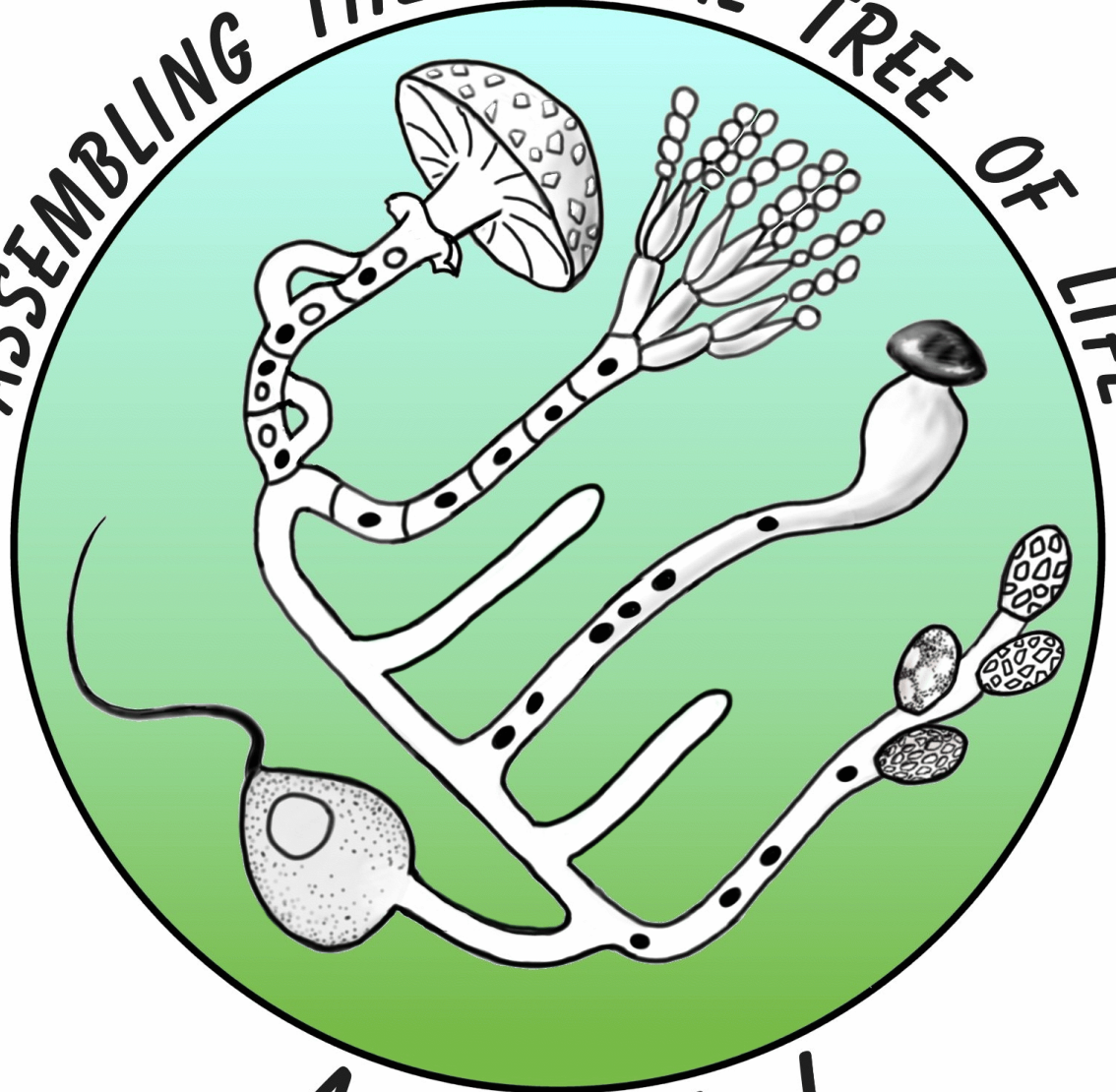


ASSEMBLING THE FUNGAL TREE OF LIFE



A F T O L

National Science Foundation Assembling the Tree of Life AToL

PROPOSAL:

***1500 species of fungi for 8 loci (\approx 10 kb) in 4 years!**

**6 nuclear loci: nucSSU rDNA, nucLSU rDNA,
ITS rDNA, *RPB1*, *RPB2*, EF-1 α**

2 mitochondrial loci: mitSSU rDNA, *ATP6*

***Ultrastructural features common to all fungi**

New data and compilation of all existing data

Starting date: January 1, 2003

See the AFToL website for more information

“ASSEMBLING THE FUNGAL TREE OF LIFE” (AFToL)

One proposal from the entire mycological community

➔ 113 collaborators from 23 countries

Strong bioinformatic & computational biology component

Preceded by an NSF Network Coordination grant “DEEP HYPHA”

“ASSEMBLING THE FUNGAL TREE OF LIFE” (AFToL)

David Hibbett (Clark University): 400 Basidiomycota

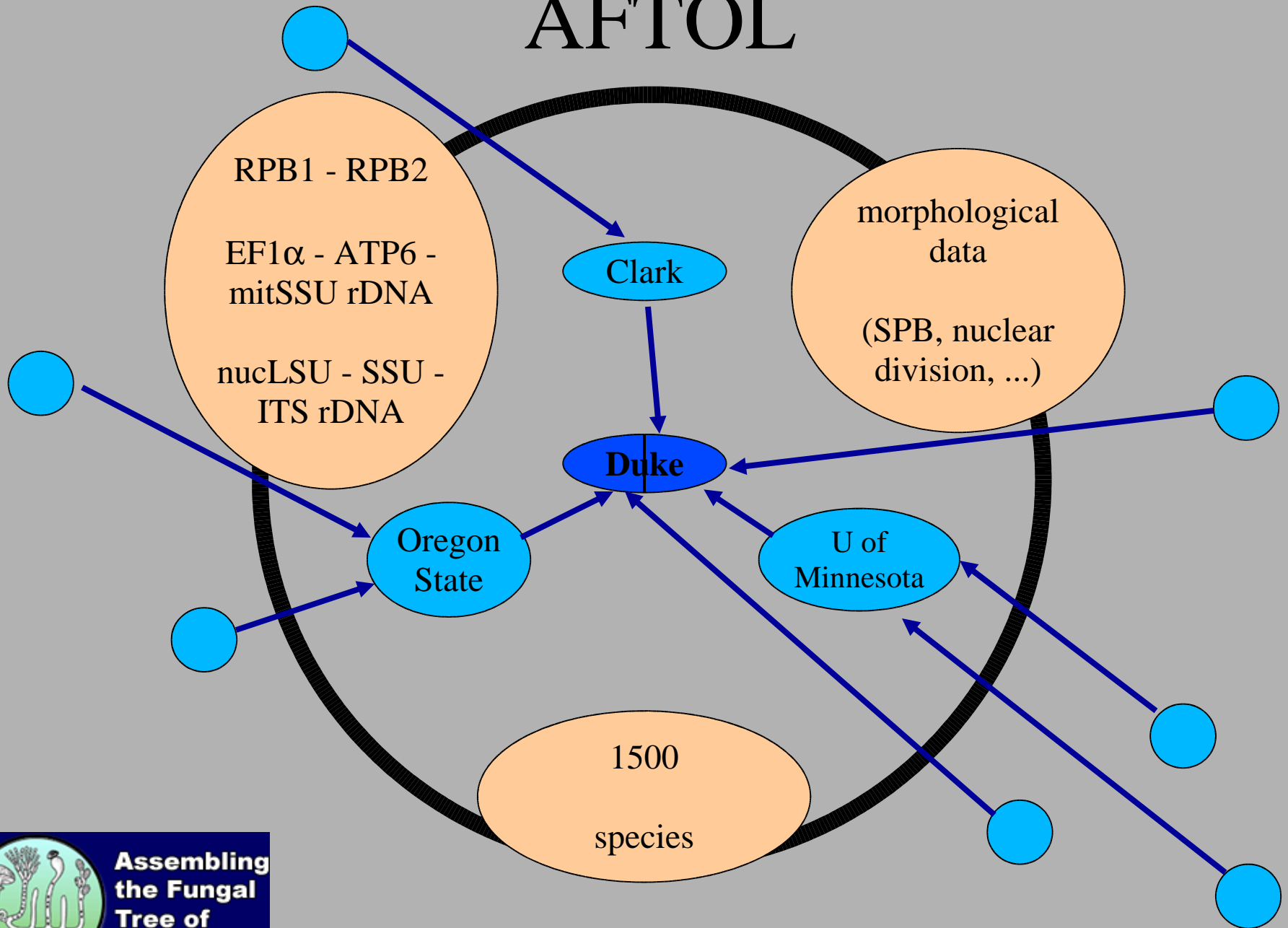
**François Lutzoni (Duke University): 400 Lichen-forming
Ascomycota et al. & Bioinformatics**

**David McLaughlin (University of Minnesota):
Subcellular characters**

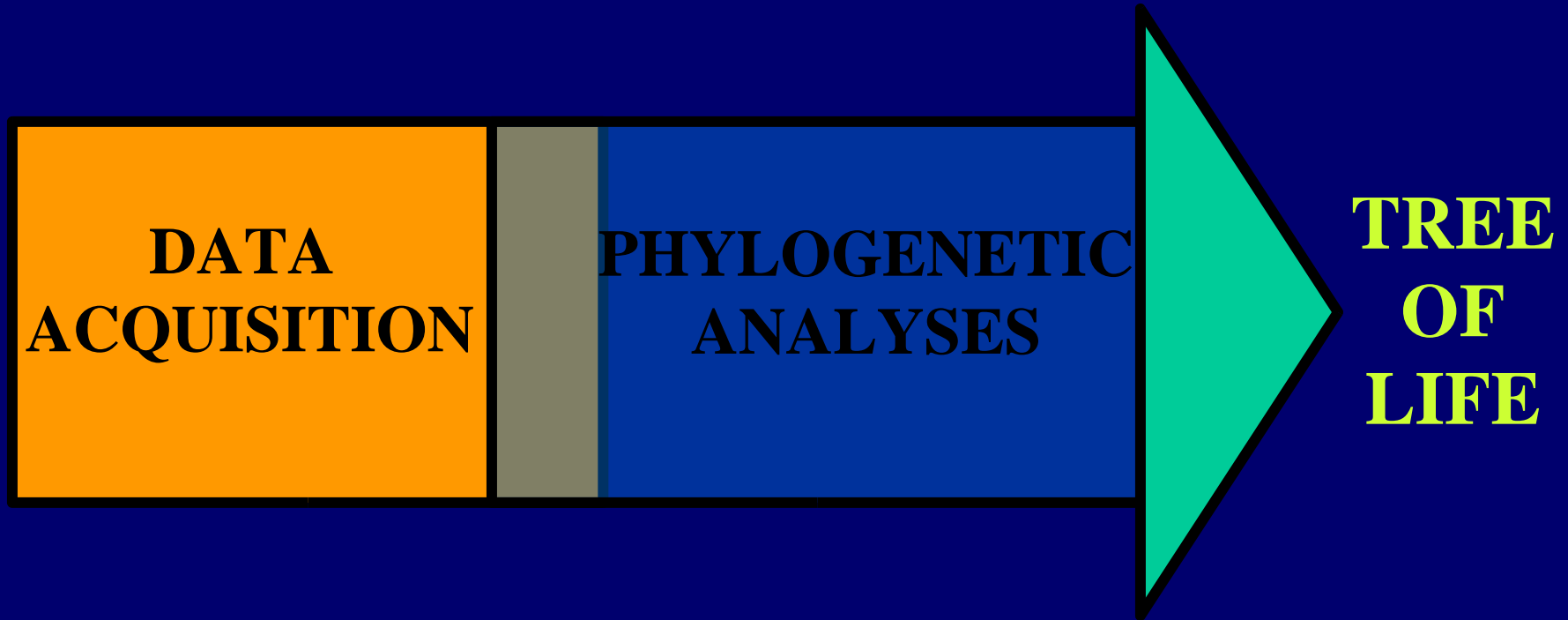
**Joseph Spatafora (Oregon State University):
400 Ascomycota**

**Rytas Vilgalys (Duke University): 300 Chytridiomycota,
Glomeromycota & Zygomycota**

AFTOL



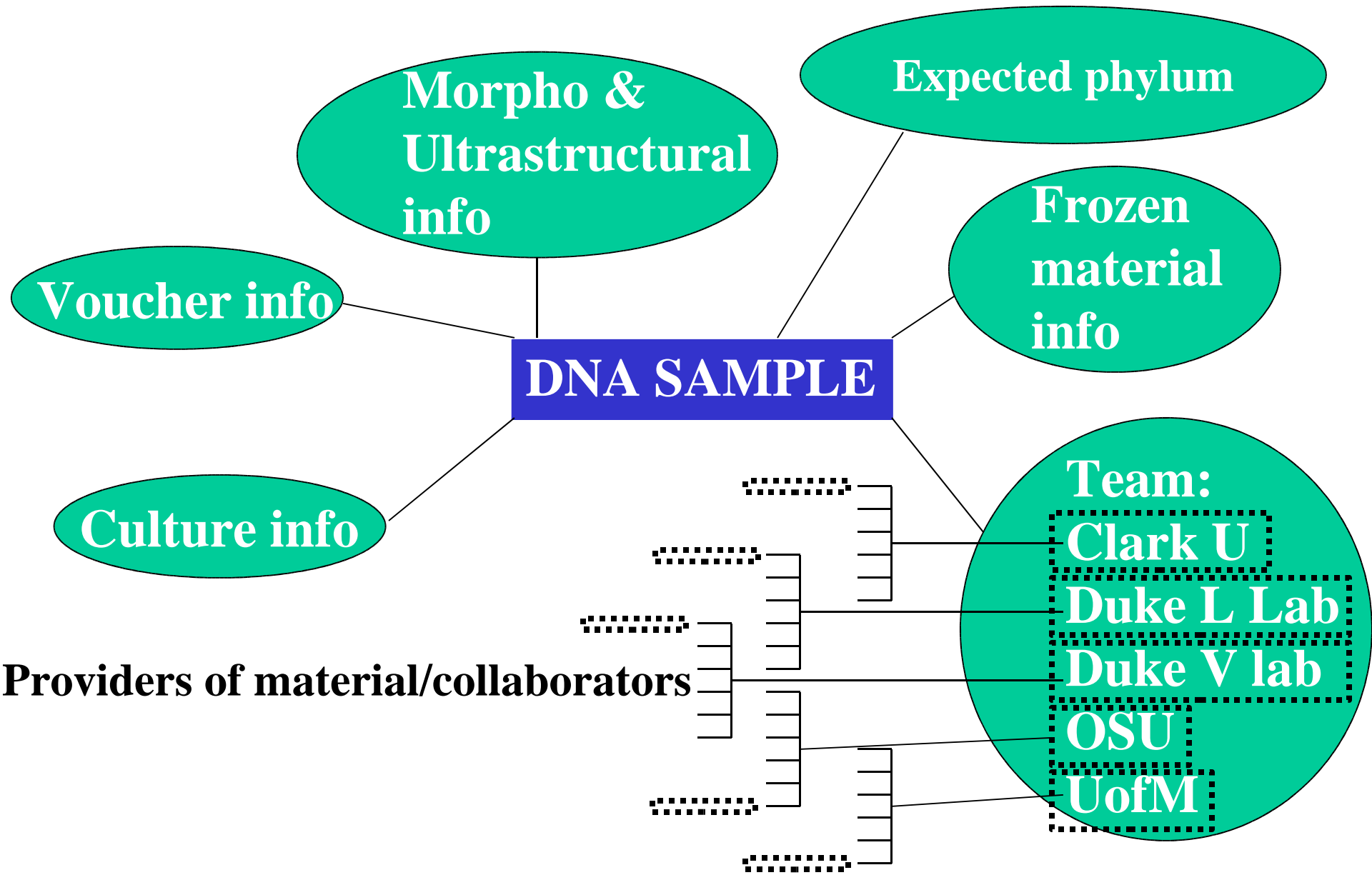
TWO MAIN OPERATIONS NEEDED FOR LARGE-SCALE PHYLOGENETIC ANALYSES

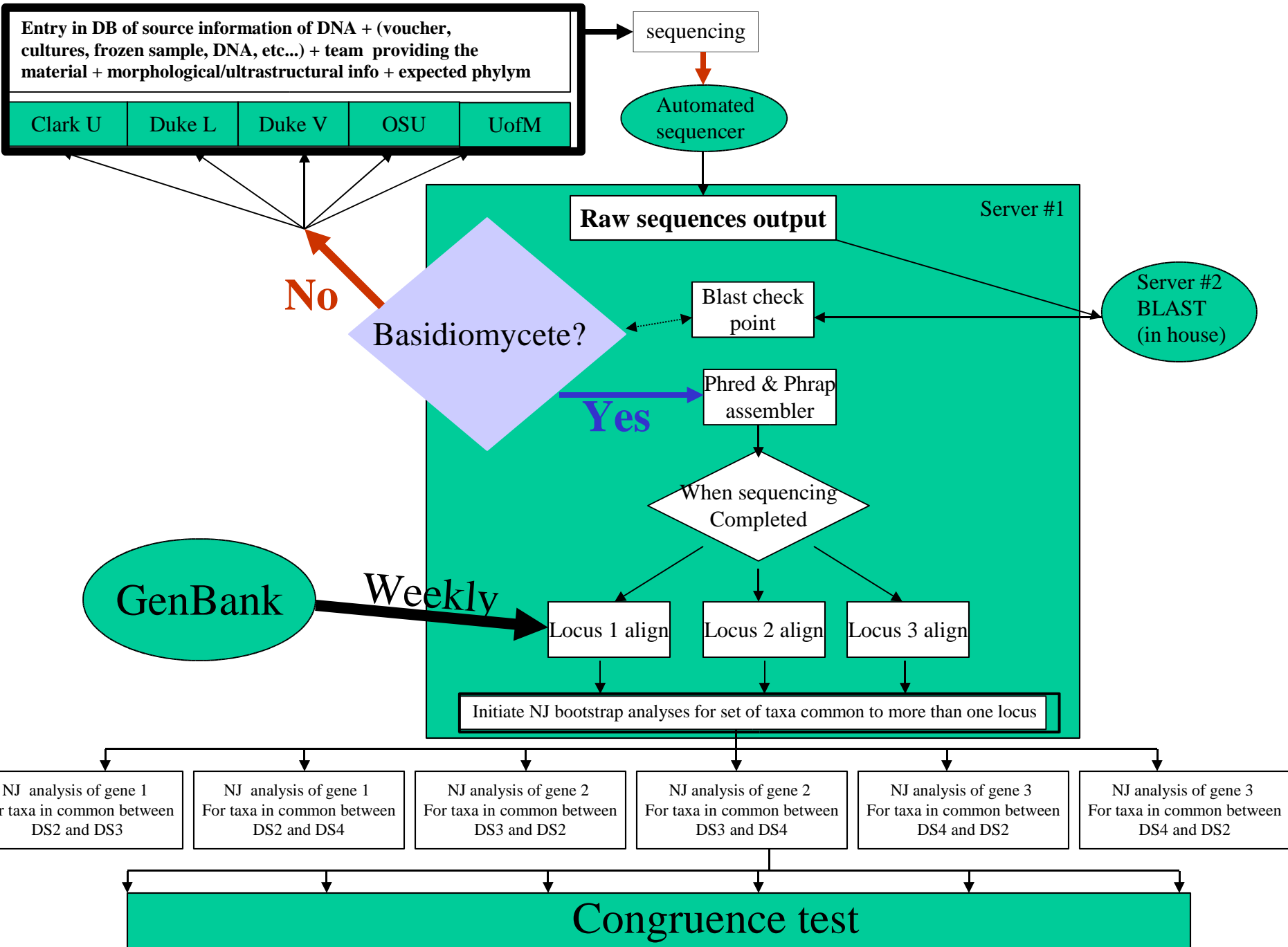


Essence of AFToL in solving data acquisition issues

- **STANDARDIZATION**
- **COMMUNICATION**
- **AUTOMATION**

Source Information of DNA Samples





Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits



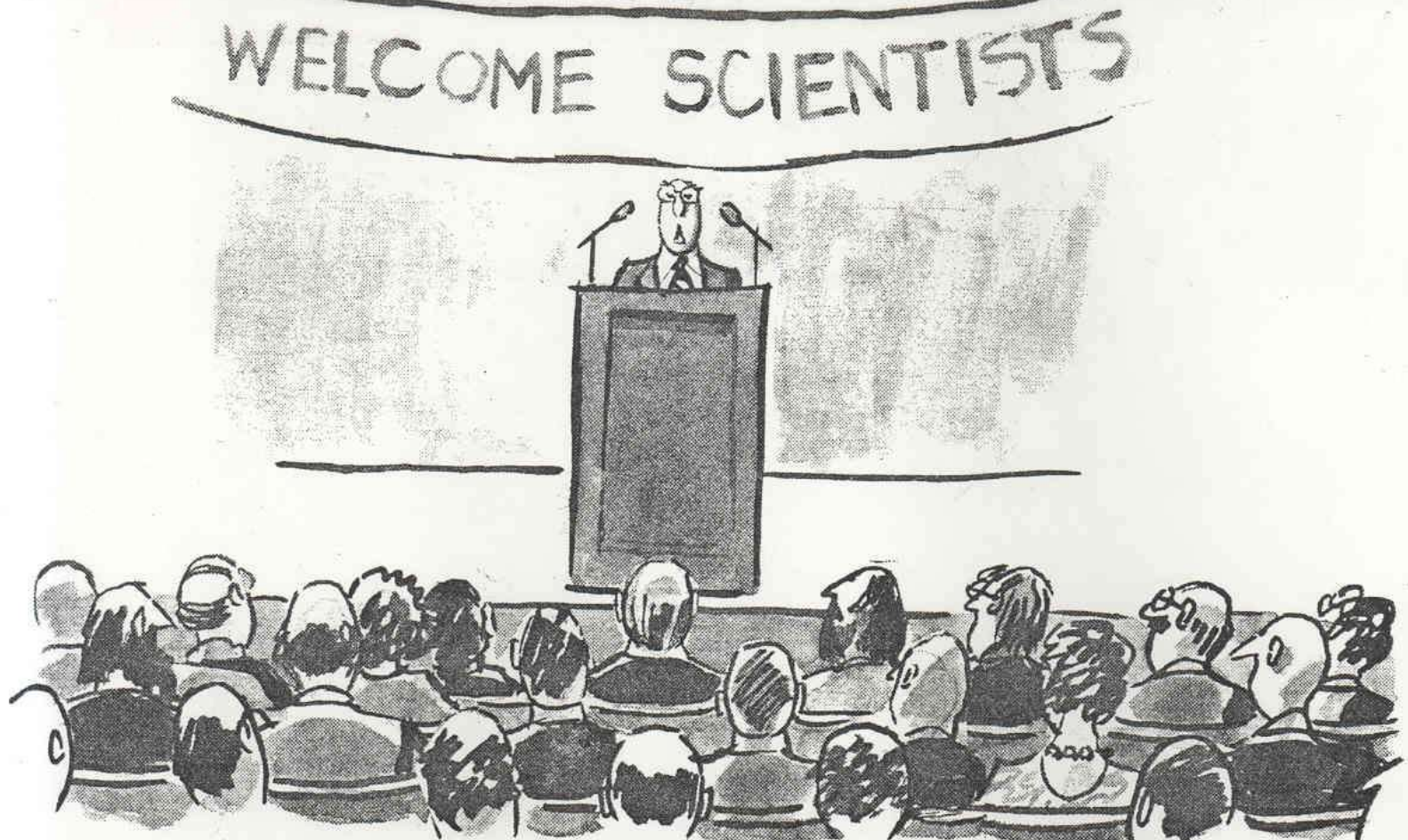
François Lutzoni, Frank Kauff, Cymon J. Cox, David McLaughlin, Gail Celio, Bryn Dentinger, Mahajabeen Padamsee, David Hibbett, Timothy Y. James, Elisabeth Baloch, Martin Grube, Valérie Reeb, Valérie Hofstetter, Conrad Schoch, A. Elizabeth Arnold, Jolanta Miadlikowska, Joseph Spatafora, Desiree Johnson, Sarah Hambleton, Michael Crockett, Robert Shoemaker, Gi-Ho Sung, Robert Lücking, Thorsten Lumbsch, Kerry O'Donnell, Manfred Binder, Paul Diederich, Damien Ertz, Cécile Gueidan, Karen Hansen, Richard C. Harris, Kentaro Hosaka, Young-Woon Lim, Yajuan Liu, Brandon Matheny, Hiromi Nishida, Don Pfister, Jack Rogers, Amy Rossman, Imke Schmitt, Harrie Sipman, Jeffrey Stone, Junta Sugiyama, Rebecca Yahr, and Rytas Vilgalys



44 authors

19 institutions

8 countries



THE CHRONICLE OF HIGHER EDUCATION

Richter
MISCHA RICHTER AND HARALD BAKKEN

*"That concludes my list of the co-authors of this paper. And now,
I see that my time is up."*

One goal of this study

Provide a phylogenetic synthesis for the Fungi and a framework for future phylogenetic studies based on previously unpublished data and all sequences available in GenBank

Taxon sampling

1) What are the loci that have been sequenced for the highest number of fungal species and appropriate for resolving deep relationships within the Fungi? **nucSSU and nucLSU rDNA**

2) A total of 13,467 GenBank sequences were considered

3) 1010 unique taxa had both sequences available

Taxonomic name associated with the sequence

4) Taxa excluded:

< 600 bp

Many errors in GenBank “definition line”

3) Unpublished sequences added from various projects and AFTOL

Total of 573 taxa

Taxon sampling (part 2)

1) What is the next locus that has been sequenced for the highest number of the 573 species selected and appropriate for resolving deep relationships within the Fungi? **mitSSU rDNA, *RPB2***

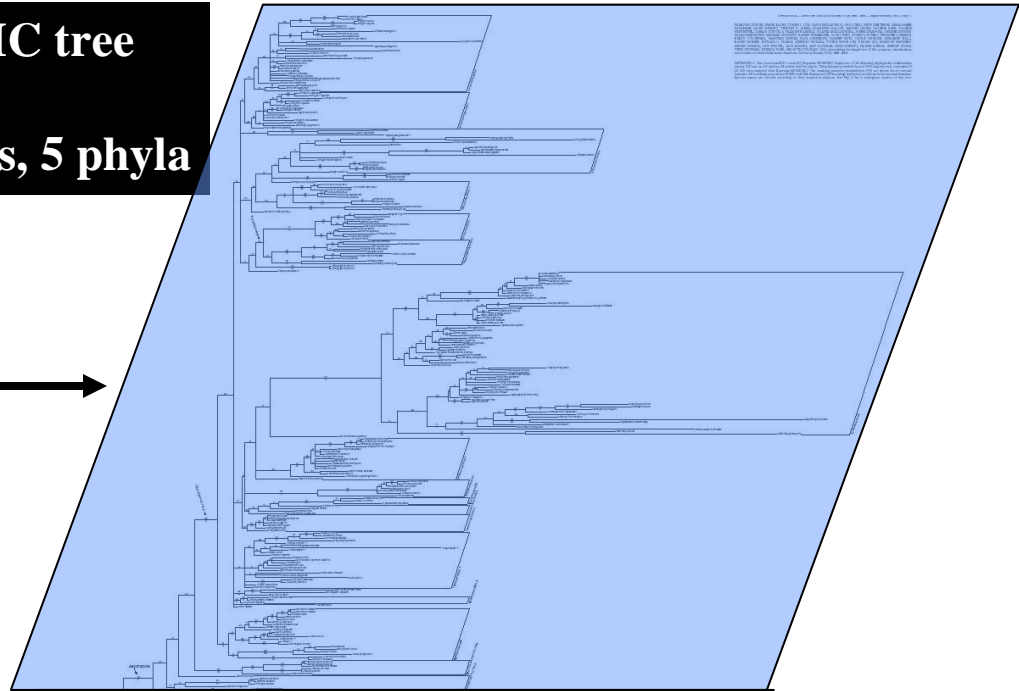
2) **nucSSU+nucLSU+mitSSU = 253 taxa (but only Asco- and Basidiomycota)**

3) **nucSSU+nucLSU+*RPB2* = 161 taxa (only Asco- and Basidiomycota)**

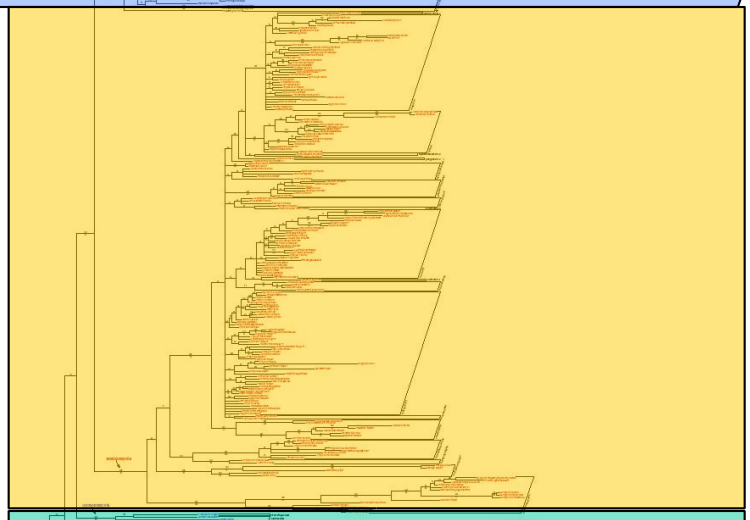
4) **nucSSU+nucLSU+mitSSU+*RPB2* = 103 taxa (only Asco- and Basidiomycota)**

**Two-locus Bayesian MCMCMC tree
nucSSU+nucLSU
558 species, 430 genera, 68 orders, 5 phyla**

Ascomycota →



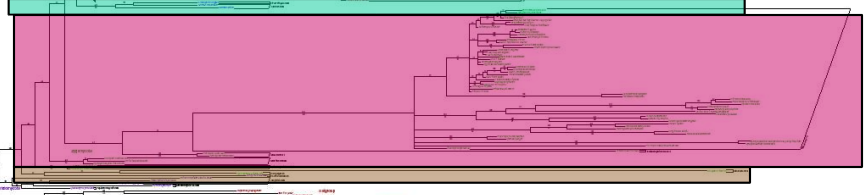
Basidiomycota →



Glomeromycota →

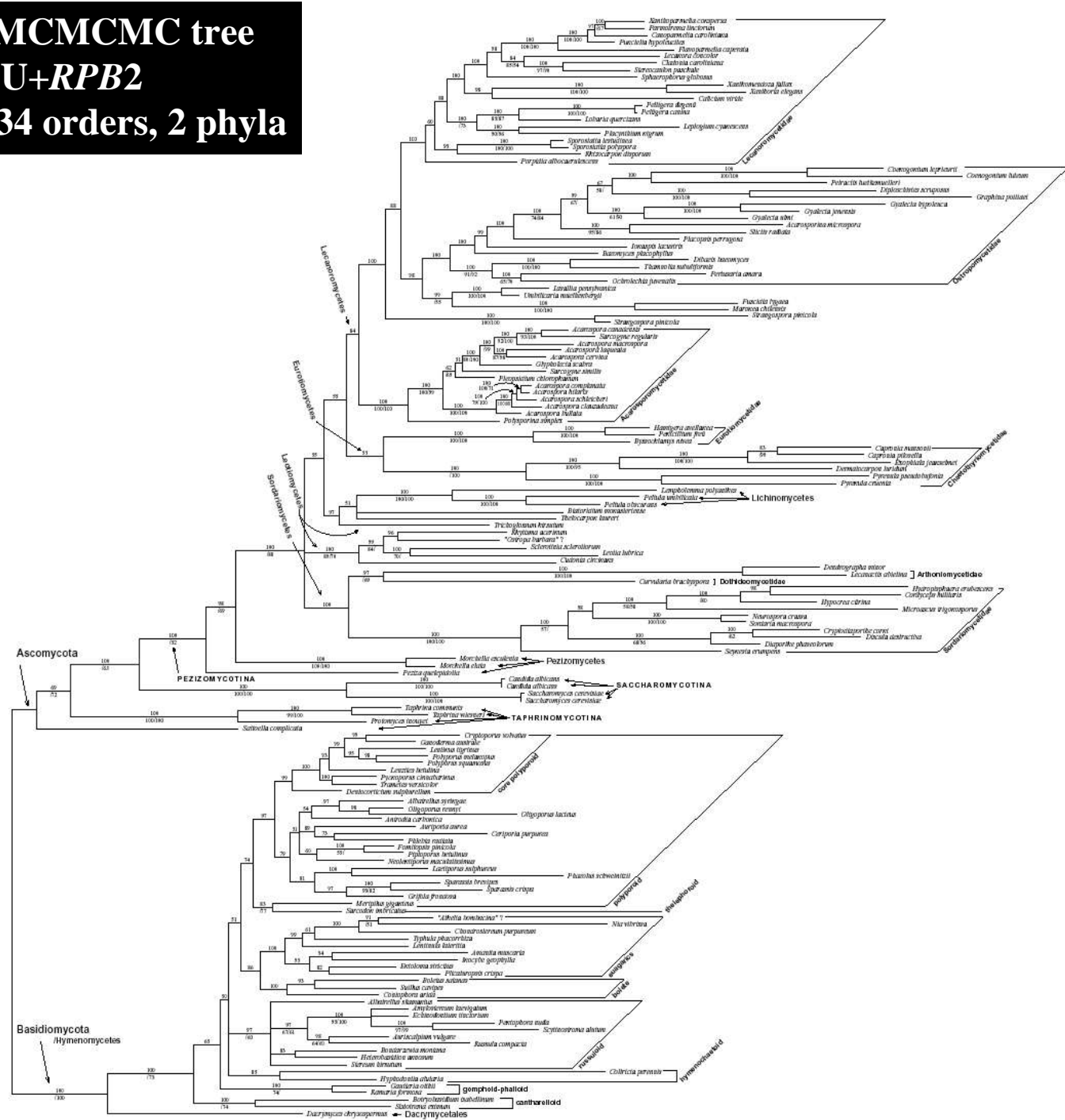
Zygomycota →

Chytridiomycota →



Three-locus Bayesian MCMCMC tree nucSSU+nucLSU+RBP2

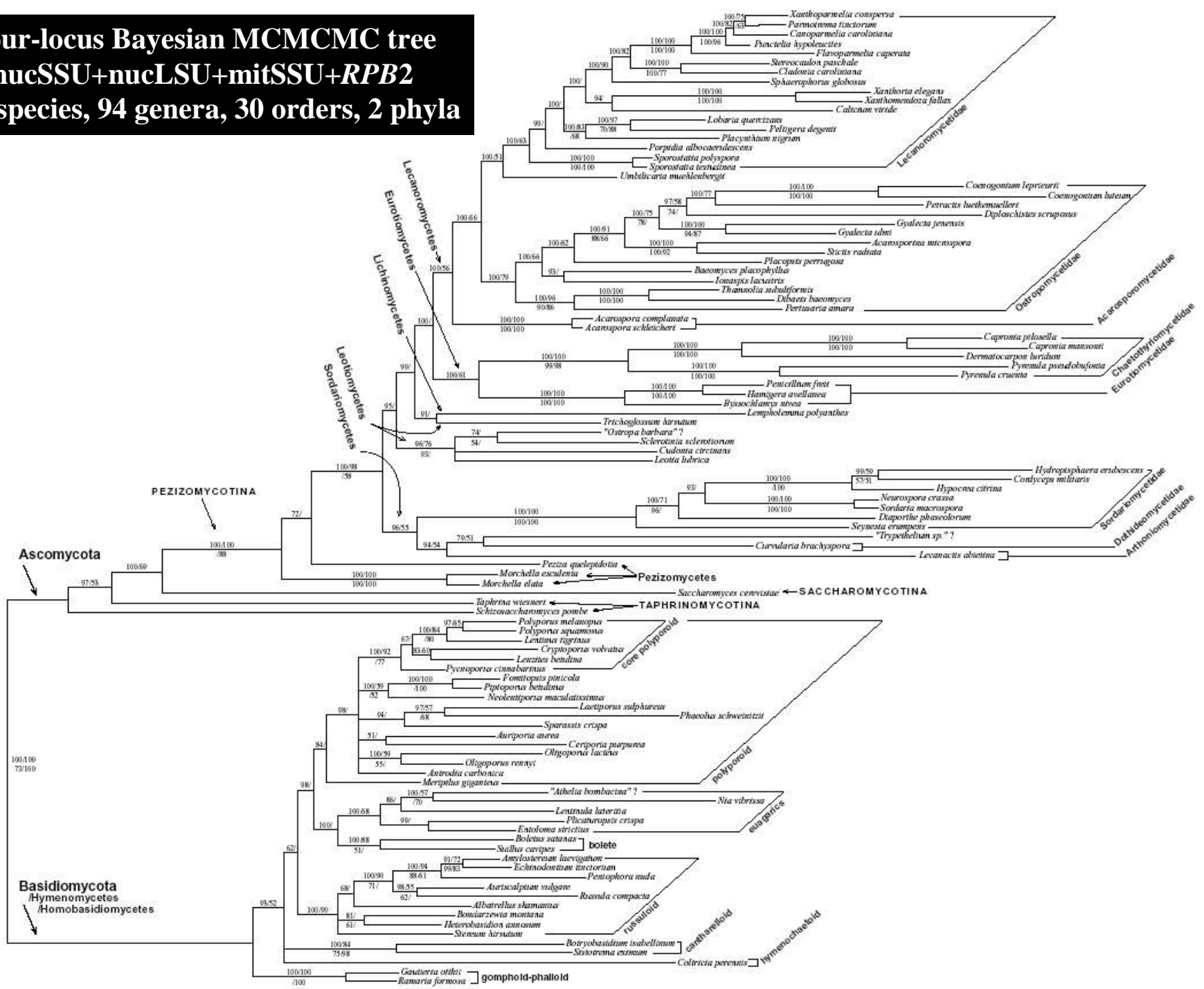
157 species, 134 genera, 34 orders, 2 phyla



Four-locus Bayesian MCMCMC tree

nucSSU+nucLSU+mitSSU+RPB2

103 species, 94 genera, 30 orders, 2 phyla



Second AFToL publication?

**150 species X 8 loci (10%; 40 lichen species)
October 30, 2004 deadline for new sequences
to be included**


Data sets are being assembled

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WWW based interface to AFTOL database

Secure access for registered users only

Possibility to enter, retrieve and change data

Each author views and modifies only his/her own data


Dynamic web page construction using Zope

AFTOL - Mozilla

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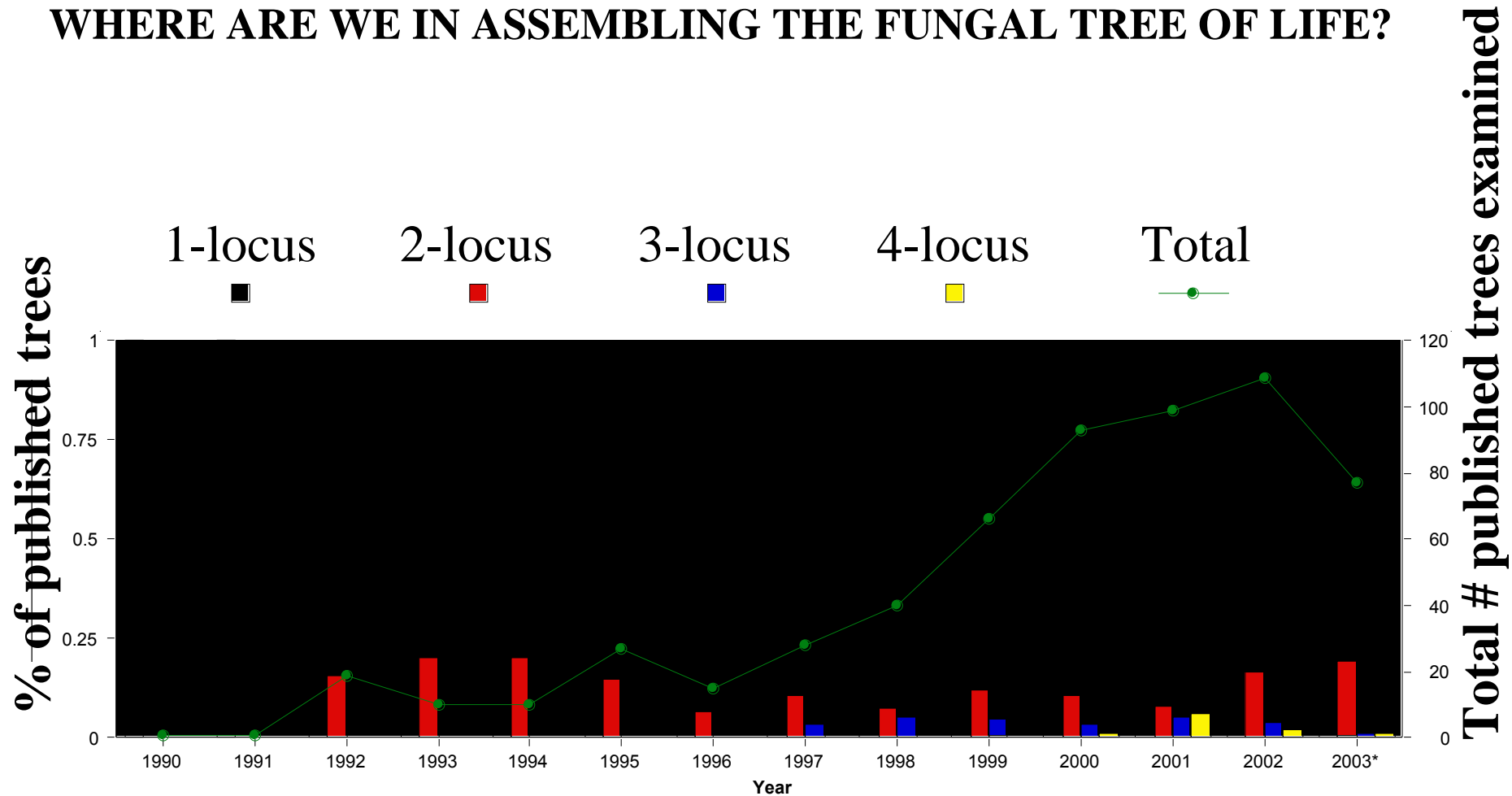


Assembling the Fungal Tree of Life

[about](#) [people](#) [participation](#) [resources](#) [data](#) [links](#)

| Taxon Binomial | AFTOL ID | nucSSU | nucLSU | RPB1 | RPB2 | ATP6 | EF1A | nucITS | mitSSU |
|--|--------------------------|------------------------|------------------------|------|------|----------------------|----------------------|------------------------|------------------------|
| Absconditella sp. | 287 | | | | | | | nucITS | |
| Acarosporina microspora | 78 | nucSSU | nucLSU | | | | | | |
| Acarosporina microsporida | 125 | | | | | | | | |
| Acrocordia subglobosum | 253 | | nucLSU | | | | | | |
| Aderkomyces heterellus | 117 | | | | | | | | |
| Agonimia repleta | 242 | | nucLSU | | | | | | mitSSU |
| Alectoria ochroleuca | 209 | | | | | | | | |
| Alectoria unknown | 232 | | | | | | | | |
| Aleuria aurantia | 65 | nucSSU | nucLSU | | | | | nucITS | mitSSU |
| Allewia eureka | 267 | | nucLSU | | | | | nucITS | mitSSU |
| Allomyces arbusculus | 300 | | | | | | | | |
| Amazonomyces farkasiae | 123 | | | | | | | | |
| Amoebidium parasiticum | 240 | | | | | | | | |
| Anisomeridium polypori | 101 | | | | | | | | |
| Anthracobia sp. | 73 | nucSSU | nucLSU | | | | | nucITS | mitSSU |
| Arthothelium spectabile | 97 | | | | | | | | |
| Asachinea scholander | 235 | | | | | | | | |
| Ascobolus carbonarius | 70 | nucSSU | nucLSU | | | | | nucITS | |
| Ascobolus crenulatus | 181 | nucSSU | nucLSU | | | | | | |
| Aspidothelium fugiens | 119 | | | | | | | | |
| Asteromassaria olivaceohirta | 268 | nucSSU | | | | | | nucITS | mitSSU |
| Aulaxina quadrangula | 116 | | | | | | | | |
| Balansia henningsiana | 188 | nucSSU | nucLSU | | | ATP6 | | | |
| Barssia oregonensis | 61 | nucSSU | nucLSU | | | | | nucITS | |
| Basidiobolus ranarum | 301 | | | | | | EF1A | | |
| Batrachochytrium dendrobatidis | 21 | | nucLSU | | | | EF1A | nucITS | |
| Belonia herculana | 256 | | nucLSU | | | | | | |
| Belonia russula | 258 | | nucLSU | | | | | | |
| Bionectria aureofulva | 187 | | nucLSU | | | | | nucITS | mitSSU |
| Bionectria ochroleuca | 154 | | nucLSU | | | | | nucITS | mitSSU |
| Bispora citrina | 269 | | nucLSU | | | | | nucITS | |
| Blastocladiella emersonii | 302 | | | | | | | | |
| Botryotinia fuckeliana | 59 | nucSSU | nucLSU | | | | EF1A | nucITS | mitSSU |

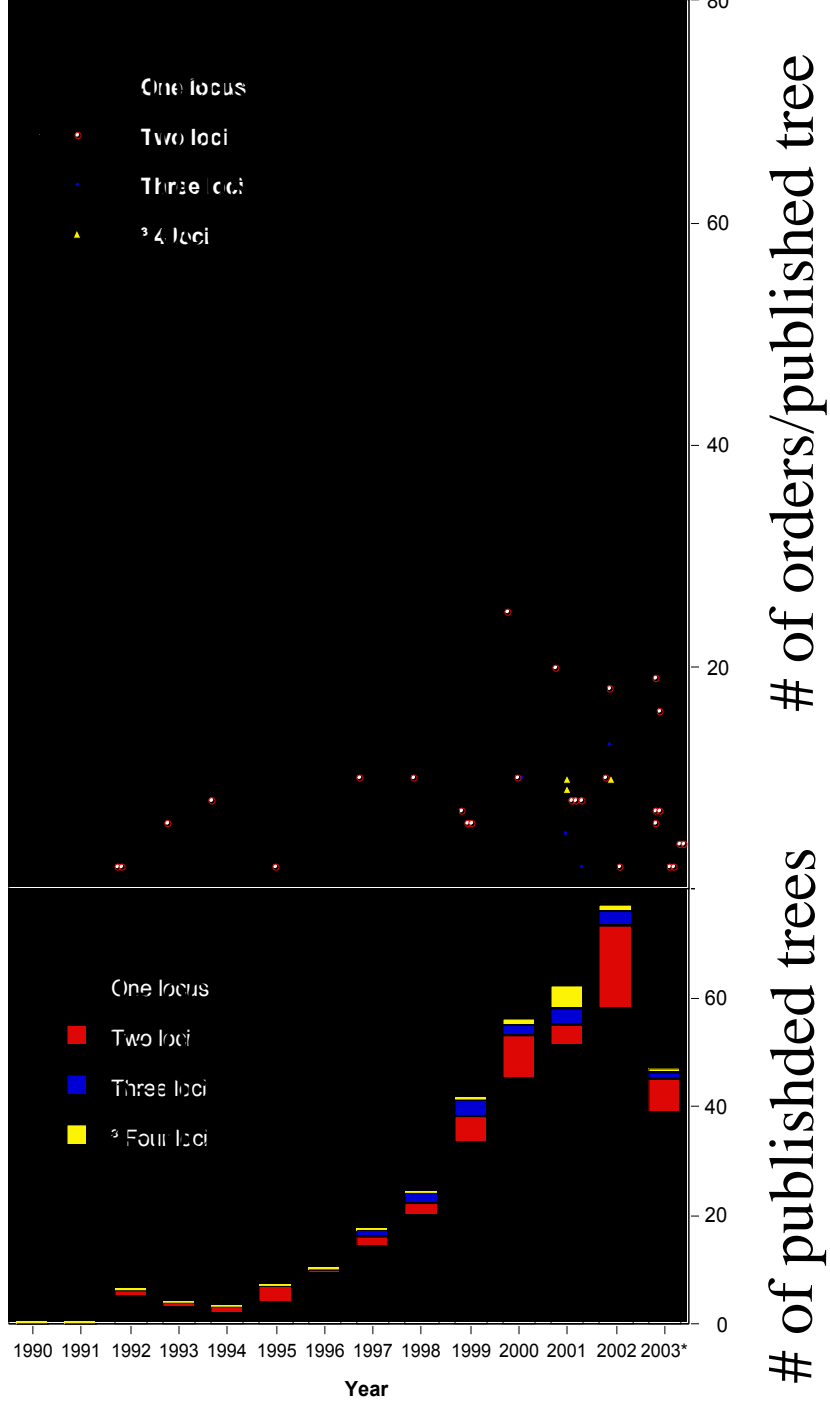
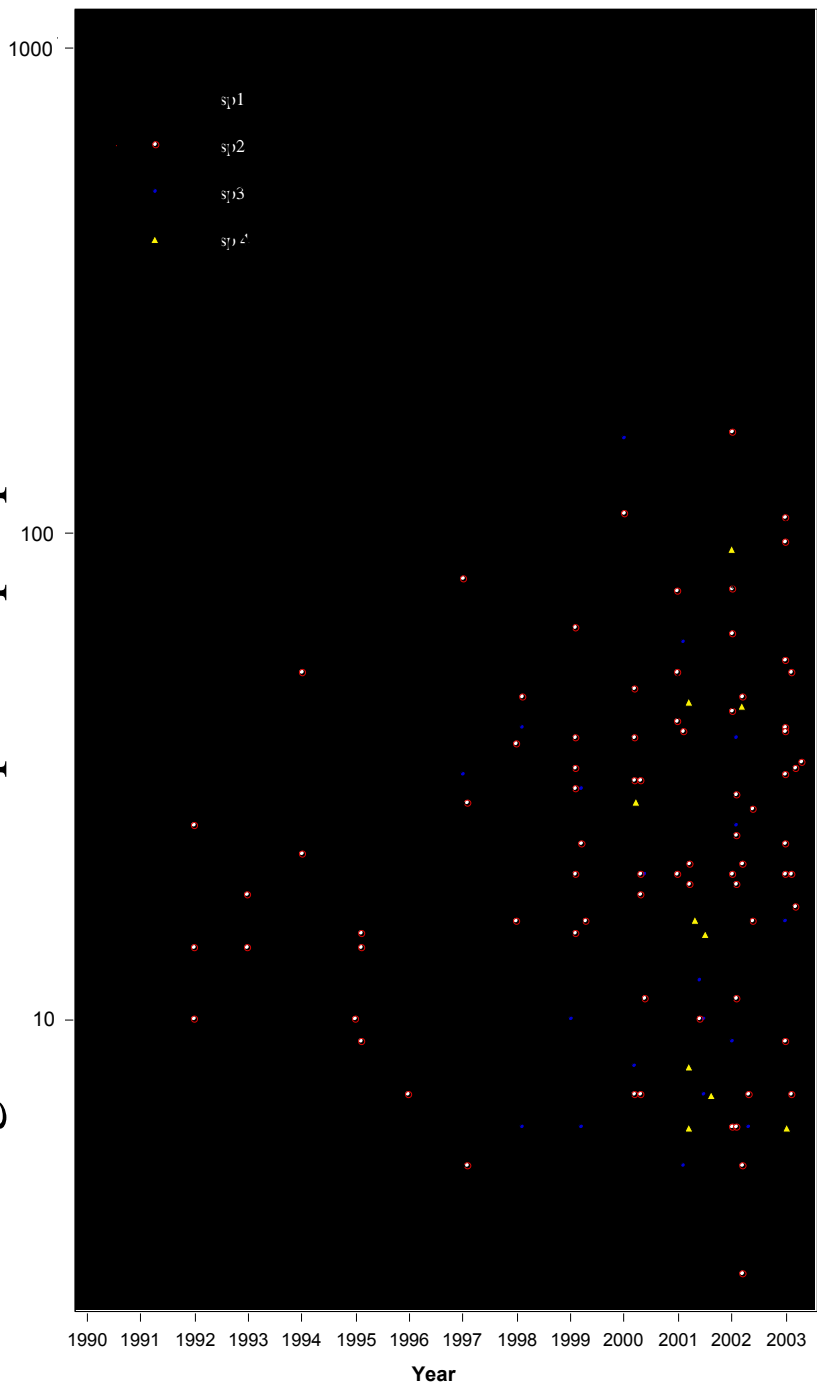
WHERE ARE WE IN ASSEMBLING THE FUNGAL TREE OF LIFE?



560 publications reporting 595 fungal phylogenetic trees: # loci, # species, # orders (Martin Grube, Elizabeth Baloch, Betsy Arnold)

489 (82.2%) trees based on single locus data set

Log number of species per published trees



Summary of survey

- 489 (82.2%) trees based on single locus data set
- 83.9% of fungal phylogenies are based exclusively on sequences from the ribosomal RNA tandem repeats.
- Although the number of species included in published trees has generally increased over time, most studies have included fewer than 100 species, with an overall mean of 34.2 ± 2.3 species/study (range: 3–1155 species)
- Few studies have focused on resolving relationships among orders of Fungi
- 354 of 595 trees examined (59.5%) conveyed relationships within single orders

Assembling the fungal tree of life: progress, classification, and evolution of subcellular traits



**Focus on progress in assembling the fungal
tree of life**

**Special issue of the *American Journal of Botany* (October 2004)
Edited by Jeff Palmer, Doug Soltis, and Mark Chase**

**How can I be an author on the next
AFTOL publication?**

Inclusion of co-authors in AFTOL publications

- ➔ **Samples (dry material, cultures, DNA) were provided and DNA sequences were obtained in time to be included in phylogenetic analyses**
- ➔ **Provided unpublished DNA sequences that could be included in phylogenetic analyses of multi-locus data sets**
- ➔ **Contributed to the article (e.g., conducting phylogenetic analyses, writing part of ms, ect.)**

Graduate students or postdocs can visit Duke University as part of this project to generate molecular data and learn phylogenetic methods

- ➔ Generate data that are essential to the visitor's and AFTOL respective project (i.e., placement of genera within the Ascomycota)**
- ➔ Visits are for a minimum of three months**
- ➔ Visitors to date:**
 - Damien Ertz (P. Diederich & E. Sérusiaux)**
 - Anja Amtoft (R. Harris)**
 - Alexandra Bachran (B. Büdel)**
 - Mónica Garcia Otálora (I. Martinez)**

Questions

What is AFTOL?

