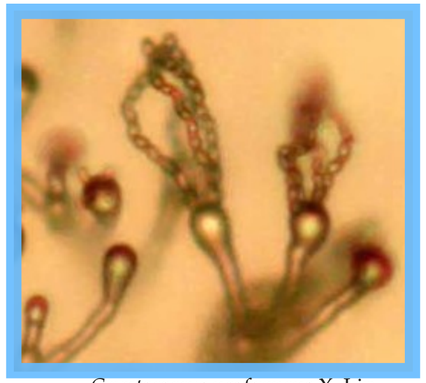
Fungal phylogenomics: Getting lost in the moldy forest

Jason E Stajich
Dept of Plant Pathology & Microbiology
University of California, Riverside

http://lab.stajich.org
http://fungalgenomes.org/blog
http://fungiDB.org
twitter{stajichlab,hyphaltip,fungalgenomes,fungidb}

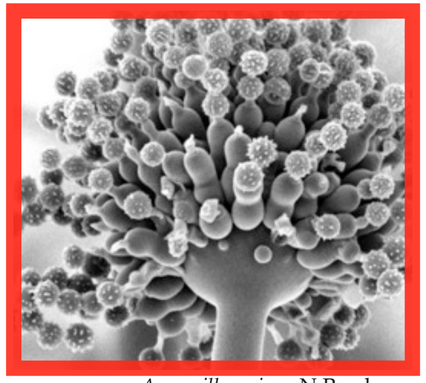
UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Fungi have diverse forms, ecology, and associations

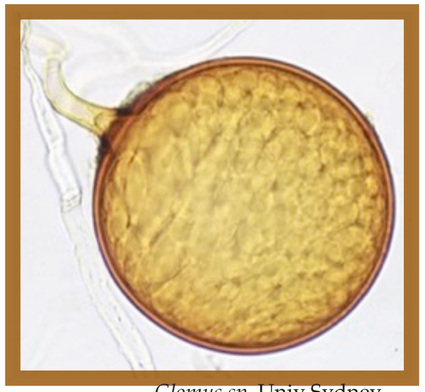


Cryptococcus neoformans X. Lin

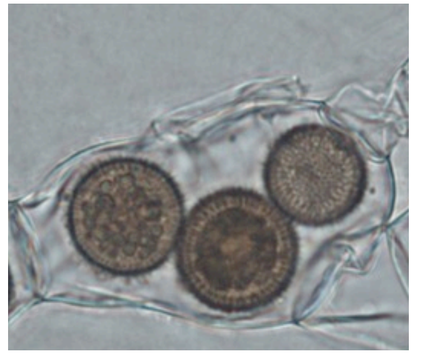
Coprinopsis cinerea Ellison & Stajich



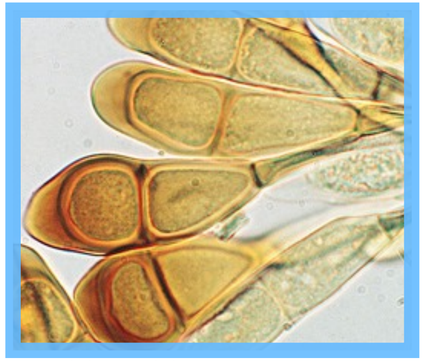
Aspergillus niger. N Read



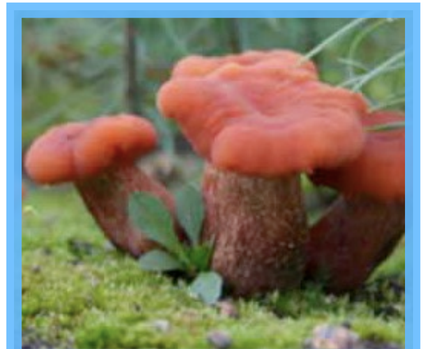
Glomus sp. Univ Sydney



Rozella allomycis. James et al



Puccinia graminis J. F. Hennen



Laccaria bicolor Martin *et al*.

Neurospora crassa. Hickey & Reed

Phycomyces blakesleansus T. Ootaki

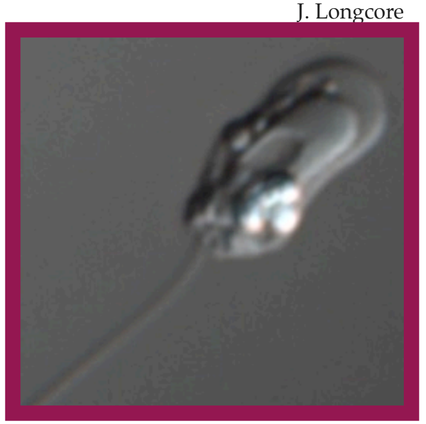
Batrachochytrium dendrobatidis J. Longcore

Ustilago maydis Kai Hirdes

Amanita phalloides. M Wood

Xanthoria elegans. Botany POtD

Rhizopus stolonifera.

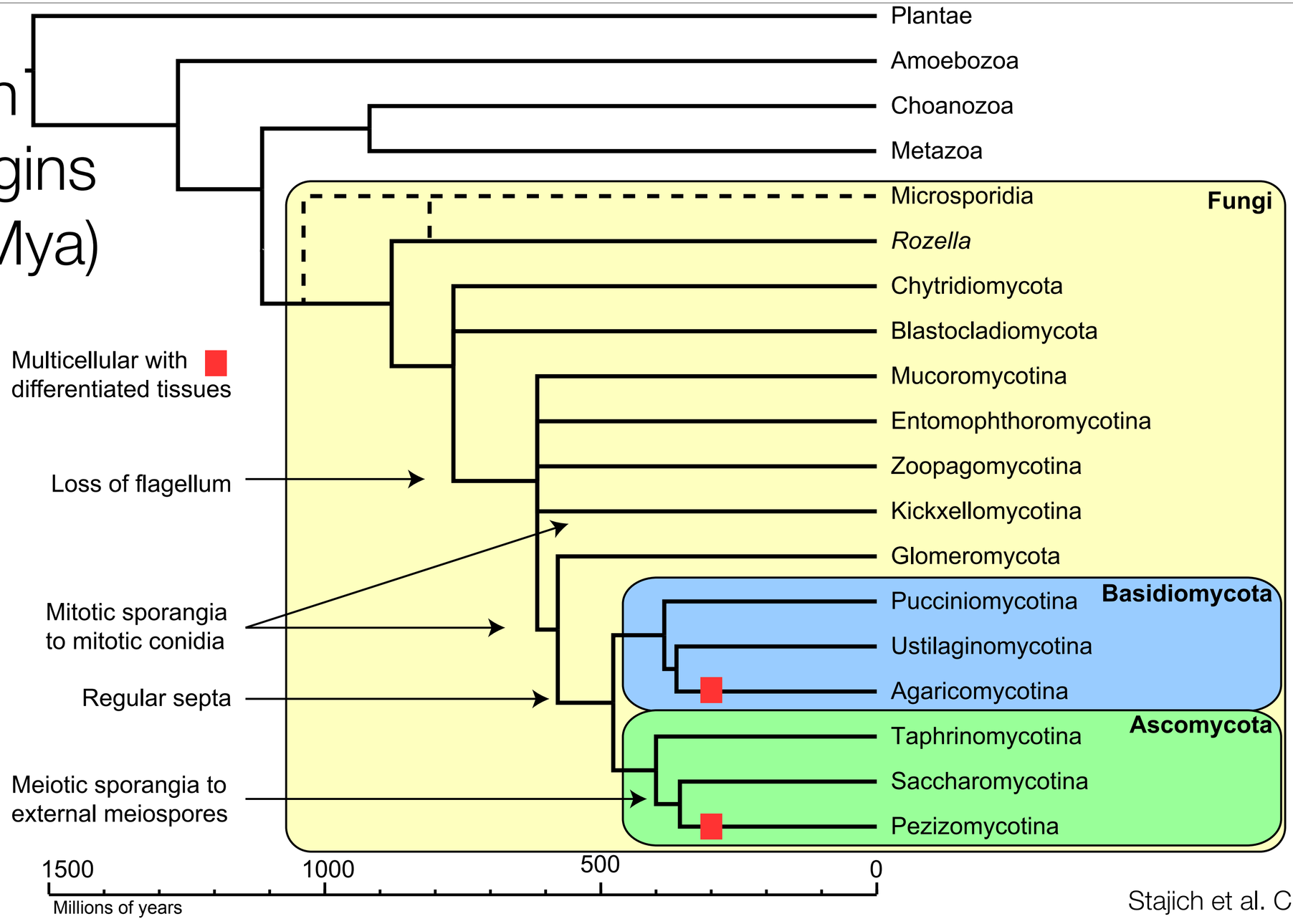


Blastocadiela simplex Stajich & Taylor

UNIVERSITY OF CALIFORNIA UCRIVERSIDE

Fungi are an old group of organisms

(Eutherian mammal origins ~ 150-180 Mya)



Stajich et al. Current Biol 2009

Awash in Fungal Genomes

- Mid-2011: Genomes from 150+ species sequenced and ~400 more in progress/pipeline

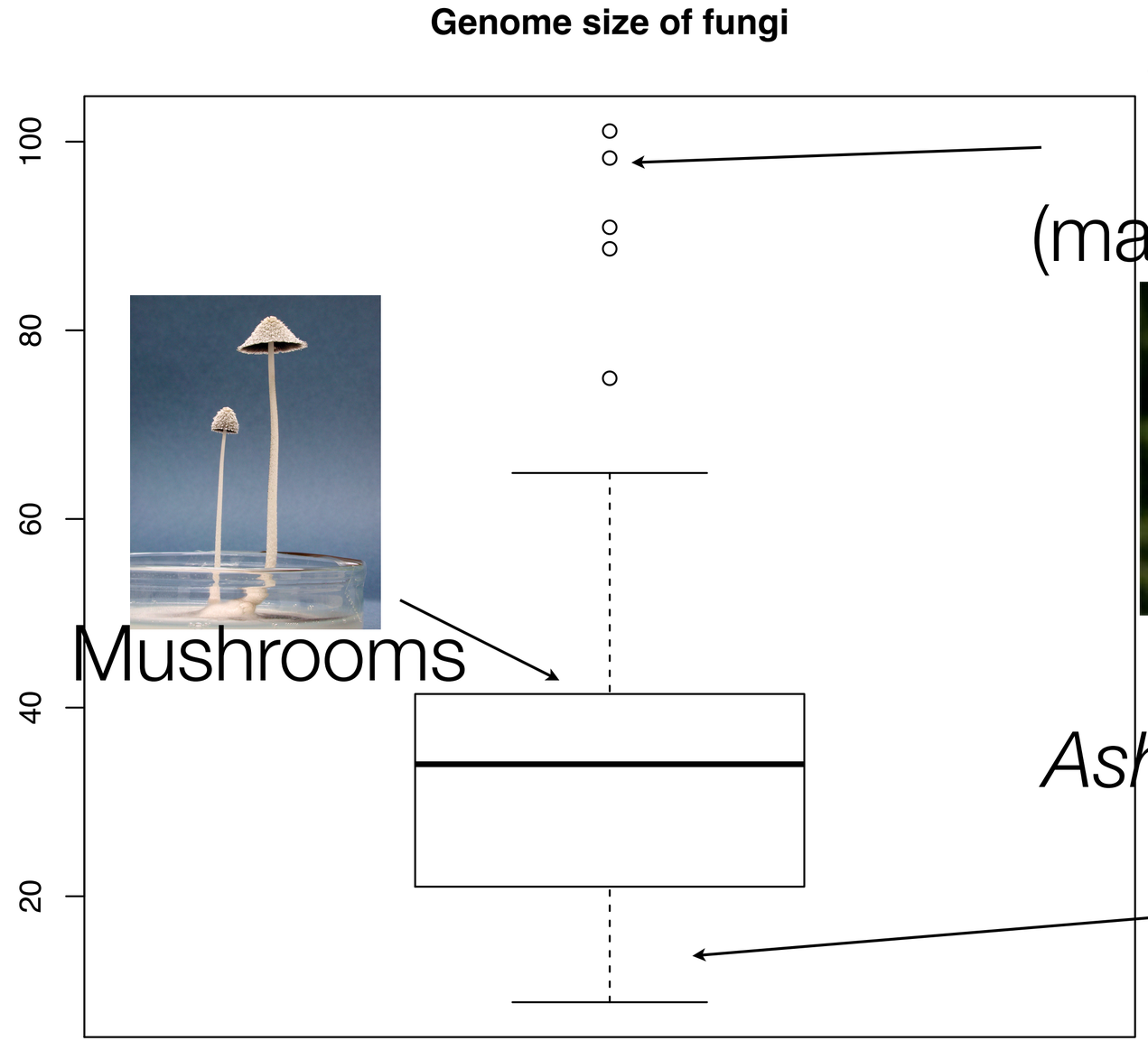
- Several multi-strain resequencing projects (*Neurospora* - Ellison PNAS 2011), Saccharomyces (Liti Nature 2009), *Coccidoides* (Neafsey Genome Res 2010) and many in progress/proposed.

- Many of sequenced genomes were focused around plant, animal pathogens, and some specific evolutionary questions.

- Now are starting to fill out the tree more to capture the diversity of kingdom and also for studies of molecular evolution among many related species.

- Also efforts targeting specific questions - pathogens and their relatives; wood rotting fungi; flagellated and non-flagellated forms; extremophiles; comparison of growth forms (e.g. yeast forms from phylogenetically very different species)

Genome sizes of fungi are 8Mb-100Mb = easy(ish) to sequence



Mushrooms

Melampsora, Blumeria, Puccinia

(many Transposable elements)

Francis Martin
Flickr:/fmartin1954/2338045504/

http://en.wikipedia.org/wiki/File:Barleypowderymildew.jpg

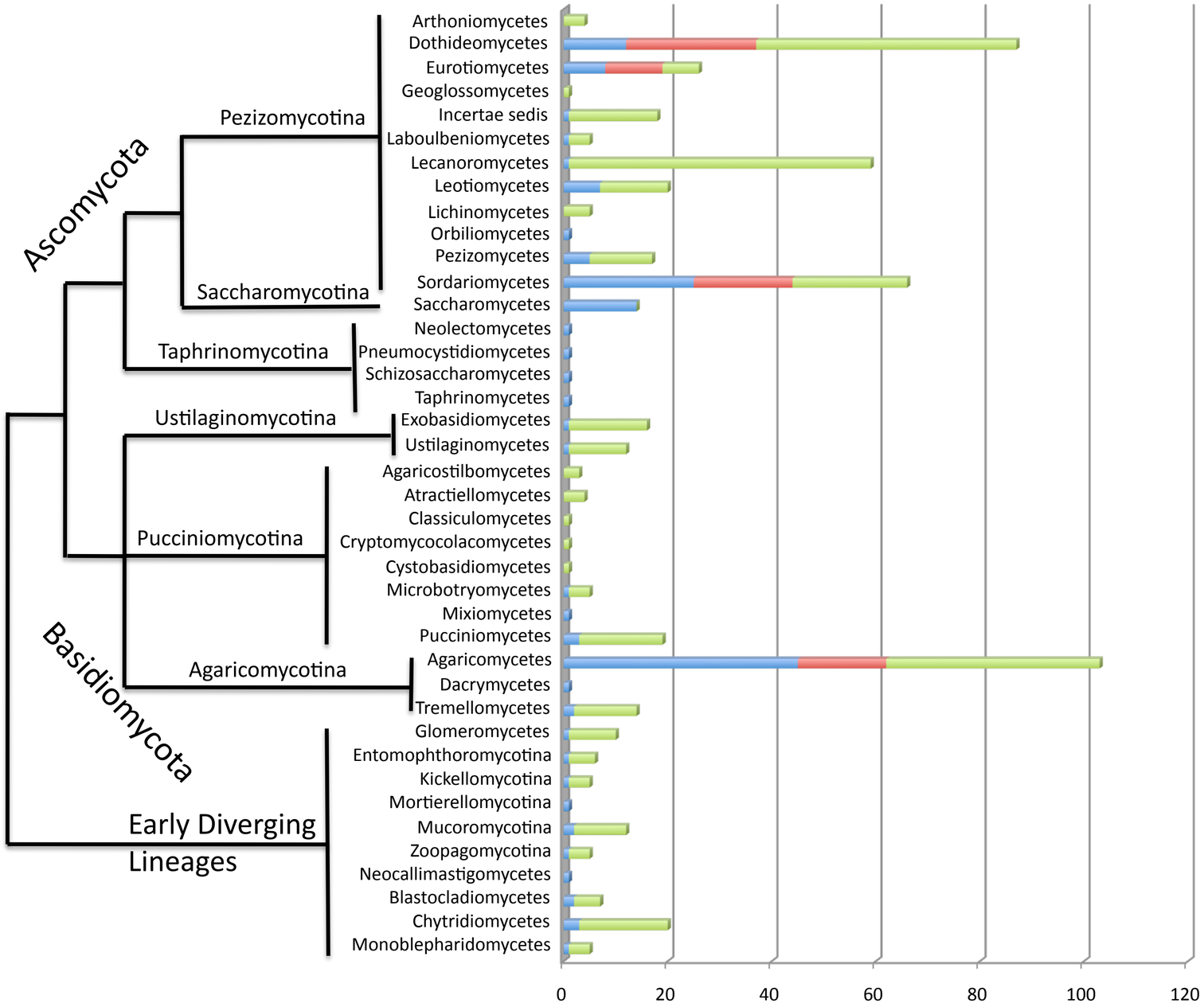
Ashbya, Malassezia, *Candida*

other yeasts

http://www.biologie.uni-osnabrueck.de/Genetik/index.php?menuid=12

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Need to cover more of the phylogenetic diversity: 1000 Fungal genomes project



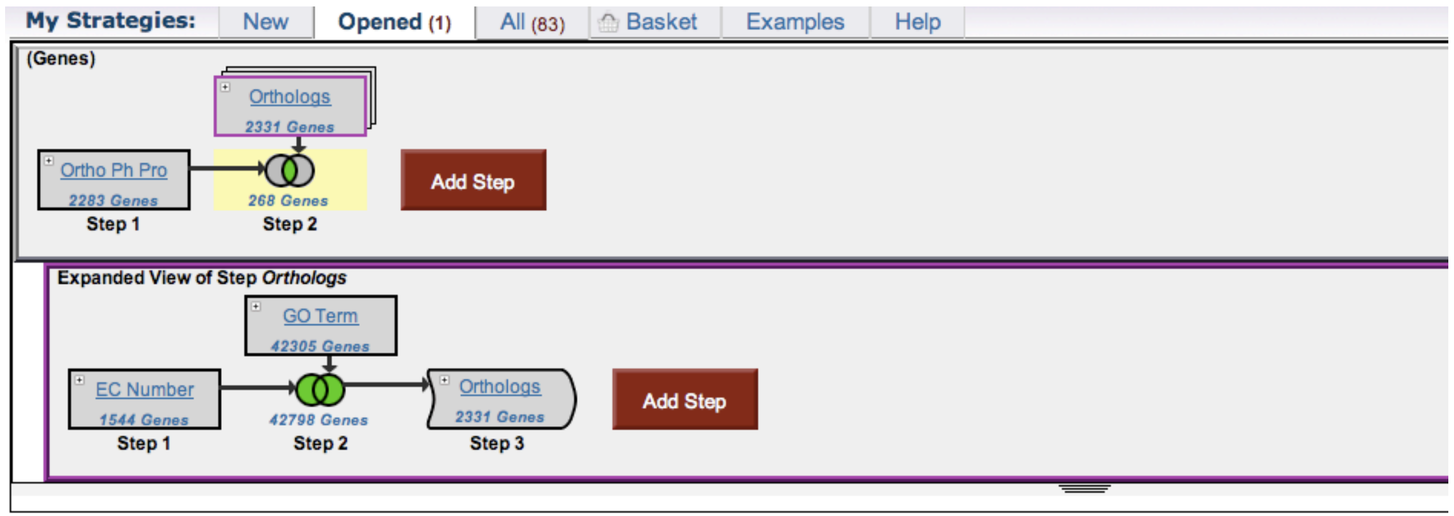
Blue = completed or in progress, Red= proposed for Tier One sampling,
Green = remaining unsampled families

Numbers or Percent of Families in each clade and their current or proposed genome sampling

Tools to access this data

- Genome databases at sequencing centers and NCBI
- Comprehensive and integrated systems are not as well developed in Fungi, but some examples of excellent tools highlighted at http://tools.fungalgenomes.org/
- Ensembl Fungi, MicrobesOnline, JGI's Mycocosm, Comparative Fungal Genomics, and some targeted to specific clades e.g. *Saccharomyces* (SGD), *Aspergillus* (AspGD), *Candida* (CGD)
- We have launched FungiDB - http://fungidb.org to support integrating functional genomics data for data mining as well as standard 'Gene' pages for genes.

Searching with FungiDB:
A strategy for drug targets



C.neoformans genes with
- no hits in other eukaryotes (excepting fungi), bacteria
- has S.cerevisiae orthologs that have EC terms OR orthologs in other fungi with GO metabolic terms associated

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
268	249	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	268	0	0

Cryptococcus Drug target? - step 2 - 268 Genes

First 1 2 3 4 5 Next Last Advanced Paging

Gene	Genomic Location	Weight	Predicted GO Function	Predicted GO Process
CneoH99__CNAG_07830	CneoH99__Chr_2.4: 1,052,305 - 1,054,670 (-)	20	DNA binding, zinc ion binding	transcription
CneoH99__CNAG_07632	CneoH99__Chr_2.6: 473,070 - 476,242 (+)	20	pyridoxal phosphate binding, transaminase activity	biosynthetic process, cellular amino acid metabolic process
CneoH99__CNAG_07589	CneoH99__Chr_2.11: 160,029 - 161,779 (-)	20	binding, catalytic activity, oxidoreductase activity, zinc ion binding	metabolic process, oxidation reduction
CneoH99__CNAG_07441	CneoH99__Chr_2.5: 1,287,517 - 1,288,271 (-)	20	4-alpha-hydroxytetrahydrobiopterin dehydratase activity	tetrahydrobiopterin biosynthetic process
CneoH99__CNAG_07011	CneoH99__Chr_2.12: 762,209 - 764,308 (+)	20	DNA binding, zinc ion binding	transcription
CneoH99__CNAG_06868	CneoH99__Chr_2.5: 29,970 - 32,039 (-)	20	phosphopyruvate hydratase activity	glycolysis
CneoH99__CNAG_06719	CneoH99__Chr_2.2: 235,880 - 239,543 (+)	20	DNA binding, zinc ion binding	transcription

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Searching with FungiDB:
A strategy for reannotation

2885 *C.neoformans* genes with desc “"conserved hypothetical protein” but 1327 can be assigned name from ortholog in any fungus with EC #, GO terms, or Pfam domains

Filter results by species *(results removed by the filter will not be combined into the next step.)*

All Results	Ortholog Groups	*Eurotiomycetes*								*Sordariomycetes*					*Saccharomycotina*		*Basidiomycota*		*Rhizopus oryzae*
		A.cla	*A.fla*	*A.fum*	*A.nid*	*A.nig*	*A.ter*	*C.imm* H538.4	*C.imm* RS	*F.gra*	*F.oxy*	*G.mon*	*M.ory*	*N.cra*	*C.alb*	*S.cer*	*C.neo*	*P.gra*	
1327	1229	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1327	0	0

Annotation(2) - step 4 - 1327 Genes

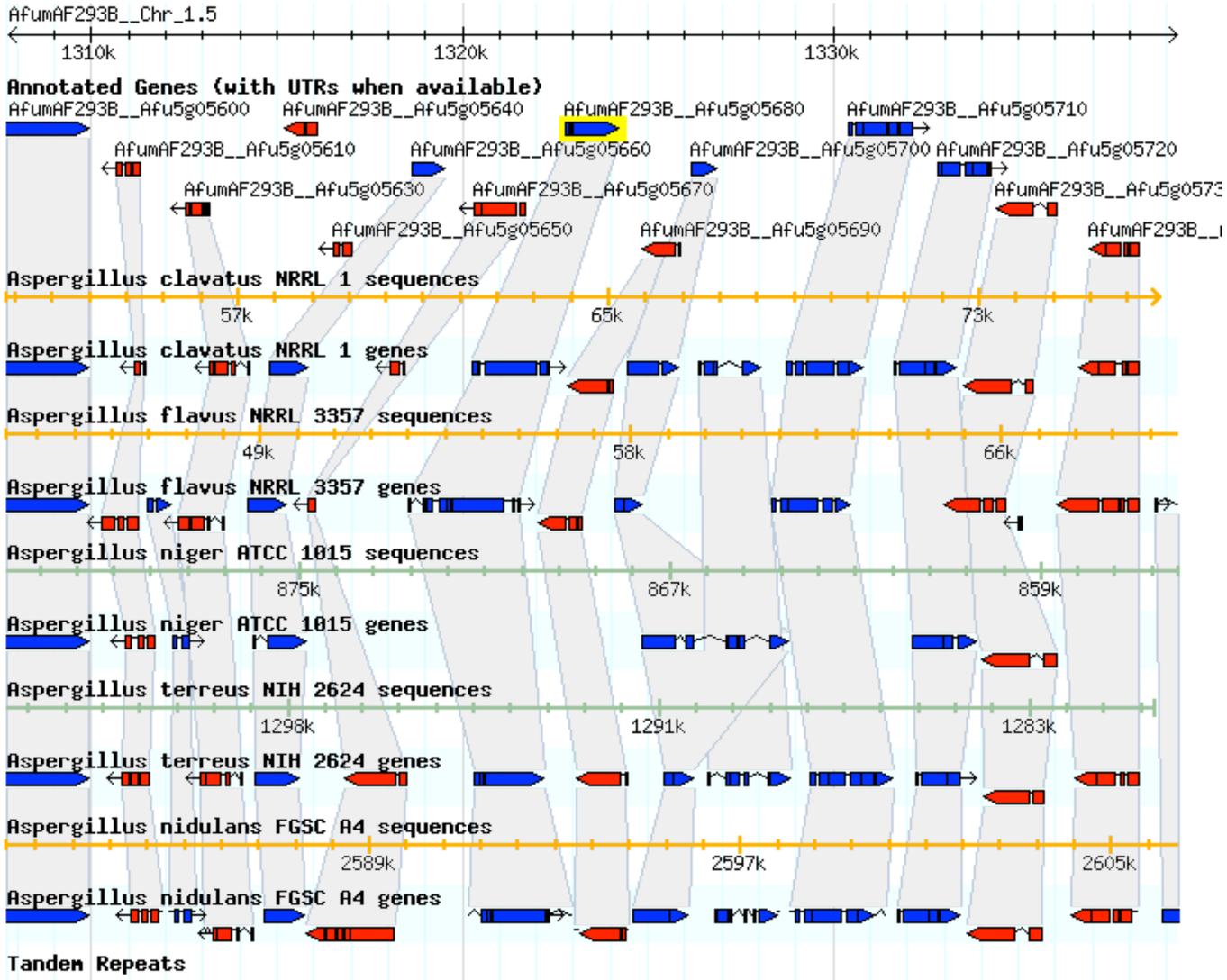
Add 1327 Genes to Basket | Download 1327 Genes

First 1 2 3 4 5 Next Last | Advanced Paging | Select Columns | Reset Columns

Gene	Genomic Location	Weight	Predicted GO Function	Predicted GO Process	Ortholog Group	SignalP Peptide
CneoH99__CNAG_07913	CneoH99__Chr_2.12: 637,812 - 638,653 (+)	10	N/A	N/A	OG5_226248	N/A
CneoH99__CNAG_07912	CneoH99__Chr_2.12: 636,724 - 637,155 (+)	10	N/A	N/A	OG5_226247	N/A
CneoH99__CNAG_07898	CneoH99__Chr_2.12: 191,256 - 192,798 (+)	10	N/A	N/A	OG5_226246	N/A
CneoH99__CNAG_07890	CneoH99__Chr_2.14: 796,716 - 797,600 (+)	10	N/A	N/A	OG5_226245	HMM: MSISKSPSLDLCLATLHELLHPSPILSLLLSALDLSAHFQLFAQQLSSDAALVSAL, NN: MSISKSPSLDLCLATLHELLHPSPILSLLLSAL...
CneoH99__CNAG_07883	CneoH99__Chr_2.14: 482,566 - 484,632 (-)	10	N/A	N/A	OG5_226244	N/A

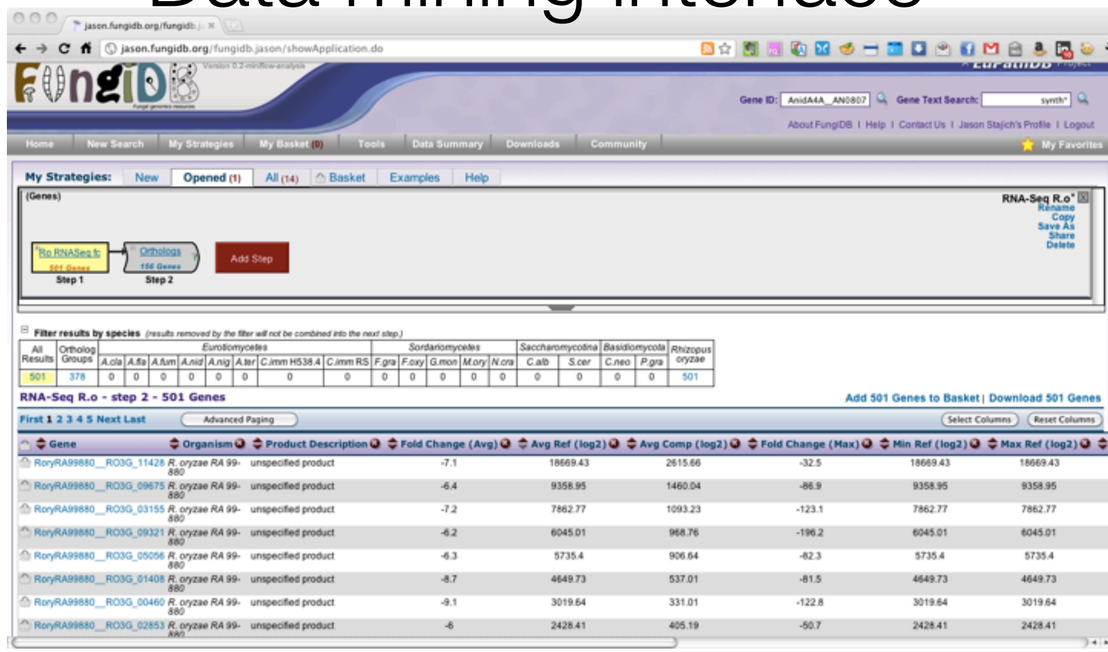
UNIVERSITY OF CALIFORNIA
UC RIVERSIDE

Synteny Views



Gene page and genome browser

Data mining interface



UNIVERSITY OF CALIFORNIA
UCRIVERSIDE

FungiDB
Fungal genomics resources

Using comparative genomics towards understand pathogen evolution

- How do traits like pathogenecity evolve?
- Can comparative genomics indicate meaningful differences that can lead to understanding the basis for pathogenesis?
- Contrasting genomes of pathogens with non-pathogens can suggest recent genomic changes that might be testable in the lab
- Gene duplication is thought to be important source for evolutionary innovation - What role might gene family size change play in adaptation?

Models for comparing gene family size changes

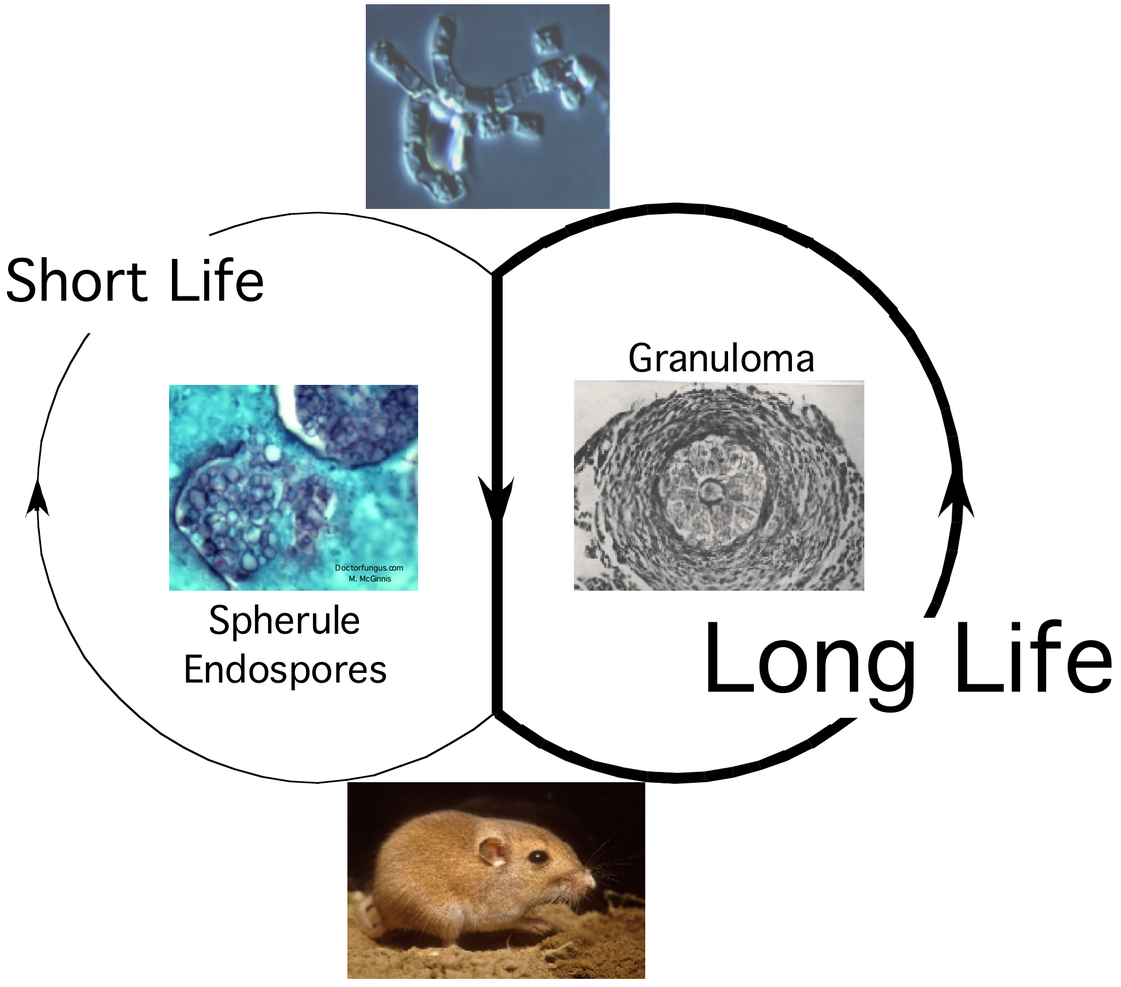
- A model for gene family size change that incorporates the birth-death process of gene families which follow a power law distribution (Hahn et al, Genome Res 2005)

- Implemented in a program called CAFE to find unexpectedly large lineage or clade-specific changes in gene family sizes (Hahn Lab @Indiana Univ) (De Bie et al, Bioinformatics 2006)

- Can screen genome family sizes across multiple species to find expectedly large changes (based on counts) which can be verified using gene tree-species tree reconciliation approaches like Notung (Chen, Durand, Farach-Colton, J Comp Bio 2000)

Coccidioides

- Fungal pathogen genomics: Gene families and appetite differences

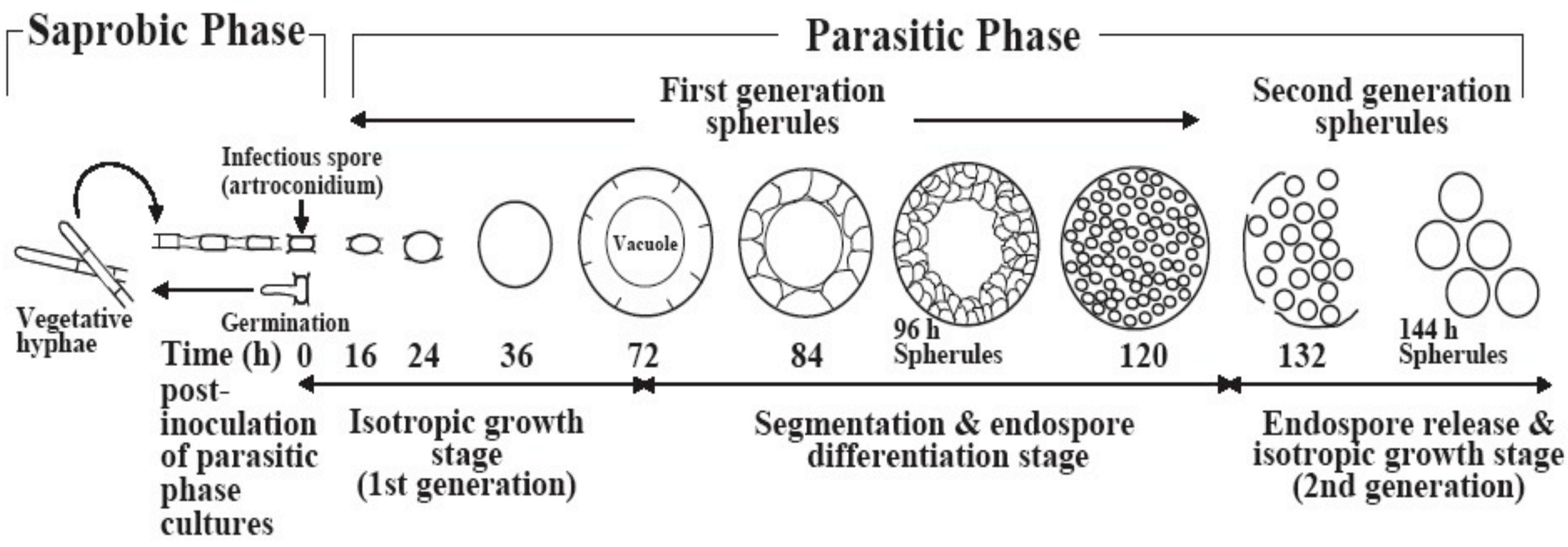


UC RIVERSIDE UNIVERSITY OF CALIFORNIA

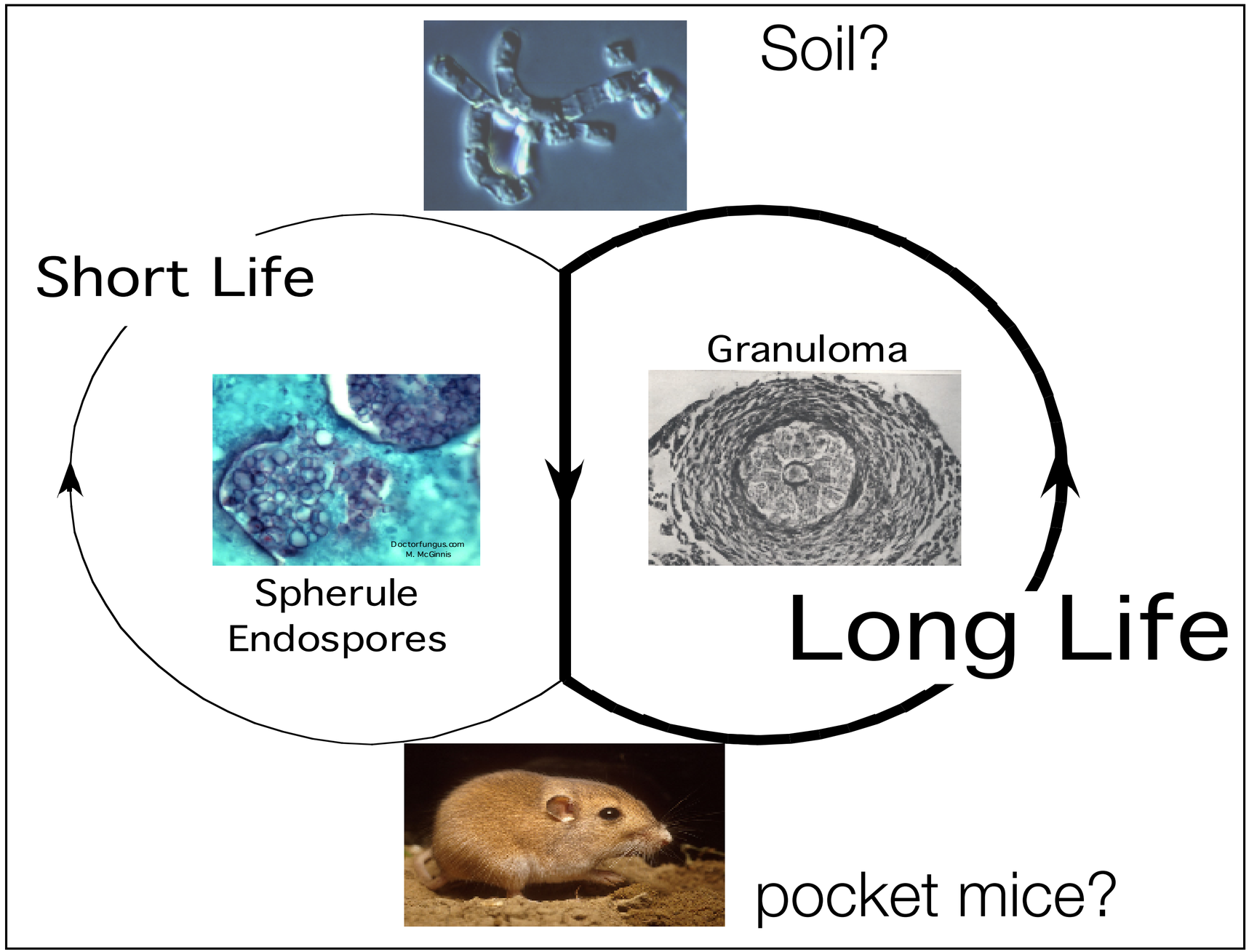
Human pathogen *Coccidioides*

- Coccidioides (Valley fever) - 2 species *C. immitis* and *C. posadasii*
    - Is a primary human pathogen - infects healthy people (most human pathogenic fungi are opportunistic)
    - Endemic in US Southwest, Mexico
        - Requires laboratory BSL3 and is a Select Agent
        - Genomes of 2 species (Sharpton et al Genome Res 2009) and then 18 strains (Neafsey et al Genome Res 2010)
- Comparative analyses of *Coccidoides* spp

Human pathogen *Coccidioides* Life cycle



Coccidioides ecology

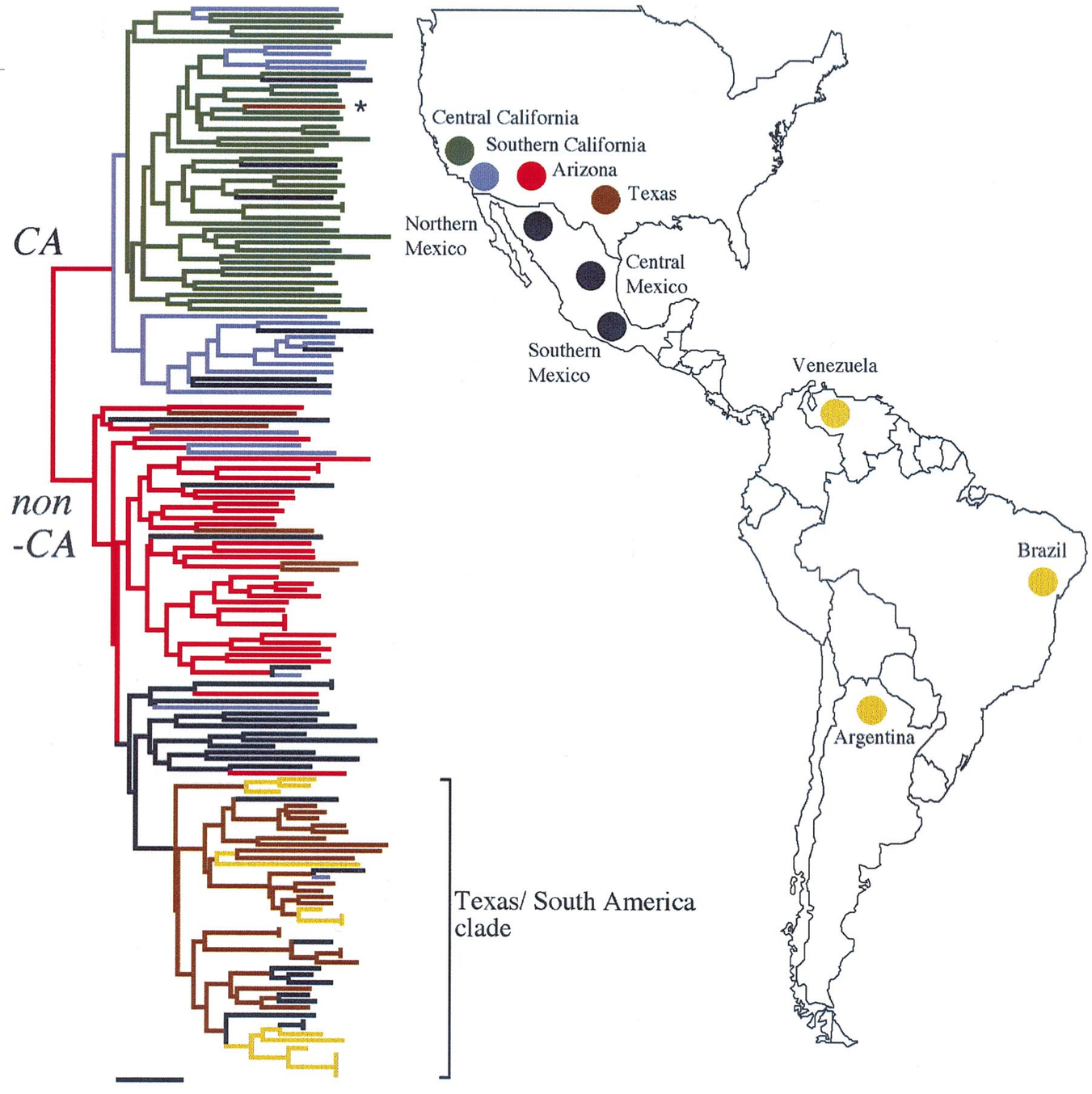


UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Two species of *Coccidioides* are allopatric

C.immitis

C.posadasii



Fisher et al, 2000

Studying the evolution of a pathogen

- Comparing sequences from two *Coccidioides* species, closely related outgroup, and more distant ougroups species:

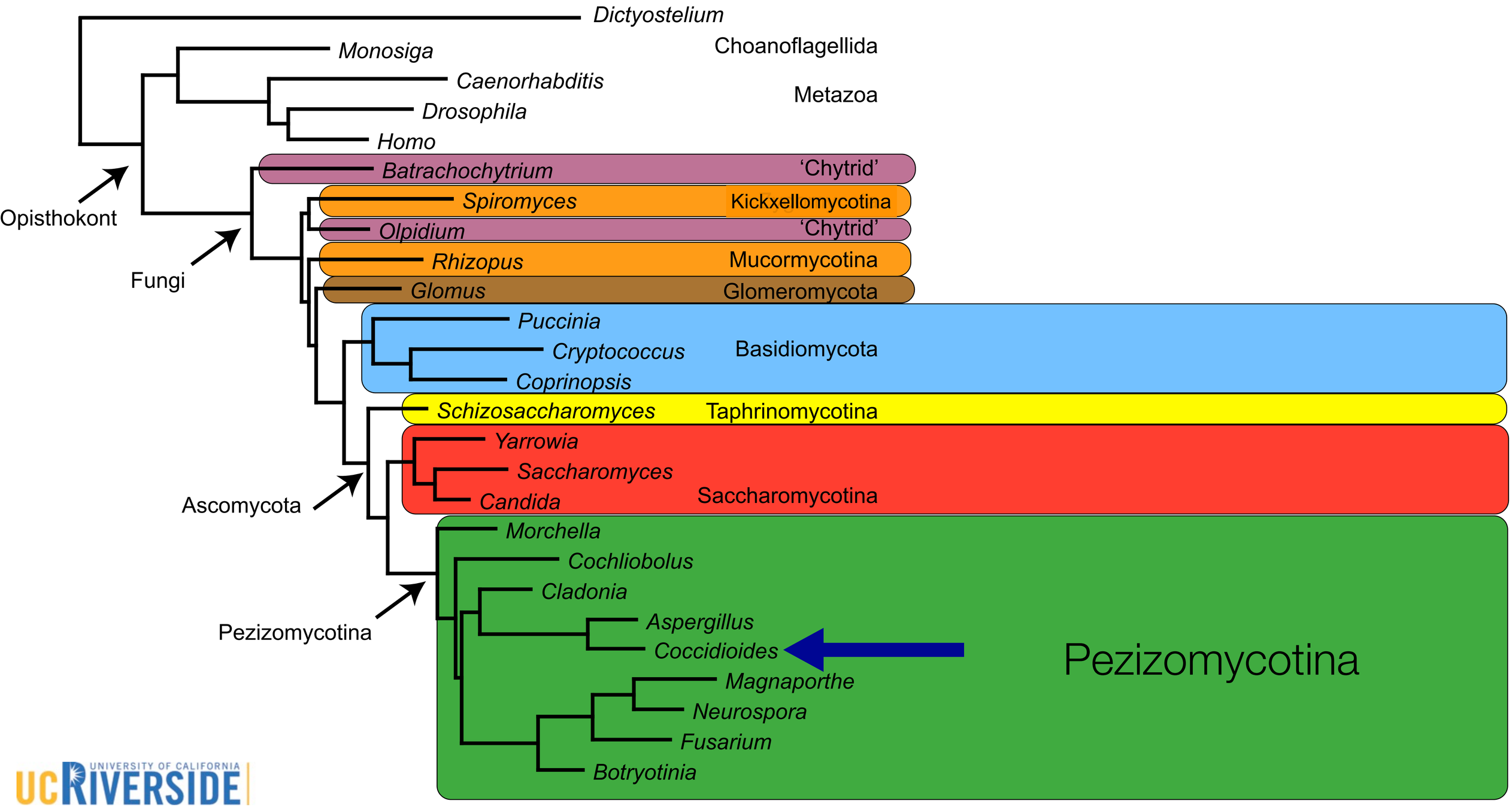
- Evidence for recent positive selection
  - What gene family differences can be identified that distinguish phenotypic groups (mammalian pathogens from non-pathogens)

- Evidence for recent introgression which contains candidate genes for pathogenesis

Gene family changes

- Another mechanism for adaptation may be changes in copy number of a gene family
    - Gene duplication is a source of novelty allowing for changes in the function of one copy if the other maintains original function
        - Expansions of copy number may also be an easy way to get more protein for a particular process
- How important is copy number change in adaptation?

Genome samples from fungi



UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Aspergillus clavatus
Aspergillus fumigatus
Aspergillus flavus
Aspergillus oryzae
Aspergillus terreus
Aspergillus niger
Aspergillus nidulans
Penicillium marneffei
Blastomyces dermatitidis
Histoplasma capsulatum 186AR
Histoplasma capsulatum 217B
Histoplasma capsulatum WU24
Paracoccidioides brasiliensis
Coccidioides immitis
Coccidioides posadasii
Uncinocarpus reesii
Fusarium graminearum
Sclerotinia sclerotiorum

Eurotiales

Eurotiomycetes

Onygenales

200
100
0
Mya

Animal Pathogen (Opportunistic)

Animal Pathogen (Primary)

Plant Pathogen

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Few protein domains for eating plant material in animal pathogens

Loss of plant saprophytic enzymes

	CBM_1	Tannase	Pec_lyase_C	NPP1	Cutinase	Cellulase	Subtilisin_N	Peptidase_S8	Peptidase_M35	Peptidase_M36	APH
Anid	6	6	6	2	4	13	2	3	3	0	9
Afum	17	5	5	2	5	10	2	5	2	1	9
Ater	15	6	6	2	8	13	2	6	2	1	29
Hcap	**0**	**0**	**0**	**0**	**2**	**2**	2	6	1	0	20
Uree	**0**	**0**	**0**	**0**	**1**	**2**	15	19	4	2	33
Cimm	**0**	**0**	**0**	**0**	**1**	**1**	13	16	7	2	38
Cpos	**0**	**0**	**0**	**0**	**1**	**1**	14	16	7	2	32
Ncra	18	1	1	4	3	6	3	6	2	0	6
Fgra	12	7	9	9	12	8	11	24	1	1	15

Animal Pathogen (Opportunistic)

Animal Pathogen (Primary)

Plant Pathogen

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton, Stajich, et al, Genome Res. 2009

Domains for eating animal material?

	CBM_1	Tannase	Pec_lyase_C	NPP1	Cutinase	Cellulase	Subtilisin_N	Peptidase_S8	Peptidase_M35	Peptidase_M36	APH
Anid	6	6	6	2	4	13	2	3	3	0	9
Afum	17	5	5	2	5	10	2	5	2	1	9
Ater	15	6	6	2	8	13	2	6	2	1	29
Hcap	0	0	0	0	2	2	2	6	1	0	20
Uree	0	0	0	0	1	2	**15**	**19**	**4**	**2**	**33**
Cimm	0	0	0	0	1	1	**13**	**16**	**7**	**2**	**38**
Cpos	0	0	0	0	1	1	**14**	**16**	**7**	**2**	**32**
Ncra	18	1	1	4	3	6	3	6	2	0	6
Fgra	12	7	9	9	12	8	11	24	1	1	15

Animal Pathogen (Opportunistic)

Animal Pathogen (Primary)

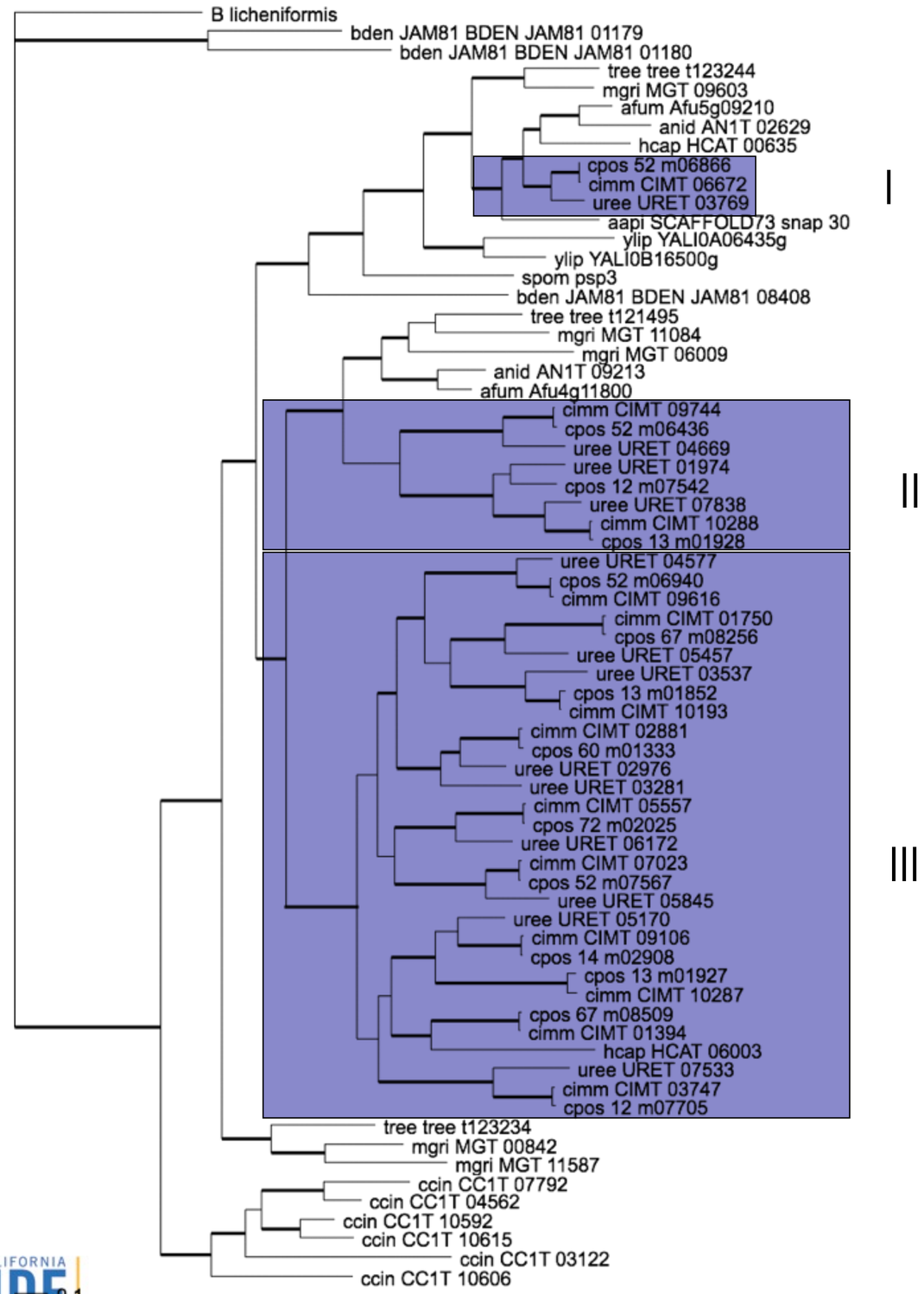
Plant Pathogen

Sharpton, Stajich, et al, Genome Res. 2009

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Keratinases in Onygenales

- Onygenales are Keratinophilic
- Domains: Peptidase S8, Subtilisin domains
- Large expansion of putative keratinases in Onygenales



Peptidase S8 expansion in Onygenales

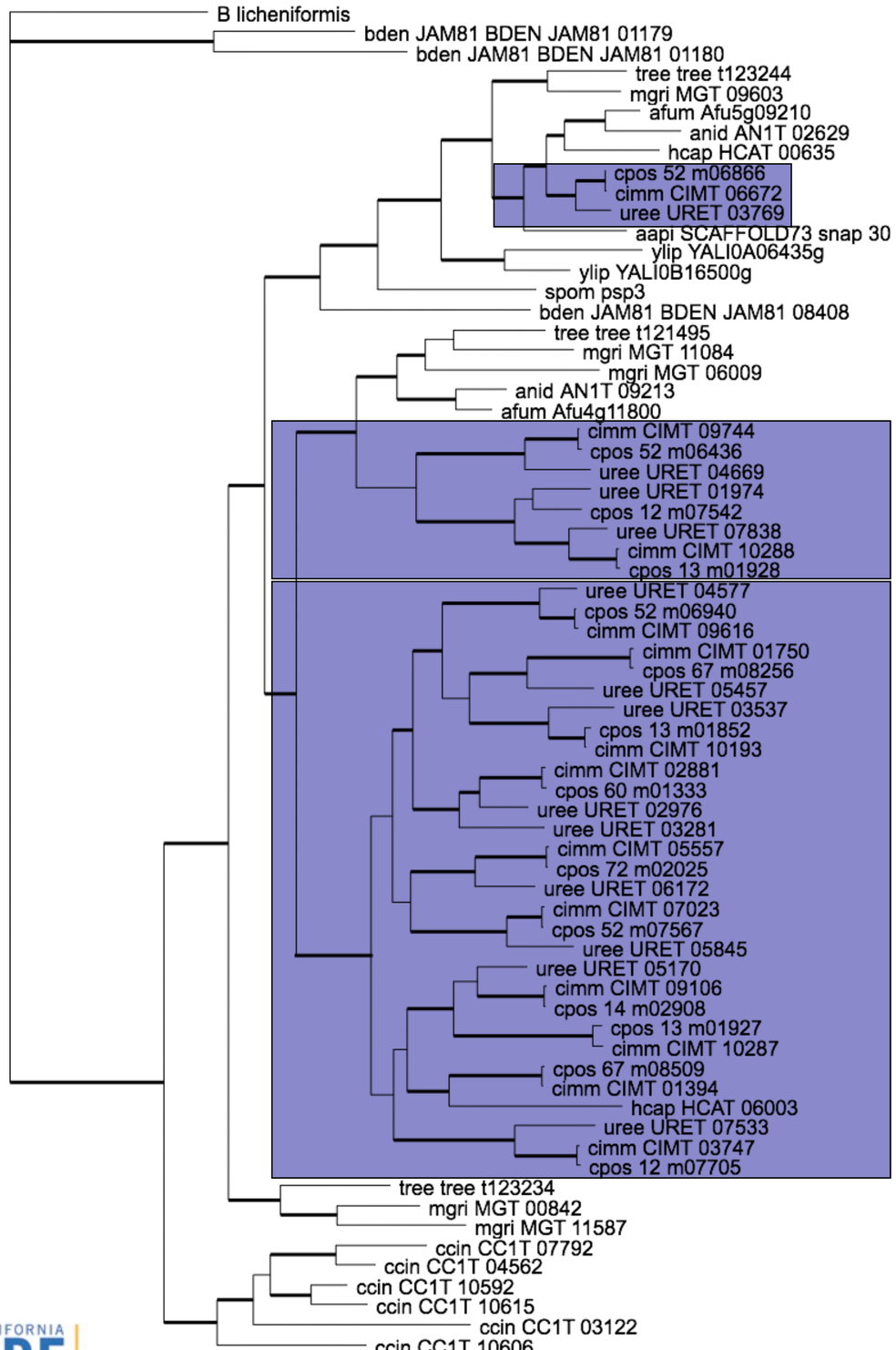
14 copies in ***Coccidioides***

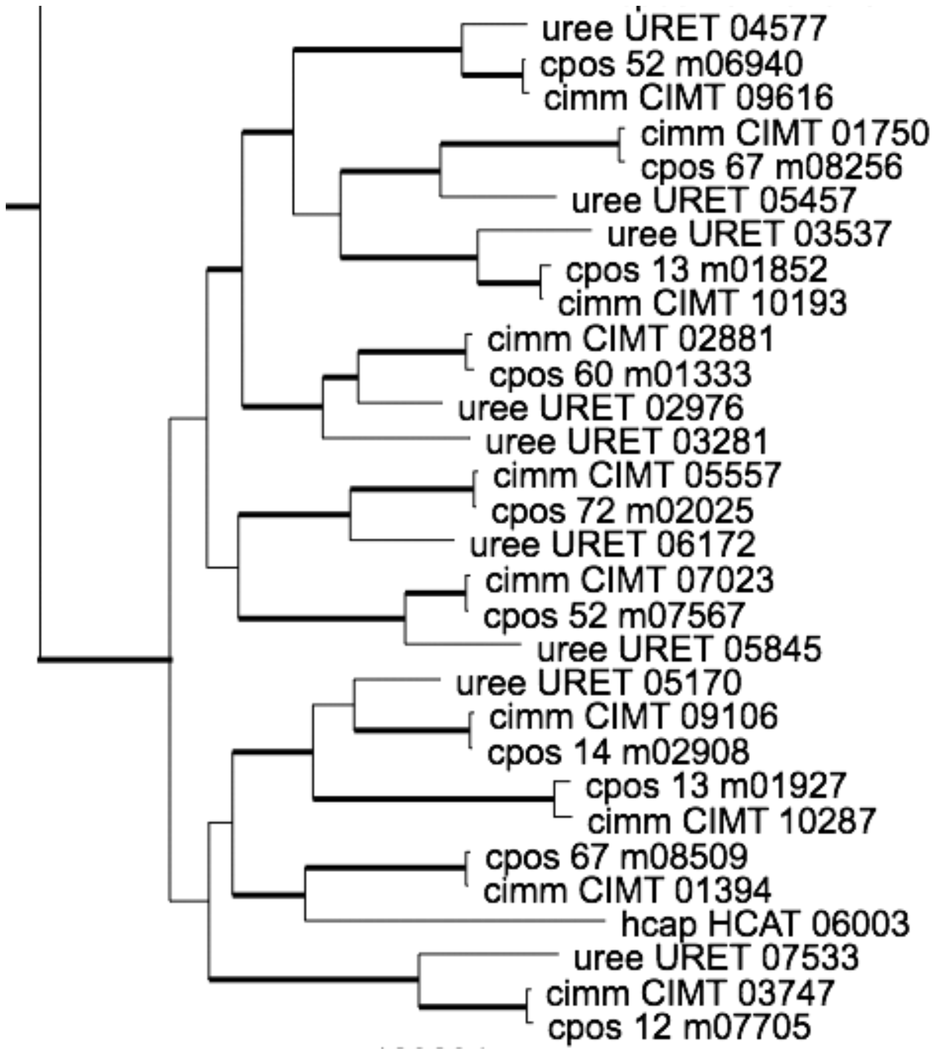
1 in ***Histoplasma***

Peptidase S8 expansion in Onygenales

14 copies in *Coccidioides*

1 in *Histoplasma*





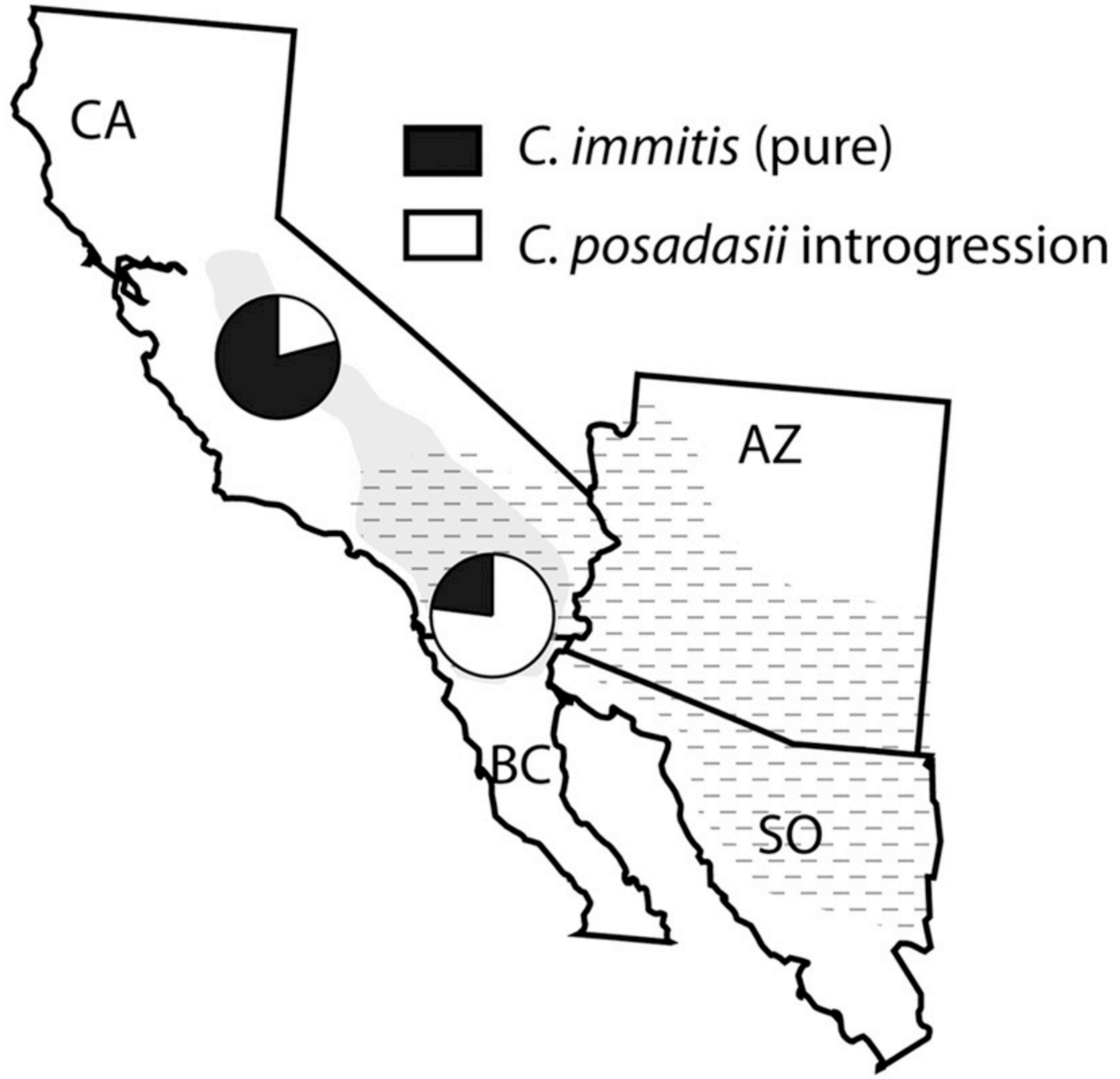
UNIVERSITY OF CALIFORNIA UCRIVERSIDE

Population genomics

- Revealed no loci with evidence for balancing selection - so little evidence for long standing host-pathogen battle as in *Plasmodium*.

- Sliding window F_{ST} analysis revealed some regions of reduced divergence and followup revealed a regions of recent intergression.
  Directionality looks to be mostly from Cp and into Ci.

- One gene implicated in pathogenesis, MEP4, is found in introgressed region



UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Towards identifying genes underlying adaptation

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

Towards identifying genes underlying adaptation

- Coccidioides is found in desert soil and associated with animals - perhaps has a long term animal association without inducing response from the host.

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

Towards identifying genes underlying adaptation

- Coccidioides is found in desert soil and associated with animals - perhaps has a long term animal association without inducing response from the host.

- Loss of genes involved in plant product metabolism suggests nutritional shift in Onygenales from relatives in Eurotiales

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

Towards identifying genes underlying adaptation

- Coccidioides is found in desert soil and associated with animals - perhaps has a long term animal association without inducing response from the host.
- Loss of genes involved in plant product metabolism suggests nutritional shift in Onygenales from relatives in Eurotiales
- Expansion of only a few gene families, seem to be involved in metabolism - none are *Coccidioides* specific though.

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

Towards identifying genes underlying adaptation

- Coccidioides is found in desert soil and associated with animals - perhaps has a long term animal association without inducing response from the host.
- Loss of genes involved in plant product metabolism suggests nutritional shift in Onygenales from relatives in Eurotiales
- Expansion of only a few gene families, seem to be involved in metabolism - none are *Coccidioides* specific though.
- From population genetics analysis - failed to find regions under balancing selection suggesting there is not a long-term arms race between host and pathogen.

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

Towards identifying genes underlying adaptation

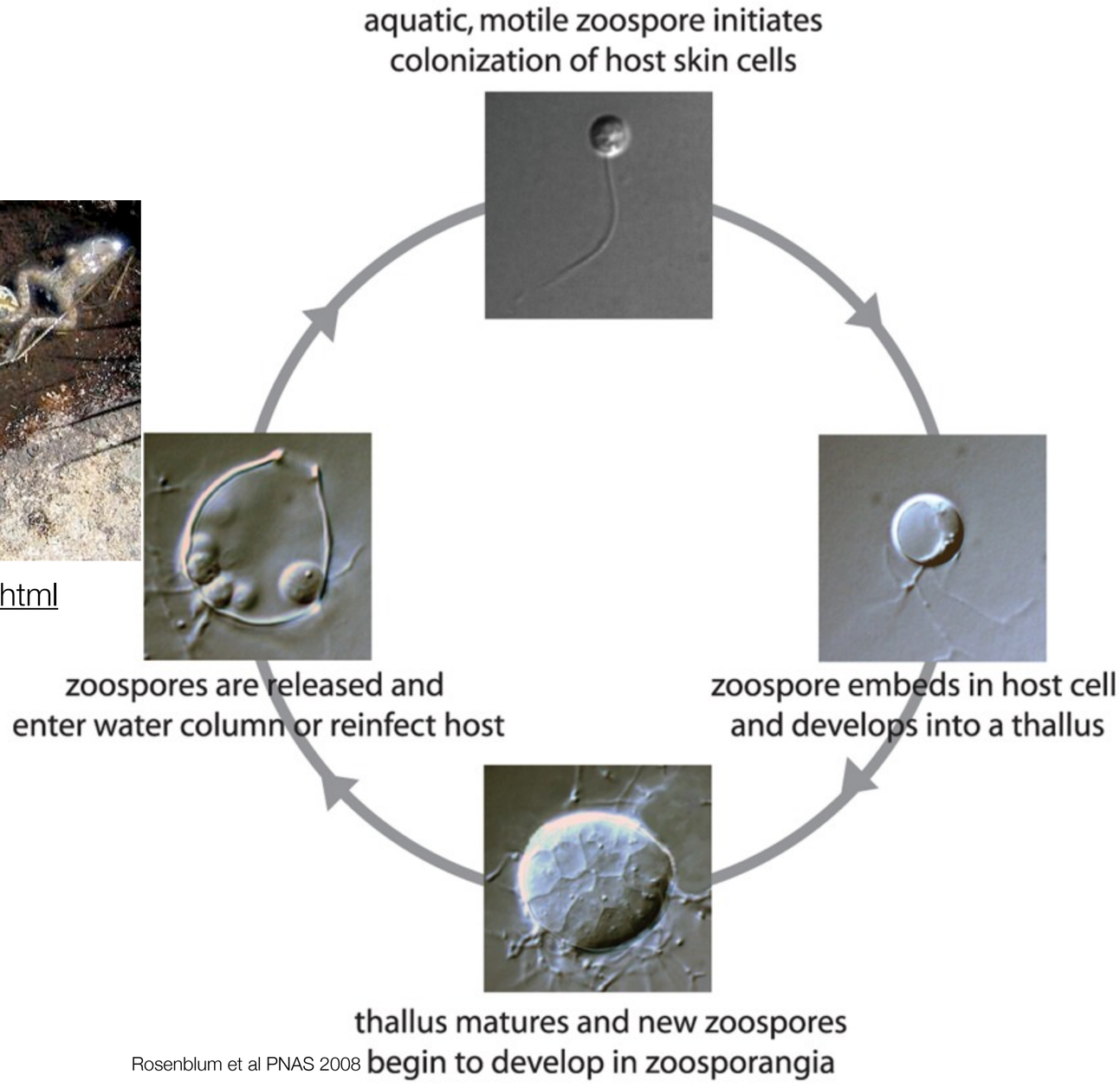
- Coccidioides is found in desert soil and associated with animals - perhaps has a long term animal association without inducing response from the host.
- Loss of genes involved in plant product metabolism suggests nutritional shift in Onygenales from relatives in Eurotiales
- Expansion of only a few gene families, seem to be involved in metabolism - none are *Coccidioides* specific though.
- From population genetics analysis - failed to find regions under balancing selection suggesting there is not a long-term arms race between host and pathogen.
- Evidence for introgression between the species and perhaps imported novel alleles that are important for adaptation in both species to their animal hosts.

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Sharpton et al. Genome Res 2009
Neafsey et al, Genome Res 2010

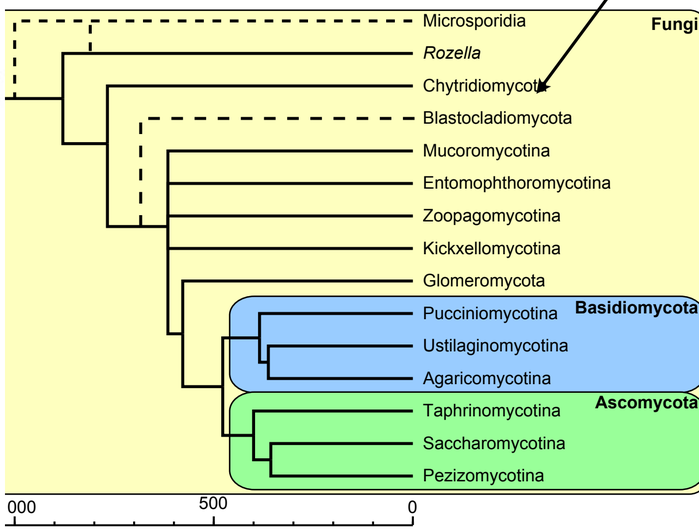
Batrachochytrium dendrobatidis (Bd)- a major cause of amphibian decline

http://cisr.ucr.edu/chytrid_fungus.html



Rosenblum et al PNAS 2008

Bd is a Chytrid fungus



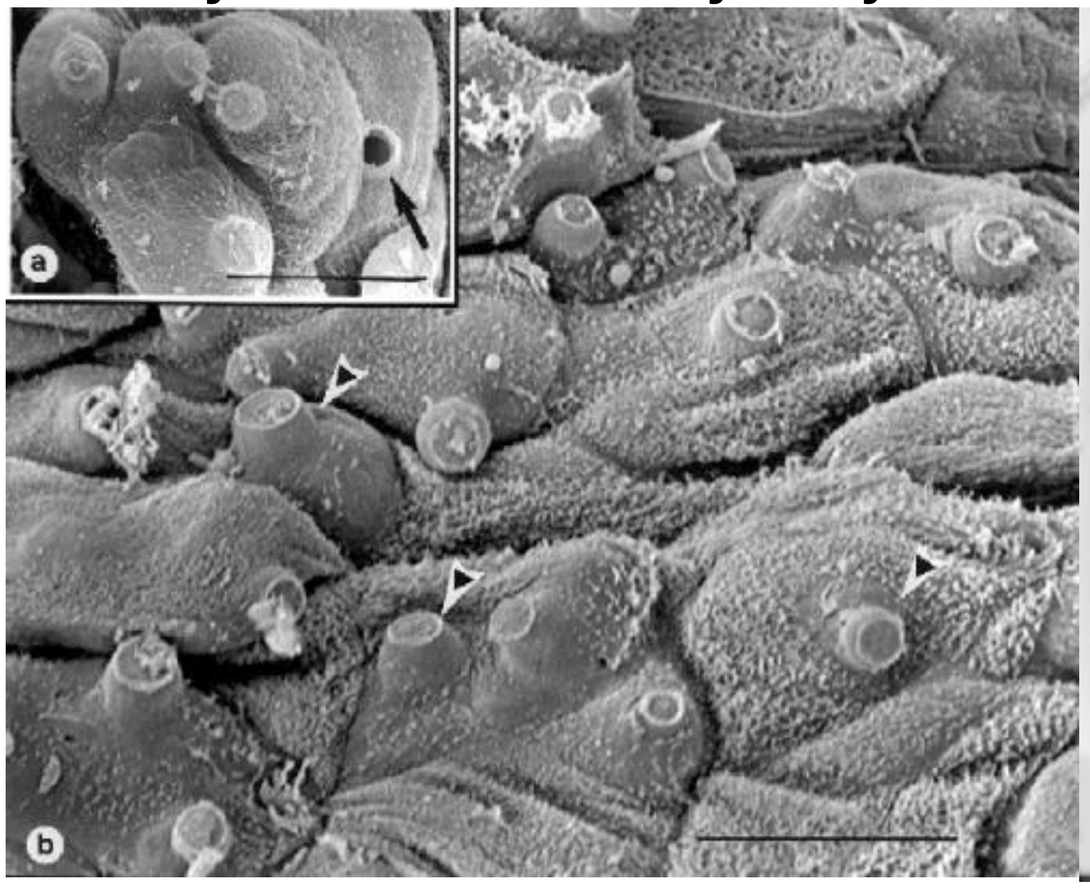
UNIVERSITY OF CALIFORNIA UCRIVERSIDE

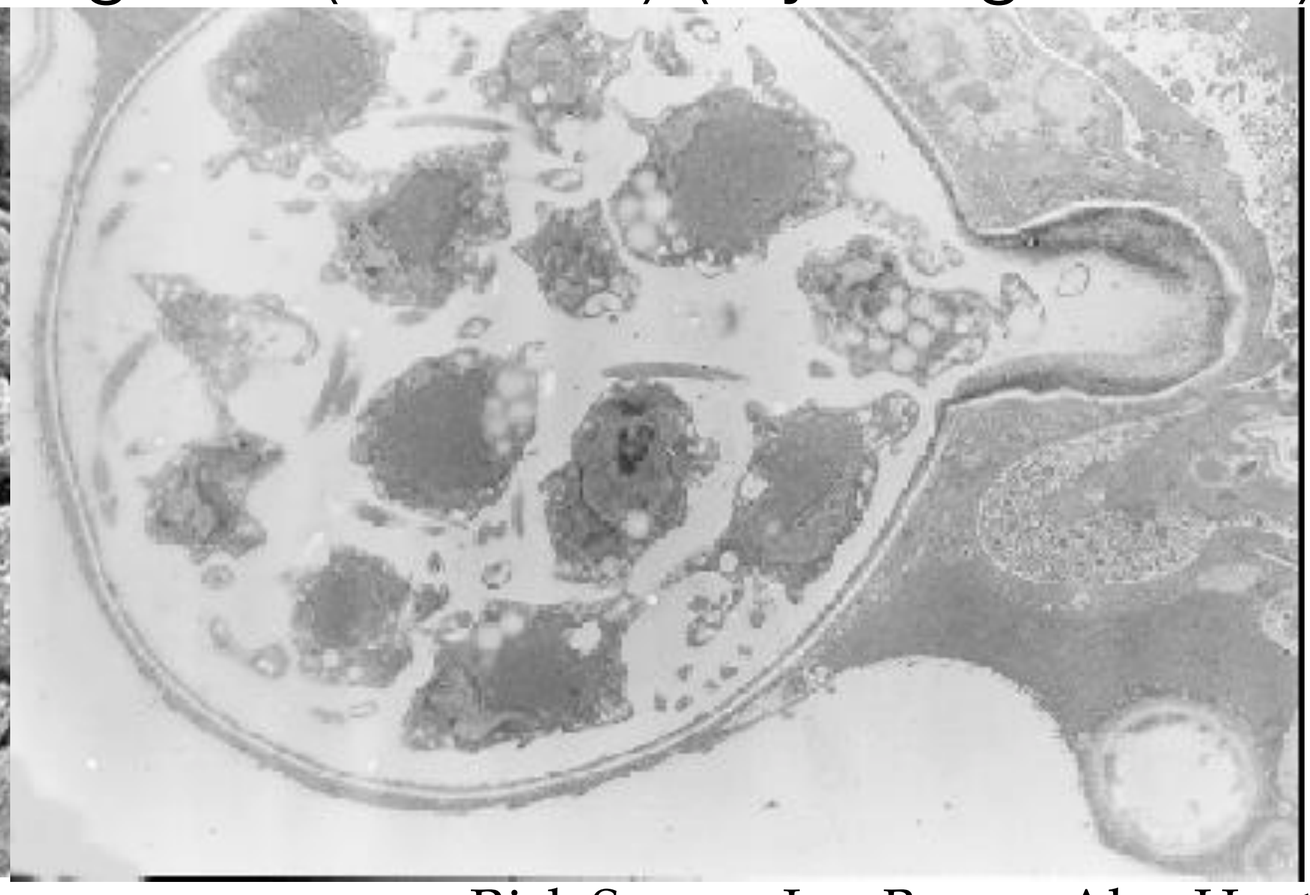
Bd genome sequence projects

- 2 strains sequenced at JGI and Broad; allow whole genome comparison between strains
- Found that genome is diploid, but with large regions with loss of heterozygocity (LOH)
- Identified gene family changes that might suggest mechanisms of pathogenecity
- Greater understanding of what the early fungus was like
- With collaborators we are sequencing 20 more strains for population genomics to better understand population dynamics, trace origin of diversity, and understand the LOH as independent or shared events.

Bd grows intercellularly

Formally described by Joyce Longcore (U Maine) (Mycologia 1999)





Rick Speare, Lee Berger, Alax Haytt

James Cook University, Townsville, Australia

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

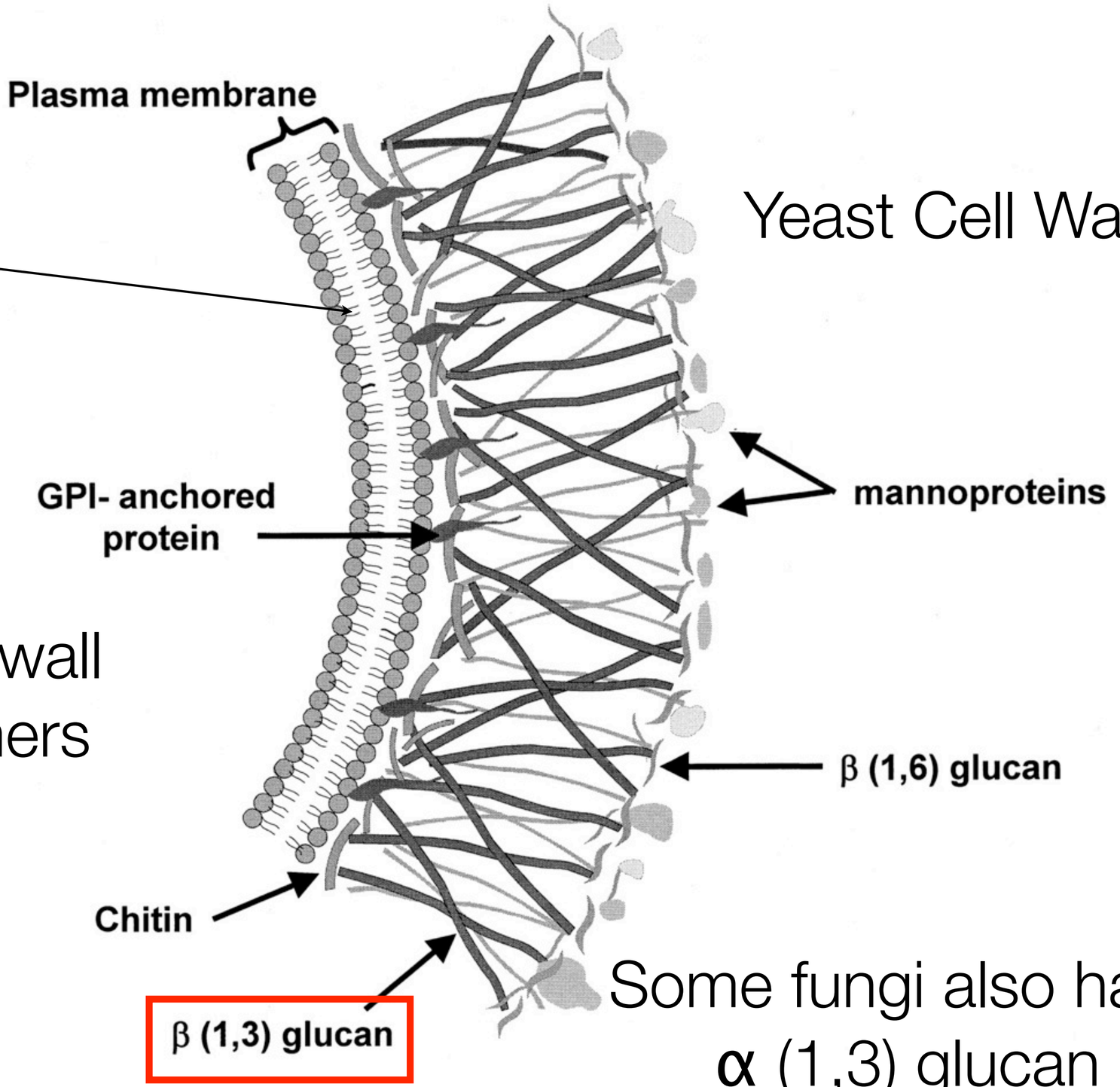
http://www.jcu.edu.au/school/phtm/PHTM/frogs/chpr1/fc13.htm

Phylogenomic profiling

- For each gene in the the target (*Bd*) genome, look to see which have homologs in other fungi, animals, plants
- Classify genes by its profile as to when it must have arisen based on identified homologs
- Also compare well-studied organisms (*S. cerevisiae*, *N. crassa*) to see which genes were missing
- For *Bd*/Chytrids several trends appeared
  - Missing: some cell wall genes, spindle-pole body
  - Present in *Bd* but not other non-chytrid fungi: Flagella, some signaling pathways, effector like proteins
  - Some expansions of gene families

Fungal cell wall evolution- a view from earliest branches

Ergosterol



Yeast Cell Wall

What is the fungal cell wall made of? Sugar polymers

Some fungi also have **α** (1,3) glucan

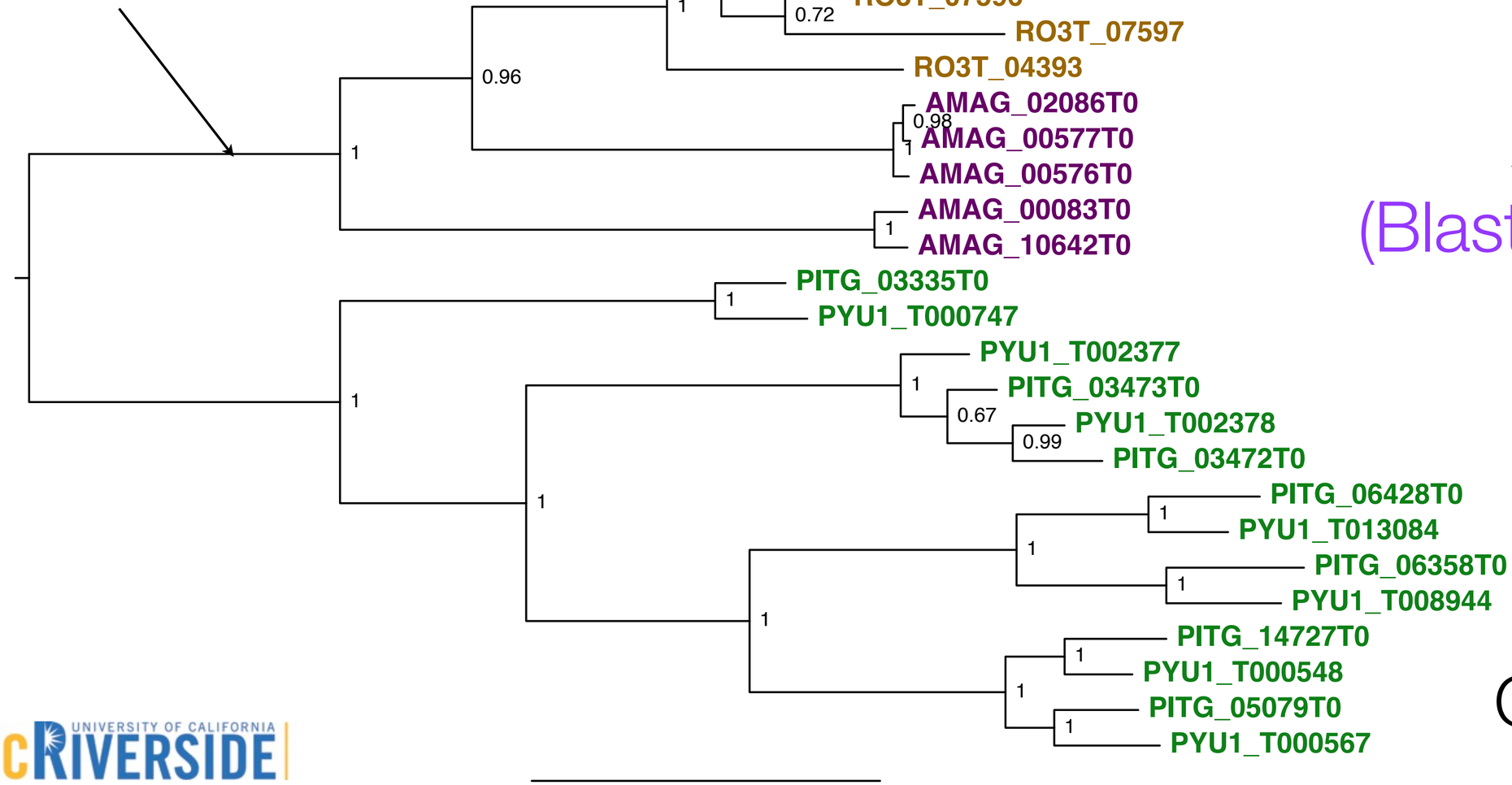
Selitrennikoff CP, AEM 2001

Evolution of β (1,3) glucan synthase

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Evolution of FKS1 [β (1,3) glucan synthetase]

No Chytridiomycota



Ascomycota

Basidiomycota

Rhizopus

Allomyces
(Blastocladiomycota)

Oomycetes

Callose synthase

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

No 1,3 Beta-glucan?

B. dendrobatidis cell wall biochemical analysis

β (1,3)-glucan	β(1,6)-glucan	α(1,3)-glucan	Cellulose β(1,4)-glucan	Chitin
X	**X**	**X**	✓	✓

A putative cellulose synthase gene can be found in genome of *Bd* but also found in *N. crassa* and other Fungi

with JP Latgé, M. Fisher

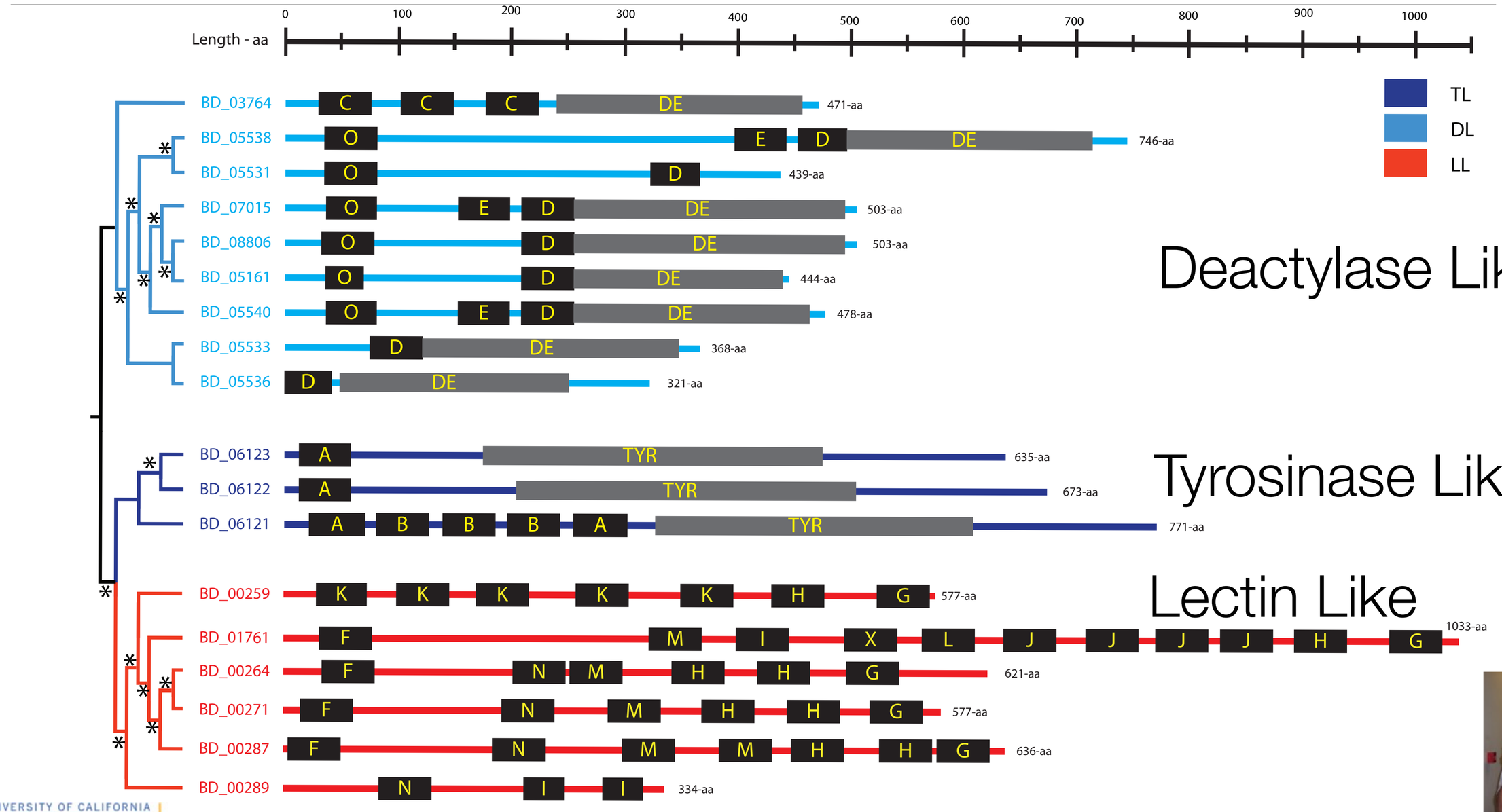
B. dendrobatidis cell wall biochemical analysis

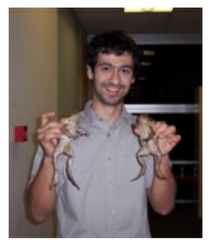
β (1,3)-glucan	β(1,6)-glucan	α(1,3)-glucan	Cellulose β(1,4)-glucan	Chitin
X	**X**	**X**	✓	✓

A putative cellulose synthase gene can be found in genome of *Bd* but also found in *N. crassa* and other Fungi with JP Latgé, M. Fisher

100X higher MIC for Caspofungin than C. albicans with N.A.R Gow & M. Fisher

Expansion of CBM18 domain - Chitin binding gene family



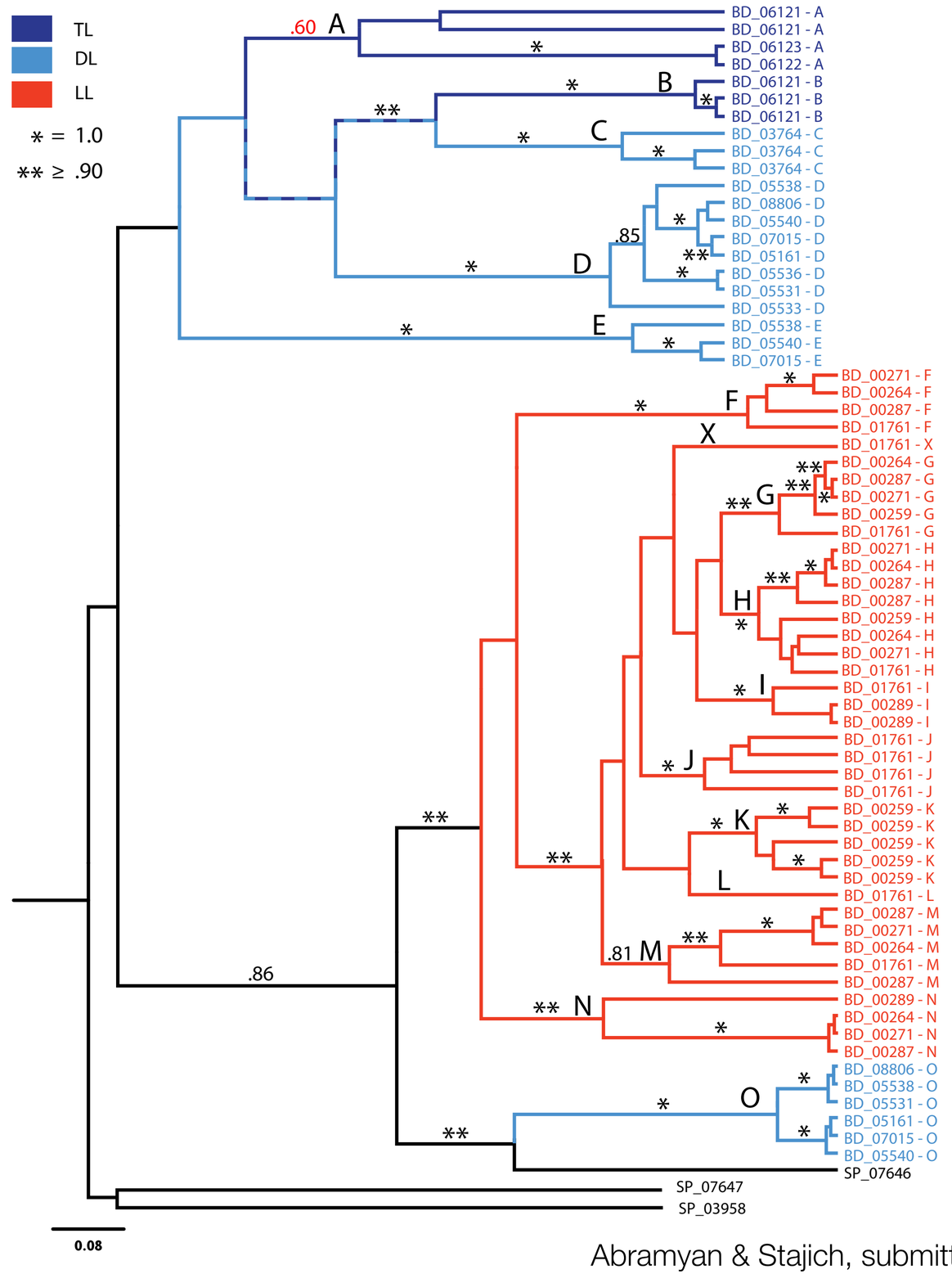


UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Abramyan & Stajich, submitted

Domain tree shows clade-specific grouping

Domains evolved from mostly tandem duplications with some intergene duplications.



Abramyan & Stajich, submitted

UNIVERSITY OF CALIFORNIA UCRIVERSIDE

CBM18 expansion

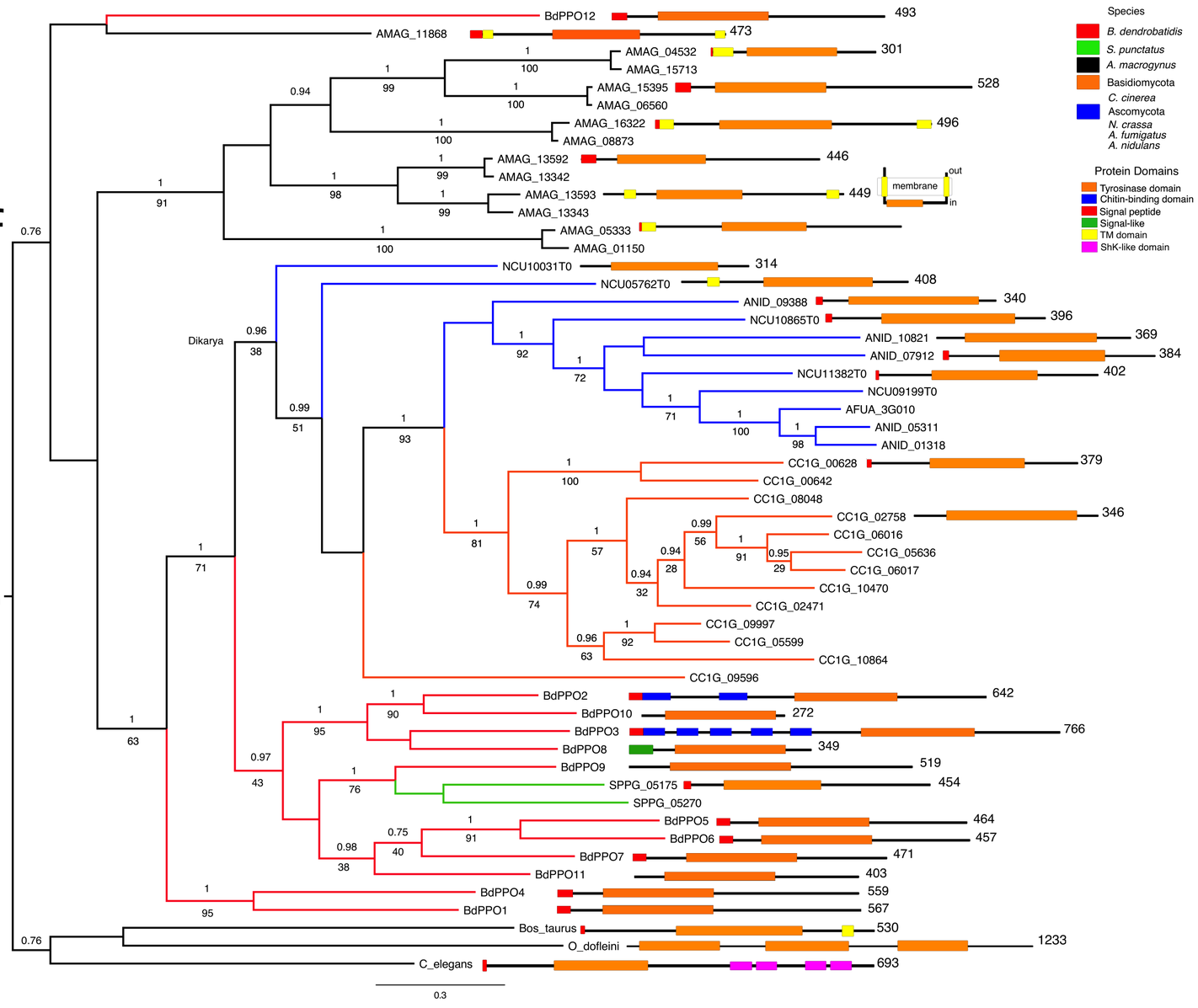
- Largest copy number of CBM18 in all fungi, and most number of domains (11) in a single locus
- Evidence for positive selection among copies of the domains based on codon analyses
- CBM18 thought to bind chitin, could be involved in binding its own chitin to cloak the cells from the host immunity
- Could also bind chitin-related molecules in animals attach more firmly to the animal cells

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Abramyan & Stajich, submitted

Tyrosinase expansions in *Bd* and other fungi

Synthesis of melanin, pigments and other polyphenols



Allomyces

H.Whistler via Liu et al BMC Evol Biol 2006

Hajime Muraguchi via Stajich et al PNAS 2010

E.Medina

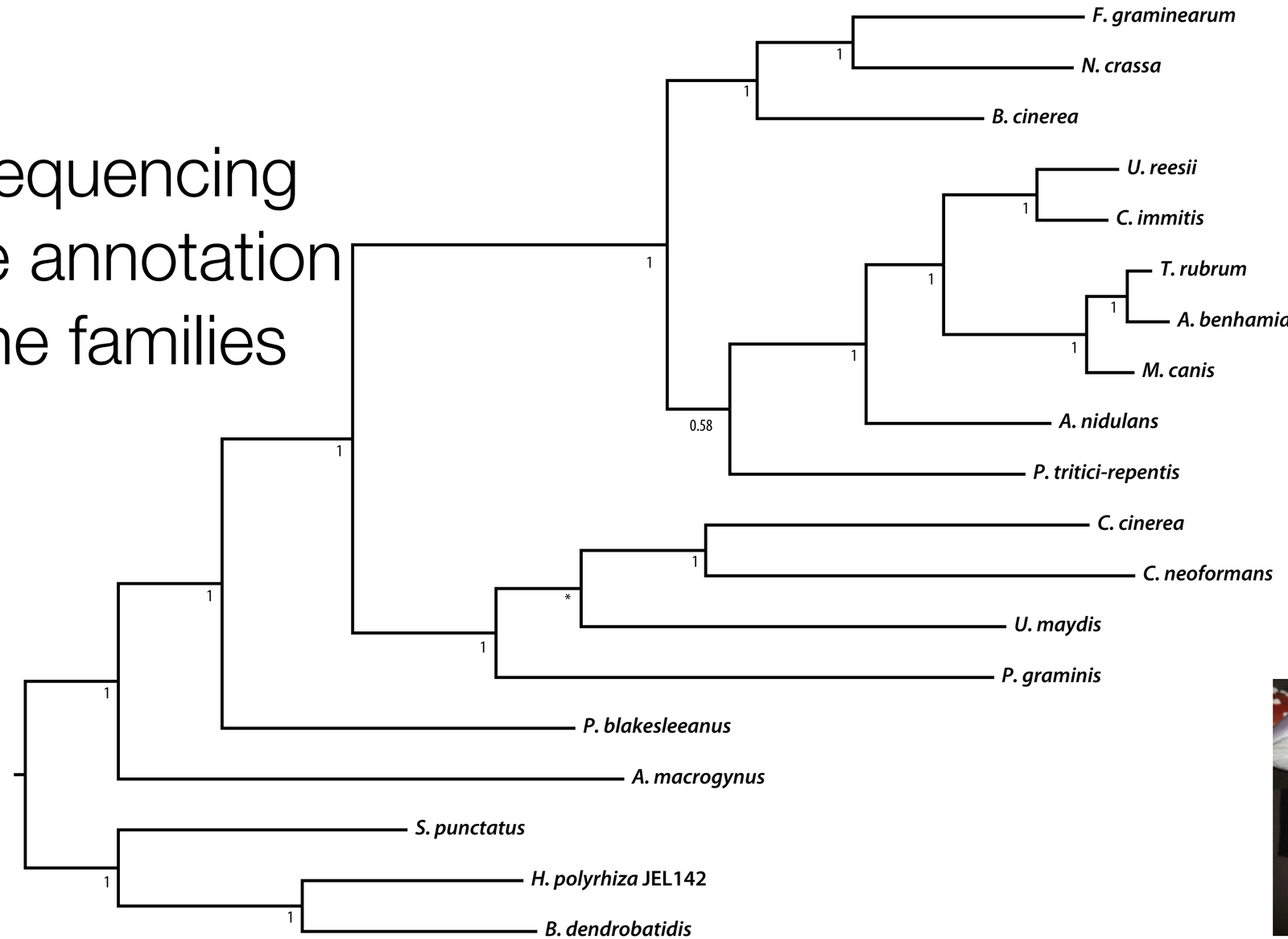
UNIVERSITY OF CALIFORNIA UCRIVERSIDE

But are these changes important?

- Just observing big families in a genome is nice, but does it mean that changes are really related to recent adaptation?
    - The branches on some gene trees are short, indicating duplications are recent
- A better is to polarize the changes to the *Bd* branch by having a closer species than 50-100 Mya...
- So is there a species closer to *Bd* we can use? ...

Homolaphylictis polyrhiza JEL142 is a close(ish) relative

454 genome sequencing
MAKER genome annotation
OrthoMCL gene families



Joneson et al, Submitted

UNIVERSITY OF CALIFORNIA UCRIVERSIDE

Contrasting some family sizes among the Chytrids

	M36	**S41**	Tyrosinase	**CBM18**
Allomyces	31	0	16	3
Spizellomyces	3	3	3	3
Hp	3-5	3	15	5
Bd	**38**	**32**	12	**14-16**

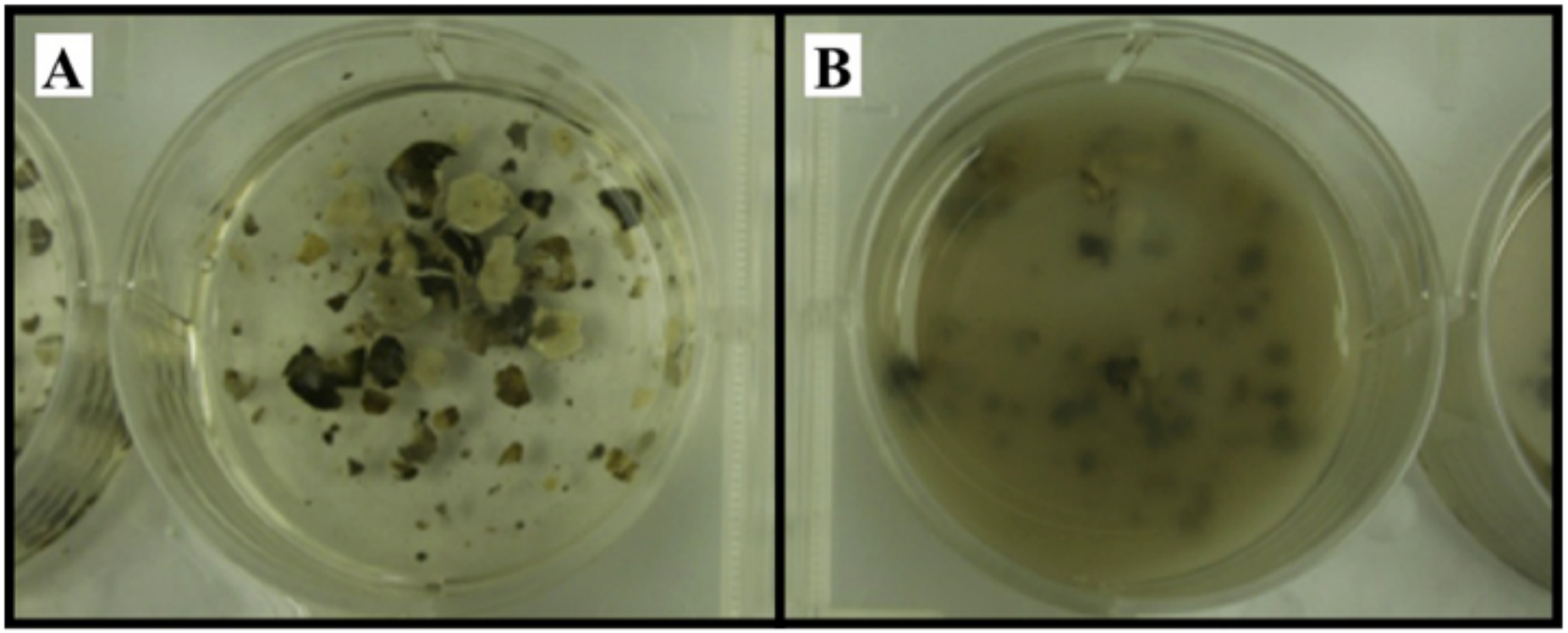
Fungalysin Serine protease

Fungalysins - thought to be keratinases (break down keratin in an amphibian skin...)

Serine protease expansions in *Coccidoides* and relatives maybe related to breaking down on animal matter

Joneson et al, Submitted

H. polyrhiza won't grow on frog skin; doesn't cause mortality in frogs



Hp- frog skin intact

Bd- frog skin degraded

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Joneson et al, Submitted

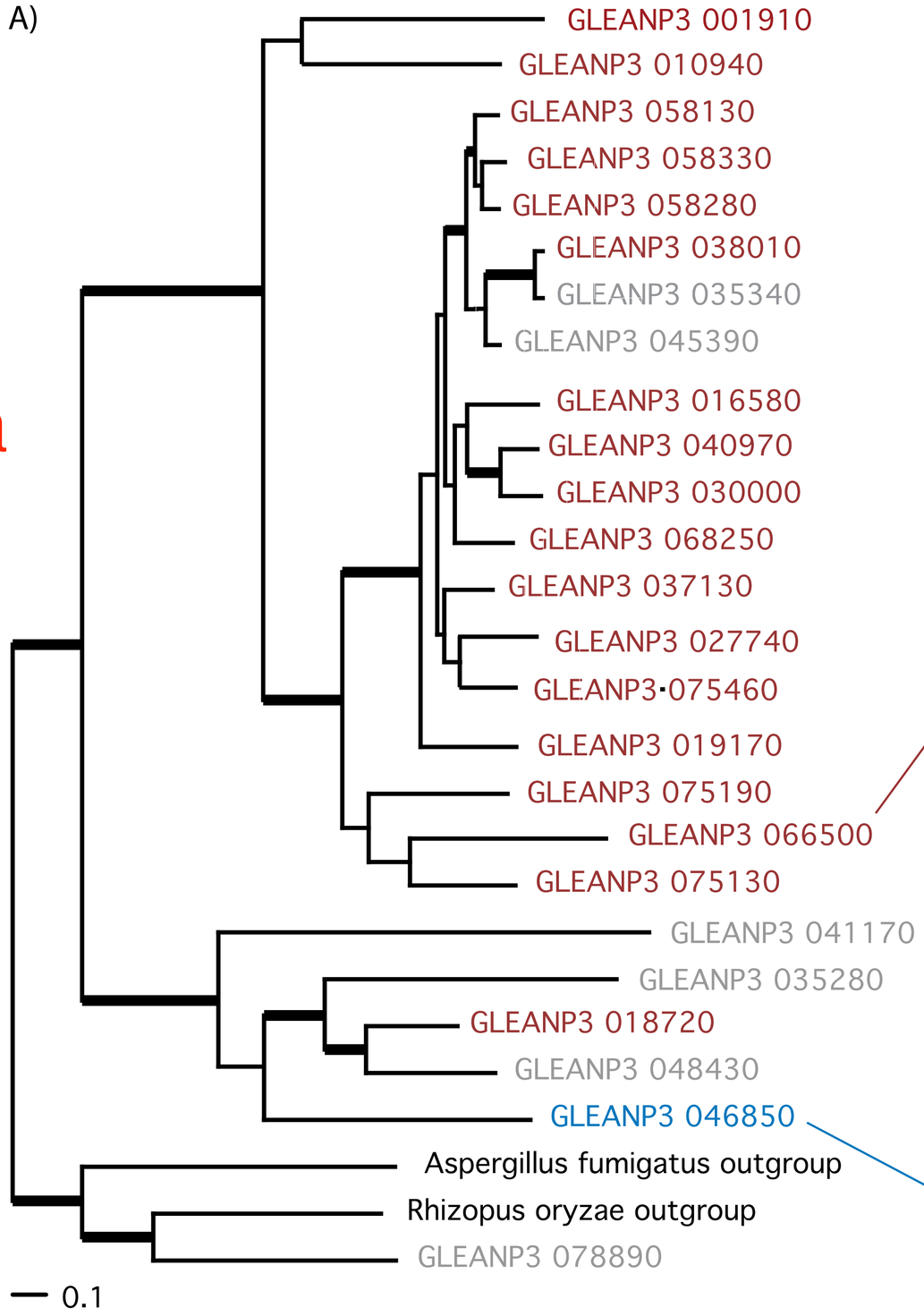
Fungalysin M36

up in sporangia

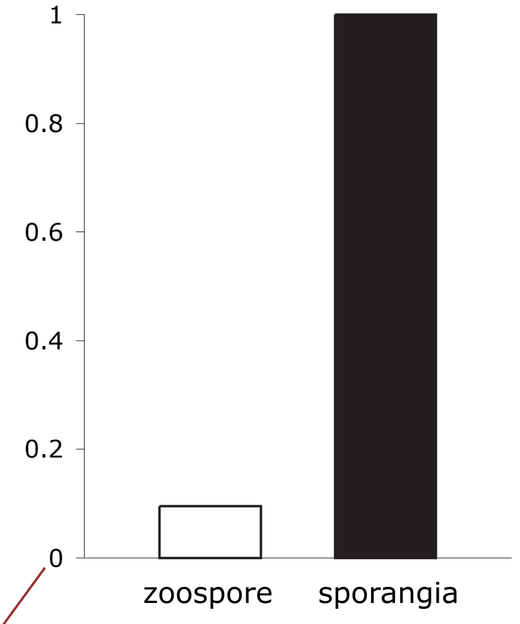
no expression diff

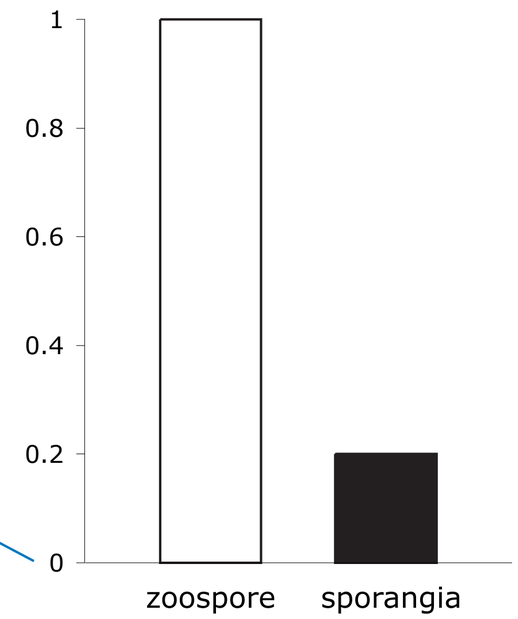
up in zoospore

A)



B)





UNIVERSITY OF CALIFORNIA UCRIVERSIDE

Rosenblum et al PNAS 2008

Bd summary

- Comparisons to close species can polarize some differences in lineage specific expansions
    - Findings of M36, S41 expansions seem to be recent to *Bd* and could be a functional link to pathogenesis
    - Expansion of Tyronsinase from counts is less compelling, but gene tree analyses suggests recent expansions on *Bd-Hp* branch
        - Lack of FKS1 in early Chytridiomycota lineages suggests a more recent origin of this gene than origin of the Fungi and predicts timing of some changes in fungal cell wall composition
        - CBM18 expansion may be related to adhesion, future experiments to test this
- Future: We are employing a population genomic approach, resequencing 24 strains of *Bd* and hope to understand more about origins and variation in the genome from these data.

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

Summary

- Unraveling the evolution of pathogens can be tricky, more so when mode of pathogenesis is not obvious (e.g. not just a toxin gene)

- Comparative genomics at the scale of gene and gene families can suggest changes that may be important in adaptation of a species.

- Connecting these molecular changes to pathogenecity is still needed to understand the role these expansions may play - but provides rich experimental fodder for the laboratory.

Acknowledgements

Coccidioides
Tom Sharpton {UCSF} John Taylor {UC Berkeley}
Dan Neafsey {Broad Institute}
Bridget Barker, Marc Orbach, Steve Rounsley {U Arizona}

Stajich lab @UCR lab
Steven Ahrendt
Divya Sain
Yizhou Wang
Yi Zhou
Jessica De Anda
Annie Nguyen

B. dendrobatidis
John Abramyan {UCR}
Edgar Medina {Universidad de Los Andes, Colombia}
Christina Cuomo {Broad Institute}
Tim James {U Michigan}
Suzanne Joneson, Tom Poorten, Erica Rosenblum {U Idaho}
Igor Grigoriev {JGI}

H. polyrhiza
Suzanne Joneson, Erica Rosenblum {U Idaho}
Shin-Han shiu {Michigan State}
Joyce Longcore {U Maine}
Tim James {U Michigan}

W.M. Keck Foundation

NSF

BURROUGHS WELLCOME FUND

ALFRED P. SLOAN FOUNDATION

UC RIVERSIDE UNIVERSITY OF CALIFORNIA

http://lab.stajich.org
http://mobedac.org
http://fungidb.org