Fungal Systematics – Current Technologies and Techniques for Fungal Identification

Sung-Oui Suh, Ph.D. Scientist, ATCC





About ATCC

- Founded in 1925, ATCC is a non-profit organization with HQ in Manassas, VA and an R&D and Services center in Gaithersburg, MD
- World's premiere biological materials resource and standards development organization
 - 5,000 cell lines
 - 80,000 microbes
 - Genomic & synthetic nucleic acids
 - Media/Reagents
- ATCC collaborates with and supports the scientific community with industry-standard and innovative biological solutions
 - Growing portfolio of products and services
 - Sales and distribution in 150 countries, 12 International distributors
- Talented team of 450+ employees; over one-third with advanced degrees

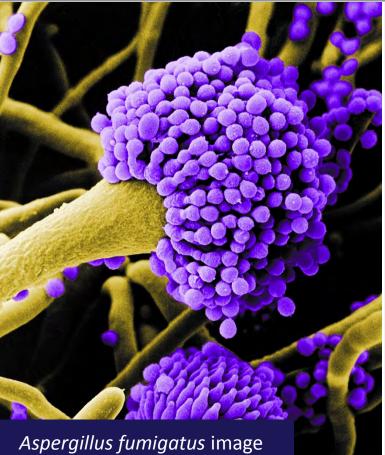


An innovative global partner for authentic biomaterials, standards, and services





Agenda



courtesy of David Gregory & Debbie Marshall

- Recent updates in Mycology
- The ATCC Mycology Collection and our QC criteria and ID methods
- Recent ATCC research on fungi and yeasts
- Summary



Recent Updates in Mycology

- Fungal taxonomy has been significantly affected by:
 - Improvements in contemporary molecular techniques
 - Identifying fungi to the species level by DNA sequencing
 - Early clinical diagnostics
 - Compare fungi as "Holomorphs"
 - Changes in nomenclatural rules
 - 2012 Melbourne Code





International Code of Nomenclature for algae, fungi, and plants

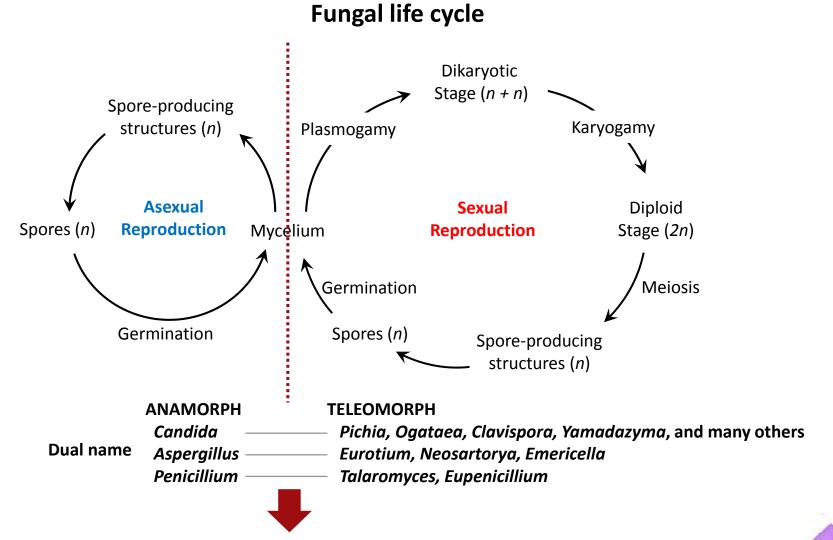
(www.iapt-taxon.org/nomen/main.php)

Recent updates

- At the International Botanical Congress in Melbourne (July 2011)
 - Major changes in the Melbourne Code started from 2012
 - Language of diagnosis (English or Latin)
 - Cultures as types (specify how the type specimens are preserved)
 - Governance of the code (set up a subcommittee on fungal nomenclature)
 - Registration of fungal names
 - The end of dual nomenclature



Dual Nomenclature to 'One fungus, One name'

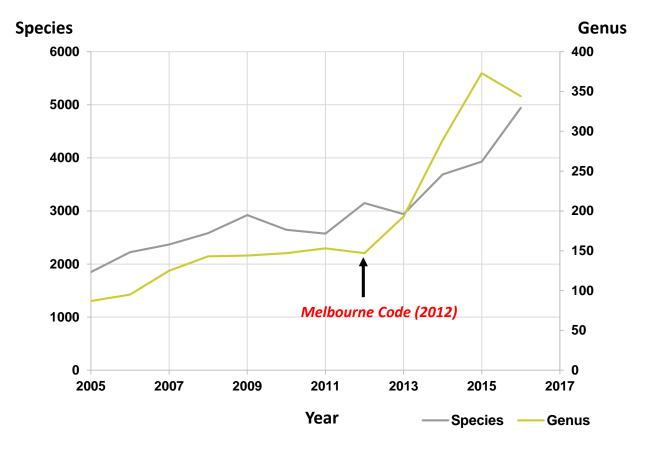




HOLOMORPH - Single name (One fungus, One name)

Number of New Fungal Taxa is Increasing

Number of fungal genera/species proposed per year



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ATCC Data is from the MycoBank database (Aug. 2017). Not all the species/genera are still valid nor accepted.

Examples of Recent Name Changes

Penicillium – Talaromyces (e.g., Samson et al. 2011, Yilmaz et al. 2014)

- No longer teleomorph-anamorph
- Represent two individual phylogenetic groups

Cryptococcus gattii/C. neoformans species complex (Hagen et al. 2015)

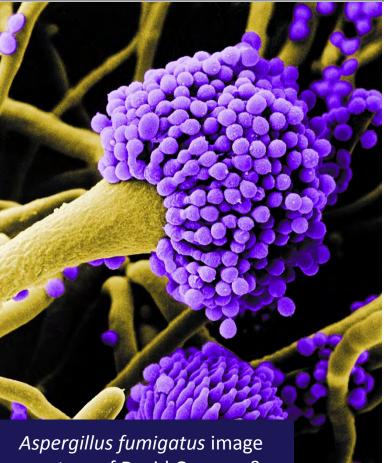
- Expanded to 7 Cryptococcus spp., including 5 novel species
- No longer use teleomorphic names Filobasidiella neoformans or Filobasidiella bacillispora

Trichophyton mentagrophytes species complex (de Hoog et al. 2017)

Transferred teleomorphic genera Arthroderma benhamiae, A. simii, and A. vanbreuseghemii to Trichophyton



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Summary



ATCC Mycology Collection

ATCC[®] is a trusted resource center housing a diverse assortment of filamentous fungi and yeasts, representing over 7,600 species.

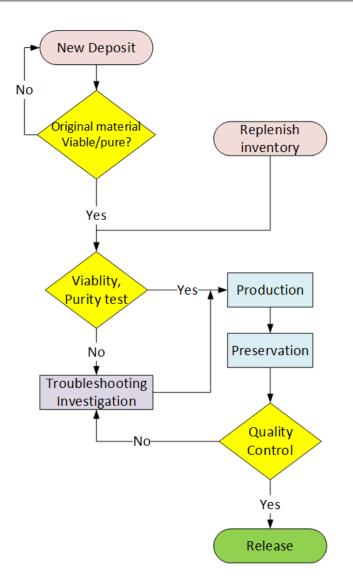
- >3,600 type strains
- ≈ 600 genome sequenced strains
- > 32,000 yeast genetic strains
- Many quality control strains for use in media testing, food microbiology, assay development, environmental testing, etc.





ATCC Mycology Accession Procedure

- All materials are evaluated for viability and purity
- Newly deposited materials are identified to the species level by ATCC scientists
- Only items confirmed to be viable, pure, and fully-identified are released to customers





QC Criteria for Yeasts and Fungi



Viability

- Recovery condition from the freeze-dried or frozen state
 Purity
- On different media at a wide temperature range
 Identification
 - Morphology macro & micro
 - DNA sequencing
 - Optional tests
 - VITEK[®] 2 YST ID card
 - VITEK[®] MS (MALDI-TOF)
 - Dropout medium test
 - API[®] test

Taxonomic References

- MycoBank Database (<u>www.mycobank.org</u>)
- Index Fungorum (<u>www.indexfungorum.org</u>)



DNA Sequencing

Default barcode genes

- ITS (Internal transcribed spacer) \approx 0.4-0.6 kb
- D1D2 region of LSU rDNA ≈ 0.5-0.7 kb

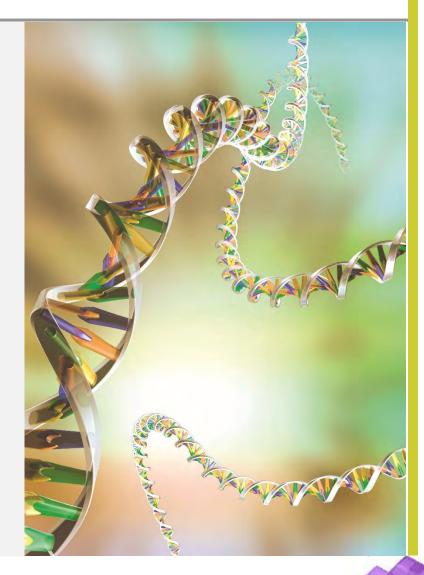
Optional genes

- SSU rDNA
- IGS (Intergenic Spacer region)
- Protein-coding genes

EF-1 α , RPB 1 & 2, calmodulin, β -tubulin, *etc*.

Reference DNA database

- GenBank (<u>www.ncbi.nlm.nih.gov/genbank</u>)
- UNITE (unite.ut.ee/index.php)





MALDI-TOF Mass Spectrometry



VITEK[®] MS system from bioMérieux

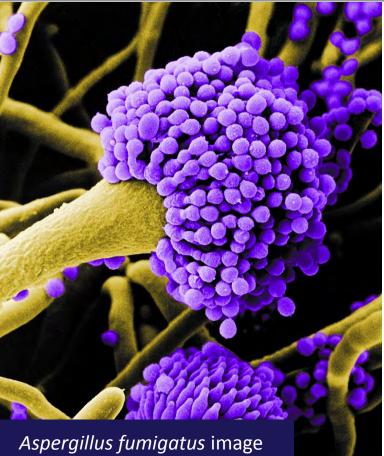


- Quick and easy to prepare test samples
- Immediate and reliable identification results
- Current database available mainly for medically relevant yeasts and fungi – but is expending

ACQ STATION

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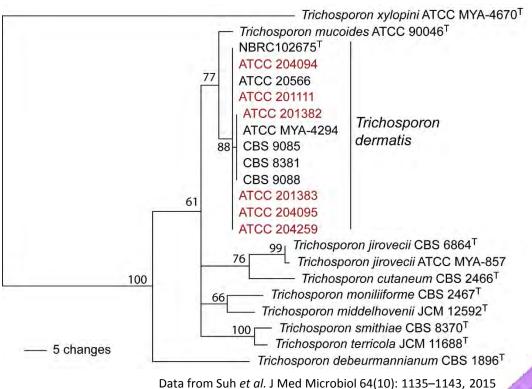


I. *Trichosporon mucoides/T. dermatis* Study

- Clinically important yeast species causes disseminated infections to humans
- The two species are closely related difficult to distinguish with conventional methods
- Many T. dermatis strains have been mistakenly identified as T. mucoides (red)



Onychomycosis caused by *Trichosporon mucoides* Rizzitelli *et al.* Int J Infect Dis 42:61-63, 2016 DOI: http://dx.doi.org/10.1016/j.ijid.2015.11.011





Data from Suh *et al.* J Med Microbiol 64(10): 1135–1143, 2015 DOI: 10.1099/jmm.0.000134

MALDI-TOF MS for *T. mucoides/T. dermatis*

- Conventional ID systems (VITEK[®] 2, VITEK[®] MS) could not distinguish the two species
- The MALDI-TOF MS successfully identified the two species with 99.9% confidence value when using customized reference spectra for each species

Strain No.	Species by DNA sequences	VITEK [®] 2 YST card (Probability)	VITEK [®] MS using the MYLA database (Confidence value)	VITEK [®] MS using customized superspectra (Confidence value)
ATCC [®] 90046 ^{™T}	T. mucoides	T. mucoides (93%)	T. mucoides (99.9%)	T. mucoides (99.9%)
NBRC 102675 ^{™ T}	T. dermatis	T. mucoides (96%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 204094 [™]	T. dermatis	T. mucoides (97%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 201382 [™]	T. dermatis	T. mucoides (99%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] MYA-4294 [™]	T. dermatis	T. mucoides (97%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 201383 [™]	T. dermatis	T. mucoides (98%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 204095 [™]	T. dermatis	T. mucoides (99%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 204259 [™]	T. dermatis	T. mucoides (99%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 20566 [™]	T. dermatis	T. mucoides (97%)	T. mucoides (99.9%)	T. dermatis (99.9%)
ATCC [®] 201111™	T. dermatis	T. mucoides (99%)	T. mucoides (99.9%)	T. dermatis (99.9%)



II. Trichophyton mentagrophytes SC Study



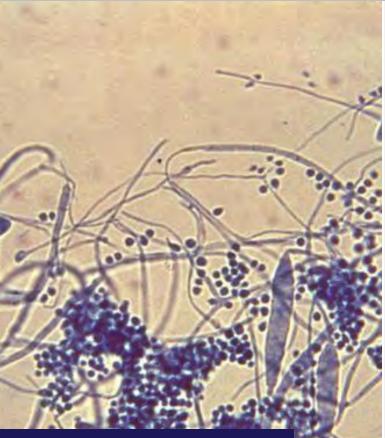
Athletes foot cause by *T. mentagrophytes.* Image courtesy of Dr. Lucille K. Georg and the CDC.

What is the *Trichophyton mentagrophytes* species complex (SC)?

- Dermatophytes causing superficial skin infections by invading the keratinized tissue of human and animal hosts, such as hair, nails, and feathers
- Common dermatophytes worldwide, but their taxonomy has not been well established
- Quick and accurate identification of these fungi is clinically relevant for providing proper treatments to patients



Taxonomic changes in the *T. mentagrophytes* SC



Trichophyton mentagrophytes image courtesy of Dr. Lucille K. Georg and the CDC Arthroderma benhamiae, A. simii, A. vanbreuseghemii and related anamorphic Trichophyton spp.
 (e.g., Gräser et al. 2008)



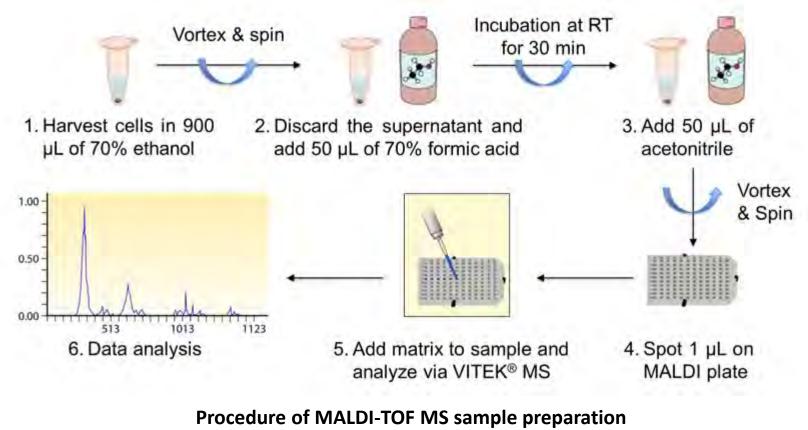
- Transferred Arthroderma spp. To Trichophyton
- No longer use teleomorphic Arthroderma in the SC
- Designated neotypes for accurate identification

(de Hoog et al. 2017)



Approach

- Multi-locus DNA sequence analysis ITS, D1D2, β-tubulin
- MALDI-TOF MS analysis rapid identification



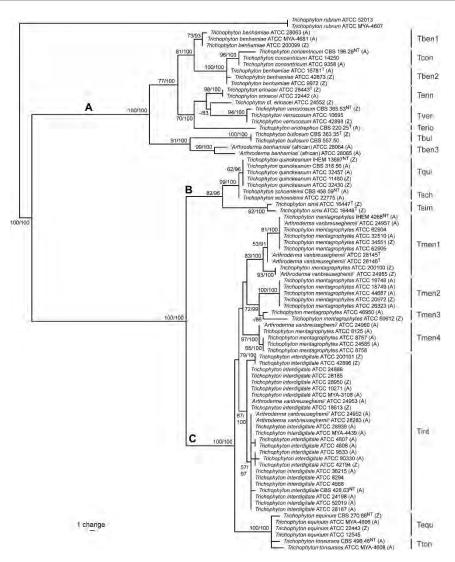
Methods summarized from Suh et al. 2017 (Submitted to Mycologia)



T. mentagrophytes SC Study – Phylogeny

Multi-locus DNA sequence analysis

- 72 ATCC strains in the T. mentagrophytes SC
- 3 major lineages (A, B, C)
- 18 phylogroups
- >65% of the tested strains required taxonomic updates





MALDI-TOF MS for *T. mentagrophytes* SC

- Developed reference spectra for each phylogroup based on the new taxonomy in the species complex
- With the customized reference spectra, each species was identified correctly with high accuracy by MALDI-TOF mass spectrometry
- Two closely related species, T. mentagrophytes and T. interdigitale, were often crossidentified

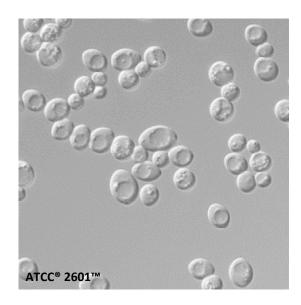
Species	Correct identification	Incorrect ID
T. benhamiae	94%	T. concentricum
T. concentricum	100%	
T. erinacei	100%	
<i>'T. benhamiae'</i> (African)	100%	
T. quinckeanum/T. schoenleinii	100%	
T. simii	100%	
T. mentagrophytes	91%	T. interdigitale
T. interdigitale	76%	T. mentagrophytes T. equinum/T. tonsurans
T. equinum/T. tonsurans	100%	

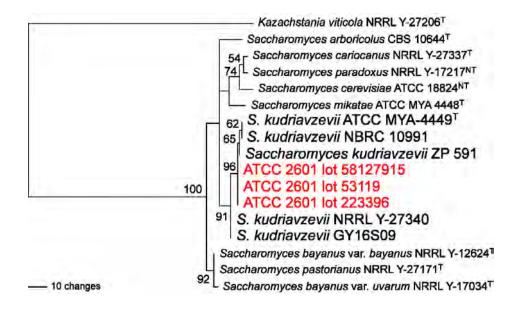


Data from Suh et al. 2017 (Submitted to Mycologia)

III. USP Drug-Testing Reference Strain ATCC[®] 2601[™]

- A reference strain designated by FDA and widely used in assays of amphotericin B fungizone and nystatin fungicidin according to U.S. Pharmacopeia General Chapters
- It has long been classified as Saccharomyces cerevisiae based on traditional taxonomic characterizations, but its barcode sequence indicated that it could be S. kudriavzevii





Data from Suh et al. PMF Newsletter19(2): 4-11, 2013

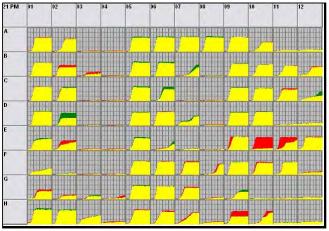


Polyphasic Approach for ATCC[®] 2601[™]

Multi-locus DNA sequence analyses

Genes	Sequence similarity		
Genes	To S. kudriavzevii	To S. cerevisiae	
ITS + D1D2 of LSU rDNA	99%	98%	
Mt SSU rDNA	100%	90%	
RPB1	99%	87%	
RPB2	99%	87%	
EF-1α	96%	98%	

Chemical sensitivity assays by Biolog PM21D Microplates



Red, ATCC[®] 2601[™] lot 58127915; Green, ATCC[®] 2601[™] lot 223396; Yellow, overlapped

Results

- ATCC[®] 2601TM is Saccharomyces kudriavzevii, not S. cerevisiae
- From the investigation on drug-susceptibility of all the previous batches, the taxonomic change of this organism will not affect its application in antifungal drug testing assays

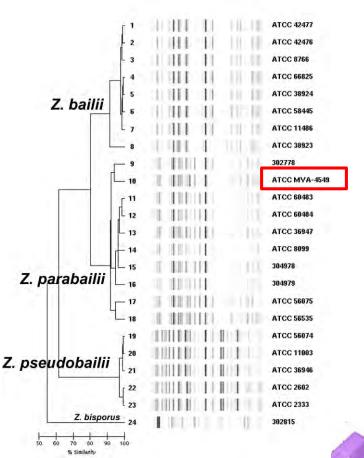


IV. Quality control strain ATCC[®] MYA-4549[™]

- Quality control strain for VITEK 2 yeast identification card for Zygosaccharomyces bailii
- DNA barcode sequence indicated that it is distinct from typical Z. bailii

Results

- Tested 23 ATCC strains that have been identified as *Z. bailii*
- Two novel species, Z. pseudobailii and Z. parabailii, were proposed based on the DNA sequence comparison and genome fingerprinting profiles
- ATCC[®] MYA-4549[™] is *Z. parabailii,* not *Z. bailii*





Dendrogram and genome fingerprinting profiles of strains in Z. bailii and the two novel species generated by DiversiLab. Data from Suh *et al.* IJSEM 63(5): 1922–1929, 2013

Future Topics



Next-generation sequencing

Antifungal-resistant *Candida* spp.

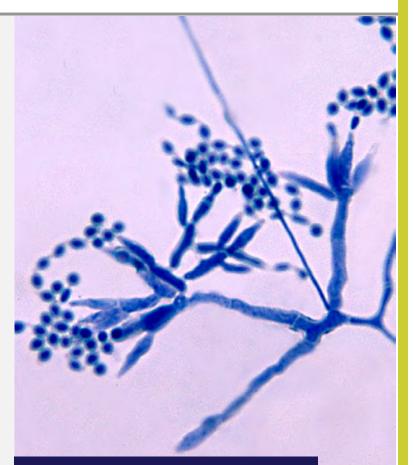
MALDI-TOF MS

 Cryptococcus gattii/C. neoformans species complex



Summary

- Fungal systematics is currently undergoing a major revision due to the improvements in contemporary molecular techniques and the new 'One fungus, One name' rule for the nomenclature code
- The quality control procedures used to evaluate and characterize ATCC mycology products meet the high standard of industrial demands
- ATCC QC strains and reference materials are authenticated using a polyphasic approach
- Recent studies support MALDI-TOF mass spectrometry as a powerful rapid identification tool for yeasts and fungi



Penicillium marneffei image courtesy of Libero Ajello and the CDC



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Check out our Mycology Culture Guide at <u>www.atcc.org/Guides</u>



Please email additional questions to tech@atcc.org

