

# Comparative genomics to assess gene age and horizontal gene transfer

Dr. Tom Hsiang

Dept. Environmental Biology

University of Guelph

[www.uoguelph.ca/~thsiang/present/2005cps.pdf](http://www.uoguelph.ca/~thsiang/present/2005cps.pdf)

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# Comparative genomics

- Comparison of genome sequence data
- Completely sequenced genomes (>95%)
  - > 200 bacterial genomes
  - > 30 fungal genomes
  - > 10 animal genomes
  - ≥ 4 plant genomes (arabidopsis, rice, poplar, corn)

# Objectives 1 & 2

- Find common fungal sequences
  - compare each yeast gene to 13 fungal genomes
- Assess how many are shared with other taxa
  - compare common fungal sequences to other animals, plants & bacteria



# 6356 Yeast predicted genes

3340 Yeast genes with homologs in 12 of 14 fungi

## Ascomycetes

*Aspergillus fumigatus*

*Magnaporthe grisea*

*Aspergillus nidulans*

*Neurospora crassa*

*Candida albicans*

*Podospora anserina*

*Gibberella zeae*

*Trichoderma reesei*

(*Saccharomyces cerevisiae*)

## Basidiomycetes

*Cryptococcus neoformans*

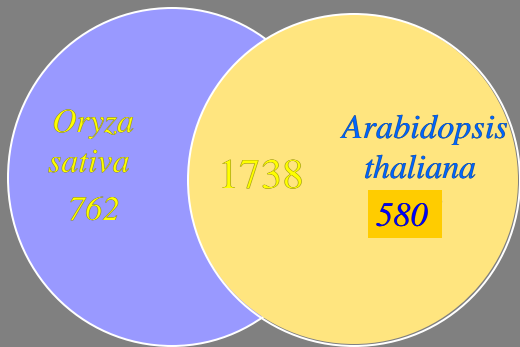
*Phakopsora pachyrhizi*

*Phanerochaete chrysosporium*

*Coprinus cinerea*

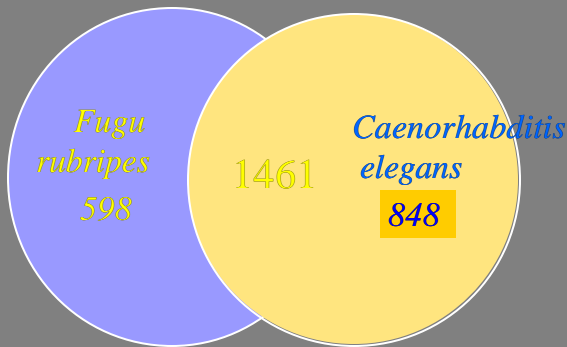
*Ustilago maydis*

3340 genes common to 12 of 14  
fungi compared to plant genomes



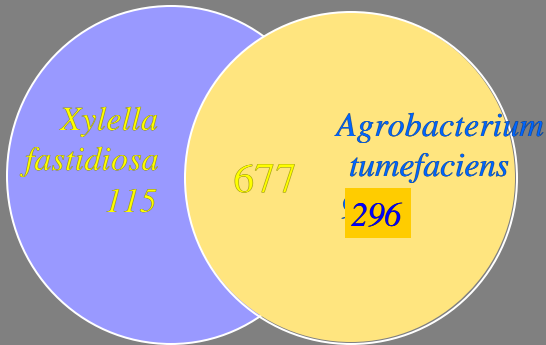
Total: 3080

3340 genes common to 12 of 14  
fungi compared to animal genomes



Total: 2907

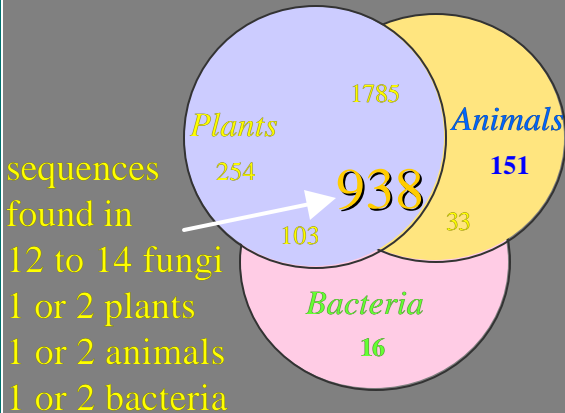
3340 genes common to 12 of 14  
fungi compared to bacterial genomes



Total: 1090



3340 genes common to 12 of 14 fungi compared to other genomes



## Objective 3

- Assess the age of fungal genes based on shared sequences and evolutionary timelines

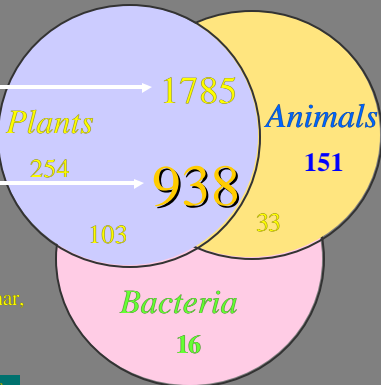
# Age of yeast genes (6356 total)

3340 common fungal genes

> 1.2 billion years old  
(asco/basidio split)

> 1.6 billion years old  
(fungi/animal/plant split)

> 2.7 billion years old  
(euk/prok split)



Timeline based on Hedges & Kumar,  
Trends in Genetics 19:200 (2003)

\* fine print: assuming no horizontal gene transfer

## Objective 4

- Look for evidence of horizontal gene transfer
  - *Magnaporthe grisea* (blast fungus) vs. rice
    - » only fungal plant pathogen + plant host combination with both genomes sequenced to date

# Horizontal Gene Transfer

- Gene acquisition not by descent
- Frequent among prokaryotes
  - » (transformation, transduction, conjugation)
- Rare with eukaryotes
- Evidence
  - best BLAST hit in another Kingdom
  - G+C content
  - codon bias
  - conflicting phylogenetic trees

## Methods: horizontal gene transfer

- Test *M. grisea* predicted genes (11k) vs. database of 13 fungi (400Mb) & rice (370 Mb)
- Find rice as top match, and rice as only match
- Confirm with TBLASTN of GenBank databases (NR, EST, GSS, HTGS)
- Check codon usage and GC content

(no *M. grisea*)

# Results (tblastn Mg vs fungi + rice)

11108 *M. grisea* protein sequences

9474 have match e-value  $\leq 1e-1$

458 have rice as top match

86 have only rice as a match

4 have only rice as a match  
at e-value  $\leq 1e-5$

# Mg matches with rice ( $e < 1e-5$ )

local tblastn rice+fungi

(Local Standalone Blast against ~1 Gb nt)

<del>■ Mg_prot1</del>	<del>Expect = 4e-18, Identities = 10/221 (4%)</del>
■ Mg_prot2	Expect = 1e-40, Identities = 106/337 (31%)
■ Mg_prot3	Expect = 1e-27, Identities = 40/62 (65%)
<del>■ Mg_prot4</del>	<del>Expect = 3e-15, Identities = 23/249 (9%)</del>



# Mg matches with rice ( $e < 1e-5$ )

3 Gb 4.5 Gb 4.5 Gb 3 Gb

tblastn NR+EST+GSS+HTGS

(GenBank Blast against 15 Gb nt, 5 Gb aa)

■ Mg\_prot2 bacterium e-86, rice e-78, no fungi

~~■ Mg\_prot3 no hits~~

# Mg matches with rice ( $e < 1e-5$ )

codon usage patterns, Mgrisea vs. Rice (diff > 0.8%)

	AAC	GCG	AUC	GUC	ACC	GAC
■ Mg - Rice	1.29	-1.05	0.97	0.86	0.83	0.82
■ Mg - Mg_prot2	-0.80	-0.85	-1.15	-0.02	-0.36	-1.76
	Mg	Rice	Mg	Mg	Mg	Mg

- number near 0 = more similar to *M. grisea*
- number closer to (Mg-Rice), more like rice

# Mg matches with rice ( $e < 1e-5$ )

	GC content
■ Rice	55.6%
■ <i>M. grisea</i>	56.5%
■ Mg_prot2	61.7%

– GC content of Mg & rice too similar?

# Conclusions

- Just over half (3340) of the genes in yeast (6356) have a homolog in 12 other fungi
- Almost 1000 common fungal genes have homologs in plants, animals and bacteria
- These 1000 genes may have originated before the origin of eukaryotes 2.7 billion years ago (ignoring horizontal gene transfer)
- Preliminary evidence of horizontal gene transfer to *Magnaporthe grisea*
  - (from rice? from bacteria?)

- J. Molec. Evol. 60:475-483 (obj. 1,2,3) available at: <http://www.uoguelph.ca/~thsiang/pubs>
- This seminar has been posted on the web at: [www.uoguelph.ca/~thsiang/present/2005cps.pdf](http://www.uoguelph.ca/~thsiang/present/2005cps.pdf)

Thank you for your attention

Any Questions?

(if time permits)