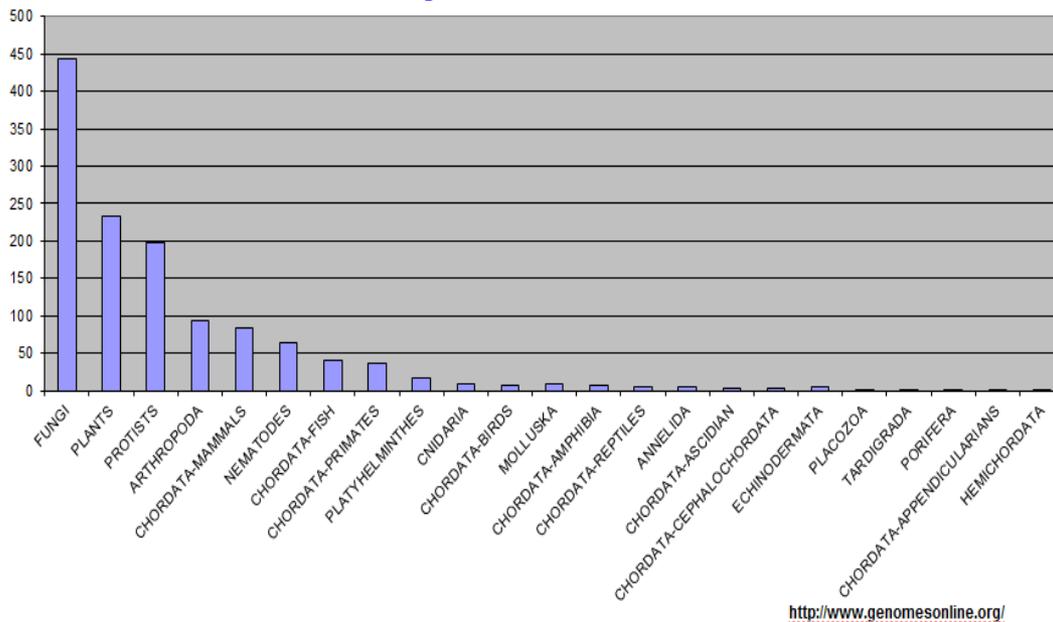


# 真菌基因组研究的发展历程



Curr. Opinion Biotechnol. 2004

### Eukaryotic Phyla with Genome Projects September 2009



2010 >500种真菌基因组被测序





### 5. 新时代（2010）？

分子生物学、组学时代？全面更新（新类群、分枝 / 新生态功能等）？

Genome > **Genome Information by Organism**

Organism name (common or scientific) or Accession (Assembly, BioProject or replicon)

Overview (33110); [Eukaryotes \(4965\)](#); [Prokaryotes \(125703\)](#); [Viruses \(12952\)](#); [Plasmids \(10916\)](#); [Organelles \(1096\)](#)

Filters **2**

Kingdom  Eukaryota (1,166)

Group  Animals (856)  **Fungi (1,166)**  Other (21)  Plants (285)  Protists (261)

Organism Name

- Fungi**
- Ajellomyces capsulatus*
  - Ajellomyces dermatitidis*
  - Alternaria brassicicola* ATCC 96836
  - Arthroderma benhamiae* CBS 112371
  - Arthroderma gypseum* CBS 118893
  - Arthroderma otae* CBS 113480
  - Ascosphaera apis* USDA-ARSEF 7405
  - Aspergillus clavatus* NRRL 1
  - Aspergillus flavus* NRRL3357
  - Aspergillus nidulans* FGSC A4
  - Aspergillus niger* CBS 513.88
  - Aspergillus terreus*
  - Blumeria graminis* f. sp. hordei DH14
  - Botryotinia fuckeliana* B05.10
  - Chaetomium globosum* CBS 148.51
  - Coccidioides immitis*
  - Coccidioides posadasii*
  - Epichloe festucae* E2368
  - Fusarium oxysporum* f. sp. lycopersici 4287
  - Gaeumannomyces graminis* var. tritici R3-111a-1
  - Gibberella moniliformis* 7600
  - Gibberella zeae* PH-1
  - Glomerella graminicola* M1.001
  - Grosmannia clavigera* kw1407
  - Magnaporthe oryzae* 70-15
  - Nectria haematococca* mpVI 77-13-4
  - Neosartorya fischeri* NRRL 181
  - Neosartorya fumigata*
  - Neurospora crassa* OR74A
  - Paracoccidioides brasiliensis*
  - Penicillium chrysogenum* Wisconsin 54-1255
  - Penicillium marneffeii* ATCC 18224

NCBI record





## Genome databases and genome browsers (7个)

- **ENSEMBL** - The web server of the European eukaryotic genome resource developed by EBI and the Sanger Institute.
- **UCSC Genome Information** - The genome browser website containing the reference sequence and working draft assemblies for a large collection of genomes at the University of California at Santa Cruz (UCSC), originally known as GoldenPath.
- **NCBI Map Viewer** - The The NCBI genomic map viewer for the visualization of completed and ongoing genome sequence.
- **NCBI Genome** - The entry portal to various NCBI genomic biology tools and resources, including the Map Viewer, the Genome Project Database and the Plant Genomes Central, etc.
- **NCBI Genome Information** - The NCBI genomic information table lists the general information of genomes for all species.
- **VISTA** - A comprehensive suite of programs and databases for comparative analysis of genomic sequences.
- **GOLD** - Genomes Online Database, a comprehensive information resource for complete and ongoing genome sequencing projects with flowcharts and tables of statistical data.

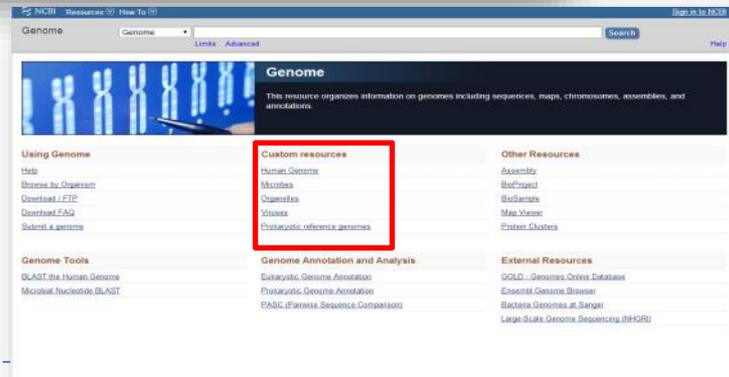
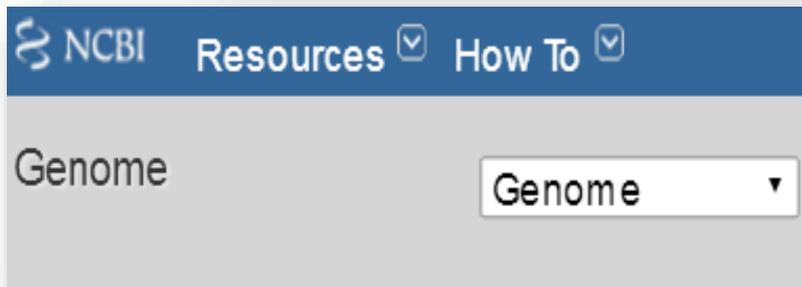


## Genome Browser



## GOLD

GENOMES ONLINE DATABASE



## Our Science

How we're contributing to bioenergy research.

[LEARN MORE](#)

## User Program Info

Everything you need to know about getting a project started.

[LEARN MORE](#)

## Data & Tools

Explore genomic data and the utilities developed by our staff.

[LEARN MORE](#)

## Our Projects

Discover projects underway and past achievements.

[LEARN MORE](#)

## Scientific Programs

### Plant Program

**植物**



The Plant Program focuses on fundamental biology of photosynthesis, conversion of solar to chemical energy.

[LEARN MORE](#)

### Fungal Program

**真菌**



This program scales up genomic sequencing and analysis to explore the diversity of fungi important for energy and the environment, and to promote system-level functional studies.

[LEARN MORE](#)

### Metagenome Program

**宏基因组**



A primary motivation for metagenomics is that most microbes found in nature exist in complex, interdependent communities and cannot readily be grown in isolation in the laboratory.

[LEARN MORE](#)

### Microbial Program

**细菌**



The Microbial Program exploits expertise and emerging technologies in sequencing, annotation and analysis, to deliver high quality and high throughput sequence-based science.

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### DNA Synthesis Science

**DNA**



Our focus is on the identification and refactoring of biological pathways with potential application in DOE mission-

### Metabolomics Technology

**代谢组学**



This group integrates metabolomics with genomic information to provide functional annotation of genomes and

## BBTools

A suite of bioinformatics tools used for DNA and RNA sequence data analysis.

[LEARN MORE](#)

## Meraculous

A distributed and scalable assembler for eukaryotic genomes.

[LEARN MORE](#)

## GOLD

An information resource for sequencing projects and associated metadata.

[LEARN MORE](#)

## Phytozome

The plant comparative genomics portal of the DOE Joint Genome Institute.

[LEARN MORE](#)

## Genome Portal

Unified access to all JGI genomic databases and analytical tools.

[LEARN MORE](#)

## MycoCosm

Access to data, visualization, and analysis tools for comparative genomics of fungi.

[LEARN MORE](#)

## IMG

A community resource for comparative analysis and annotation.

[LEARN MORE](#)

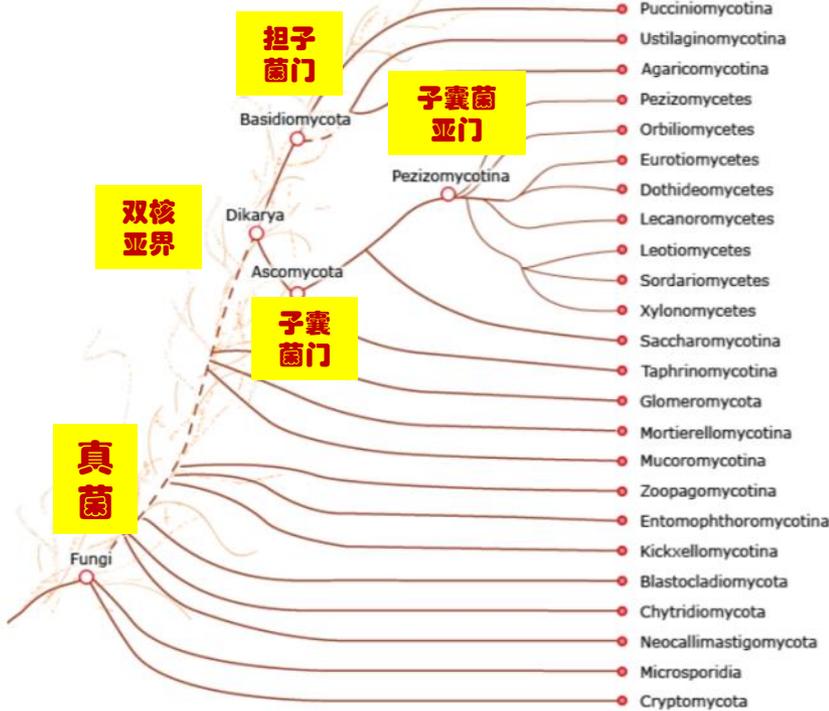
Plant Program

Fungal Program

- MycoCosm
- Genomic Encyclopedia of Fungi
- 1000 fungal genomes
- Benchmarks
- Search the Fungal Program Project List
- Fungal Publications
- Recent Fungal Genome Releases

# Fungal Program

The Fungal Program scales up sequencing and analysis of fungal genomes to explore the diversity of fungi important for energy and the environment, and to promote functional studies on a system level. Encoded in the genomes of the organisms of the kingdom Fungi are biological processes with high relevance to the Department of Energy missions in bioenergy production, carbon cycling and biogeochemistry. Combining new sequencing technologies and comparative genomics analysis, we work on large and complex sequencing projects such as surveying the broad phylogenetic and ecological diversity of fungi, and capturing genomic variation in natural populations and engineered strains. This approach allows us to build a foundation for translating the genomic potential of fungi into practical applications.



界 → 门 → 纲 → 目 → 科 → 属 → 种

-mycota -mycetes

-mycotina



## Our Science

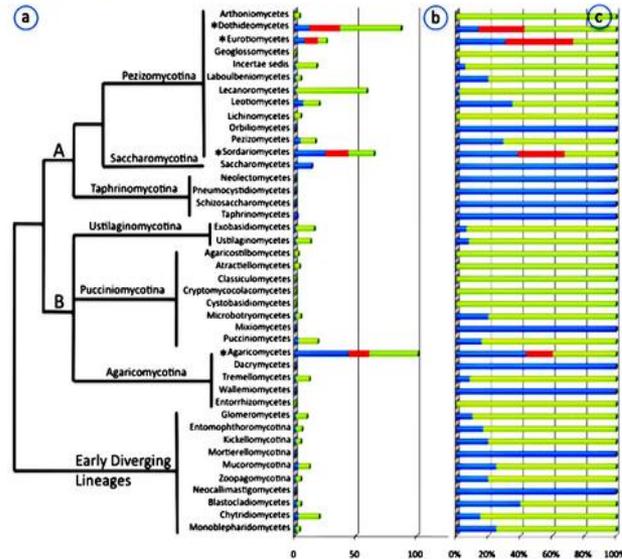
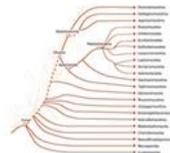
Home > Our Science > Science Programs > Fungal Program > 1000 fungal genomes

### 1000 fungal genomes

[Nominatate a genome to sequence](#)

- Plant Program
- Fungal Program
  - MycCosm
  - Genomic
  - Encyclopedia of Fungi
  - 1000 fungal genomes**
  - Benchmarks
  - Search the Fungal Program Project List
  - Fungal Publications
  - Recent Fungal Genome Releases
- Metagenome Program
- Microbial Program
- DNA Synthesis Science Program
- Emerging Science Program

[MycCosm Web Portal](#)



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.



### 1000 Fungal Genomes

This project aims to provide genomic information for every family of fungi. The list below includes sequenced fungal genomes, those in progress, and selected nominations. You can [log in](#) and nominate new species for genome sequencing in the families with no (green) or only one (yellow) reference genome if you can provide DNA/RNA samples for their sequencing (see [JGI User Guidelines](#)). If you know additional fungal species being sequenced somewhere but not reflected on this list, please register these projects in GOLD (use [Add to GOLD](#) link) or [let us know](#).

Phylum: all | Subphylum: all | Class: all | Order: all | Family: all | [Search](#) [Reset](#)

Show families with  No genomes  Single genome  Many genomes

Genome project(s), 864 nomination(s).  
Nominated for sequencing by community are marked with asterisk.

Phylum name	Subphylum name	Class name	Order name	Family name	Genome Projects
Ascomycota	Incertae sedis	Incertae sedis	Incertae sedis	Incertae sedis	<ul style="list-style-type: none"> <li><a href="#">Ascomycete sp.</a>  WGS</li> <li><a href="#">Calcarisporiella thermophila</a>  WGS</li> <li><a href="#">Cerataphis brasiliensis yeast-like symbiont</a>  WGS</li> <li><a href="#">Helminthosporium solani</a>  WGS</li> <li><a href="#">Nilaparvata lugens yeast-like symbiont</a>  WGS</li> <li><a href="#">* Stanjemonium griseum</a>  WGS</li> <li><a href="#">Symbiotaphrina kochii</a>  WGS</li> </ul>

Kathryn Bushley, University of Minnesota





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[Science Programs](#)

[Science Highlights](#)

## Our Science

[Home](#) > [Our Science](#) > [Science Programs](#) > [Fungal Program](#) > Recent Fungal Genome

Releases

Plant Program

Fungal Program

[MycoCosm](#)

[Genomic Encyclopedia of Fungi](#)

[1000 fungal genomes](#)

[Benchmarks](#)

[Search the Fungal Program Project List](#)

[Fungal Publications](#)

[Recent Fungal Genome Releases](#)

## Recent Fungal Genome Releases

2017-12-08

[Oliveonia pauxilla KC1149 v1.0](#)

2017-12-08

[Paraphoma chrysanthemicola PD 92/468 v1.0](#)

2017-12-08

[Fusarium oxysporum FOX64 v1.0](#)

2017-12-08

[Paecilomyces variotii CBS 101075 v1.0](#)

2017-12-08

[Achaetomium strumarium CBS333.67 v1.0](#)

查询于  
2017.12.9



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NCBI Resources How To

q90 MyNCBI Sign Out

RefSeq

RefSeq

Search



### RefSeq: NCBI Reference Sequence Database

A comprehensive, integrated, non-redundant, well-annotated set of reference sequences including genomic, transcript, and protein.

#### Using RefSeq

[About RefSeq](#)

[Human Reference Genome](#)

[Prokaryotic RefSeq Genomes](#)

[FAQ](#)

[NCBI Handbook](#)

[Factsheet](#)

#### RefSeq Access

[Human Genome Resources and Download](#)

[RefSeq FTP](#)

[RefSeq genomes FTP](#)

[New RefSeq genomic \(last 30 days\)](#)

[New RefSeq transcripts \(last 30 days\)](#)

[New RefSeq proteins \(last 30 days\)](#)

[Searching for RefSeq records \(Queries\)](#)

#### RefSeq projects

[Consensus CDS \(CCDS\)](#)

[RefSeq Functional Elements](#)

[RefSeqGene](#)

[Targeted Loci](#)

[Virus Variation](#)

**全面的、集成的、  
非冗余的、注释过的**

**基因组、转录本、蛋白质**





## /genomes/refseq/ 的索引

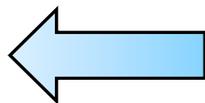
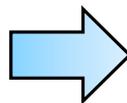
名称	大小	修改日期
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<a href="#">assembly_summary_refseq.txt</a>	0 B	2017/12/9 9:43:00
<a href="#">assembly_summary_refseq_historical.txt</a>	0 B	2017/12/9 9:43:00
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<a href="#">fungi/</a>		2017/12/9 11:37:00
<a href="#">invertebrate/</a>		2017/12/9 11:37:00
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<a href="#">viral/</a>		2017/12/9 11:37:00

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<a href="#">Alternaria_alternata/</a>		2017/12/9 11:25:00
<a href="#">Anthracocystis_flocculosa/</a>		2017/12/9 11:26:00
<a href="#">Arthrotrrys_oligospora/</a>		2017/12/9 11:25:00
<a href="#">Ascoidea_rubescens/</a>		2017/12/9 11:26:00
<a href="#">Aspergillus_aculeatus/</a>		2017/12/9 11:25:00
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<a href="#">Bipolaris_victoriae/</a>		2017/12/9 11:26:00
<a href="#">Bipolaris_zeicola/</a>		2017/12/9 11:25:00

## /genomes/refseq/fungi/Botrytis\_cinerea/latest\_assembly\_versions/GCF\_0

名称	大小	修改日期
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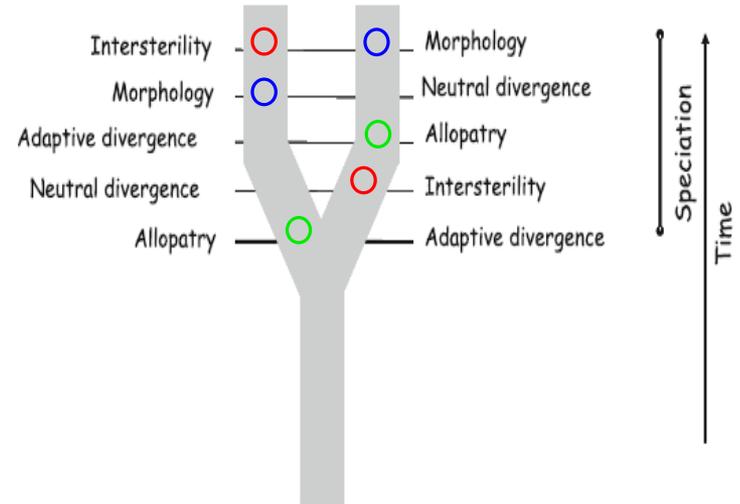
# What is species?

物种，简称“种”，是生物**分类学**研究的基本单元与核心，不同物种之间存在**生殖隔离**。



Allopatric speciation

Sympatric speciation



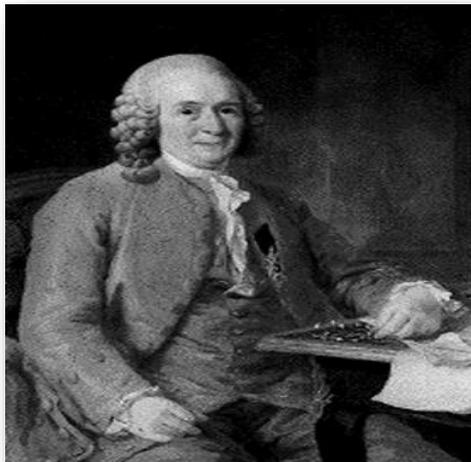
物种形成是一个长期过程，通过**表型与基因型**特征综合物种形成标志性事件科学认识物种

(Fungal Divers. 50:121-133, 2011)



# 物种概念的进化

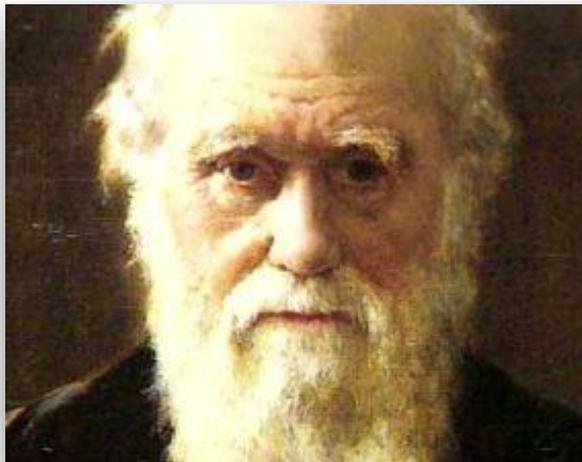
形态物种



**CLASSIFICATION  
BASED ON  
SIMILARITY**

Carolus Linnaeus  
(1707-1778)

Group organisms  
according to phenotypic  
resemblance



**EVOLUTION**

Charles Darwin  
The Origin of Species  
(1859)

Organisms descend with  
modification from  
common ancestors;  
variations are heritable in  
any species

系统演化物种



**CLASSIFICATION  
BASED ON  
GENEALOGY**

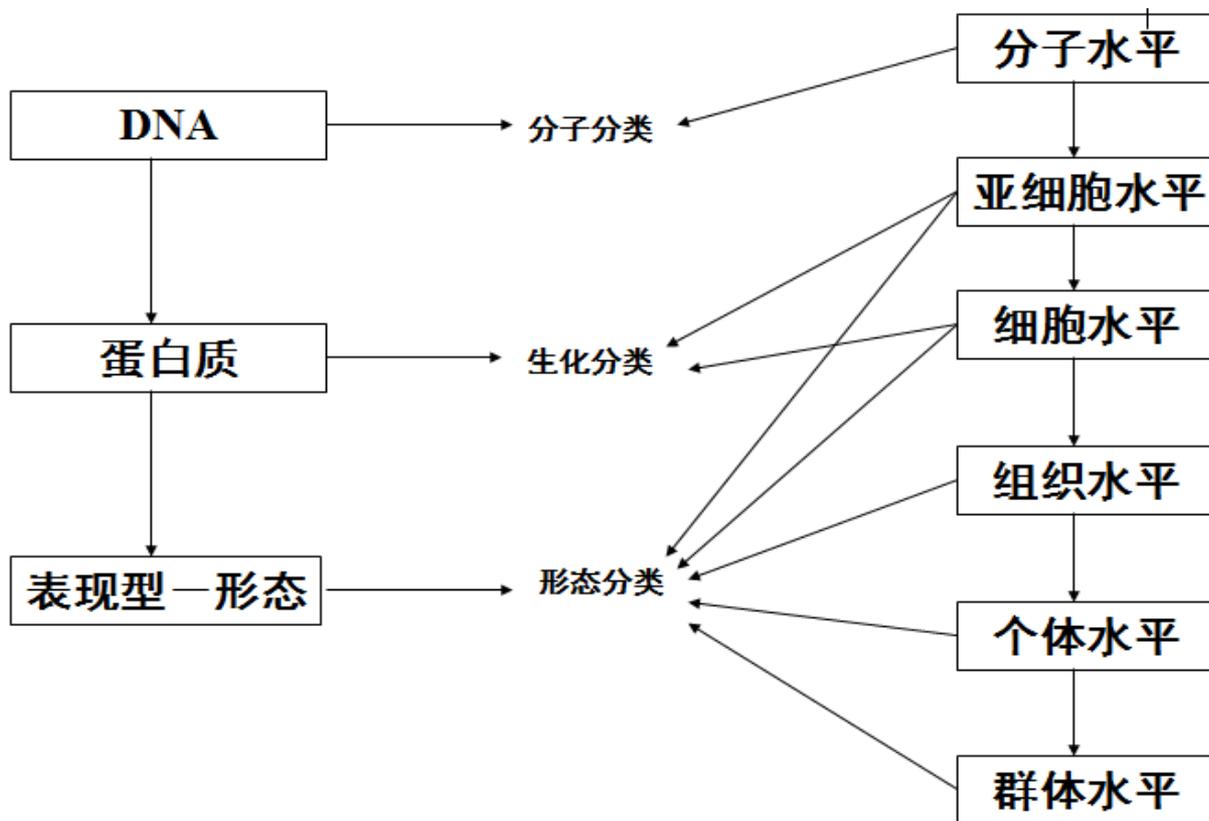
Willi Hennig  
Phylogenetic Systematics  
(1966)

Proposed the use of  
sister-group relationships





### 物种分类原理:



many phylogenetic characters are now derived from DNA sequence





### ***Are molecular characters superior to morphological characters for phylogenetic inference?***

- ▶ yes and no...
  - ▶ **strengths of molecular characters:**
  - ▶ very numerous
  - ▶ allow explicit coding (A/C/G/T)
  - ▶ can be compared in organisms **with no morphological similarities**
  - ▶ models of evolution based on genetic code and biochemical attributes of DNA can be built into **analytical** methods
  - ▶ **weaknesses of molecular characters:**
  - ▶ cannot be obtained from **fossils** (except very rarely )
  - ▶ requires **expensive** laboratory equipment (this becomes less and less significant all the time)
  - ▶ does not provide characters for field identification (this too may change)
  - ▶ most of the approximately 2 million **described species** have not yet to be studied using molecular tools, so in a sense, taxonomy is still primarily based on morphology.
- 



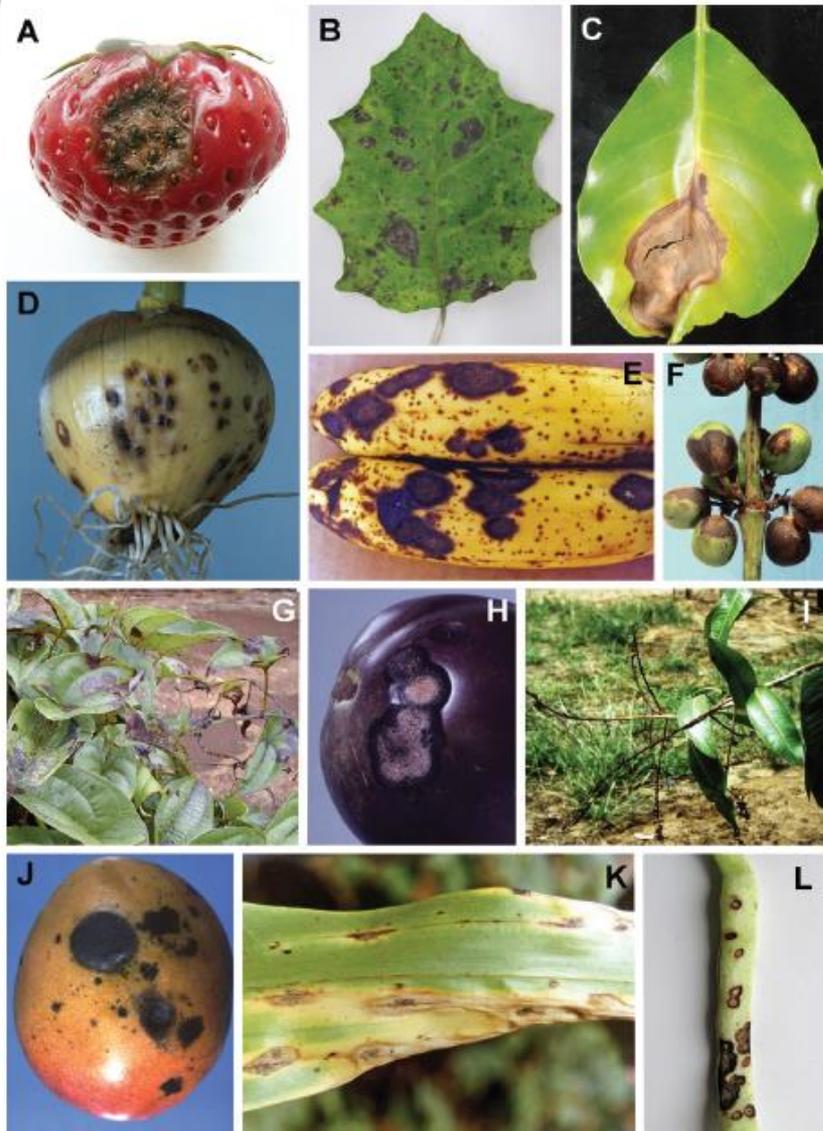


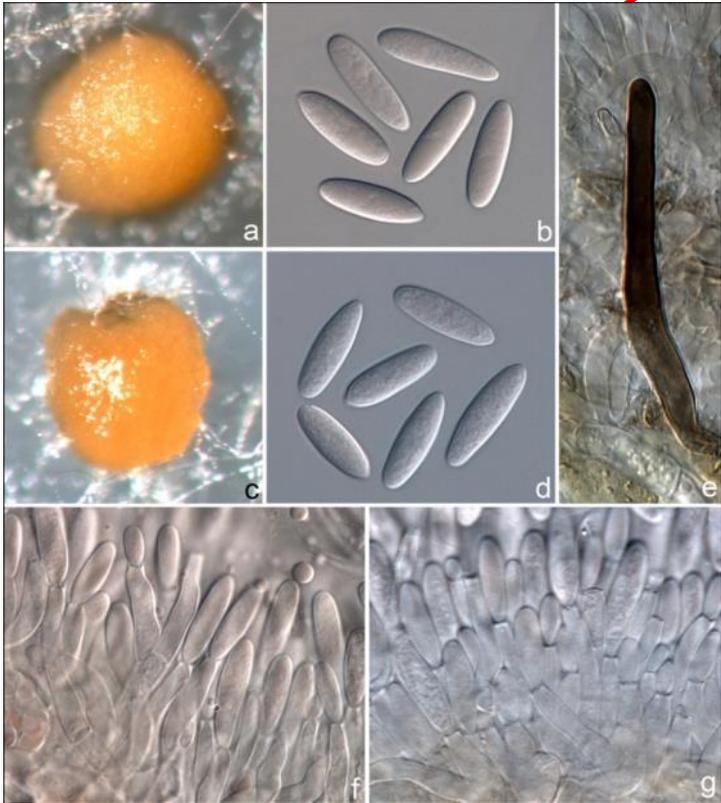
### 炭疽菌属

▶ 寄主专化性 (生态物种概念) 750

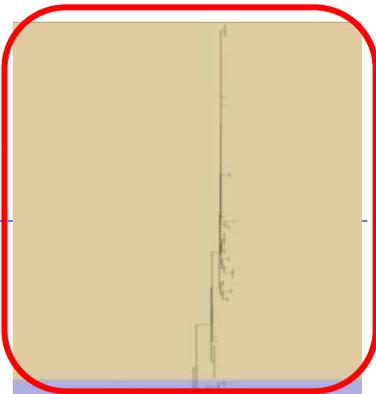
▶ 形态学 (形态物种概念) 11

▶ 进化谱系 (系统演化物种概念) 150





*Colletotrichum proteae*  
 Conidia cylindrical to clavate ,  
 7–22(–37) × 3–6 μm



*Colletotrichum acutatum*  
 Conidia cylindrical to clavate ,  
 6.5–13 × 2.5–4 μm



Morphologically similar,  
 phylogenetically distinct

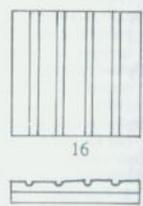
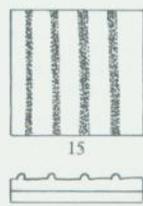
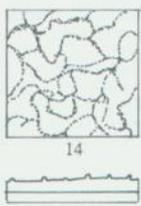
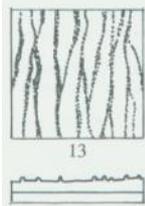
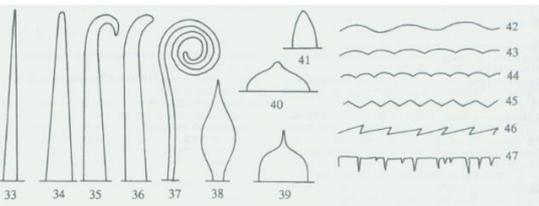
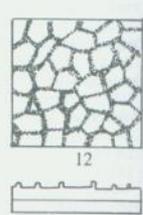
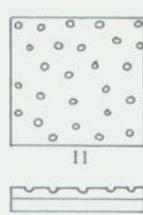
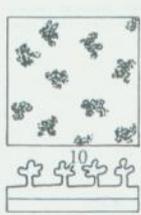
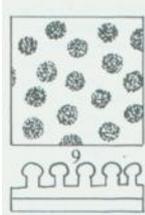
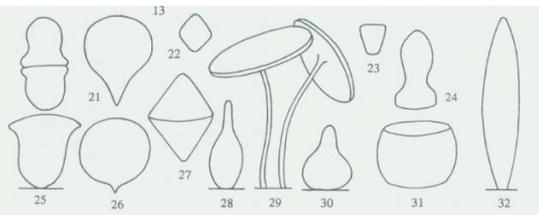
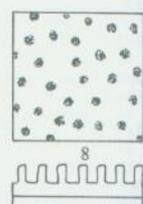
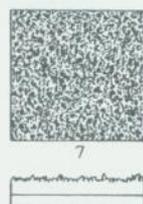
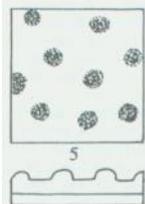
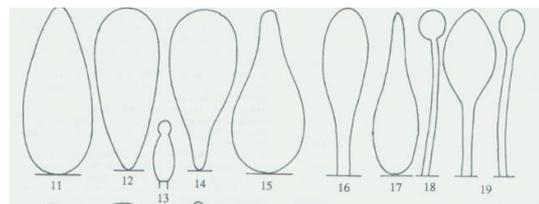
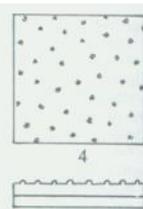
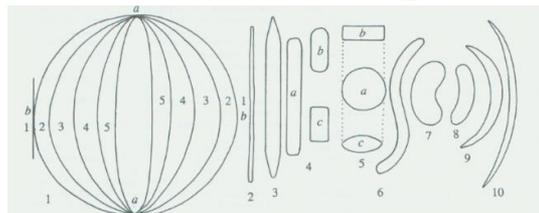




### 形态学鉴别指标:

#### 形态 Shapes

#### 纹饰 Ornamentation



大小  
Size

颜色  
Color

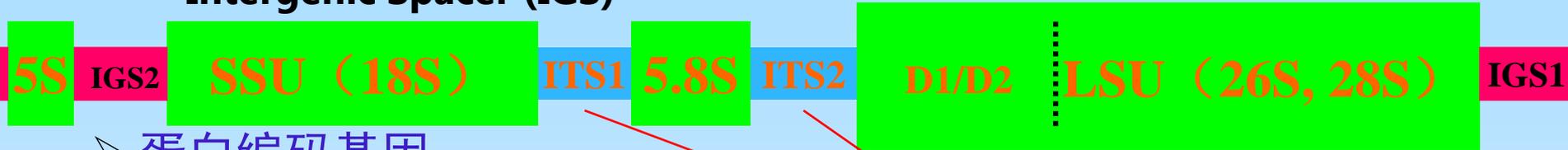
排列  
Arrangement

etc.

# 真菌分子系统发生学研究 常用基因和DNA片段

## ➤ 细胞核rRNA基因(rDNA)及其间非编码区

- Small Subunit (SSU) rDNA (18S)
- Large Subunit (LSU) rDNA (26S, 28S)
- **Internal Transcribed Spacer (ITS)**
- Intergenic Spacer (IGS)



## ➤ 蛋白编码基因

- $\beta$ -tublin gene
- elongation factor-1 $\alpha$  (EF- 1 $\alpha$  )
- RNA polymerase II 等等

## ➤ 线粒体mitochondrial (mt) DNA

- mtSSU and LSU rRNA genes
- mitochondrial cytochrome b (cytb)
- cytochrome oxidase I and II (COX I, COX II) 等等

非编码区  
承受的选择压力较小  
相对变化较大



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### NCBI-Taxonomy

NCBI Resources  How To  Sign in to NCBI

Taxonomy    [Limits](#) [Advanced](#) [Help](#)



### Taxonomy

The Taxonomy Database is a curated classification and nomenclature for all of the organisms in the public sequence databases. This currently represents about 10% of the described species of life on the planet.

#### Using Taxonomy

- [Quick Start Guide](#)
- [FAQ](#)
- [Handbook](#)
- [Taxonomy FTP](#)

#### Taxonomy Tools

- [Browser](#)
- [Common Tree](#)
- [Statistics](#)
- [Name/ID Status](#)
- [Genetic Codes](#)

#### Other Resources

- [GenBank](#)
- [LinkOut](#)
- [E-Utilities](#)
- [Batch Entrez](#)
- [INSDC](#)

You are here: NCBI > Taxonomy > Taxonomy

NCBI Resources  How To

Taxonomy    [Create alert](#) [Limits](#) [Advanced](#)

Display Settings:

**Colletotrichum**  
 genus, ascomycetes  
[Nucleotide](#) [Protein](#)

Search for  as complete name  lock

- Display  levels using filter: none
- Nucleotide  Nucleotide EST  Nucleotide GSS  Protein  Structure  Genome  Popset  SNP
  - Domains  GEO Datasets  UniGene  PubMed Central  Gene  HomoloGene  SRA Experiments  Probe
  - Assembly  MapView  LinkOut  BLAST  TRACE  Bio Project  Bio Sample  Bio Systems
  - Clone DB  dbVar  GEO Profiles  PubChem BioAssay  Protein Clusters  Host

Lineage (full): [root](#); [cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Fungi](#); [Dikarya](#); [Ascomycota](#); [saccharomyceta](#); [Pezizomycotina](#); [Leotiomyceta](#); [sordariomyceta](#); [Sordariomycetes](#); [Hypocreomycetidae](#); [Glomerellales](#); [Glomerellaceae](#)

[Colletotrichum](#) *Click on organism name to get more information.*

- [Colletotrichum abscissum](#)
- [Colletotrichum acerbum](#)
- [Colletotrichum aciculare](#)
- [Colletotrichum acutatum](#)
- [Colletotrichum cf. acutatum FSU 10150](#)
- [Colletotrichum cf. acutatum MU-2009](#)
- [Colletotrichum cf. acutatum RI](#)
- [Colletotrichum aenigma](#)
- [Colletotrichum aescyhoenenes](#)
- [Colletotrichum agaves](#)
- [Colletotrichum alatae](#)
- [Colletotrichum alcornii](#)
- [Colletotrichum alienum](#)
- [Colletotrichum americanae-borealis](#)
- [Colletotrichum ampelinum](#)
- [Colletotrichum annellatum](#)
- [Colletotrichum anthrisci](#)
- [Colletotrichum antirrhinicola](#)
- [Colletotrichum aotearoa](#)
- [Colletotrichum arxii](#)
- [Colletotrichum asianum](#)
- [Colletotrichum australe](#)
- [Colletotrichum axonopodi](#)
- [Colletotrichum beeveri](#)
- [Colletotrichum bidentis](#)
- [Colletotrichum bletillum](#)
- [Colletotrichum boninense](#)
- [Colletotrichum cf. boninense Col](#)
- [Colletotrichum aff. boninense LA79](#)
- [Colletotrichum cf. boninense UFMGCB 5024](#)
- [Colletotrichum brasiliense](#)
- [Colletotrichum brassicae](#)
- [Colletotrichum brassicicola](#)
- [Colletotrichum brevisporum](#)
- [Colletotrichum brisbanense](#)
- [Colletotrichum bryoniicola](#)
- [Colletotrichum camelliae](#)
- [Colletotrichum capsici](#)
- [Colletotrichum carthami](#)
- [Colletotrichum caudasporum](#)
- [Colletotrichum caudatum](#)

Search for  as complete name  lock

Display  levels using filter: none

### Colletotrichum abscissum

Taxonomy ID: 1671311

Scientific name: *Colletotrichum abscissum* Pinho & O.L. Pereira, 2015  
 holotype: VIC 42850  
 holotype: COAD 1877

Inherited blast name: [ascomycetes](#)

Rank: species

Genetic code: [Translation table 1 \(Standard\)](#)

Mitochondrial genetic code: [Translation table 4 \(Mold Mitochondrial\)](#); [Protozoan Mitochondrial](#);

[Coelenterate Mitochondrial](#); [Mycoplasma](#); [Spiroplasma](#)

Other names:

includes: [Colletotrichum sp. DBP2015](#)

Lineage (full)

[cellular organisms](#); [Eukaryota](#); [Opisthokonta](#); [Fungi](#); [Dikarya](#); [Ascomycota](#); [saccharomyceta](#); [Pezizomycotina](#); [leotiomyceta](#); [sordariomyceta](#); [Sordariomycetes](#); [Hypocreomycetidae](#); [Glomerellales](#); [Glomerellaceae](#); [Colletotrichum](#)

Entrez records	
Database name	Direct links
Nucleotide	<a href="#">255</a>
Protein	<a href="#">234</a>
Popset	<a href="#">12</a>
PubMed Central	<a href="#">2</a>
Taxonomy	<a href="#">1</a>

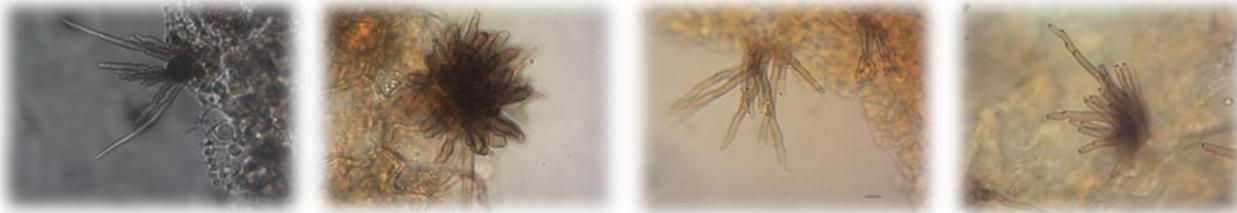




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# What is Molecular Phylogenetics of Fungi?





## 基本概念

### 系统发生 (*Phylogeny*)

指任何**生物实体**（基因、物种、种上阶元、个体和种群）的**起源和演化**。

### 系统发生学 (*Phylogenetics*)

研究生物间**亲缘关系及演化的学科**。依靠对取样物种的性状进行**数学推论**，推断**系统树**，**重建演化历史**。**准确性**依赖于对性状演化的**假设和模型**。

### 分子系统发生 (*Molecular phylogeny*)

利用各种**分子性状**构建生物实体之间的起源和演化关系。采用的分子数据主要是**DNA和蛋白质序列**，也包括**其它类型**的分子数据。

### 系统学/系统分类学 (*Systematics*)

研究生物的分类与命名的科学。

附属学科：分类学 Taxonomy

命名法 Nomenclature



# Why do we perform phylogenetic analysis?

- Find **evolutionary** ties between organisms  
(Analyze changes occurring in different organisms during evolution)
- Find (understand) **relationships** between an ancestral sequence and its descendants  
(Evolution of family of sequences)
- Estimate **time of divergence** between a group of organisms that share a common ancestor





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3,163 Studies 97,085 Species



### TIMETREE

THE TIMESCALE of LIFE

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Search

TimeTree (Taxa Group)

Group:

fungi

X

Search

Group:

Fungi (Fungi)

Update

Rank:

phylum (3)

Show Timetree

Spacing  
1x 2x 3x

Line Color

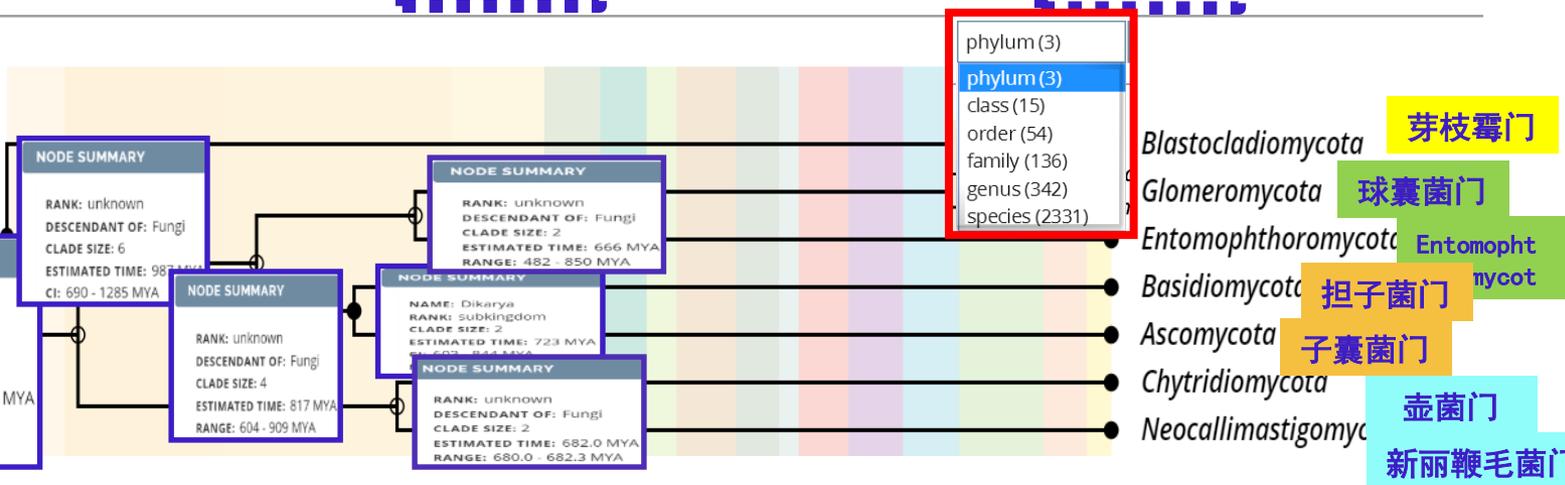
#000000

Tim

Linear

**NODE SUMMARY**

NAME: Fungi  
RANK: kingdom  
CLADE SIZE: 7  
ESTIMATED TIME: 1055 MYA  
CI: 779 - 1331 MYA  
NCBI LINK: Fungi

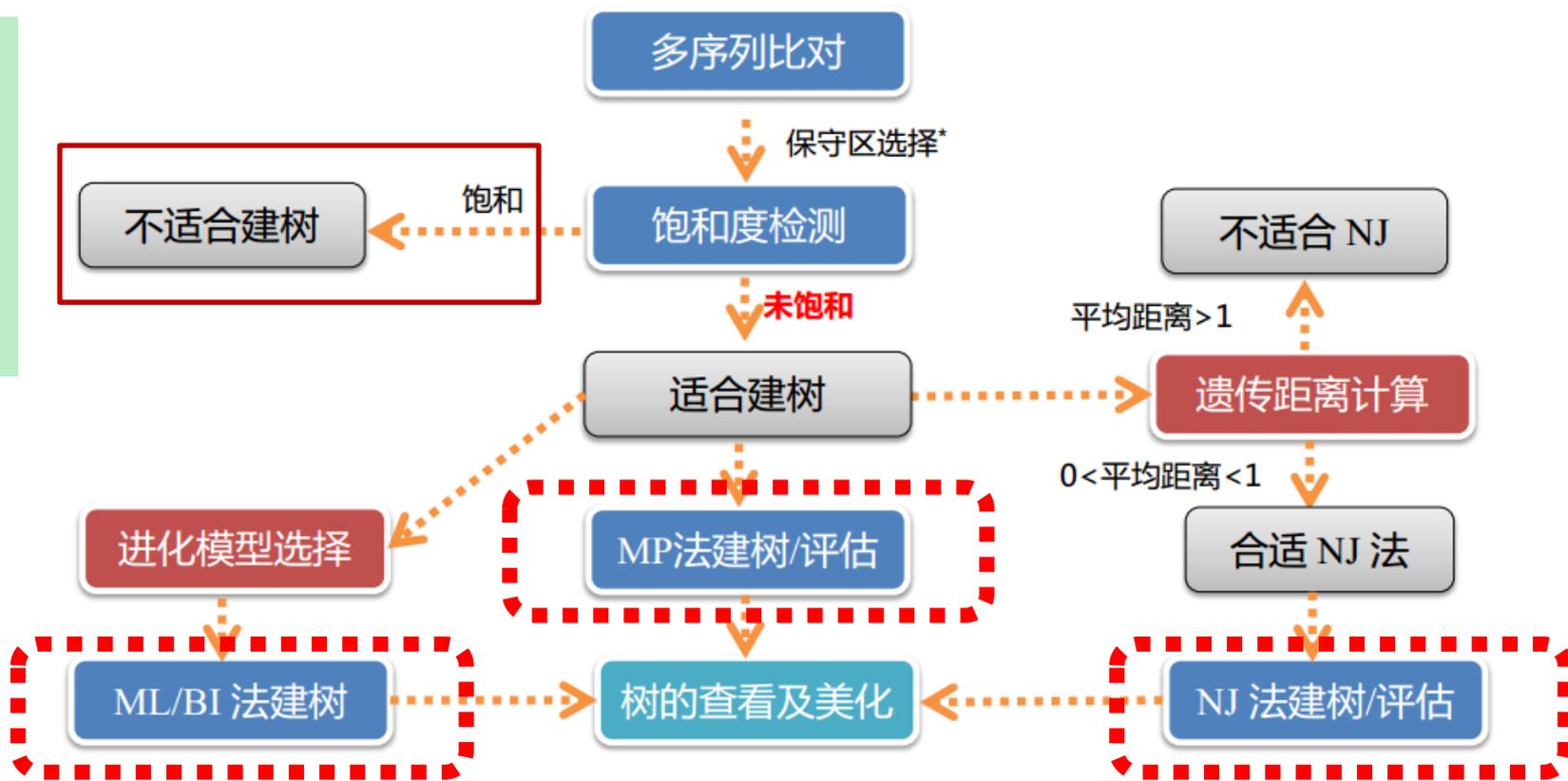






### How to perform phylogenetic analysis?

规范流程



\* 保守区选择，主要用于优化多重比对质量，仅适用于信息位点足够多的长序列。

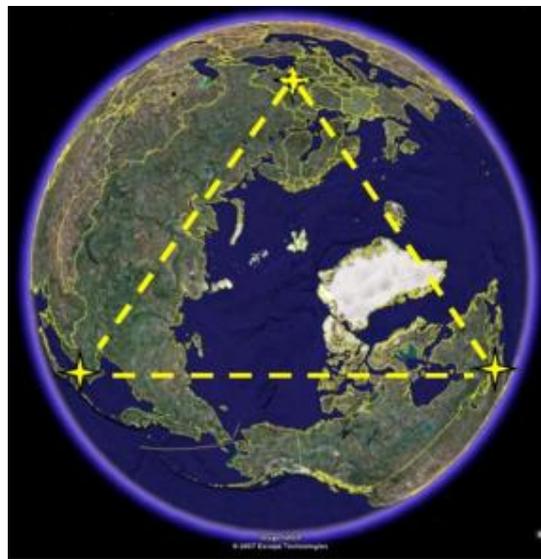
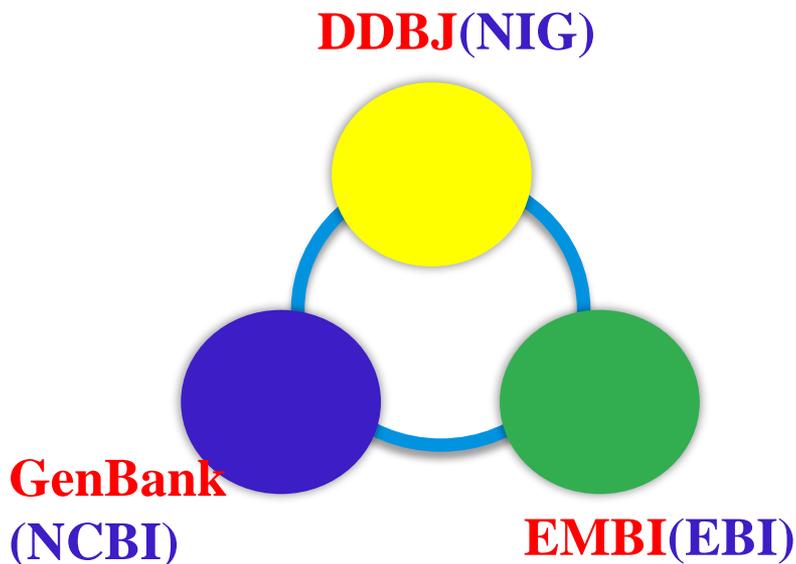


# 准备工作

### ➤ 序列片段拼接和正反链校正

常用软件 Lasergene (DNAStar) 、 **BioEdit** (免费软件)

### ➤ 从国际**核酸序列数据库**(GenBank/DDBJ/EMBL)中搜索(BLAST)和下载同源序列





## 多重序列比对

速度：**Muscle** > MAFFT > Clustal W > T-Coffee

准确性：**MAFFT** > Muscle > T-Coffee > Clustal W

## 进化模型的选择

### 核苷酸替换模型

- MrModeltest (24种)
- Modeltest (56种)
- jModelTest (24-1624种)
- **ModelGenerator (56种)**

### 进化模型

MEGA 自带模型选择

### 氨基酸替换模型

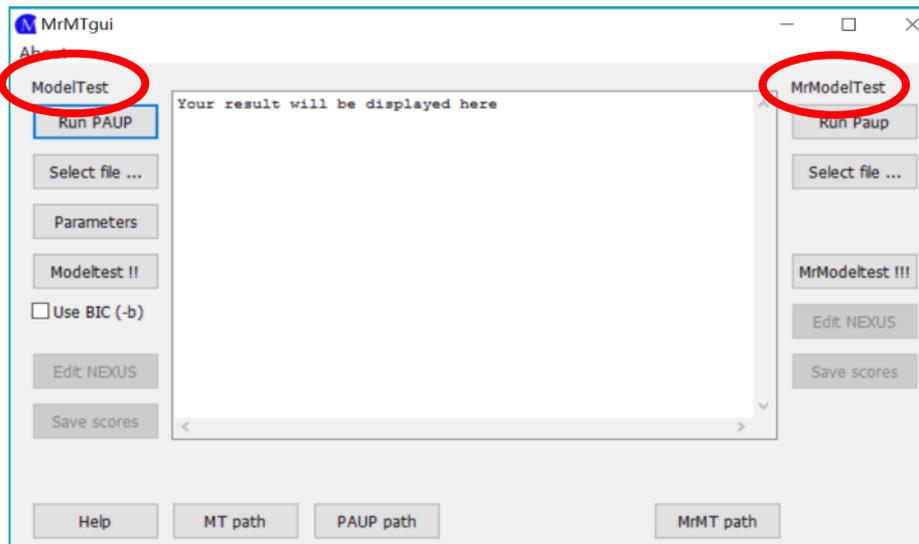
- Protest (15?种)
- **ModelGenerator (96种)**

**注意：模型越多越准确，但前提是建树软件能支持，否则模型再多，也无用！**

**使用BI法时，推荐 Mrbayes + Mrmodeltest 与 BEAST+ jModelTest 组合。**



## MrMTgui 主界面

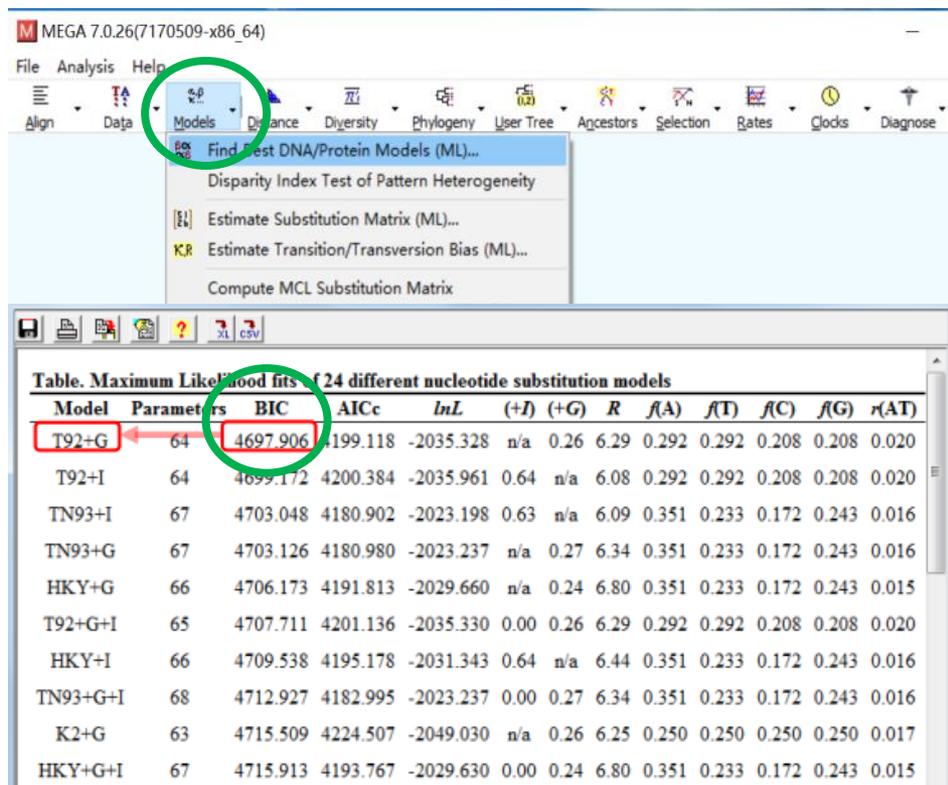


```

BEGIN MRBAYES;
  Lset nst=6 rates=invgamma;
  Prset statefreqpr=dirichlet(1,1,1,1);
END;
  
```

模型参数的MrBayes 模块

## MEGA篇



MEGA中采用BIC标准，  
BIC 值最低的对应模型为最佳。



# 建树软件

## 主要软件:

MrBayes **(BI)**

MEGA **(ML/NJ/MP)**

PHYLIP **(ML/NJ)**

PAUP **(ML/MP)**

RaxmlGUI **(ML)**

PhyML **(ML)**

## 辅助软件

### 多重比对

ClustalX/ClustalW

MAFFT

MUSCLE

### 模型选择

ModelTest 3.7

MrModelTest 2.3

jModelTest

### 系统树的可视化

TreeView

TreeGraph(JAVA)

FigTree(JAVA)



# Phylogeny Programs

 **CIPRES** Cyberinfrastructure for Phylogenetic Research 

[Home](#) [About](#) [Help](#) [Links](#) [News](#)

[home](#) »

All submissions are working normally.

- Codes
- Requirements
- Limitations
- Architecture
- Known Issues
- Usage Statistics
- User Locations
- Survey Results
- Publications

## The CIPRES Science Gateway V. 3.3

The CIPRES Science Gateway [V. 3.3](#) is a public resource for inference of large phylogenetic trees. It is designed to provide all researchers with access to NSF [XSEDE](#)'s large computational resources through a simple browser interface. You can now also access these same capabilities programatically with the [CIPRES REST API](#).

High Performance Parallel Codes for Large Tree Inference and Sequence Alignment on XSEDE: [RAxML](#); [MrBayes](#); [BEAST](#); [BEAST2](#); [GARLI](#); [MAFFT](#); [DPPDIV](#); [FastTree](#); [iModelTest2](#); [PAUP](#); [ParallelStructure](#); [PartitionFinder2](#); and [Migrate-N](#). If you need access to [PhyloBayes](#), please inquire.

Serial Codes for Tree Inference: [PAUP\\*](#) (Inference by Parsimony); [Poy](#) (Alignment and Inference);

Serial Codes for Sequence Alignment: [ClustalW](#); [Conatrigon](#); [MUSCLE](#); [PROBCONS](#); [PROBALIGN](#)

**在线建树**



## 建树方法

邻接法 (Neighbor-Joining, NJ)

最大似然法 (Maximum Likelihood, ML)

最大简约法 (Maximum Parsimony, MP)

贝叶斯法 (Bayesian inference, BI)



## 邻接法 (Neighbor-Joining, NJ)

### 特点:

NJ 法是**基于最小进化原理**经常被使用的一种算法，它构建的树相对准确，假设少，**计算速度快**。

### 缺点:

序列上的所有位点等同对待，且所分析的**序列的进化距离**不能太大。

### 适用:

**进化距离不大，信息位点少**的短序列。





# 最大似然法 (Maximum Likelihood, ML)

## 原理:

将每个位点所有可能出现的残基替换概率进行累加，产生特定位点的**似然值**，对所有可能的系统发育树都计算似然函数，**似然函数值最大**的那颗树即最可能的系统发育树。

## 优点:

在进化模型确定的情况下，ML法是与**进化事实吻合最好**的建树算法。

## 缺点:

**计算强度**非常大，**极为耗时**。



## 最大简约法 (Maximum Parsimony, MP)

### 特点:

基于进化过程中**碱基替代数目最少**这一假说。

### 缺点:

推测的树不是唯一的，**变异大的序列**可能会导致建树错误。

### 适用:

序列残基差别小，具有近似变异率，包含**信息位点比较多**的**长序列**。





### 信息位点：

在**两个及以上分类单元**（的序列）中存在**差异**，且其中至少有**两种变异类型**在该位点出现**两次及以上**。

序列位点及性状

Pos	1	2	3	4	5	6	7	8	9
Seq1	A	A	G	A	G	T	G	C	A
seq2	A	G	C	C	G	T	G	C	G
seq3	A	G	A	T	A	T	C	C	A
seq4	A	G	A	G	A	T	C	C	G
	×	×	×	×	✓	×	✓	×	✓





# 贝叶斯法 ( Bayesian inference, BI)

## 特点:

基于进化模型的**统计推论法**，具有完整而坚实的数学和统计学基础，可以处理复杂而接近实际情况的进化模型，可以将现有的系统发育知识整合或体现在先验概率中，通过**后验概率**直观反映出各分支的可靠性，而不需要通过自举法检验。

## 缺点:

**对进化模型比较敏感**，BI法中指定的每个氨基酸的后验概率建立在许多**假说条件**下，在现实中可能不成立。

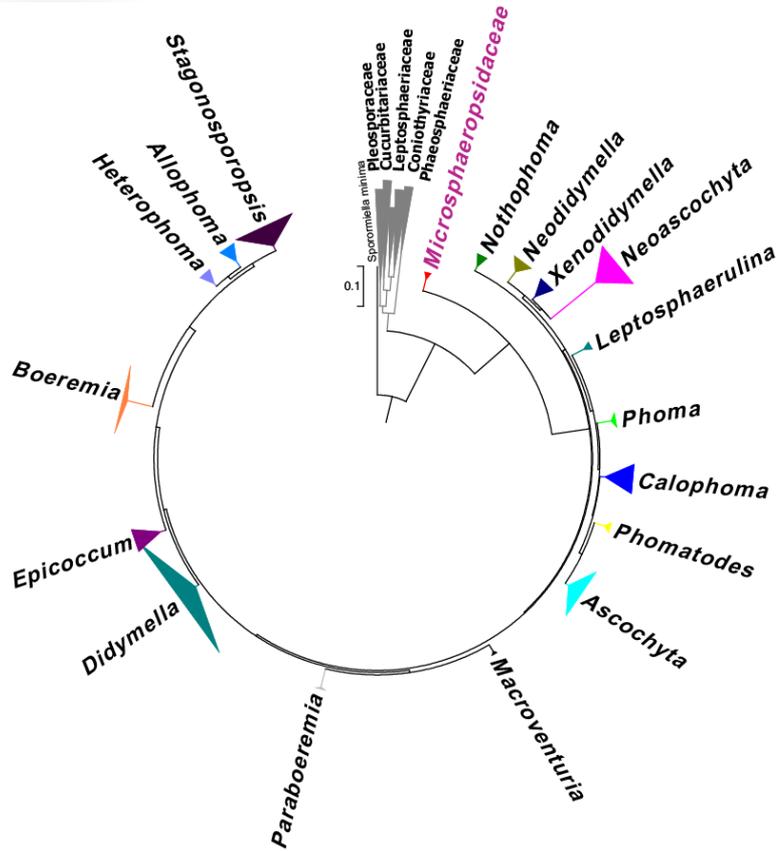
## 适用:

**大或复杂的数据集。**

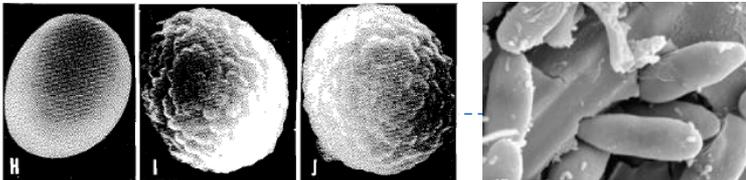




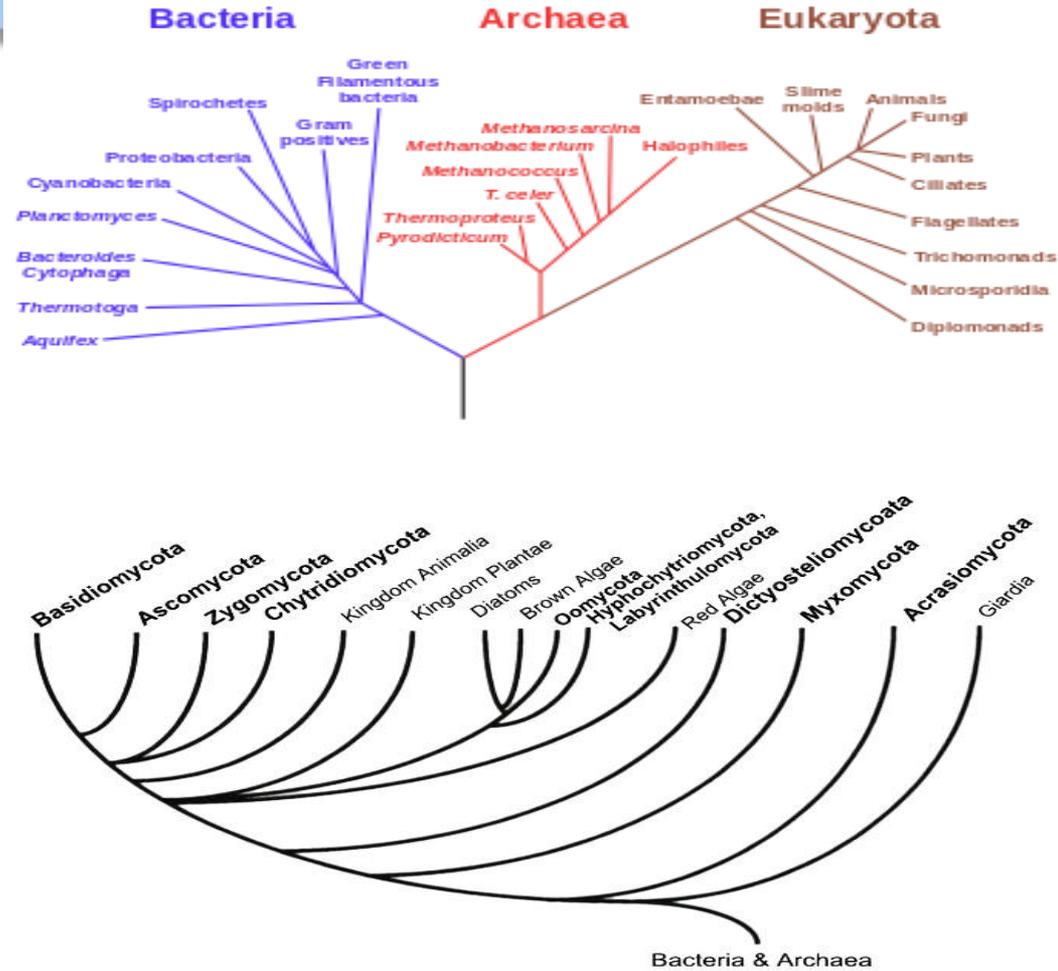
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**Microsphaeropsidaceae** fam. nov.  
 模式属: *Microsphaeropsis* Höhn.



# Phylogenetic Tree of Life



## 系统演化树

真菌界各类生物(粗体)间的相互关系

**Half day on the Web,  
saves you half month in the lab!**





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# 致 谢

指导老师：罗静初 教授

组员：何国仁、贺飞燕、武语笛

同学：ABC课程全体同学



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Thank you!

